

DNA Barcoding of Selected Medicinal Plant Species from Jordan Using *matK*, *rbcL*, and *rpoC1* Genes

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Abstract— Medicinal plants play an essential role in preventing and treating several diseases. Classical taxonomic tools generally carry out medicinal plant identification and characterization. Unfortunately, conventional methods need well-trained taxonomists and could give a false identity for closely related species. Jordanian flora is rich in a variety of plant species. The phylogeographic architecture of Jordanian medicinal plant samples was not explored yet. This study aims to recruit DNA barcoding using *matK*, *rbcL*, and *rpoC1* genes to identify different selected medicinal plants species from Jordan. These are *Maerua crassifolia*, *Ziziphus spina-christi*, *Balanites aegyptiaca*, *Senna italica*, and *Moringa peregrina*. Plant samples were collected from the Dead Sea area (Jordan), and three DNA barcode regions were amplified, sequenced, and analyzed using different bioinformatic tools. Twelve sequences were obtained and deposited in Genbank. These sequences showed a very good discrimination capacity with sequences retrieved from related species. The phylogenetic analysis illustrated that DNA barcoding could successfully identify the selected medicinal plant species using different chloroplast genes (*rbcL*, *matK*, and *rpoC1*). Further analysis for other plants species is recommended to explore the genetic relationship and the phylogeographic architecture for Jordanian flora.

Keywords— DNA barcoding, *Maerua crassifolia*, *Ziziphus spina-christi*, *Balanites aegyptiaca*, *Senna italica*, *Moringa peregrina*.

I. INTRODUCTION

Jordanian flora is rich in various plant species; at least 2498 species belong to 813 genera, and 112 plant families were reported [1]. Among these, 485 species are

recognized as medicinal plant species with many therapeutic and antioxidant properties [2, 3]. Identifying medicinal plant species depends on the classical taxonomic methods, contingent mainly on plant morphological characteristics and the researchers' own experience. The classical ways of plant identification could be subjected to human errors; due to the inability of discriminating related plant species and the lack of expertise. Moreover, medicinal plant species authentication is impressively recommended to ensure the therapeutic efficacy and safety of the plant species [4, 5]. DNA barcoding is considered as an effective emerging tool to overwhelmed authentication challenges in herbal medicine [6]. DNA barcoding technology was proposed earlier in 2003 for species molecular identification using standardized DNA markers (Loci) for several genes or regions (mainly mitochondrial and chloroplast) [7]. The standard barcode region in most animals is the mitochondrial gene cytochrome oxidase I (*COI*). Meanwhile, the chloroplast genes maturase K (*matK*) and ribulose 1,5-bisphosphate carboxylase oxygenase large subunit (*rbcL*) were recommended as more efficient DNA barcode in plant species [8, 9]. Other DNA markers/regions in plants include different combinations of different genes or intergenic regions. In addition, nuclear segments are also engaged in plant DNA barcoding [10]. DNA barcoding is considered an effective emerging tool to overwhelmed authentication challenges in herbal medicine [6]. The main two goals of plant DNA barcoding are identifying unknown samples and classifying new species [11]. Moreover, DNA barcoding can be used to evaluate the quality of food products [12], authenticating medicinal plants [13], and endangered species identification [13-15]. In this study, we are aiming to use DNA barcoding to confirm the identity of the following selected medicinal plant species from Jordan: *Maerua crassifolia*, *Ziziphus spina-christi*, *Balanites aegyptiaca*, *Senna italica*, and *Moringa peregrina*, which were collected from Jordanian flora using *matK*, *rbcL* and *rpoC1* as barcoding candidates.

II. MATERIALS AND METHODS

A. Sampling and DNA Extraction

Five selected plant species were collected from the Dead Sea area, the eastern part of Jordan valley (Locality 31.600195482086015, 35.564421360045024). A specialized plant taxonomist did collect fresh leaves of each studied species. Scientific names of the selected species are *Maerua crassifolia*, *Ziziphus spina-christi*, *Balanites aegyptiaca*, *Senna italica*, and *Moringa peregrina*. Samples were kept frozen (-80 °C) till DNA was extracted. Leaves were ground separately using sterile ceramic mortars and pestles with the aid of liquid nitrogen. DNA was extracted using a plant mini kit (Qiagen, Germany) according to the instructions provided by the manufacturer. The quality and quantity of DNA were assayed spectrophotometrically and via electrophoresis in 1% agarose gel.

B. PCR Amplification, Sequencing, and Bioinformatic Analysis

Primers for *matK*, *rbcL*, and *rpoC1* genes (Table 1) were recruited for PCR amplification. PCR reactions were performed using 5x HOT FIREPol® Blend master mix (30 µl total reaction). The amplification steps were Initial denaturation step (95 °C) for 5 minutes, followed by 40 cycles (30 seconds each) of denaturation (95° C), annealing (54 °C for all loci), and extension at 72° C. A final extension step for 5 minutes was applied for all PCR reactions. PCR amplification successfulness was confirmed using gel electrophoresis (2 % agarose), and the amplified PCR products were purified and sequenced using Sanger method (Macrogen company, Korea), applying ABI PRISM® kit and sequencer. DNA sequences were read using Finch program [16]. Sequences were later searched using the NCBI-BLAST online tool to check related sequences in the nucleotide database. Moreover, five related sequences with a high matching score and significant E value for each plant sample were obtained from NCBI- Nucleotide Entrez using the BLAST tool [17]. Selected genes were extracted from complete chloroplast genomes using early published Python code [18]. Phylogenetic trees were constructed using Mega-X software [19]. Numbers at branches represent the evolutionary distances, calculated using the *p*-distance method via the number of base differences per site [20].

<i>rpoC1</i> [23]	F-GGCAAAGAGGGAAGATTTTCG
	R-CCATAAGCATATCTTGAGTTGG

III. Results

A. Barcode Amplification

The three barcode loci (*matK*, *rbcL*, and *rpoC1*) were amplified and sequenced for the five selected plant species. The amplification of the chosen barcoding loci was accomplished in 12 out of 15 loci. Table 2 lists the successful barcode amplification in each selected plant along with the amplified length in bp. The *matK* sequences length range was from 590 bp to 724 bp with an average length of 685.4 bp. Meanwhile, the *rbcL* sequence length range was from 654 bp to 674 bp, with an average length of 669.25.

Moreover, the *rpoC1* sequence length ranges from 454 bp to 495 bp, with an average length of 469 bp. The obtained length of sequences was within the previously reported ranges of the selected genes. Barcode sequences were deposited through BankIt to the GenBank database, and the deposited accession numbers are shown in Table 2. Appendix A shows the sequence data deposited in the GenBank database.

Table 1. List of selected barcode regions along with primers recruited for PCR amplification.

Locus	Primer Sequences (5' 3')
<i>matK</i> [21]	F-CCCRTYCATCTGGAAATCTTGGTTC
	R-GCTRTRATAATGAGAAAAGATTTCTGC
<i>rbcL</i> [22]	F-ATGTCACCACAAACAGAAAC
	R-TCGCATGTACCTGCAGTAGC

Table 2. List of successful sequences for (*matK*, *rbcL*, and *rpoC1*) barcode loci of the five selected plant species along with the length of each amplified locus and the accession numbers of the deposited sequences at GenBank along with the list of available barcode sequences of the selected plant species deposited earlier in the GenBank.

Plant Species	Parameter	Genes		
		<i>matK</i>	<i>rbcL</i>	<i>rpoC1</i>
<i>Maerua crassifolia</i>	Sequence length (bp)	685	X *	458
	Deposited accession number	OK340593	X	OK340602
	Related GenBank accession	N/A	MH598876.1	N/A
<i>Ziziphus spina-christi</i>	Sequence length (bp)	590	674	X
	Deposited accession number	OK340596	OK340598	X
	Related GenBank accession	MH211048.1	KX298996.1	N/A
<i>Balanites aegyptiaca</i>	Sequence length (bp)	713	654	495
	Deposited accession number	OK340592	OK340599	OK340603
	Related GenBank accession	KR735118.1	KX298999.1	N/A
<i>Senna italica</i>	Sequence length (bp)	715	673	X
	Deposited accession number	OK340595	OK340600	X
	Related GenBank accession	KX119408.1	KY464111.1	N/A
<i>Moringa peregrina</i>	Sequence length (bp)	724	676	454
	Deposited accession number	OK340594	OK340597	OK340601
	Related GenBank accessions	LC547439.1	JX091933.1	N/A

X * Unsuccessful amplification or low-quality sequence obtained.

A. Pairwise alignment (BLAST)

The obtained sequences of the five selected plant species were searched against the GenBank database [24] to detect similar sequences.

About 9 of the obtained sequences were reported earlier in the GenBank database. The *rpoC1* amplified sequences were not reported earlier in the GenBank database, along with the *matK* sequence of *Maerua crassifolia* which was also not deposited. Pairwise alignment using the BLAST tool [24] was performed for all amplified sequences and previously deposited corresponding sequences at the GenBank database. Figure 1 shows the pairwise alignment of obtained *matK* gene sequences and corresponding sequences; the range of identity 98% - 99%. The higher identity percentage was 99 % in *Senna italica* KX119408.1 (Query) with *Senna italica* (Subject), *Moringa peregrina* LC547439.1 (Query) with *Moringa peregrina* (Subject), and between *Ziziphus spina-christi* (Query: MH211048.1) with *Ziziphus spina-christi* (Subject). However, the lower reported percent of identity (98%) was in *Balanites aegyptiaca* KR735118.1 (Query) *Balanites aegyptiaca* (Subject) in *matK* sequence. Similarly, *rbcL* pairwise alignment showed 91-100% identity percent; the lower reported percent of identity was 91 % in case *Balanites aegyptiaca* KX298999.1 (Query) compared to *Balanites aegyptiaca* sample (Subject). Otherwise, the reported *rbcL* pairwise alignment identity percentage was higher than 99 % (Figure 2).

B. NCBI-BLAST results

The NCBI-BLAST search shows other related sequences for our sequences, results of the top five related species for each barcode loci are shown in (Appendix A). *RpoC1* sequences for different selected species were obtained by analyzing the complete chloroplast genome via python coding.

Results for *matK* locus show the highest percent identity was found to be (100.00%) among *Maerua crassifolia matK* and *Maerua angolensis* reported earlier in databases, while the lowest percentage of identity was reported in *Moringa peregrina matK* (92.63%) and *Bretschneidera sinensis*.

