

Article

The First Complete Chloroplast Genome Sequence and Phylogenetic Analysis of Pistachio (*Pistacia vera*)

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Abstract: Pistachio is one of the most economically important nut crops worldwide. However, there are no reports describing the chloroplast genome of this important fruit tree. In this investigation, we assembled and characterized the complete pistachio chloroplast sequence. The *Pistacia vera* chloroplast genome was 160,598 bp in size, similar to other members of Anacardiaceae (149,011–172,199 bp) and exhibited the typical four section structure, including a large single copy region (88,174 bp), a small single copy region (19,330 bp), and a pair of inverted repeats regions (26,547 bp). The genome contains 121 genes comprised of 87 protein-coding genes, 30 tRNA genes and 4 rRNA genes. Thirteen intron-containing genes were identified in the genome wherein two genes had more than two introns. The genomic patterns of GC content resembled those for other Anacardiaceae. *P. vera* displayed the highest number of simple sequence repeats (SSRs) among the genera studied, which may be useful for molecular marker development and future population studies. Amino acid analysis revealed that Leucine is the most frequent (10.69%) amino acid in the chloroplast genome followed by Isoleucine (8.53%) and Serine (7.77%). Cysteine (1.30%) and Tryptophan (1.74%) were the least frequent amino acids. Phylogenetic analysis revealed *P. vera* is most like its taxonomically close relative *P. weinmannifolia*, followed by *Rhus chinensis*; all placed taxonomically in the tribe Rhoeeae. Members of Anacardiaceae were most closely related to Rhoeeae, followed by members of Spondieae. The reports of this chloroplast genome will be useful for future conservation studies, genetic evaluation and breeding of *P. vera*, and more comprehensive phylogenetic analysis of the *Pistacia* species and its closely-related genera.

Keywords: taxonomic; chloroplast genome; phylogenetic relationship; sequence assembly; SSR



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1. Introduction

Pistachio (*Pistacia vera* L.), a deciduous nut species, is the most economically important member of the Anacardiaceae family, with at least eleven species [1]. This diploid ($2n = 2x = 30$), dioecious, wind-pollinated fruit species is believed to originate from the Iranian plateau region spanning from northeast Iran to north Afghanistan and the central Asian republic [2]. Wild pistachio forests still exist in northeast Iran [3]. *P. atlantica* subsp. *mutica* and *P. khinjuk* are closely related to pistachio, but are mainly used as *P. vera* rootstocks and are naturally distributed throughout Iran, primarily in the Zagros Mountain range [3,4]. As the main center of pistachio origin, Iran has the largest pistachio cultivation area in the world. According to available statistics, the United States, Iran, and China are the three main producers of this nut crop, respectively [5]. Boasting a considerable number of branched

and essential amino acids, vitamins, unsaturated fatty acids, antioxidant compounds, and additional minerals, pistachio is superior to other nut bearing species and is a healthy food source, rich in beneficial nutrients [6]. In addition to its nutritional benefits, pistachio is considered an economically important nut species worldwide. Estimates of pistachio economic values indicated roughly \$2.811 billion of pistachio are exported around the world annually [7]. The United States and Iran lead with pistachio exports appropriating 32.2% (\$1.084 billion) and 24.43% (\$686 million) of total world exports, respectively [7].

Chloroplasts are oval, green organelles that are widely distributed in the cytoplasm of photosynthetic plant cells and contribute to the photosynthetic characteristics of the species. Chloroplasts, along with the nucleus and mitochondria, constitute the three main genetic systems in plant cells and are derived through endosymbiosis from co-evolution of cyanobacterium and ancient plants [8]. Although photosynthesis is considered to be the main role of these organelles, chloroplasts are also actively associated with other aspects of plant metabolism, including nucleotides, fatty acid, starch, phytohormones, pigment, vitamins, and amino acid synthesis [9]. Chloroplasts are also involved in the synthesis of several metabolites that play vital roles in plant defense against various biotic and abiotic stresses [10,11]. Chloroplasts are semi-autonomous and have independent genetic material, mostly encoding the genes involved in photosynthesis, transcription, and translation [12].

Due to the mono-parental nature of their inheritance, chloroplast genomes are highly valuable tools to investigate the molecular evolutionary and phylogenetic relationships of different plant lineages, as well as to estimate the effects of pollen and seeds on total gene flow [13].

Chloroplast genome sequences provide more reliable information about the phylogenetic relationship among different plant genera [14]. Chloroplast genomes have sufficient informative sites, which exhibit substantial variation either within or between plant species and enable scientists to improve their knowledge about the phylogeny and evolutionary adaptation of different taxa [15–17]. The whole chloroplast sequence is a highly valuable tool for providing insights into the phylogenetic relationships among different plant lineages [18,19]. In addition, maternal inheritance of the chloroplast genome, and lack of cross recombination, make this subcellular organelle a good platform for genetic engineering studies.

The size of chloroplast DNA (cpDNA) is variable among different plant species. According to available records, *Cathaya argyrophylla* has the smallest chloroplast genome size (107 kb), while *Pelargonium* has the largest (218 kb) [15]. Despite the overall high variation in size, chloroplast genomes are highly conservative and have similar structural organization, including gene content and gene order, in different plant species [20]. This circular, double-stranded DNA molecule comprises of four sections, including two copies of inverted repeats (IRs) with the same length (20–28 kb) that separate the large single copy (LSC) (80–90 kb) and the small single copy (SSC) (16–27 kb) regions [15]. The cpDNA contains 110–130 genes that are involved in photosynthesis and gene expression (about 80 genes), as well as translation (4 rRNAs and 30 tRNAs) with overall conservation in their composition and arrangement [15]. However, there is considerable diversity in regulatory sequences of non-coding intergenic spacer regions, as well as occurrence of structural rearrangements, point mutation, gene/intron gains and losses, translocations, IR expansion and inversions, and insertion loss among different species [15,21]. This small variability in the chloroplast genome provides a valuable resource for investigation of plant phylogenetic and evolutionary events. Moreover, in cpDNA there are many repeated sequences, such as simple sequence repeats (SSRs), homo-polymeric repeats and long repeats, which can serve as a good source for designing molecular markers, one of the powerful tools for the evaluation of population genetic structures and phylogenetic relationships among different samples [22].

