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Two chloroplast genomes with reduced inverted repeat regions in *Mammillaria* series *Stylothelae* (Cactaceae)

Juan Pablo Ortiz-Brunel[1,2], Michael R. McKain[3], Pilar Zamora-Tavares[1,4], Eduardo Ruiz-Sanchez[1,4], Daniel Sánchez[4,5], Isaac Sandoval-Padilla[2], Bryan N. MacNeill[3], and Aarón Rodríguez[1,4]*

[1] Departamento de Botánica y Zoología, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Zapopan, Jalisco, Mexico.
[2] Doctorado en Ciencias en Biosistemática, Ecología y Manejo de Recursos Naturales y Agrícolas, Universidad de Guadalajara, Zapopan, Jalisco, Mexico
[3] Department of Biological Sciences, The University of Alabama, Tuscaloosa, USA.
[4] Laboratorio Nacional de Identificación y Caracterización Vegetal (LaniVeg), Instituto de Botánica, Universidad de Guadalajara, Zapopan, Jalisco, Mexico.
[5] CONAHCYT-Universidad de Guadalajara, Departamento de Botánica y Zoología, Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Zapopan, Jalisco, Mexico.
*Author for correspondence: aaron.rodriguez@academicos.udg.mx

Abstract
Background: The chloroplast genomes of Cactaceae exhibit boundary modifications in the inverted repeat regions (IRs), gene inversions, and deletions. Among nine *Mammillaria* species, three distinct chloroplast structures have been identified, although not all of these correspond to the morphology-based classification of the genus.
Question: Is there a distinct chloroplast genome structure in the species of *Mammillaria* series *Stylothelae*?
Studied species: *Mammillaria bocasana* and *M. erythrosperma*.
Study site and dates: Mexico from 2019 to 2023.
Methods: Chloroplast DNA was sequenced, and chloroplast genomes were *de novo* assembled using the Fast-Plast program. Complete plastome sequences were annotated and verified. The sequences were aligned in MAUVE program to detect possible structural changes. A maximum likelihood phylogeny was executed to evaluate the relationships of the studied species.
Results: The plastomes ranged from 107,368 bp in *Mammillaria bocasana* to 108,069 bp in *M. erythrosperma*. Both presented a quadripartite structure and contained 108 genes. The IRs were ~ 1,600 bp long and included the genes *rpl*2, *rpl*23 (pseudo), and *trn*I-CAU. MAUVE identified a ~ 21 kb inversion in the large single copy containing a block of genes related to photosynthesis. The phylogenetic analysis placed both species in a single clade separated from the other species within *Mammillaria* subg. *Mammillaria*.
Conclusions: The studied species of *Mammillaria* series *Stylothelae* exhibited a different and synapomorphic chloroplast genome structure. Other *Mammillaria* chloroplast genome structures have evolved independently in different lineages.
Keywords: isomeric plastomes, *ndh* genes, plastome, structure.

Resumen
Antecedentes: Los genomas de cloroplasto de Cactaceae exhiben modificaciones en los límites de las regiones repetidas inversas (IRs), inversiones de genes y deleciones. En nueve especies de *Mammillaria*, se han encontrado tres estructuras de cloroplasto distintas, aunque no todas corresponden a las clasificaciones basadas en morfología.
Pregunta: ¿Existe una estructura de genoma de cloroplasto distinta en las especies de *Mammillaria* serie *Stylothelae*?
Especies estudiadas: *Mammillaria bocasana* y *M. erythrosperma*.
Sitio y años de estudio: México, de 2019 a 2023.
Métodos: ADN de cloroplasto fue secuenciado y los plastomas fueron ensamblados *de novo* usando el programa Fast-Plast. Las secuencias completas fueron anotadas y verificadas. Las secuencias fueron alineadas en el programa MAUVE para detectar posibles cambios estructurales. Un análisis filogenético con máxima verosimilitud evaluó las relaciones de las especies estudiadas.
Resultados: Los plastomas variaron desde 107,368 pb de longitud en *Mammillaria bocasana* hasta 108,069 pb en *M. erythrosperma*. Ambos presentaron una estructura cuadripartita y contuvieron 108 genes. Las IRs tuvieron ~1,600 pb y contuvieron los genes *rpl2, rpl*23 (pseudo) y *trn*I-CAU. MAUVE identificó una inversión de ~21 kb en la región larga de copia única que contiene genes relacionados con la fotosíntesis. El análisis filogenético recuperó a ambas especies como grupos hermanos dentro de *Mammillaria* subg. *Mammillaria*.
Conclusiones: Las dos especies estudiadas de *Mammillaria* serie *Stylothelae* presentaron una estructura de plastoma sinapomórfica. Otras estructuras de plastomas de *Mammillaria* han evolucionado independientemente en linajes diferentes.
Palabras clave: plastomas isoméricos, estructura, genes *ndh*, plastoma.