RbcL locus shows the highest percent identity was (100.00%) between *Ziziphus spina-christi rbcL* and *Ziziphus jujuba* and *Ziziphus spina-christi*, while the lowest percent identity was (97.86%) between *Balanites aegyptiaca rbcL* and *Sisyndite spartea*.

RpoC1 locus shows the highest percent identity (99.34%) between *Moringa peregrina rpoC1* and *Moringa oleifera*, while the lowest percent identity was

(96.00%) between *Balanites aegyptiaca rpoC1* and *Loropetalum subcordatum*.

Further phylogenetic analysis Using Mega X software was performed to construct phylogenetic trees using available sequences and their corresponding sequences at the GenBank database. The phylogenetic trees for the selected plant species using the three barcode loci (*matK*, *rbcL*, and *rpoC1*) are shown in Figures (3-5).

Figure 3 shows the phylogenetic trees for *matK* sequences with retrieved related species sequences. The phylogenetic trees were constructed using the Neighbor-Joining method between selected medicinal plant species sequences. The retrieved related species sequences have branch length equal 0.02209131 for *Maerua crassifolia*, 0.01016949 for *Ziziphus spina-christi*, 0.02633712 for *Balanites aegyptiaca*, 0.55517366 for *Senna italica* and 0.52923977 for *Moringa peregrina*. Moreover, Figure 4 shows the phylogenetic trees for *rbcL* sequences with retrieved related species sequences. The Neighbor-Joining trees show summation of optimal branch length equal (0.00744048, 0.02527006, 0.02353051, and 0.01037037) for *Ziziphus spina-christi*, *Balanites aegyptiaca*, *Senna italica* and *Moringa peregrina* representatively. In addition, Figure 5 shows the phylogenetic trees for *rpoC1* sequences with retrieved related species sequences. The Neighbor-Joining trees show summation of optimal branch length equal (0.64875566, 0.59414226, and 0.61360837) for *Maerua crassifolia*, *Balanites aegyptiaca*, and *Moringa peregrina* representatively.

(A)						(B)					
Score	Expect	Identities	Gaps	Strand		Score	Expect	Identities	Gaps	Strand	
1057 bits(572)	0.0	584/590(99%)	0/590(0%)	Plus/Plus		1234 bits(668)	0.0	698/713(98%)	0/713(0%)	Plus/Plus	
Query	95	TACTCCaaaaaaTCTATTtctttttttGAAAGTAATCAAGATTTTTCTGTCTC		154		Query	3	CTCCTCTTGCACTTTAAGACTTTTATCCATGAGTATTGTAATGGAATAGTCTTAT		62	
Sbjct	1		60		Sbjct	1		60	
Query	155	ATATAATTCTCATGTTTATGAATACGAATCCATCTTACTTTTTCTCGTAACCGATCTC		214		Query	63	TACCCCCAAAAATCTATTTCTATTTTTCAAAAAAGATCCAAAGTCTTTTTATTCTC		122	
Sbjct	61		120		Sbjct	61	C.....A.G.....T.....		120	
Query	215	TCATTTACGATTAACTCTCTGGGTAATTTTGAAGCAATTTATTTCTATGAAAAAT		274		Query	123	ACATAATTCTATGTATGTAATACGAATCAATTTTTCTTTTCTCGTAACCAATCTC		182	
Sbjct	121		180		Sbjct	121	.T.....A.....C.....		180	
Query	275	AAAACATCTGTACAAGAAGTCTTTCTAATGATTTCCAGCGTCTTATGGTCTTCAC		334		Query	183	TCATTTACGATCAACATCTCTGGGGCTCTTGACCGAATATATTTCTATCGAAAAAT		242	
Sbjct	181T.....		240		Sbjct	181		240	
Query	335	GGAGCCTTTCATGCATTATGTTAGATACAAGGAAATCTATTTGGTTCAAAAGATAC		394		Query	243	AGAACATTTGTAGAAAGCTTTGCTAATGATTTTCAGACTATCTTATGGTGTCAAAGA		302	
Sbjct	241A.....		300		Sbjct	241		300	
Query	395	GCCCCCTCTAATGAATAAATGGAAATTTTTCTGTCTTTATGGCAATGTCATTTTTA		454		Query	303	TCCTTTATGCATTATGTTAGATACAAGCAAAATCAATCTGTCTCAAAGATAGCTC		362	
Sbjct	301A.....		360		Sbjct	301		360	
Query	455	TGTGTGGGCTCAACCAGGAAGGATCTATATAAACCAATTAGCCAACCATCTTCCGGTT		514		Query	363	TCCTCTGATGAATAAATGGAATCTTATTTGTCAATTTATGGCAATGTCATTTTTATG		422	
Sbjct	361C.....		420		Sbjct	361A.....		420	
Query	515	TTTAGGCTATCTTTAAGTGTGCGACTAAATCTTTCAGTGTGCGAGTGAATGCTAGA		574		Query	423	GTGGTCAACCCGAAAGGCTATATAAACCAATTATATAAGCAATCCCTCCATTTTTT		482	
Sbjct	421		480		Sbjct	421C.....		480	
Query	575	AAATTCATTTATAATGGATAATGCTATAAAGAGCTTGATACATTAGTTCCAATTAGCCC		634		Query	483	AGGTATTTTTCAAATGCGACTAAATCTTCAGTGGTCCGAAGTCAAATGCTAGAAAA		542	
Sbjct	481A.....		540		Sbjct	481G.....		540	
Query	635	AATGATGGATCATTGGCTAAAAGAAATTTTTGAACGATTAGGACACC		684		Query	543	TTTATATAATAGATAATGTTATGAAGAAGCTCGATAACATAGTCCAATTTCTCTT		602	
Sbjct	541G.....		590		Sbjct	541T.....		600	
						Query	603	GATGGATCATTAGCTAAAGCGAAATTTGTAATACATTAGGGTATCCCGTAGCAACC		662	
						Sbjct	601G.....		660	
						Query	663	GACCTGGCCGATTCATCAGATCTGATATTATCGACCGATTTGGTGTATAT		715	
						Sbjct	661C.....		713	

(C)						(D)					
Score	Expect	Identities	Gaps	Strand		Score	Expect	Identities	Gaps	Strand	
1312 bits(710)	0.0	712/713(99%)	0/713(0%)	Plus/Minus		1332 bits(721)	0.0	723/724(99%)	0/724(0%)	Plus/Plus	
Query	31	TTCTGCATCTCCGCAAAATCGGTCAATAATCAAAATCGGATGAATCGGCCAGACCG		98		Query	36	GATGCTCTCTTTGCACTTTAATACGGTCTGTCTACAAGTATTGTAATGGAAGAGT		95	
Sbjct	713G.....		654		Sbjct	36		60	
Query	91	GCTTACTAATGGGATGCCATAACATACAAAATCTGCTTTAGCCAATGATCTAATTA		150		Query	96	CTTATTACTCAAAGAAATcttttttAATCCAAAGTTTTCTTGTCTTATATAATTCT		155	
Sbjct	653		594		Sbjct	61		120	
Query	151	GTGGAATAATTGGAATTTGATGTAAGCCTTTTATAACATTTCAATTAGAAATGAAT		210		Query	156	CATGTATGTGAATACGAATCCATCTATTTTTCTCGCAACCAATCTCTCATTACGA		215	
Sbjct	593		534		Sbjct	121		180	
Query	211	TTTCCAGCATTTGACTCGGTACCCTGAAGGATTTAACCGCACATTTGAAAAATAGCCCA		270		Query	216	TCAACATCTCGGGAGTCTCTTGAGCGCAttttttCTATGGAAAAATAGAACATCTT		275	
Sbjct	533		474		Sbjct	181		240	
Query	271	AAAAGTAAAATGAATGCTCAGATAATTGGTTTATATGGATCTTTCTGGTTGAGACCAA		330		Query	276	ATAAAAAACACATCTATAAAAAACCTTTGTTAATGGTTTTCCAGGACATCTATGCTTGTTC		335	
Sbjct	473		414		Sbjct	241		300	
Query	331	CAGAAAAATGACATTTGCCATAAACGGATAAGATAGATTTCATTTATTCATCAAAAAGG		390		Query	336	AAGGATCTTTCATGCATTATGTAGATACAAGGAAATCCATTTGGCTCAAAGAT		395	
Sbjct	413		354		Sbjct	301		360	
Query	391	GCGTATTGTTGAAGCCAAATGGATTTCTTGTATCTAACATAATGAATGAAAGGGT		450		Query	396	ACGCCCTCTGATGAATAAATGGAATATFACTTTGTCAATTTATGGCAATGTCATTT		455	
Sbjct	353		294		Sbjct	361		420	
Query	451	CCTTGAAGAACCATAGGGTGGACGAAAAATCTTATCAAGACTCTACAAAATGTTCTA		510		Query	456	TACGTGTGGTCAATCAGGAAGGTCGTATAAACCAATTATCAAAGATTATCTAGAC		515	
Sbjct	293		234		Sbjct	421		480	
Query	511	TTTTTGATAGAAAATAGATTGCTCAAAAAGGACTTAGAAGATGTTAATCGTAAATAAG		570		Query	516	TTTTGGGCTATTTTTCAAGTTTGGGATTTAATCCGTTAGTGGTACGGACCAAATGCTA		575	
Sbjct	233		174		Sbjct	481G.....		540	
Query	571	AAGATTGTTACGAGAAAAAAGATAGATTGATTCATACATACATAAAAATATATA		630		Query	576	GAAAACATTTATAATAGATAATGCTATAAAGAAAGTTCGATAACAAAATTCCAATATT		635	
Sbjct	173		114		Sbjct	541		600	
Query	631	GGAACAGGAAGAACTTGGATTCTTTTGAAAAAGTAGAAATCCAttttttGGAGTAA		690		Query	636	CCTATGATGCATCATTGGCTAAGCGAGATTTGTAATACATTAGGCGATCCCATTAGT		695	
Sbjct	113		54		Sbjct	601		660	
Query	691	TAAGACTATTTCCAATTAATACTATAAAGAAAGGCCTTAATAAATGAAAA		743		Query	696	AAGCCGACTGGGCGATTTCATCAGATCTGATATTATCGACCGATTTGGTGTATATGC		755	
Sbjct	53		1		Sbjct	661		720	
						Query	756	AGAA		759	
						Sbjct	721		724	

Fig. 1 Pairwise alignment of previously worked plant sequences in GenBank database against selected plant species sample sequences of *matK* barcode region. (A) *Ziziphus spina-christi* MH211048.1 (Query) *Ziziphus spina-christi* (Subject) (B) *Balanites aegyptiaca* KR735118.1 (Query) *Balanites aegyptiaca* (Subject) (C) *Senna italica* KX119408.1 (Query) *Senna italica* (Subject) (D) *Moringa peregrina* LC547439.1 (Query) *Moringa peregrina* (Subject).