Despite being one of the most economically important nut species across the world, pistachio has not been subjected to comprehensive sequencing and there is no chloroplast sequence information about this plant species. In this study, we assembled, described, and characterized the complete chloroplast genome sequence of *Pistacia vera*. In addition, we compared and analyzed the chloroplast sequence of pistachio with other known chloroplast genomes, including those of its closely related species to determine their phylogenetic relationships. Results of the present study should provide good information about the phylogenetic relationship of the *Pistacia* species, as well as providing a theoretical basis for genetic improvement of this important nut crop.

2. Materials and Methods

2.1. Chloroplast Genome Assembly and Validation

Chloroplast genome data (paired-end read data, Illumina HiSeq 2000) was downloaded from the NCBI database (SRR4453367) [23]. The deposited sequences were derived from *P. vera* cv. 'Siirt' [23]. A multi-step pipeline involving the following was applied for assembly: Burrows-Wheeler aligner (bwa) [24]; Picard-tools, and Genome Analysis Tool-Kit (GATK) [25] and variant calling tools [26,27]. The pistachio chloroplast genome was used as a reference for chloroplast assembly.

2.2. Gene Annotation and Sequence Analysis

Structural features of the chloroplast genome were illustrated by OGDRAW v1.2 [28]. CpGAVAS [29] and DOGMA [30] were used to annotate the sequences, while analyses of sequence composition were performed by MEGA 6 software.

2.3. Simple Sequence Repeats (SSR) Analysis

MIcroSATellite (MISA) was used to detect simple sequence repeats in the chloroplast genome of *Pistacia* and its closely-related genera [31]. The parameters for SSRs were set as follows: a minimum number of 10, 5, 4, 3, 3 and 3 repeat units was adjusted for identification of perfect mono-, di-, tri-, tetra-, penta-, and hexa-nucleotides motifs, respectively. In addition to the whole chloroplast genome, SSRs were separately analyzed in different regions of genomes.

Tandem repeat finder (<https://tandem.bu.edu/trf/trf.submit.options.html>, accessed on 27 April 2022) was used to identify tandem repeats in the chloroplast genomes. The alignment parameters were set 2 for match and 7 for indels and mismatch. Palindromic and forward repeats were detected by REPuter software [32]. The minimum sizes for repeat elements and the sequence identity were considered to be 30 bp and more than 90% (hamming distance of 3), respectively.

2.4. Phylogenetic Analysis

The phylogenetic analysis was performed using 17 complete chloroplast genomes, including *P. vera* and its 14 closely related species, from the Sapindales order, as well as two outgroups, including *Nicotiana tabacum*, as a plant model, and *Prunus davidiana*, as a fruit tree species (Table 1). The chloroplast genomes were aligned with clustalW [33] and a neighbor-joining tree was created with Geneious software [34]. The genetic differences among chloroplast genomes were computed using Geneious software [34]. All sequences were obtained from the NCBI Organelle Genome and Nucleotide Resources database where complete sequences were used to analyze their affinity.

Table 1. List of plant species with published chloroplast genomes used for phylogenetic cluster analysis.

Order	Family	Tribe	Genus	Species	NCBI Accession No.	Reference
Sapindales	Anacardiaceae	Rhoeae	Pistacia	<i>P. vera</i>	-	Current study
Sapindales	Anacardiaceae	Rhoeae	Pistacia	<i>P. weinmannifolia</i>	NC_037471.1	[35]
Sapindales	Anacardiaceae	Rhoeae	Rhus	<i>R. chinensis</i>	NC_033535.1	[36]
Sapindales	Anacardiaceae	Anacardiaceae	Anacardium	<i>A. occidentale</i>	NC_035235.1	[37]
Sapindales	Anacardiaceae	Anacardiaceae	Mangifera	<i>M. indica</i>	NC_035239.1	[37]
Sapindales	Anacardiaceae	Spondieae	Spondias	<i>S. tuberosa</i>	NC_030527.1	[38]
Sapindales	Burseraceae	Bursereae	Commiphora	<i>C. wightii</i>	NC_036978.1	unpublished
Sapindales	Burseraceae	Bursereae	Boswellia	<i>B. sacra</i>	NC_029420.1	[39]
Sapindales	Sapindaceae	Nephelieae	Litchi	<i>L. chinensis</i>	NC_035238.1	[37]
Sapindales	Sapindaceae	Sapindeae	Sapindus	<i>S. mukorossi</i>	KM454982.1	[40]
Sapindales	Simaroubaceae	-	Leitneria	<i>L. floridana</i>	NC_030482.1	[41]
Sapindales	Meliaceae	Swietenieae	Swietenia	<i>S. mahagoni</i>	NC_040009.1	unpublished
Sapindales	Meliaceae	Swietenieae	Khaya	<i>K. senegalensis</i>	NC_037362.1	[42]
Sapindales	Rutaceae	Aurantieae	Citrus	<i>C. sinensis</i>	DQ864733.1	[43]
Sapindales	Rutaceae	Zanthoxyleae	Zanthoxylum	<i>Z. bungeanum</i>	NC_031386.1	[44]
Rosales	Rosaceae	Pruneeae	Prunus	<i>P. davidiana</i>	NC_039735.1	[45]
Solanales	Solanaceae	Nicotianeae	Nicotiana	<i>N. tabacum</i>	Z00044.2	[46]

3. Results

3.1. Structural Features of *P. vera* Chloroplast Genome

The *Pistacia vera* chloroplast genome is 160,598 bp in length with a typical quadruple structure comprising of an LSC region (88,174 bp; 54.90%), an SSC section (19,330 bp; 12.04%) and two IR regions (26,547 bp; 33.06%) (Figure 1). Within the genome, 121 genes were recognized, among which 18 genes were duplicated in the invert repeat regions, making a total number of 139 genes (Table 2). These genes included 4 rRNA genes, 30 tRNA genes and 87 protein-coding genes. Among the 87 protein-coding genes, photosynthesis-related genes were the most prevalent (43 genes), followed by proteins for subunits of ribosomal proteins (21 genes) and RNA polymerase-coding genes (4 genes). Ten protein-coding genes were categorized as genes with other functions, including protease, translational initiation factor, maturase, subunit acetyl-CoA-carboxylase, envelope membrane protein, c-type cytochrome synthesis gene, and four hypothetical open reading frames. Most of the predicted genes (90 genes) were localized to the LSC region. All of the rRNA genes and 10 tRNA genes were among those localized to the IR regions, while most NADH dehydrogenase genes were in the SSC region.

Table 2. Functions of genes identified from the *P. vera* chloroplast genome.

Category	Gene Group	Gene Names
Self replication	Large subunit of ribosomal protein genes	rpl32, rpl23 ^a , rpl2 ^{*a} , rpl33, rpl20, rpl36, rpl14, rpl16, rpl22
	Small subunit of ribosomal protein genes	rps7 ^a , rps12 ^{*a} , rps15, rps19 ^a , rps16 [*] , rps2, rps4, rps14, rps18, rps11, rps8, rps3
	DNA-dependent RNA polymerase genes	rpoA, rpoB, rpoC1 [*] , rpoC2
	Ribosomal rRNA genes	CGW73_pgr008 ^a , (16S); CGW73_pgr007 ^a , (23S); CGW73_pgr008 ^a , (4.5S); CGW73_pgr0085, (5S)
	tRNA genes	trnM-CAU ^a , trnI-CAU ^a , trnL-CAA ^a , trnV-GAC ^a , trnI-GAU ^{*a} , trnA-UGC ^{*a} , trnR-ACG ^a , trnR-ACG ^a , trnR-ACG ^a , trnN-GUU ^a , trnL-UAG, trnH-GUG, trnH-GUG, trnH-GUG, trnK-UUU [*] , trnQ-UUG, trnS-GCU, trnT-CGU [*] , trnG-UCC, trnR-UCU, trnD-GUC, trnD-GUC, trnY-GUA, trnE-UUC [*] , trnE-UUC [*] , trnT-UGU, trnS-GGA, trnM-CAU, trnM-CAU, trnS-UGA, trnG-GCC, trnG-GCC, trnT-GGU, trnL-UAA [*] , trnF-GAA, trnV-UAC [*] , trnM-CAU, trnW-CCA, trnP-UGG, trnP-UGG, trnE-UUC [*]

Table 2. Cont.

Category	Gene Group	Gene Names
Photosynthesis	Photosystem I	psaA, psaB, psaJ, psaC
	Photosystem II	psbA, psbk, psbI, psbM, psbZ, psbC, psbD, psbJ, psbL, psbF, psbE, psbB, psbT, psbN, psbH
	Cytochrome b/f complex	petN, petA, petL, petG, petB, petD
	ATP synthase	atpA, atpF *, atpH, atpI, atpE, atpB
	NADH dehydrogenase	ndhB *, ^a ndhF, ndhD, ndhE, ndhG, ndhI, ndhA *, ndhH, ndhJ, ndhK, ndhC
	RubisCo large subunit	rbcL
Other genes	Protease	clpP *
	Translation initiation factor	infA
	Maturase	matK
	Acetyl-CoA-carboxylase (subunit)	accD
	Envelope membrane protein	cemA
	Cytochrome synthesis (C-Type)	ccsA
	Chloroplast reading frames (<i>hypothetical</i>)	ycf2 ^a , ycf1, ycf3 *, ycf4

* Genes containing introns; ^a duplicated genes.

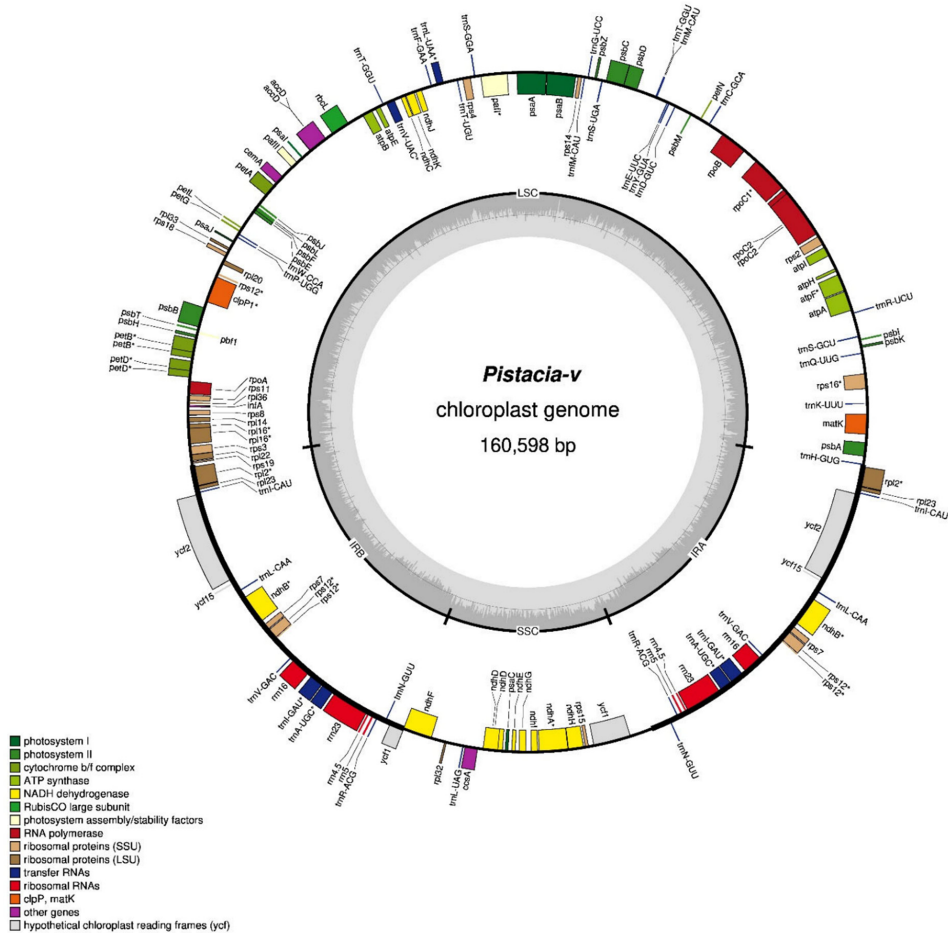


Figure 1. Chloroplast genome map of *P. vera* depicted with OGDRAW software. Genes identified inside the circle are transcribed clockwise and those drawn outside of the circle are transcribed counter-clockwise. Genes having similar functions are shown in the same colors. The inner circle illustrates nucleotide compositions (light grey, AT content; dark grey, GC content). Itron containing genes are marked with '*'.