Fig. 2 Pairwise alignment of the previously worked plant sequences in GenBank database against selected plant species sample sequences of *rbcl* barcode region. (A) KX298996.1 *Ziziphus spina-christi* (Query) *Ziziphus spina-christi* sample (Subject) (B) KX298999.1 *Balanites aegyptiaca* (Query) *Balanites aegyptiaca* sample (Subject) (C) KY464111.1 *Senna italica* (Query) *Senna italica* sample (Subject) (D) JX091933.1 *Moringa peregrina* (Query) *Moringa peregrina* sample (Subject).

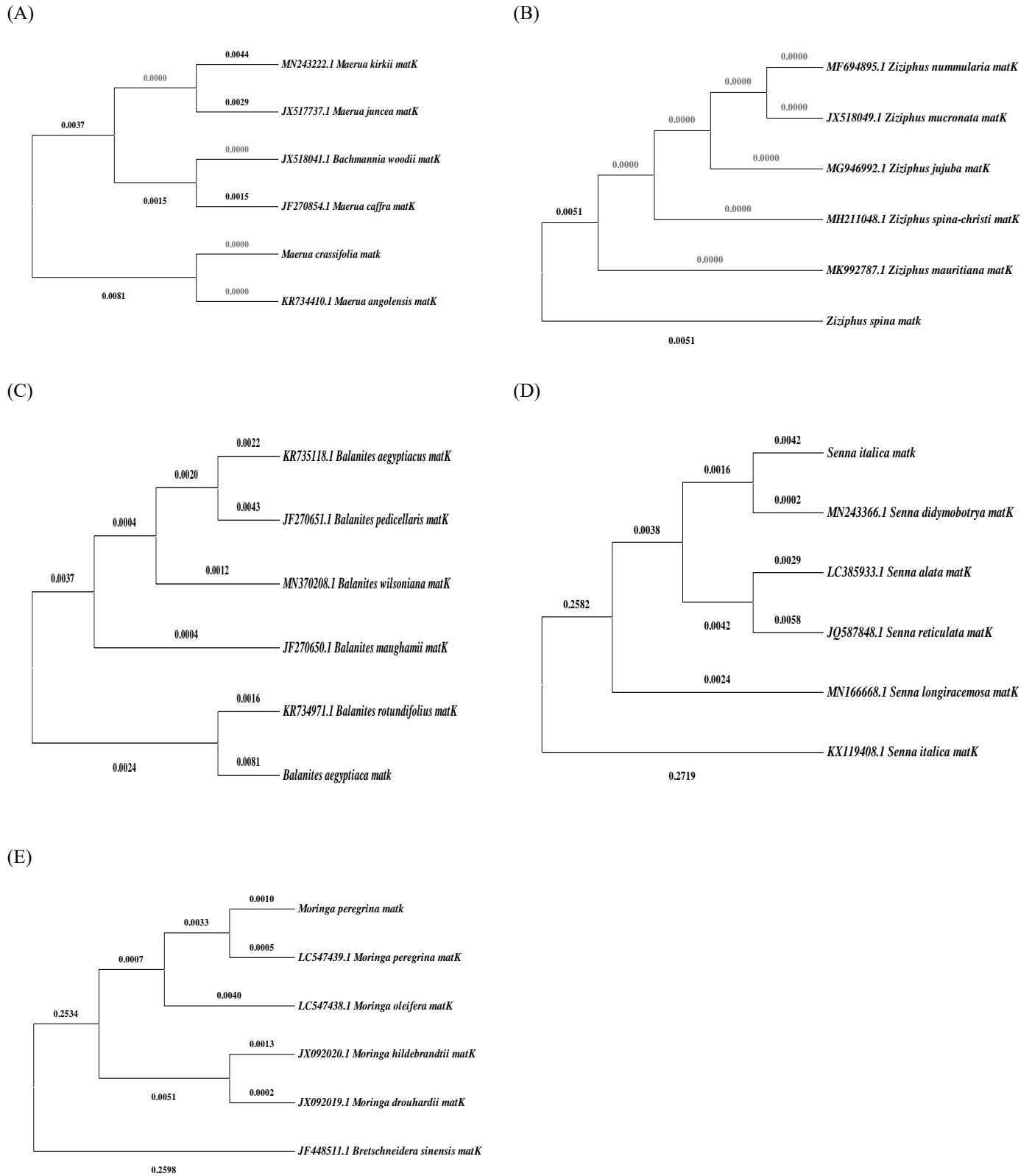


Fig. 3 The phylogenetic tree of obtained *matK* sequences with related species sequences retrieved from NCBI-BLAST. (A) *Maerua crassifolia* (B) *Ziziphus spina-christi* (C) *Balanites aegyptiaca* (D) *Senna italica* (E) *Moringa peregrina*.

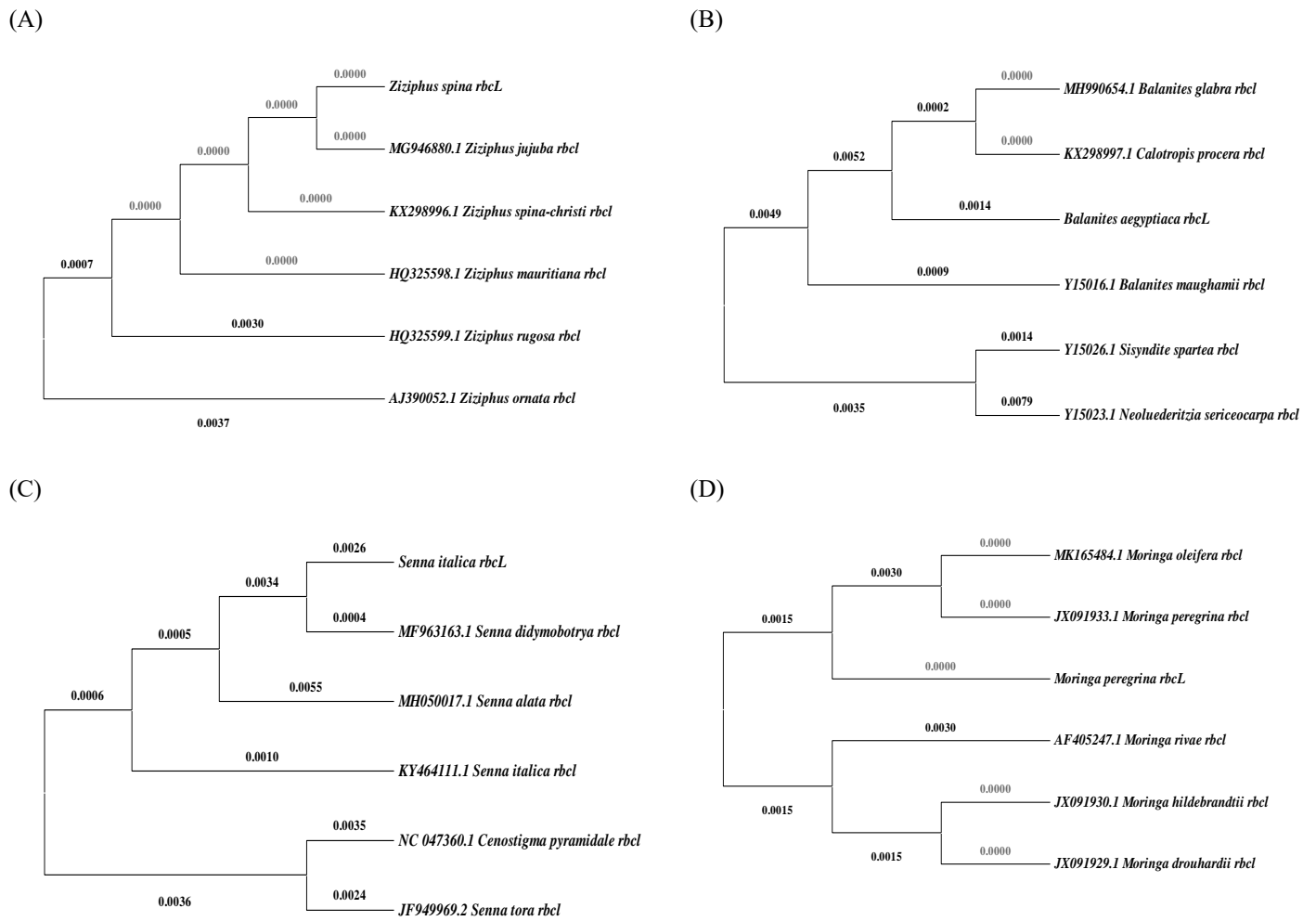


Fig. 4 The phylogenetic tree of obtained *rbcL* sequences with related species sequences retrieved from NCBI-BLAST. (A) *Ziziphus spina-christi* (B) *Balanites aegyptiaca* (C) *Senna italica* (D) *Moringa peregrina*.