The highest nucleotide proportion of the *P. vera* chloroplast genome was dedicated to protein coding genes (76,749 bp; 47.80%), followed by intergenic spacers (IGSs) (67,561; 42.06%), introns (9031 bp; 5.65%), rRNA (9048 bp; 5.62%) and tRNA (2897 bp; 1.80%) genes,

respectively (Table 3). The overall chloroplast genome GC content was 37.87%. However, nucleotide distribution was highly variable among different parts of the *P. vera* chloroplast genome with IR regions having the highest GC content (42.94%), followed by LSC (33.13%) and SSC (32.36%). Nucleotide composition was also highly variable among different gene classes. The rRNA-related sequences had the highest GC content (54.52%) among the chloroplast genes, while intergenic regions (34.07%) and intron sequences (36.68%) had the lowest GC content, respectively (Table 3). The GC content of tRNA genes was also relatively high (52.50%), but much lower (38.56%) in the protein coding genes.

Table 3. Nucleotide composition of specific *P. vera* chloroplast genome regions.

	T(U)	A	C	G	GC Content	SSRs	Length (bp)	%
Whole Genome	31.37	30.76	19.26	18.61	37.87	91	160,598	100
LSC	30.67	36.20	16.89	16.24	33.13	64 (70.33%)	88,174	54.9
SSC	33.72	33.92	16.81	15.55	32.36	15 (16.48%)	19,330	12.04
IR	28.38	28.67	20.67	22.27	42.94	12 (13.19%)	26,547	16.53
tRNA	26.64	23.23	22.25	27.88	50.13	0	2346	1.46%
rRNA	21.20	24.28	26.14	28.38	54.52	0	10,642	6.63%
Intron	33.02	30.30	19.42	17.26	36.68	4 (4.4%)	9099	5.65%
Intergenic space	33.16	32.77	17.28	16.79	34.07	78 (85.71%)	67,561	42.06

Thirteen intron-containing genes were identified in the *P. vera* chloroplast genome, including 10 protein-coding genes, two tRNA genes and one rRNA gene (Table 4). Among these genes, eleven contained one intron while *clp* and *ycf3* genes had more than one intron. In addition, five intron-containing genes were duplicated in the inverted regions. The longest intron sequence (1124 bp) was recorded in the *ndhA* genes, the only intron-containing gene located in the SSC region.

Table 4. Intron containing genes obtained from CPGAVAS analysis of the *P. vera* chloroplast genome.

Gene	Location	Strand	Start	End	Exon 1	Intron 1	Exon II	Intron II	Exon III
					Base Pair (bp)				
trnR-TCT	LSC	-	127	351	35	152	38		
atpF	LSC	-	13,218	14,526	148	694	467		
rpoC1	LSC	-	22,314	25,133	435	777	1608		
trn-CTA	LSC	-	39,132	39,262	38	56	37		
psaA	LSC	-	42,601	44,742	1788	30	324		
ycf3	LSC	-	45,534	47,564	126	724	230	801	150
clpP	LSC	-	73,656	75,702	74	818	290	641	224
rpl2	IR	-	88,274	89,760	394	626	467		
ycf2	IR	+	92,992	97,260	2404	57	1808		
ycf15	IR	+	97,351	97,948	155	292	151		
ndhB	IR	-	98,944	101,154	870	588	753		
rrn23S	IR	+	108,235	111,706	160	38	3274		
ndhA	SSC	-	125,134	127,349	556	1124	536		
rrn23S	IR	-	136,889	140,360	160	38	3274		
ndhB	IR	+	147,441	149,654	777	681	756		
ycf15	IR	-	150,650	151,244	158	289	148		
ycf2	IR	-	151,338	155,633	2428	33	1835		
rpl2	IR	+	158,853	160,342	391	629	470		

The frequency of amino acid usage was inferred for the chloroplast genome of *P. vera* (Table 5). In general, 25,708 codons were identified in pistachio chloroplast genes. Based on the analysis of codon usage frequency, leucine was the most prevalent amino acid and comprised 2742 codons (10.69%) of amino acids, followed by isoleucine with 2195 (8.53%). Contrarily, cysteine (320 codons, 1.30%) and tryptophan (447 codons, 1.74%) were the

two least frequent amino acids found in proteins coded by the *P. vera* chloroplast genome. ATT (isoleucine) was the most frequent codon (1072) among the codons of *P. vera* chloroplast genome.

Table 5. Frequency and patterns of codon usage and codon–anticodon recognition in the chloroplast genome of *P. vera*.

Amino acid	Genome (%)	Codon	No.	RSCU *	tRNA	Amino Acid	Genome (%)	Codon	No.	RSCU *	tRNA
Ala	5.6	GCA	399	1.13	trnA-UGC	Ile	8.53	ATA	673	0.94	trnI-UAU
		GCC	235	0.66				ATC	450	0.62	trnI-GAU
		GCG	174	0.49				ATT	1072	1.47	
Cys	1.3	GCT	633	1.79	trnC-ACA	Lys	4.91	AAA	946	1.5	trnK-UUU
		TGT	228	1.43				AAG	319	0.5	
		TGC	107	0.67				CTA	409	0.89	trnL-UAG
Asp	3.86	GAT	769	1.55	trnD-GUC	Leu	10.69	CTC	202	0.44	
		GAC	226	0.45				CTG	201	0.44	
Glu	4.79	GAA	917	1.49	trnE-UUC			CTT	557	1.21	trnL-UAA
		GAG	317	0.51				TTA	841	1.83	
Phe	5.71	TTC	519	0.71	trnF-GAA			TTG	541	1.18	trnL-CAA
		TTT	952	1.29				ATG	584	1	trnM-CAU
Gly	7.16	GGA	718	1.56	trnG-UCC	Met	2.49	AAC	297	0.5	trnN-GUU
		GGC	192	0.42				AAT	886	1.5	
		GGG	329	0.71		Pro	4.08	CCA	311	1.18	trnP-UGG
		GGT	603	1.31				CCC	205	0.78	
His	2.56	CAC	172	0.52	trnH-GUG			CCG	143	0.54	
		CAT	487	1.48				CCT	392	1.49	
								Gln	3.34	CAA	642
Thr	5.19	ACA	405	1.21	trnT-UGU	Arg	5.96	CAG	219	0.51	
		ACC	275	0.82				AGA	466	1.82	trnR-UCU
		ACG	149	0.45				AGG	166	0.65	
Val	5.49	ACT	507	1.52	trnT-CGU			CGA	342	1.34	trnR-ACG
		GTA	519	1.47				CGC	114	0.45	
		GTC	192	0.54				CGG	131	0.51	
		GTG	192	0.54				CGT	316	1.24	
		GTT	511	1.45				AGC	117	0.35	trnS-GCU
Trp	1.74	TGG	467	1	trnW-CCA	Ser	7.77	AGT	417	1.25	
Tyr	3.65	TAC	209	0.44	trnY-GUA			TCA	389	1.17	trnS-UGA
		TAT	731	1.56				TCC	345	1.03	trnS-GGA
Stop	0.57	TAA	63	1.28				TCG	186	0.56	trnS-CGA
		TAG	42	0.85				TCT	547	1.64	
		TGA	43	0.87							

* Relative Synonymous Codon Usage.

3.2. Comparison of *P. vera* Chloroplast Genome to Other Members of Anacardiaceae

The *P. vera* chloroplast genome size was comparable to other Anacardiaceae (Table 6). Among the six Anacardiaceae family chloroplast genomes, *Rhus chinensis* and *Anacardium occidentale* were the smallest (149,011 bp) and largest (172,199 bp), respectively. However, *P. vera* size was most like *P. weinmanniifolia* (160,767 bp). Irrespective of the sequence length, the LSC was the most variable chloroplast genome region (Table 6), and *Rhus chinensis* and *Anacardium occidentale* had the longest (96,882 bp) and the shortest (87,727 bp) LSC regions, respectively. Accordingly, the LSC chloroplast region of Anacardiaceae showed the highest variation in GC content (SD = 3.27%) compared to other parts of the chloroplast genome. Compared with LSC, the SSC had lower variation and ranged from 19,330 bp in *P. vera* to 18,349 bp in *M. indica*. The length of IRs exhibited the greatest variation (SD = 11.98%) among different parts of the sequenced chloroplast genomes in Anacardiaceae and varied from 25,792 bp in *M. indica* to 33,474 bp in *Rhus chinensis*. The numbers of genes in the genome were also variable in these species and *P. weinmanniifolia* (131 genes) and *M. indica* (112 genes) had the maximum and minimum numbers of genes, respectively. The tRNA-related genes were the most variable among different gene classes in the genome and were the main cause of higher numbers of genes in this plant. However, rRNA gene numbers were the least variable (SD = 0) among different classes of chloroplast genes.

Table 6. Sequence comparison of the *P. vera* chloroplast genome sequence with other Anacardiaceae family members.

Species	<i>Pistacia vera</i>	<i>Pistacia weinmannifolia</i>	<i>Anacardium occidentale</i>	<i>Mangifera indica</i>	<i>Rhus chinensis</i>	<i>Spondias tuberosa</i>	Variation	SD
Single-copy region (large)								
Length (bp)	88,174	88,402	87,727	86,673	96,882	89,550	10,209 bp	4.13
G + C (%)	33.13	36	35.7	36	36.2	35.8	3.0%	3.27
Length (%)	54.9	54.98	50.94	54.93	65.02	55.26	14.0%	8.41
Single-copy region (small)								
Length (bp)	19,330	19,129	19,046	18,349	18,647	18,399	981 bp	2.17
G + C (%)	32.36	32.9	32	32.4	32.5	32.2	1.0%	0.94
Length (%)	12.04	11.9	11.06	11.63	12.51	11.36	1.0%	4.38
Inverted repeat								
Length (bp)	26,547	26,618	32,713	25,792	33,474	27,045	7,684 bp	11.98
G + C (%)	42.94	42.9	43	43	45.4	42.7	3.0%	2.36
Length (%)	16.53	16.56	19	16.34	22.47	16.69	6.1%	6.53
Total								
Length (bp)	160,598	160,767	172,199	157,780	149,011	162,039	23,188 bp	4.65
G + C (%)	37.87	36.8	38.1	37.9	37.7	37.7	1.0%	1.21
Length (%)	100	100	100	100	100	100	0.0%	0
Total genes	132 (136 (+121))	131	126	112	120	117	20	6.5
Protein-coding genes								
genes	87	87	79	78	84	83	9	4.64
tRNA	30	37	29	30	32	30	3	9.4
rRNA	4	4	4	4	4	4	0	0
Intron-containing genes (# with 2 introns)								
	13 (2 with 2)	16 (2 with 2)	12 (3 with 2)	16 (2 with 2)	13 (2 with 2)	14 (3 with 2)	-	9.56
SSRs/Compound SSRs								
	91/12	86/9	78/8	73/8	76/8	14/3	19	11.95

3.3. Repeat Sequences Analysis

The chloroplast genome of *P. vera* and its related genera were screened for SSR sequences. The number of SSRs in the chloroplast genomes of the six analyzed species varied from 72 (*Anacardium occidentale*) to 91 (*Pistacia vera*) (Table 6). Mononucleotide repeats were the most frequent motifs found in all analyzed genomes and comprised 66.67% (*Anacardium occidentale*) to 78.02% (*Pistacia vera*) of all SSR sequences, followed by tetranucleotide motifs (8.79–16.67%). Pentanucleotide SSRs were not detected in *Anacardium occidentale* and hexanucleotide repeats were not found in *P. vera*, *P. weinmannifolia* and *Rhus chinensis* (Figure 2). The most frequent SSRs were A/T repeats that comprised 75.82% of the total SSRs identified in the pistachio chloroplast genome. In addition, the majority of SSRs (70.33%) were found in the LSC region. Intergenic spacer sequences had the highest SSR numbers (85.71%), followed by coding sequences (13.19%), and introns (4.4%). No SSRs were detected in tRNA and rRNA coding sequences.

The chloroplast genome of *P. vera* and its closely-related genera were also screened for long repeat sequences. Tandem repeats were the most frequent type of long repeats in the chloroplast of studied genera (Figure 2). Most (37.78%) tandem repeat sequences were in the range of 16–20 bp. The maximum (53) and the minimum (21) numbers of tandem repeats were detected in the *Pistacia weinmannifolia* and *Spondias tuberosa*, respectively. Number of forward repeats varied from 10 (*Anacardium occidentale*) to 20 (*P. vera*, *P. weinmannifolia* and *Rhus chinensis*) in the different genera studied, while palindromic repeats ranged from 17 (*Rhus chinensis*) to 32 (*Mangifera indica*) (Figure 2). Lengths of many forward (75.24%) and palindromic (69.03%) repeats were in the range of 30–50 bp. There were 20 forward, 30 palindromic and 45 tandem repeats in the chloroplast genome of *P. vera*. The chloroplast genome of *Pistacia weinmannifolia*, also had the same number of forward

(20) and palindromic repeats (30) as the *P. vera*; however, the tandem repeats were more prevalent in the chloroplast genome of *P. weinmannifolia*, compared with *P. vera* (53).