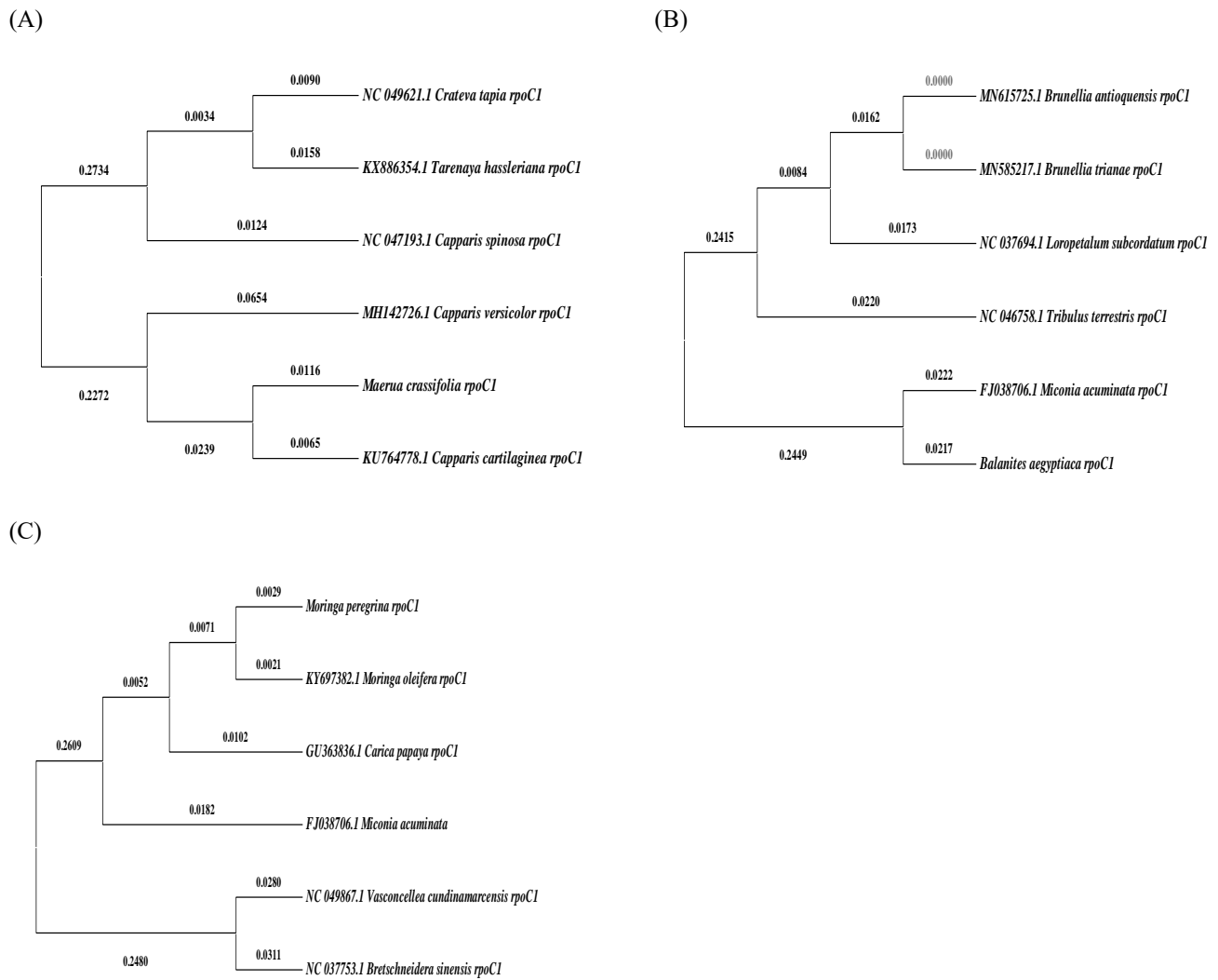


Fig. 5 The phylogenetic tree of obtained *rpoC1* sequences with related species sequences retrieved from NCBI-BLAST. (A) *Maerua crassifolia* (B) *Balanites aegyptiaca* (C) *Moringa peregrina*.

IV. DISCUSSION

Jordanian flora was intensively studied classically in the last century. Among the comprehensive reports is the flora Palaestina [25], which includes almost most plant species in the geo-botanical subunit between the eastern coast of the Mediterranean and the Syrian and Jordanian deserts, bordered by the mountains of Lebanon and the desert of Sinai [25]. The traditional methods of plant species identification could be misleading unless experts in this field perform it. DNA barcoding could serve as a helpful tool for species identification and help solve taxonomic dilemmas and doubting in clades organization and labeling concerns. Integrating DNA barcoding into the identification and phylogenetic characterization of different medicinal plants could help prevent medicinal products adulteration, fabrication, or product mislabelling. In addition, DNA barcoding could be a pivotal application to conserve natural resources and documentation of phylogeographic architecture.

DNA barcoding strategies were recruited successfully for different applications in the Middle East, including both plants and animal subjects [26-28]. Recently, selected medicinal plant species in Saudi Arabia and the United Arab Emirates were barcoded [29, 30]. Moreover, an effective barcode tool was developed to discriminate between different wheat species in Egypt [18]. In Jordan, Medicinal plants play a vital role in folk medicine [31]. However, DNA barcoding in plant species is still an emerging field that needs to be developed and recruited to identify plant species correctly. This study is the first draft of DNA barcoding in plant species in Jordan, and the selected plant species were successfully identified through different barcoding loci. This study showed that DNA barcoding could be successfully recruited for identifying different medicinal plant species. In addition, it indicates the ability to recruit different barcode loci to differentiate between the selected medicinal plant species by adding new sequences to the GenBank database. In this study the five selected plant species were selected according to their therapeutic/ antioxidant properties or their usage in folk medicine. These are as the following:

A. *Maerua crassifolia*

Maerua crassifolia which belongs to the *Capparaceae* family is a native plant reported in Africa and tropical Arabia and abundantly found in Saharan Africa. There are different common names of the plant, such as 'Jega' in Nigeria; and 'agargar' in the Niger Republic. Traditionally it is used as a camel's fodder during dry seasons. It was reported that *Maerua crassifolia* is used to treat camel diseases [32, 33]. The antibacterial activity and antioxidant activities of *Maerua*

crassifolia methanolic leaf extract were reported earlier [34], along with phytochemical and Anti-diarrhoeal properties [35] and antimalarial potency of the methanolic extract [36]. Leaves of *Maerua crassifolia* are known for the treatment of malaria, intestinal diseases, and toothache. Leaves are also used for other treatment purposes, including anti-inflammatory, analgesic, antipyretic, antibacterial, and antioxidant. The acute and subacute oral toxicity of the leaf ethanol extract was investigated in rats. Similarly, the ethanol extract was determined safe [35]. Our obtained sequences of *Maerua crassifolia* were aligned using blastn database. The results showed a high similarity with an early deposited whole chloroplast complete genome of *Maerua crassifolia* (Sequence ID: MN603029.1 Length: 155685 Number of Matches: 1). The partial coding sequences (CDS) showed identical DNA and protein sequence with GenBank Sequence ID: MN603029.1 for matK with 24 hits *Maerua* belonging to 12 organisms (NCBI Taxonomy browser via blastn alignment). Similarly, rpoC1 showed 100 % query coverage (99.78 % percent identity with Sequence ID: MN603029.1 (Length: 155685 Number of Matches: 1). The CDs information showed an identical protein sequence with our obtained accession [24] number. Only two hits and two organisms belonging to *Maerua* genus were retrieved from the NCBI taxonomy browser, indicating that our obtained sequences are among the first sets of sequences deposited for *Maerua crassifolia* in GenBank.

B. *Senna italica*

Senna italica belongs to *Fabaceae*, a perennial herb that could reach 60 cm. according to Indian culture, *Senna italica* is traditionally used for hair treatment and is known as "neutral henna". Moreover, it is used to treat sexually transmitted diseases and constipation. The phytochemical composition of the acetone extract revealed vanillin-sulphuric acid and *p*-anisaldehyde reagents. Roots inhibited the growth of Jurkat T cells in a dose- and time-dependent manner. It also had antioxidant and antibacterial. It is considered a CNS depressant and used for anti-nociception and sedation. Chemical constituents of the different plant's part revealed alkaloids, quinines, and anthraquinones [37]. Alkaloids, steroids, and flavonoids were also identified in different extracts [38]. Worth mentioning that the plant's root ethyl acetate extract exhibited anti-tick activity against adults of *Hyalomma marginatum rufipes* [39]. In addition, chloroform extract of pods had insecticidal activity [40]. The antibacterial activity of the leaf and root extracts of *Senna italica* showed potent activity against several bacterial species [38]. Two sequences were obtained (*matK* and *rbcL*) for *Senna italica*. The two sequences were successfully deposited at

GenBank database (OK340596 and OK340596, respectively). Running *Senna italica matK* sequence in blastn retrieved 99 % query coverage and 99.86 % identity. Different partial CDs were found at the GenBank database for *Senna italica matK* (Sequence IDs: KX119408.1, JQ024997.1, JQ301884.1). The number of hits (NCBI taxonomy browser) was found to be 96 hits belonging to 29 organisms from the genus *Senna*. Similarly, *rbcL* obtained sequence showed 100 % query coverage (99.26 % identity) with other deposited sequences (e.g. Sequence ID: KY464111.1). Moreover, reviewing the taxonomy [24] browser showed a total of 55 hits belonging to 16 organisms from genus *Senna*. *Senna italica* was found to be extensively studied due to their medicinal use applications.

C. *Ziziphus spina-christi*,

Ziziphus spina-christi, which belongs to the *Rhamnaceae* family known as 'Sedr' and 'Christ's Thorn Jujube', is a native plant species in tropical and subtropical regions in the Middle East region. The ripe fruit of *Ziziphus spina-christi* is edible, and the honey produced by bees feeding on *Ziziphus spina-christi* is found to have antibacterial activity against selected pathogenic bacteria [41]. It was also reported that the leaf extract *Ziziphus spina-christi* suppressed mercury chloride-induced renal toxicity [42]. In addition, *Ziziphus spina-christi* was reported as a good candidate for cytotoxicity of tumor cell lines [43]. It has been used as a food and in alternative medicine to treat asthma, ocular diseases, digestive disorders, weakness, liver complaints, obesity, urinary troubles, inflammation, pain, fever, dandruff, anorexia, insomnia, wounds, and wounds ulcers. It was reported to have antioxidant, antibacterial, antifungal, anti-hyperglycemic, and anti-nociceptive activities. The seeds are mainly sedative and taken with buttermilk. The main active components in this plant are flavonoids, alkaloids and saponins. Leaf volatile oil contains geranyl acetone, methyl hexadecanoate, methyl octadecanoate, farnesyl acetone C, hexadecanol and ethyl octadecanoate. It belongs to the *Rhamnaceae* family (order of Rosales). This plant is a shrub, and sometimes it is a tall tree of 20 m height. *Z. spina-christi* extract has also been reported to possess protective effect against aflatoxicosis [44]. The antioxidant capacity of ethanol and hexane extract of *Z. spina-christi* leaves were investigated in vitro using hydroxyl radical, DPPH radical, lipid peroxidation, and superoxide radical standardization methods. The ethanol extract has better antioxidant activity than the hexane extract. The study also identified glycosides, polyphenols, saponins, and tannins in both extracts, which acting singly or in synergy as antioxidants [45].