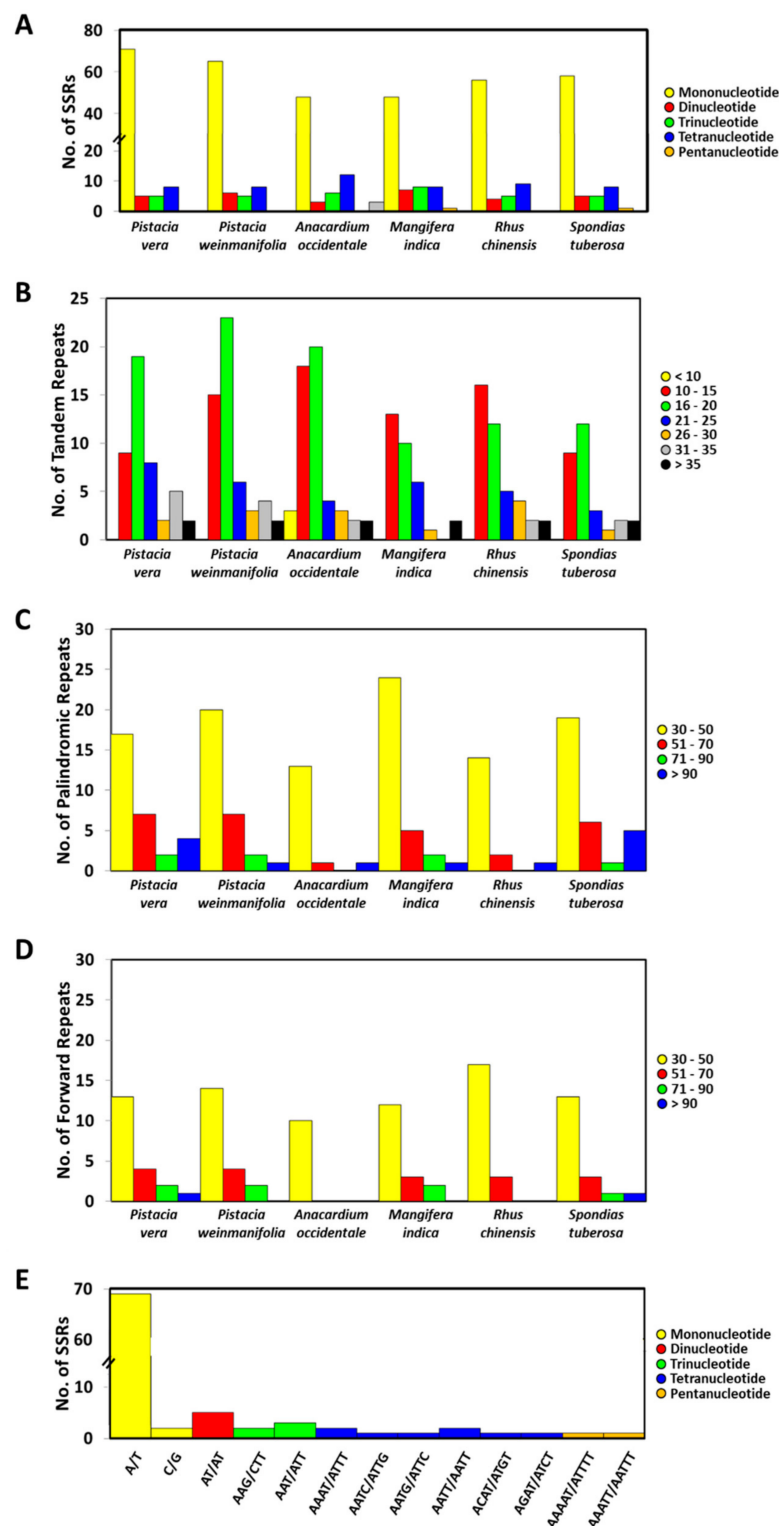


Figure 2. Statistics describing SSR (A) motif type and frequency, (B) number of tandem repeats, (C) number of palindromic repeats, (D) and number of forward repeats in the chloroplast genomes of different Anacardiaceae family members. (E) SSR repeat frequency within the *P. vera* chloroplast genome.

3.4. Phylogenetic Analysis

To build a phylogenetic tree (Figure 3), the complete chloroplast genome of *P. vera* was compared with 14 chloroplast sequences of other members of the Sapindales order published in NCBI (Table 6). In addition to the species in the Sapindales order, *Nicotiana tabacum* and *Prunus davidiana* from Solanaceae and Rosaceae were used as outgroup samples. Based on cluster analysis, all 17 chloroplast genomes were divided into three main groups. The first group consisted of six Anacardiaceae members (*P. vera*, *P. weinmannifolia*, *Rhus chinensis*, *Anacardium occidentale*, *Mangifera indica*, *Spondias tuberosa*) and two members of Burseraceae (*Commiphora wightii* and *Boswellia sacra*). Two members of Meliaceae (*Khaya senegalensis* and *Swietenia mahagoni*) and two members of Rutaceae (*Citrus sinensis* and *Zanthoxylum bungeanum*) were clustered together. Two members of Sapindaceae (*Litchi chinensis* and *Sapindus mukorossi*), along with *Leitneria floridana* from the Simaroubaceae family, were clustered with *Nicotiana tabacum* (Solanaceae) and *Prunus davidiana* (Rosaceae); two outgroup samples were used in this analysis. According to the generated tree, *P. vera* clustered with three other members of Anacardiaceae, from which the complete sequences of chloroplast were available in NCBI. However, *P. vera* was closest to *Pistacia weinmannifolia*. These two species, along with Rhoeeae tribe member, *Rhus chinensis*, formed a sub-cluster, separate from other Anacardiaceae members, including the Anacardiaceae and Spondieae tribes.

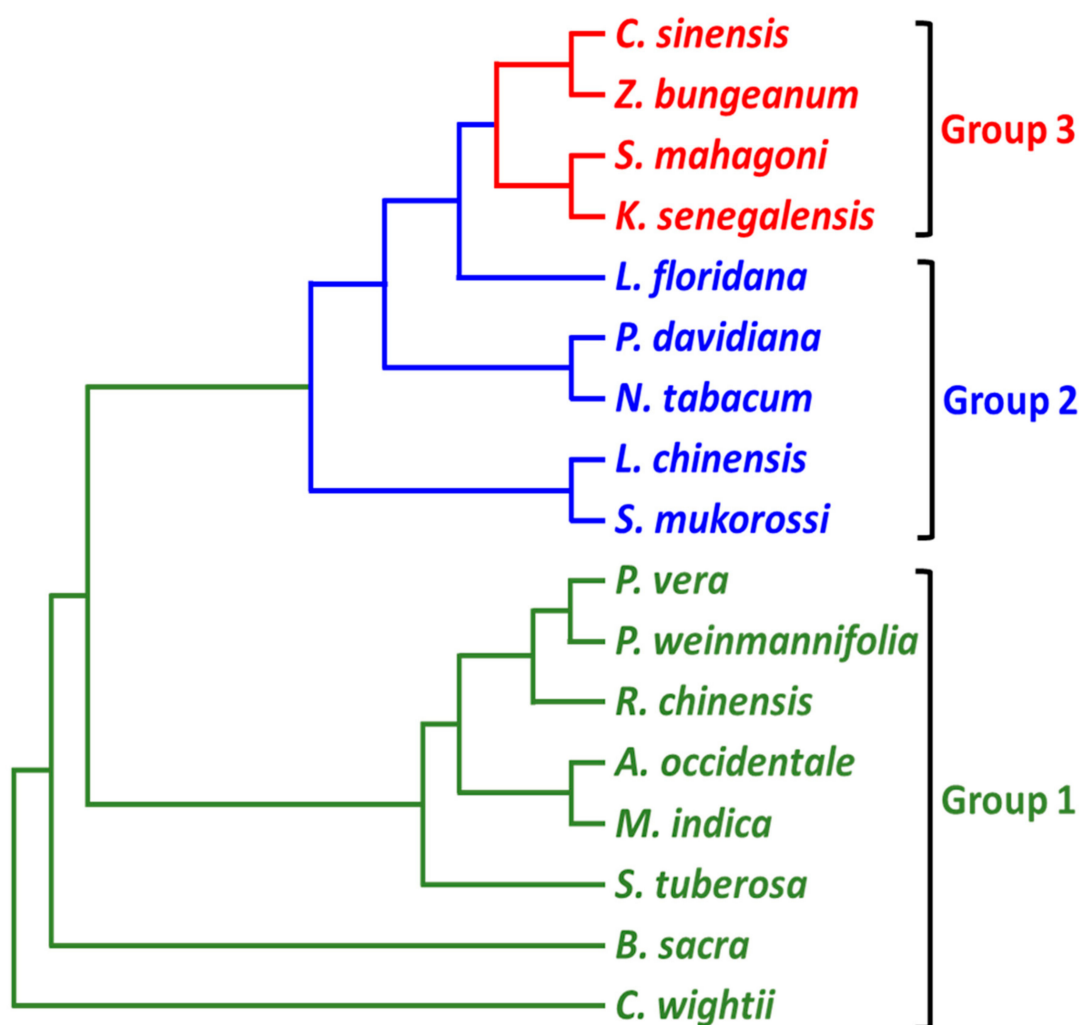


Figure 3. Phylogenetic relationships constructed from the complete chloroplast genome sequences of the members of the Spindales order.

As expected, the two outgroup samples were completely distinct and separated from other members of the Sapindales order. These two genera showed the highest genetic differences within Sapindales (Supplementary Table S1). *Nicotiana tabacum* was the species most distinct from *P. vera* (genetic dissimilarity = 0.085), followed by *Prunus davidiana* (0.075) (Supplementary Table S1). However, *Prunus davidiana*, as a tree species sample, showed higher genetic similarity with members of Sapindales order than herbaceous *Nicotiana tabacum*.

4. Discussion

4.1. Structural Features of *P. vera* Chloroplast Genome

Information about the organization and evolution of chloroplast genomes is beneficial, both for improving plant yield and for providing more accurate insights into plant phylogeny. In this study, the chloroplast genome of *P. vera* was assembled using high throughput next generation sequences. The complete chloroplast genome of *P. vera* is 160,598 bp, which is within the range of chloroplast genomes of other angiosperm plants [15]. The chloroplast genome of *P. vera* is highly conserved and is composed of a four-section circular DNA with similar structure, gene content, and order with other angiosperms [47–50]. Inverted repeat sections were the most size-variable (SD = 11.01%) chloroplast genome regions among different members of the Sapindales order. Expansion and contraction of invert repeat sections is considered the main reason for variation in the length of the chloroplast genome [51].

GC content is an important index for determining kinship relationships among different species [52,53]. *P. vera* chloroplast GC content resembled that of other genera within Anacardiaceae and was most similar to *M. indica*. As was typical in other plant chloroplast genomes, the highest GC content was detected in the IR regions [54]. This could be attributed to the high numbers of rRNA and tRNA genes that are aggregated in these regions [55,56].

Intron containing gene numbers were lower in the *P. vera* compared with other closely-related species and two genes *clp* and *ycf3*, had more than one intron. Finding multiple introns for *clp* and *ycf3* was also disclosed in studies of other chloroplast genomes [48–50,54]. It has been reported that *ycf3* is required for stable accumulation in the photosystem I complex [57] and the additional introns may be beneficial for studies of photosynthesis evolution [54].

Amino acid codons were highly biased towards a specific codon in *P. vera* chloroplast genome sequences. Codon degeneracy has an important biological role in higher organisms and can decrease the detrimental effects of point mutations [58–60]. On the other hand, uneven codon distribution of certain amino acids in the genome indicates nucleotide mutation is not random and there exists mutation preference and selective pressure, resulting in synonymous codon usage bias [47]. As noted in reports of nucleic acid composition for other angiosperm plants [47,49,50,54], codons ending in amino acids A and U(T) were most prevalent in synonymous codons and represented the highest value for relative synonymous codon usage (RSCU). An informative indicator to calculate level of codon preference, RSCU values ranged from 0.35 (AGC of serine) to 1.83 (TTA of leucine). RSCU index values may vary from 0.09 to 1.92 [61] and codon preference can be categorized into four groups, including no preference ($\text{RSCU} \leq 1.0$), low preference ($1.0 < \text{RSCU} < 1.2$), moderate preference ($1.2 < \text{RSCU} < 1.3$) and intense preference ($\text{RSCU} > 1.3$) [47]. Of the 64 codons responsible for coding 20 amino acids in the *P. vera* plastid genome, 20 showed high preference ($\text{RSCU} > 1.3$) and 6 showed moderate preference ($1.2 < \text{RSCU} < 1.3$). The amino acids tryptophan and methionine showed no codon preference ($\text{RSCU} = 1.0$). Most amino acids with multiple codons were highly biased towards one or two A/T ending codons, except phenylalanine, which showed moderate preference. Codon preference is highly pervasive among different plant genes and is considered the primary reason for sequence conservation among chloroplast genes in different plants [47].