Running obtained *matK* sequence of *Ziziphus spina-christi* on blastn database retrieved a number partial CDs. Among the

matches there is MH211048.1 accession number [24] with 100 % query coverage and 98.98 % identity. Furthermore, number of hits with *Ziziphus* genus were 71 hits belonging to 18 organisms (taxonomy browser via blastn (NCBI). Alignment results (BLASTN) of obtained *Ziziphus spina-christi* showed the ability of the barcode sequence to locate *Ziziphus spina-christi* within their genus correctly, along with the ability to differentiate different species within dendrograms of related species within the results section. Similarly, obtained *rbcL* barcode shows 100 % identity with a corresponding region of early deposited whole chloroplast genome (*Ziziphus spina-christi* voucher ZSC20161128 chloroplast, complete genome, GenBank NCBI). The number of hits obtained through running taxonomy tool within blastn results were 35 hits belonging to 12 organisms of *Ziziphus* genus.

D. *Balanites aegyptiaca* Del.

Balanites aegyptiaca Del. (*Zygophyllaceae*), known as 'Desert date' is widely grown in dry areas of Africa, South Asia, and parts of the Middle East. It exists as a shrub or tree of 10 m in height. It is usually used to treat fever, jaundice, asthma, intestinal worm infection, wounds, malaria, syphilis, epilepsy, dysentery, constipation, diarrhea, hemorrhoid, and stomach aches. Seeds of the *Balanites aegyptiaca* is used as an expectorant, antibacterial, and antifungal, and the bark is used as spasmolytic. Moreover, their fruits are used in whooping cough and skin diseases, and the extract of fruit pulp causing hyperglycemia and inducing testicular dysfunction in dogs [46]. The oil of *Balanites aegyptiaca* has antiviral activity against the Herpes simplex virus and antimicrobial activity against selected strains of bacteria and *Candida* [46]. Different plant parts are confirmed to be utilized as antidiabetic, antimicrobial, antioxidant, anticancer, antiviral, and anti-inflammatory to treat various diseases [47]. *Balanites aegyptiaca* maturase K (*matK*) gene partial cds were documented earlier at the GenBank database (Sequence ID: KR735118.1, Length: 726). The query coverage was 100% with 97.9 %, showing slight differences in the nucleotide sequence between obtained *matK* and the early deposited one. The reported organisms in the taxonomy browser belonging *Balanites* were only six organisms with a total of six hits. Running obtained *rbcL* barcode via blastn showed that no earlier submissions were deposited *Balanites aegyptiaca* by other research groups. Similarly *rpoC1* obtained accession of *Balanites aegyptiaca* Del is considered novel since no corresponding accessions were reported to *Balanites aegyptiaca*. The lower the number of hits belonging *Balanites aegyptiaca* indicates

that this organism is not intensively studied at the molecular (Phylogenetic) level.

E. *Moringa peregrina* (Forssk.) Fiori

Moringa peregrina (Forssk.) Fiori (family: *Moringaceae*) is a small desert tree distributed in tropical and subtropical regions, from Africa to East India, including the Middle East. *Moringa peregrina* has diverse traditional, medicinal, industrial, spiritual, and religious values [48]. In Folk medicine, different plant parts have been recruited for different medicinal purposes, including diabetes, hypertension, wound healing and skin problems, fever, and many other reported uses [49-51]. It was reported that Persian *M. peregrina* (Forssk.) usage of leaves and seeds daily could improve the recommended dietary allowance of vitamins C and A, calcium, and potassium [52]. It has natural antioxidants that have a role in preventing many age-related diseases and the promotion of health. Methanolic leaf extract identified flavonoid glycoside, rutin, tocopherols, carotenoids, vitamin C, and chelating agents [53]. Its bright yellow oil, with a pleasant taste, has been compared in quality with olive oil. The oil proved effective against different bacterial strains [54]. In addition, different extracts of aerial parts of *Moringa peregrina* revealed a noticeable antioxidant activity [55]. It has natural antioxidants that have a role in preventing many age-related diseases and promoting of health. Methanolic leaf extract identified flavonoid glycoside, rutin, tocopherols, carotenoids, vitamin C and chelating agents [53]. *Moringa peregrina matK* hits (Taxonomy browser) were reported to be 3, with other reported hits of 17 for other related species *Moringa oleifera*. The highest percent of the identity of *Moringa peregrina matK* was 99.86 % (GenBank accession: LC547439.1). Similarly, the *rbcl* barcode was detected through blastn database with a number of hits equal to two (*Moringa peregrina*). Other hits belong to related species *Moringa oleifera*. *rpoC1* obtained from *Moringa peregrina* was not reported earlier on GenBank database. The closest sequence was reported for *Moringa oleifera* (GenBank accession MK726020.1), with a percent identity of 99.34 % and zero gaps. Although *Moringa peregrina* has vast therapeutic and daily applications, however, it is not reported till to date as a whole chloroplast genome sequencing in the GenBank database. And all sequences present uptodate are partial CDs or chloroplast intergenic spacers.

V. CONCLUSION

It is crucial to correctly identify different medicinal plant species using effective technology as DNA barcoding. Accordingly, about 12 sequences of plant species samples

were newly added to GenBank databases, and a high percentage of similarity between data deposited previously in the database and our study. The results indicate the importance of DNA barcoding in the molecular identification of different plant species according to molecular sequences previously deposited at the GenBank database. Further studies in medicinal plants should be done to performed to add more sequences to databases. Thus, exploring the phylogenetic architecture of different species in the tree of life. Further studies are recommended to select more species related to Jordanian Flora and nearby countries in the Middle East.

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Contribution of Individual Authors to the Creation of a Scientific Article (Ghostwriting Policy)

Almuthanna K Alkaraki: Conceptualization, Formal analysis, Resources, Supervision, Project administration, Writing - Original Draft.

Maisam Aldmoor: Methodology, Validation, Formal analysis, Investigation, Writing - Original Draft.

Jamil Lahham: Collecting Plant materials, taxonomical identification, Writing - Review & Editing..

Shreen D. Nusair: Writing - Original Draft, Writing - Review & Editing, Visualization.

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VI. APPENDIX

A. DNA SEQUENCES AND GENBANK SUBMITTED DATA

LOCUS *matK* 713 bp DNA linear PLN 27-SEP-2021
DEFINITION , maturase K, *matK*, partial cds.
VERSION
KEYWORDS .
SOURCE chloroplast *Balanites aegyptiaca*
ORGANISM *Balanites aegyptiaca*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Zygophyllales; Zygophyllaceae;
Tribuloideae; Balanites.
REFERENCE 1 (bases 1 to 713)
AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.
TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

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BASE COUNT      210 a      128 c      106 g      269 t
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541 ttcatttata atagataatg ttatgaagaa gctcgataca atagttccta ttattccttt  
601 gatgggatca ttagctagag cgaaattttg taatacatta gggatccccg ttagcacatc  
661 gacctgggcc gattcatcag attctgatat tatcgaccgc tttgtgcgta tat
```

//

```
LOCUS      matK                      679 bp      DNA      linear      PLN 27-SEP-2021
```

```
DEFINITION , maturase K, matK, partial cds.
```

VERSION

```
KEYWORDS .
```

```
SOURCE      chloroplast Maerua crassifolia
```

```
ORGANISM    Maerua crassifolia
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```


*Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; malvids; Brassicales; Capparaceae; Maerua.*

REFERENCE 1 (bases 1 to 679)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

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/lab_host="Yarmouk University, Irbid, Jordan"

/country="Jordan"

/identified_by="Jamil Lahham"

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GSSHLRSTSSGILFERIFFY GKIEHLVKVFN NFQDILGLFKDPFVHYVRYHGKCILA

TKDTPLLMNKWKY YFVNLWQWHFSIWFQS QKVHINQLSKANLDFLGYLSSLRLNPLVV

RSQMLENSFLIDNVRKKFDTKIPISSIIGSLAKERFCNVLGHPISKSTWMDSSDSDIL

DRFVRICR"

BASE COUNT 216 a 101 c 111 g 251 t

ORIGIN

1 tgtctatatg agtattggaa ttggaagaat ttttatactc aaaaaaatc aattttaaat

61 acaagatttt tcttgttctt atataattct catgtatgtg aatatgaatc catcttattt
121 tttctacgca aggggtcttc tcatttacga tcgacatctt ctggaattct ttttgagcga
181 atctttttct atggaaaaat agaacatctt gtaaaagttt ttgttaataa ttttcaggac
241 atcctaggat tgttcaagga tcccttcgta cattatgtta gatatcacgg aaaatgcatt
301 ctggcaacaa aggatacgcc gcttctgatg aataaatgga aatattactt tgtaattta
361 tggcaatggc atttttccat atggtttcaa tcgcaaaagg tccatataaa tcaattatct
421 aaagctaatt tagactttct gggctatctt tcaagtttgc gattaaatcc tttagtggta
481 cgtagtcaaa tgctagaaaa ctcaatttcta atagataatg ttagaaagaa attcgataca
541 aaaattccaa tttcttctat tattgggtca ttggctaaag aaaggttttg taatgtatta
601 ggatcatcca ttagtaaadc gacctggatg gattcatcag attctgatat tctcgaccga
661 tttgtacgta tatgcagaa

//

LOCUS matK 724 bp DNA linear PLN 27-SEP-2021

DEFINITION , matK gene, maturase K, partial cds.

VERSION

KEYWORDS .

SOURCE chloroplast *Moringa peregrina*

ORGANISM *Moringa peregrina*

*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; malvids; Brassicales; Moringaceae; Moringa.*

REFERENCE 1 (bases 1 to 724)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

COMMENT Bankit Comment: ALT EMAIL:alkaraki@gmail.com

Bankit Comment: TOTAL # OF SEQS:5

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

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source      1..724
            /organism="Moringa peregrina"
            /organelle="plastid:chloroplast"
            /mol_type="genomic DNA"
            /db_xref="taxon:161031"
            /lab_host="Yarmouk University, Irbid, Jordan"
            /country="Jordan"
            /identified_by="Jamil Lahham"

gene        <1..>724
            /gene="matK"

CDS         <1..>724
            /gene="matK"
            /note="[intronless gene]"
            /codon_start=1
            /transl_table=11
            /product="maturase K"
            /translation="DASSLHLLRFCLYKYCNWKSLLITPKKSFFNPRFFFLYNSHVCE
            YESILFFLRNQSSHLRSTSSGVLLERIFFYKGIEHLIKTHLIKTFVNGFQDILCLFKD
            PFMHYVRYQGKSILASKDTPLLMNKWKYYFVNLWQCHFVWSQSRRVRINQLSKDYLD
            FLGYFSSLRFNPLVRSQMLENSFIIDNAIKKFDTKIPIIPMIASLAKARFCNTLGHP
            ISKPTWADSSDSIDIIDRFVRCR"
```

BASE COUNT 214 a 130 c 117 g 263 t

ORIGIN

```
1 gatgcctctt ctttgcattt attacggttc tgtctctaca agtattgtaa ttggaagagt
61 cttattactc caaagaaatc tttttttaat ccaaggtttt tcttgttctt atataattct
121 catgtatgtg aatacgaatc catcttattt tttctccgca accaatcttc tcatttacga
181 tcaacatctt cgggagtcct tcttgagcgc atttttttct atggaaaaat agaacatctt
241 ataaaaacac atcttataaa aacctttggt aatggttttc aggacatctt atgcttggtc
301 aaggatcctt tcatgcatta tgtagatat caaggaaaat ccattttggc ttcaaagat
361 acgcctcttc tgatgaataa atggaaatat tactttgtca atttatggca atgtcatttt
421 tacgtgtggt ctcaatcacg aagggtccgt ataaaccaat tatccaaaga ttatctagac
481 tttctgggct atttttcaag tttgcgattt aatccgtagg tggtagggag ccagatgcta
```

541 gaaaactcat ttataataga taatgctata aagaagtctg atacaaaaat tccaattatt
601 cctatgattg catcattggc taaagcgaga ttttgtaata cattagggca tcccattagt
661 aagccgacct gggccgattc atcagattct gatattatcg accgatttgt gcgtatatgc
721 agaa

//

LOCUS *matK* 715 bp DNA linear PLN 27-SEP-2021

DEFINITION , maturase K (*matK*) gene, partial cds; chloroplast.

VERSION

KEYWORDS .

SOURCE chloroplast *Senna italica*

ORGANISM *Senna italica*

*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Fabales; Fabaceae; Caesalpinioideae;
Cassia clade; Senna.*

REFERENCE 1 (bases 1 to 715)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..715
/organism="*Senna italica*"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/db_xref="taxon:346974"
/lab_host="Yarmouk University, Irbid, Jordan"
/country="Jordan"
/identified_by="Jamil Lahham"
gene <1..>715

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        /gene="matK"  
CDS      <1..>715  
        /gene="matK"  
        /note="[intronless gene]"  
        /codon_start=2  
        /transl_table=11  
        /product="maturase K"  
        /translation="FHLLRFLYEFNWNLSLITPKKWISTFSKRNPFFFLYLYNFYVC  
EYESIFLFLRNKSSYLRLTSSRVLFERIYFYAKIEHFVEVFDKDFPSTLWFFKDPFIH  
YVRYQGKSILASTNTPFLMNKWKYYLIRLWQCHFSVWSQPEKIHINQLSEHSFYFLGY  
FSNVRLNPSVRSQMLENSFLIENVMKRLDTIPIIPLIRSLAKARFCNVLGHPISKP  
VWADSSDLDIIDRFLRRCRI"
```

BASE COUNT 210 a 122 c 111 g 272 t

ORIGIN

```
1 ttttcattta ttaaggctct ttctttatga gtattttaat tggaaatagtc ttattactcc  
61 aaaaaaatgg atttctactt tttcaaaaag gaatccaaga ttcttcctgt tcctatataa  
121 tttttatgta tgtgaatagc aatctatctt tctttttctc cgtaacaaat cttcttattt  
181 acgattaaca tcttctagag tcctttttga gcgaatctat ttctatgcaa aaatagaaca  
241 ttttgtagaa gtctttgata aagatthtcc gtccacccta tggttcttca aggacccttt  
301 cattcattat gttagatatac aaggaaaatc cattttggct tcaacgaata cgcccttttt  
361 gatgaataaa tggaaatact atcttatccg tttatggcaa tgtcattttt ctgtttggtc  
421 tcaaccagaa aagatccata taaaccaatt atctgagcat tcattttact ttttgggcta  
481 tttttcaaat gtgvcggttaa atccttcagt ggtacggagt caaatgctgg aaaattcatt  
541 tctaattgaa aatgttatga aaaggcttga tacaataatt ccaattatc cactaattag  
601 atcattggct aaagcgagat tttgtaatgt attagggcat cccattagta agccggctctg  
661 ggccgattca tccgatttgg atatcattga ccgatttttg cggagatgca gaatc
```

//

LOCUS *matK* 590 bp DNA linear PLN 27-SEP-2021

DEFINITION *maturase K (matK) gene, partial cds; chloroplast.*

VERSION

KEYWORDS .

SOURCE chloroplast *Ziziphus spina-christi*

ORGANISM *Ziziphus spina-christi*

*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Rosales; Rhamnaceae; Paliureae;
Ziziphus.*

REFERENCE 1 (bases 1 to 590)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..590

/organism="Ziziphus spina-christi"

/organelle="plastid:chloroplast"

/mol_type="genomic DNA"

/db_xref="taxon:264981"

/lab_host="Yarmouk University, Irbid, Jordan"

/country="Jordan"

/identified_by="Jamil Lahham"

gene <1..>590

/gene="matK"

CDS <1..>590

/gene="matK"

/note="[intronless gene]"

/codon_start=2

/transl_table=11

/product="maturase K"

/translation="TPKKSISFFLKNSRFFFLYNSHVYEYESILLFLNRSSHLRL

TSSGVFFERIYFYGKIKHPVQEVFSNDFPAVLWFFTEPFMHYVRYQGKSILVSKDTPL

LMNKWKYFLVLLWQCHFVWAQPGRIYINQLANHSFGFLGYLLSVRLNLSVVRSEMLE

NSFIMDNAIKKLDTLVPIRPMIGSLAKMKFCNALGH"

BASE COUNT 179 a 98 c 93 g 220 t

ORIGIN

```
1 tactccaaaa aaatctatth cttttttttt gaaaagtaat tcaagattht tcttgthctt
61 atataattct catgthttatg aatacgaatc catcttactt thtctccgta accgatcttc
121 tcatttacga ttaacatctt ctgggggtatt thttgagcga atthatttct atggaaaaat
181 aaaacatcct gtacaagaag thtttttctaa tgatthttcca gcggtcttat ggttcttcac
241 ggagcctthc atgcattatg taagatatca aggaaaatct atthttggtht caaaagatac
301 gcccctacta atgaataaat ggaaatatht tcttgthctt ttatggcaat gtcattthta
361 tgtgtgggcc caaccaggaa ggatctatat aaaccaatta gccaacctt thttcggctt
421 thtaggctat thtttaagtg tgcgactaaa thtttcagtg gtacggagtg aatgctaga
481 aaattcattt ataatggata atgctataaa gaagcttgat acattagthc caattagacc
541 aatgattgga tcattggcta agatgaaatt ttgtaacgca ttaggacacc
```

//

LOCUS *rbcL* 676 bp DNA linear PLN 27-SEP-2021

DEFINITION , ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, *rbcL*, partial cds.

VERSION

KEYWORDS .

SOURCE chloroplast *Moringa peregrina*

ORGANISM *Moringa peregrina*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae; Pentapetales; rosids; malvids; Brassicales; Moringaceae; Moringa.

REFERENCE 1 (bases 1 to 676)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..676

/organism="*Moringa peregrina*"

/organelle="plastid:chloroplast"

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/mol_type="genomic DNA"
/db_xref="taxon:161031"
/lab_host="Yarmouk University, Irbid, Jordan"
/country="Jordan"
/collected_by="Jamil Lahham"
gene <1..>676
/gene="rbcL"
CDS <1..>676
/gene="rbcL"
/note="[intronless gene]"
/codon_start=2
/transl_table=11
/product="ribulose-1,5-bisphosphate carboxylase/oxygenase
large subunit"
/translation="YKLTYYTPDYETKDTDILAAFRVTPQPGVPPEEAGAAVAESST
GTWTTVWTDGLTSLDRYKGRCYHIEPIAGEENQFIAYVAYPLDLFEEGSVTNMFTSIV
GNVFGFKALRALRLEDLRIIPPAYSKTFQPPHGIQVERDKLNKYGRPLLGCITKPKLG
LSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKAQAETGEIKG
HYLNATA"
```

BASE COUNT 188 a 142 c 149 g 197 t

ORIGIN

```

   1 ttataaattg acttattata ctctgacta tgaacccaaa gatactgata tcttggcagc
  61 attccgagta actcctcaac cggagttcc acctgaggaa gcaggggccg cggtagctgc
 121 tgaatcttct actggtacat ggacaactgt gtggaccgat gggcttacca gccttgatcg
 181 ttacaaagga cgatgctacc acatcgagcc cattgctgga gaagaaaatc aatttattgc
 241 ttatgtagct tacccttag acctttttga agaaggttct gttactaaca tgtttacttc
 301 tattgtgggt aatgtatttg ggttcaaagc cctgcgcgct ctacgtctag aggatctgcg
 361 aatccctcct gcttattcta aaactttcca gggaccacct catggtatcc aagttgaaag
 421 agataaattg aacaagtatg gccgtcccct attaggatgt actattaaac ctaaattggg
 481 tttatccgct aagaactacg gtagagcggg ttatgaatgt ctacgcggtg gacttgattt
 541 taccaaagat gatgagaatg tgaactcca accatttatg cgttgagag accgtttctt
 601 attttgtgcc gaagctatth ataaagcaca ggctgaaaca ggtgaaatca aagggcatta
```


661 tttgaatgct actgcg

//

LOCUS *rbcL* 674 bp DNA linear PLN 27-SEP-2021

DEFINITION , ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
gene, *rbcL*, partial cds.

ACCESSION *rbcL*
VERSION

KEYWORDS .

SOURCE chloroplast *Ziziphus spina-christi*

ORGANISM *Ziziphus spina-christi*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Rosales; Rhamnaceae; Paliureae;
Ziziphus.

REFERENCE 1 (bases 1 to 674)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..674
/organism="*Ziziphus spina-christi*"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/db_xref="taxon:264981"
/lab_host="Yarmouk University, Irbid, Jordan"
/country="Jordan"
/collected_by="Jamil Lahham"
gene <1..>674
/gene="*rbcL*"
CDS <1..>674