4.2. Repeat Sequences

Repetitive sequences are highly important in the recombination and rearrangement of the chloroplast genome, as they promote genetic variation through slipped strand mispairing during DNA replication [62] and illegitimate recombination [17,22,63]. SSRs are a valuable tool for phylogenetic analysis, ecological studies, distinguishing between closely-related plant species, and plant breeding [64]. With a highly polymorphic nature or copy number variation, repetitive elements serve as powerful molecular markers for genetic diversity, phylogenetic and population genetic studies [49,65,66]. Most previous phylogenetic investigations in plant species were conducted using a small number of loci, which may be insufficient for precise understanding of evolutionary relationships, especially at low taxonomic levels and in controversial plant species [16,48]. In the present study, 91 SSRs were detected in the *P. vera* chloroplast genome which was higher than other closely related taxa, with poly A/T repeats being the most frequent repeat units. Most previous reports indicated mononucleotide SSRs as more common in the chloroplast genome of different plant lineages with a strong A/T bias in their base composition [48–50,54]. No six-nucleotide repeats were detected in three Rhoëae tribe members, which indicates the presence of pattern similarities among repeat units of closely related species.

In accordance with previous reports, most chloroplast SSRs were in the intergenic spacer regions, and only about 13% of detected SSRs were in the coding sequences. These observations support the idea that intergenic spacer regions are highly variable and crucial hotspots for reconfiguration of the chloroplast genome [52]. According to Eguluz et al. [67], SSRs in the non-coding sequences of chloroplasts are usually short mononucleotide repeats and are highly intraspecific variables in repetitive units.

Considering chloroplast SSRs are informative molecular markers for genetic evaluation of phylogenetic relationships, some of the detected SSR loci will be extremely useful for genetic diversity studies in *P. vera*. Use of SSRs may improve discrimination efficiency among controversial taxonomic classifications of *P. vera* and its close relatives, such as *P. khinjak*, *P. atlantica*, *P. lentiscus*, and *P. integerrima* [68], and, subsequently, may increase the power of interspecific discriminating, possibly in combination with other nuclear genomic SSRs.

4.3. Phylogenetic Reconstruction

Chloroplast genomes provide a good platform for resolving controversial phylogenetic relationships among different species, even at lower taxonomic levels [16,17]. Approaches such as morphological resemblance, molecular markers, and different barcode systems have been used to assign uncertain genera to proper families. In fact, many previous phylogenetic analyses were conducted based on a small number of loci, which were insufficient for delineating accurate phylogenetic relationships, especially for closely related species [48]. However, development of next generation sequencing technologies has expedited sequencing and assemblage of plastid genomes from varied plant species, compared to traditional sequencing methods. These advancements have enabled researchers to assign controversial species to their appropriate genera and species more accurately.

Phylogenetic analysis based on the complete chloroplast sequence of *P. vera* and its relatives revealed this species is most closely-related to *P. weinmannifolia*. *Pistacia* is genetically most like the *Rhus* genus. These two genera are placed in the Rhoëae tribe within Anacardiaceae. Our results were consistent with those of previous phylogenetic studies, based on nuclear markers, plastid DNA barcodes, and chloroplast genome sequences, which describe *Rhus* as a sister group of *Pistacia* [35,69]. Moreover, our results revealed Rhoëae is more closely-related to Anacardiaceae than Spondiëae, two other tribes in the Anacardiaceae family. Based on morphological differences, special features of flower structure, pollen, and flower style, it has been suggested that *Pistacia* be separated from Anacardiaceae and placed into Pistaciaceae instead [69]. As low taxon sampling may result in differing cluster topology [67], supplementary studies with additional samples from various tribes within Anacardiaceae are needed to obtain a more reliable picture of

phylogenetic relationships among the tribes in this family. Incidentally, all members of Anacardiaceae formed a highly supported clade in the cluster analysis.

We used previously sequenced chloroplast genomes from different families in Sapindales to investigate among-family relationships. Based on the phylogenetic analysis, the Anacardiaceae family is more similar to Burseraceae than other families in Sapindales, including Sapindaceae, Simaroubaceae, Meliaceae and Rutaceae. The chloroplast sequence divergence among the three main groups in this cluster was substantial, representing high genetic dissimilarities between different members of the main groups. However, we should bring to mind that great genetic diversity was reported among pistachio samples from different regions [3,70] and sequencing more pistachio cultivars, as well as its closely-related species, will shed more light on the phylogenetic relationships among *Pistacia* and its close genera.

Our results indicated two outgroup samples used in this study diverged from Sapindales members and formed an individual clade. Notably, these two outgroups were genetically similar to some Sapindales order members and clustered with Simaroubaceae and Sapindaceae family members. Sequences of the entire chloroplast genome may not reveal sufficient discrimination among highly similar species, and, therefore, informative loci from the nuclear genome should also be included for evolutionary analysis of young lineages [71].

Altogether, it seems that by increasing chloroplast sequence data in this family and scientific awareness of the relationship between different genera in Sapindales, a comprehensive revision of the order may be unavoidable. However, supplementary phylogenetic studies using sequence data from other members of the Sapindales order and its different sub-divisions, including family, subfamily and tribe, are needed to shed light on the phylogenetic relationships within this populous order and reach a more decisive conclusion regarding member assignment.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/d14070577/s1>, Supplementary Table S1. Genetic differences among different plant species used for cluster analysis.

Author Contributions: All authors contributed to the study conception and design. A.E. designed the project, assembled the genome and analyzed the data. A.Z. drafted the manuscript and analyzed and interpreted the data. S.L. edited and revised the critically the manuscript for important intellectual content and did data visualization. S.M. revised the manuscript and analyzed data. All authors have read and agreed to the published version of the manuscript.

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