```
/gene="rbcL"  
/note="[intronless gene]; [intronless gene]"  
/codon_start=1  
/transl_table=11  
/product="Ribulose-1,5-bisphosphate carboxylase/oxygenase  
large subunit"  
/translation="DYKLTYYTPDYETKDTDILAAFRVTPQPGVPPEEAGAAVAEES  
TGTWTTVWTDGLTSLDRYKGRCYGLEPVAGEENQYIAYVAYPLDLFEEGSVTNMFTSI  
VGNVFGFKALRALRLEDLRIPTAYTKTFQGGPHGIQVERDKLNKYGRPLLGCTIKPKL  
GLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKAQAETGEIK  
GHYLNAT"
```

BASE COUNT 182 a 138 c 156 g 198 t

ORIGIN

```
1 gattataaat tgacttatta cactcctgac tatgaaacca aagatactga tatcttgcca  
61 gcgtttcgag taactcctca acctggagtt cgcctgagg aagcaggggc cgcggtagct  
121 gctgaatctt ctactggtac atggacaact gtatggactg acgggcttac cagtcttgat  
181 cgttacaaag gtcgatgcta cggccttgag cccgttgctg gagaagaaaa tcaatatatt  
241 gcttatgtag cttaccctt agacctttt gaagaaggtt ctgttactaa catgtttact  
301 tccattgtgg gtaatgtttt tgggttcaag gccctgcgcg ctctacgttt ggaggatttg  
361 cgaatcccta ctgcttatac taaaactttc caaggaccgc ctcatggcat ccaggttgaa  
421 agagataaat tgaacaagta tggccgcccc ctattgggat gtactattaa acctaaattg  
481 gggttatctg ctaagaatta cggtagagca gtttatgaat gtcttcgcgg tggacttgat  
541 ttaccxaaag atgatgagaa cgtgaattcc caaccattta tgcgttggag agaccgtttc  
601 ttatcttgat ccgaagccat ttataaagca caggctgaaa caggtgaaat caaagggcat  
661 tacttgaatg ctac
```

//

LOCUS rbcL 654 bp DNA linear PLN 27-SEP-2021

DEFINITION , ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
gene, rbcL, partial cds.

VERSION

KEYWORDS .

SOURCE chloroplast *Balanites aegyptiaca*

ORGANISM *Balanites aegyptiaca*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Zygophyllales; Zygophyllaceae;
Tribuloideae; Balanites.

REFERENCE 1 (bases 1 to 654)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source	1..654 /organism=" <i>Balanites aegyptiaca</i> " /organelle="plastid:chloroplast" /mol_type="genomic DNA" /db_xref="taxon:886265" /lab_host="Yarmouk University, Irbid, Jordan" /country="Jordan" /collected_by="Jamil Lahham"
gene	<1..>654 /gene="rbcL"
CDS	<1..>654 /gene="rbcL" /note="[intronless gene]; [intronless gene]" /codon_start=1 /transl_table=11 /product="Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit" /translation="DYKLTYYTPEYETKDTDILAAFRVTPQPGVPPPEEAGAAVAEES TGTWTTVWTDGLTSLDRYKGRCYHIEPVAGEENQYIAYVAYPLDLFEEGSVTNMFTSI VGNVFGFKALRALRLEDLRIPTSYIKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKL

GLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEALYKAQAETGEIK

"

BASE COUNT 184 a 130 c 148 g 192 t

ORIGIN

```
1 gattataaat tgacttatta tactcctgaa tatgaaacaa aggatactga tattttggca
61 gcattccgag taactcctca acctggagtt ccacctgagg aagcaggggc tgcggtagca
121 gctgaatctt ctactggtac atggacaact gtgtggactg atgggcttac tagtcttgat
181 cgttacaaag gacgatgcta ccacatcgag cccgttgctg gagaagaaaa tcaatatatt
241 gcttatgtag cttaccctt agacctttt gaagaagggt ctgttactaa catgtttact
301 tccattgtgg gtaatgtatt tgggttcaaa gccctacgcg ctctgcttct ggaggatttg
361 cgaatcccta cttcttatat taaaactttc caagggccgc ctcacggtat ccaagttgag
421 agagataaat tgaataagta tggccgtccc ctattgggat gtactattaa acctaaattg
481 gggctatccg ctaaaaatta cggtagagca gtttatgaat gtcttcgagg tgggcttgat
541 tttaccaaag atgatgagaa cgtgaactcc caaccattta tgcgttgagg agaccgtttc
601 ttattttgtg ccgaagcact ttataaagca caggcagaaa ctggtgaaat caaa
```

//

LOCUS rbcL 673 bp DNA linear PLN 27-SEP-2021

DEFINITION , ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
gene, rbcL, partial cds.

ACCESSION rbcL

VERSION

KEYWORDS .

SOURCE chloroplast *Senna italica*

ORGANISM Senna italica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Fabales; Fabaceae; Caesalpinioideae;
Cassia clade; Senna.

REFERENCE 1 (bases 1 to 673)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

```
FEATURES             Location/Qualifiers
     source            1..673
                        /organism="Senna italica"
                        /organelle="plastid:chloroplast"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:346974"
                        /lab_host="Yarmouk University, Irbid, Jordan"
                        /country="Jordan"
                        /collected_by="Jamil Lahham"
     gene              <1..>673
                        /gene="rbcL"
     CDS                <1..>673
                        /gene="rbcL"
                        /note="[intronless gene]"
                        /codon_start=3
                        /transl_table=11
                        /product="Ribulose-1,5-bisphosphate carboxylase/oxygenase
                        large subunit"
                        /translation="KLTYYPDYETKDTDILAAFRVTPQPGVPPEEAGAAVAESSTG
                        TWTTVWTDGLTSLDRYKRCYGIIEPVAGEENQYIAYVAYPLDLFEEGSVTNMFTSIVG
                        NVFGFKALRALRLEDLRIPTSYIKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGL
                        SAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAI FKAQAETGEIKGH
                        YLNATA"
```

```
BASE COUNT      185 a      138 c      152 g      198 t
```

ORIGIN

```
1 ataaattgac ttattatact cctgactatg aaaccaaaga tactgatatc ttggcagcat
61 tccgagtaac tcctcaacca ggagttccgc ctgaagaagc aggtgccgcg gtagctgctg
121 aatcttctac tggtagatgg acaactgtgt ggaccgatgg gcttaccagt cttgatcggt
181 acaaaggacg atgctacggc atcgagcccg ttgctggaga agaaaatcaa tatattgctt
241 atgtagctta tcccttagac ctttttgaag aaggttctgt tactaacatg tttacttcca
```

301 ttgtgggtaa tgtatttggga ttcaaggccc tgcgcgctct acgtctggag gatttgcgaa
361 tccctacttc ttatattaaa actttccaag gtccgcctca cggcatccaa gttgagagag
421 ataaattgaa caagtatggc cgtcccctat tgggatgtac tattaaacct aaattggggt
481 tatctgctaa gaattacggg agagcagttt atgaatgtct ccgcggtgga cttgatttta
541 ccaaagatga tgagaatgtg aattccaac catttatgcg ttggagagac cgtttcttat
601 tttgtgccga agctatTTTT aaagcacagg ccgaaacagg tgaaatcaaa gggcattact
661 tgaatgctac tgc

//

LOCUS rpoC1 454 bp DNA linear PLN 27-SEP-2021

DEFINITION , DNA-directed RNA polymerase subunit beta (rpoC1) gene, rpoC1,
partial cds.

VERSION

KEYWORDS .

SOURCE chloroplast *Moringa peregrina*

ORGANISM *Moringa peregrina*

*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; malvids; Brassicales; Moringaceae; Moringa.*

REFERENCE 1 (bases 1 to 454)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..454

/organism="*Moringa peregrina*"

/organelle="plastid:chloroplast"

/mol_type="genomic DNA"

/db_xref="taxon:161031"

/lab_host="Yarmouk University, Irbid, Jordan"

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                /country="Jordan"  
                /collected_by="Jamil Lahham"  
gene            <1..>454  
                /gene="rpoC1"  
CDS             <1..>454  
                /gene="rpoC1"  
                /note="[intronless gene]"  
                /codon_start=1  
                /transl_table=11  
                /product="DNA-directed RNA polymerase subunit beta"  
                /translation="VIVVGPSLSLHRCGLPREIAIELFQTFVIRGLIRQHLSNIGVA  
KSKIREKGPVWEILQDVMRGHPVLLNRAPTLHRLGIQAFQPILVEGRAICLHPLVRK  
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BASE COUNT 114 a 90 c 105 g 145 t

ORIGIN

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1 gtcattgtcg ttggaccttc actttcatta catcgttgtg gattgcctcg cgaaatagca  
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121 ataggagttg ctaagagtaa aattcgggaa aaagggccga ttgtatggga aataacttcaa  
181 gacgttatgc gggggcatcc tgtattgctg aatagagcgc ctactctgca tagattaggc  
241 atacaggcat tccaacccat tttagtggaa ggacgtgcta tttgtttaca tccattagtt  
301 cgtaagggat tcaatgcaga ctttgatggg gatcaaatgg ctgttcatgt gcctttatct  
361 ttagaggctc aagcggaggc tcgtttactt atgttttctc atatgaatct cttgtctcca  
421 gctattgggg atcccatttc ggtaccaact cagc
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LOCUS rpoC1 458 bp DNA linear PLN 27-SEP-2021

DEFINITION , DNA-directed RNA polymerase subunit beta (rpoC1) gene, rpoC1,
partial cds.

VERSION

KEYWORDS .

SOURCE chloroplast *Maerua crassifolia*

ORGANISM *Maerua crassifolia*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;

Pentapetalae; rosids; malvids; Brassicales; Capparaceae; Maerua.

REFERENCE 1 (bases 1 to 458)
AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.
TITLE Direct Submission

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers
source 1..458
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/organelle="plastid:chloroplast"
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/db_xref="taxon:1198337"
/lab_host="Yarmouk University, Irbid, Jordan"
/country="Jordan"
/collected_by="Jamil Lahham"
gene <1..>458
/gene="rpoC1"
CDS <1..>458
/gene="rpoC1"
/note="[intronless gene]"
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/transl_table=11
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BASE COUNT 121 a 92 c 100 g 145 t

ORIGIN

1 tctgtcattg tcgttgacc ttcacttca ttacatcgct gtggattgcc tcgggaata

61 gcaatagagc ttttcagac atttgaatt cgtggtctaa ttagacaaca tctggcttcg
121 aacataggag ttgctaagag taaaattcgg gaaaaaaggc cgattgtctg ggaaatactt
181 caagaagtta tgcaggggca tcccgtattg ctgaatagag cacctactct acatagatta
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301 gtttgcaagg gattcaatgc agactttgat ggggatcaaa tggctgttca tgtgccttta
361 tcttttagagg ctcaagcgga ggctcgttta cttatgtttt ctcatatgaa tctcttgtct
421 ccagctattg gagatcccat ttctgtacca actcaaga

//

LOCUS *rpoC1* 495 bp DNA linear PLN 27-SEP-2021

DEFINITION , DNA-directed RNA polymerase subunit beta (*rpoC1*) gene, *rpoC1*,
partial cds.

ACCESSION *rpoC1*
VERSION

KEYWORDS .

SOURCE chloroplast *Balanites aegyptiaca*

ORGANISM *Balanites aegyptiaca*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
Pentapetalae; rosids; fabids; Zygothylales; Zygothylaceae;
Tribuloideae; Balanites.

REFERENCE 1 (bases 1 to 495)

AUTHORS Alkaraki,A.K., Lahham,J.N. and Aldmoor,M.A.

TITLE Direct Submission

COMMENT Bankit Comment: ALT EMAIL:alkaraki@gmail.com

Bankit Comment: TOTAL # OF SEQS:3

##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..495

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/organelle="plastid:chloroplast"

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CDS     <1..>495
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VPTQN"
BASE COUNT      124 a      93 c      121 g      157 t
ORIGIN
      1 gggggagttg ggcacggggt tgattattcg gggcgttctg tcattgtcgt aggaccctca
     61 ctttcattac atcaatgtgg attgcctcgc gaaatagcaa tagagctttt ccagacattt
    121 gtaattcgtg gtctaattag acagcatctt gcttcgaaca taggagttgc taagagtaaa
    181 attcgggaaa aagaaccgat tgtatgggaa atacttcagg aagttatgcg ggggcatcct
    241 gttttgctga atagagcgcc cactctgcat agattaggaa tacaggcatt ccaaccatt
    301 ttagtggaag ggcgtgctat ttgtttacat cccttagttt gtaagggatt caatgcagac
    361 tttgatggag atcaaatggc tgttcatgta cttttatfff tggaggctca agcagaggct
    421 cgtttactta tgttttctca tatgaatctc ttgtctccag ctattgggga tcccatttct
    481 gtaccaactc agaat
//
```

B. The NCBI-BLAST results for retrieved sequences. The scoring results of sequences alignment, sequence coverage (QC), sequences identity reveals genes with high similarity to our retrieved sequences.

Plant species	Gene	Related species	QC	EV	Identity	Accession
<i>Maerua crassifolia</i>	<i>Matk</i>	<i>Maerua angolensis</i>	100%	0.0	100.00%	KR734410.1
	<i>Matk</i>	<i>Bachmannia woodii</i>	100%	0.0	98.67%	JX518041.1
	<i>Matk</i>	<i>Maerua juncea</i>	99%	0.0	98.67%	JX517737.1
	<i>Matk</i>	<i>Maerua caffra</i>	100%	0.0	98.53%	JF270854.1
	<i>Matk</i>	<i>Maerua kirkii</i>	100%	0.0	98.38%	MN243222.1
<i>Ziziphus spina-christi</i>	<i>Matk</i>	<i>Ziziphus spina-christi</i>	100%	0.0	98.98%	MH211048.1
	<i>Matk</i>	<i>Ziziphus mauritiana</i>	100%	0.0	98.98%	MK992787.1
	<i>Matk</i>	<i>Ziziphus nummularia</i>	100%	0.0	98.98%	MF694895.1
	<i>Matk</i>	<i>Ziziphus jujuba</i>	100%	0.0	98.98%	MG946992.1
	<i>Matk</i>	<i>Ziziphus mucronata</i>	100%	0.0	98.98%	JX518049.1
<i>Balanites aegyptiaca</i>	<i>Matk</i>	<i>Balanites wilsoniana</i>	99%	0.0	98.03%	MN370208.1
	<i>Matk</i>	<i>Balanites aegyptiacus</i>	100%	0.0	97.90%	KR735118.1
	<i>Matk</i>	<i>Balanites maughamii</i>	99%	0.0	98.03%	JF270650.1
	<i>Matk</i>	<i>Balanites pedicellaris</i>	92%	0.0	97.65%	JF270651.1
	<i>Matk</i>	<i>Balanites rotundifolius</i>	86%	0.0	99.03%	KR734971.1
<i>Senna italica</i>	<i>Matk</i>	<i>Senna didymobotrya</i>	99%	0.0	99.86%	MN243366.1
	<i>Matk</i>	<i>Senna italica</i>	99%	0.0	99.86%	KX119408.1
	<i>Matk</i>	<i>Senna alata</i>	99%	0.0	99.02%	LC385933.1
	<i>Matk</i>	<i>Senna longiracemosa</i>	99%	0.0	98.16%	MN166668.1
	<i>Matk</i>	<i>Senna reticulata</i>	99%	0.0	98.74%	JQ587848.1
<i>Moringa peregrina</i>	<i>Matk</i>	<i>Moringa peregrina</i>	100%	0.0	99.86%	LC547439.1
	<i>Matk</i>	<i>Moringa oleifera</i>	100%	0.0	99.16%	LC547438.1
	<i>Matk</i>	<i>Moringa drouhardii</i>	100%	0.0	96.96%	JX092019.1
	<i>Matk</i>	<i>Moringa hildebrandtii</i>	100%	0.0	95.72%	JX092020.1
	<i>Matk</i>	<i>Bretschneidera sinensis</i>	100%	0.0	92.63%	JF448511.1
<i>Maerua crassifolia</i>	<i>rbcL</i>	No significant similarity found.				
<i>Ziziphus spina-christi</i>	<i>rbcL</i>	<i>Ziziphus jujuba</i>	100%	0.0	100%	MG946880.1
	<i>rbcL</i>	<i>Ziziphus spina-christi</i>	100%	0.0	100%	KX298996.1
	<i>rbcL</i>	<i>Ziziphus mauritiana</i>	100%	0.0	99.70%	HQ325598.1
	<i>rbcL</i>	<i>Ziziphus rugosa</i>	100%	0.0	99.70%	HQ325599.1

	<i>rbcL</i>	<i>Ziziphus ornate</i>	100%	0.0	99.55%	AJ390052.1
<i>Balanites aegyptiaca</i>	<i>rbcL</i>	<i>Calotropis procera</i>	100%	0.0	99.85%	KX298997.1
	<i>rbcL</i>	<i>Balanites glabra</i>	98%	0.0	99.85%	MH990654.1
	<i>rbcL</i>	<i>Balanites maughamii</i>	100%	0.0	99.24%	Y15016.1
	<i>rbcL</i>	<i>Sisyndite spartea</i>	100%	0.0	98.32%	Y15026.1
	<i>rbcL</i>	<i>Neoluederitzia sericeocarpa</i>	100%	0.0	97.86%	Y15023.1
<i>Senna italica</i>	<i>rbcL</i>	<i>Senna didymobotrya</i>	100%	0.0	99.70%	MF963163.1
	<i>rbcL</i>	<i>Senna italica</i>	100%	0.0	99.26%	KY464111.1
	<i>rbcL</i>	<i>Senna alata</i>	99%	0.0	98.81%	MH050017.1
	<i>rbcL</i>	<i>Cenostigma pyramidale</i>	100%	0.0	98.66%	NC_047360.1
	<i>rbcL</i>	<i>Senna tora</i>	100%	0.0	98.66%	JF949969.2
<i>Moringa peregrina</i>	<i>rbcL</i>	<i>Moringa peregrina</i>	99%	0.0	99.70%	JX091933.1
	<i>rbcL</i>	<i>Moringa oleifera</i>	99%	0.0	99.70%	MK165484.1
	<i>rbcL</i>	<i>Moringa hildebrandtii</i>	99%	0.0	99.56%	JX091930.1
	<i>rbcL</i>	<i>Moringa drouhardii</i>	99%	0.0	99.56%	JX091929.1
	<i>rbcL</i>	<i>Moringa rivae</i>	99%	0.0	99.41%	AF405247.1
<i>Maerua crassifolia</i>	<i>rpoC1*</i>	<i>Capparis versicolor</i>	100%	0.0	98.69%	MH142726.1
	<i>rpoC1*</i>	<i>Tarenaya hassleriana</i>	99%	0.0	98.90%	KX886354.1
	<i>rpoC1*</i>	<i>Crateva tapia</i>	100%	0.0	98.47%	NC_049621.1
	<i>rpoC1*</i>	<i>Capparis spinosa</i>	100%	0.0	98.25%	NC_047193.1
	<i>rpoC1</i>	<i>Capparis cartilaginea</i>	99%	0.0	98.24%	KU764778.1
<i>Ziziphus spina-christi</i>	<i>rpoC1</i>	No significant similarity found.				
<i>Balanites aegyptiaca</i>	<i>rpoC1*</i>	<i>Tribulus terrestris</i>	95%	0.0	97.89%	NC_046758.1
	<i>rpoC1</i>	<i>Miconia acuminata</i>	94%	0.0	96.6%	FJ038706.1
	<i>rpoC1*</i>	<i>Brunellia antioquiensis</i>	95%	0.0	96.21%	MN615725.1
	<i>rpoC1*</i>	<i>Brunellia trianae</i>	95%	0.0	96.21%	MN585217.1
	<i>rpoC1*</i>	<i>Loropetalum subcordatum</i>	95%	0.0	96.00%	NC_037694.1
<i>Senna italica</i>	<i>rpoC1</i>	No significant similarity found.				
<i>Moringa peregrina</i>	<i>rpoC1</i>	<i>Moringa oleifera</i>	99%	0.0	99.34%	KY697382.1
	<i>rpoC1*</i>	<i>Bretschneidera sinensis</i>	99%	0.0	98.67%	NC_037753.1
	<i>rpoC1*</i>	<i>Vasconcellea cundinamarcensis</i>	99%	0.0	97.57%	NC_049867.1
	<i>rpoC1</i>	<i>Carica papaya</i>	97%	0.0	97.97%	GU363836.1
	<i>rpoC1</i>	<i>Miconia acuminata</i>	98%	0.0	96.64%	FJ038706.1