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While the chloroplast genome (plastome) remains highly conserved in most angiosperms (Daniell *et al*. 2016), there are exceptions characterized by significant structural changes. These variations have been reported in some species-rich groups such as Fabaceae, Passifloraceae, and Malpighiales (Cauz-Santos *et al.* 2020, Jin *et al.* 2020, Lee *et al.* 2021), often observed in parasitic plants (Wolfe *et al.* 1992, Braukmann *et al.* 2013, Frailey *et al.* 2018, Su *et al.* 2021) or species adapted to extreme environments (McCoy *et al.* 2008, Silva *et al.* 2016, Wei *et al.* 2021). In this scenario, the Cactaceae family serves as a prominent example within the Caryophyllales order. Plastomes in Caryophyllales members usually range from 151 to 155 kb and exhibit the typical quadripartite structure divided into a large single copy (LSC), a small single copy (SSC), and two inverted repeats (IRa and IRb) regions (Yao *et al.* 2019). Nevertheless, numerous structural arrangements have been identified within Cactaceae. These arrangements involve plastome reduction derived from expansion/reduction or loss of the inverted repeat regions (IRs), and gene losses (Sanderson *et al.* 2015, Majure *et al.* 2019, Köhler *et al.* 2020, Morais Da Silva *et al.* 2021, Köhler *et al.* 2023, Yu *et al.* 2023).

Chloroplast genomes within Cactaceae exhibit a wide range in length, spanning from 107 to 162 kb, and their IRs vary from around 350 bp to 37 kb (Solórzano *et al.* 2019, Köhler *et al.* 2023, Yu *et al*. 2023). It is worth noting that *Carnegiea gigantea* (Engelm.) Britton & Rose (the saguaro) and *Lophocereus schoottii* (Engelm.) Britton & Rose, lack the IRs (Sanderson *et al.* 2015, Solórzano *et al.* 2019), as well as other Opuntioideae such as *Quiabentia verticillata* (Vaupel) Borg (Köhler *et al*. 2020). Within the genus *Mammillaria* Haw., nine chloroplast genomes have been sequenced with lengths ranging from 107 to 116 kb and three distinct structural variations (Solórzano *et al.* 2019, Hinojosa-Alvarez *et al.* 2020, Yu *et al.* 2023).

In *Mammillaria*, the structure of the chloroplast genome displays variation. Solórzano *et al.* (2019) assembled chloroplast genomes for seven species representing three out of the eight subgenera proposed by Hunt *et al*. (2006): *Krainzia*, *Mammillaria*, and *Phellosperma*. Interestingly, species from different subgenera share the same chloroplast genome structure (Solórzano *et al.* 2019). Consequently, the different chloroplast genome structures seem to not be related to the morphology-based classification. Given the variation of the plastome structure in *Mammillaria*, other unknown structures may exist in the remaining subgenera or in other groups within the subgenus *Mammillaria*.

Plastome sequences and information are lacking for the *Mammillaria* series *Stylothelae*, which is part of *M*. subg. *Mammillaria* and encompasses 19 taxa (Hunt 2016, González-Zamora *et al.* 2023, Ortiz-Brunel *et al.* 2023). This series can be distinguished by the presence of axillary bristles, slightly embedded flowers and fruits, generally uncinated central spines, and the production of Luethy's alkaloid. The combination of these characters differentiates *Stylothelae* from the other series (Fitz-Maurice & Fitz-Maurice 2006, Hunt *et al*. 2006). Additionally, all species of *M.* series *Stylothelae* share the absence of the *rpl*16 intron, which is proposed as a synapomorphy of the group (Butterworth & Wallace 2004, Butterworth *et al.* 2007). This could be an indicator of chloroplast structure variation. Based on this evidence, we anticipate that species of *M.* subg. *Mammillaria* series *Stylothelae* may exhibit a different chloroplast genome structure.

Analyses of chloroplast genome structures and phylogenetic hypothesis based on whole chloroplast sequences have demonstrated their utility in elucidating phylogenetic relationships within *Mammillaria* and its related genera (Solórzano *et al.* 2019, Breslin *et al.* 2021, Chincoya *et al.* 2023). Our objective was to sequence and assemble the plastome of *M. bocasana* Poselg. and *M. erythrosperma* Boed., which belong to *M*. subg. *Mammillaria* series *Stylothelae* (Hunt *et al*. 2006). Additionally, we also compared their structures with those previously described for the genus to gain insights into a broad overview of plastome evolution within the genus.

Material and methods

Sampling. Two living individuals of *Mammillaria bocasana* (*J. P. Ortiz-Brunel 922,* IBUG) and two of *M. erythrosperma* (*J. P. Ortiz-Brunel 410,* IBUG) (herbarium acronym according to Thiers 2023) were collected nearby their type locality (Figure 1). The morphology of the specimens was compared with the morphological descriptions to corroborate their identity (Bravo-Hollis & Sánchez-Mejorada 1991, Reppenhagen 1991, Fitz-Maurice & Fitz-Maurice 2006). We preserved the plants in a greenhouse at the University of Guadalajara until tissue collection.

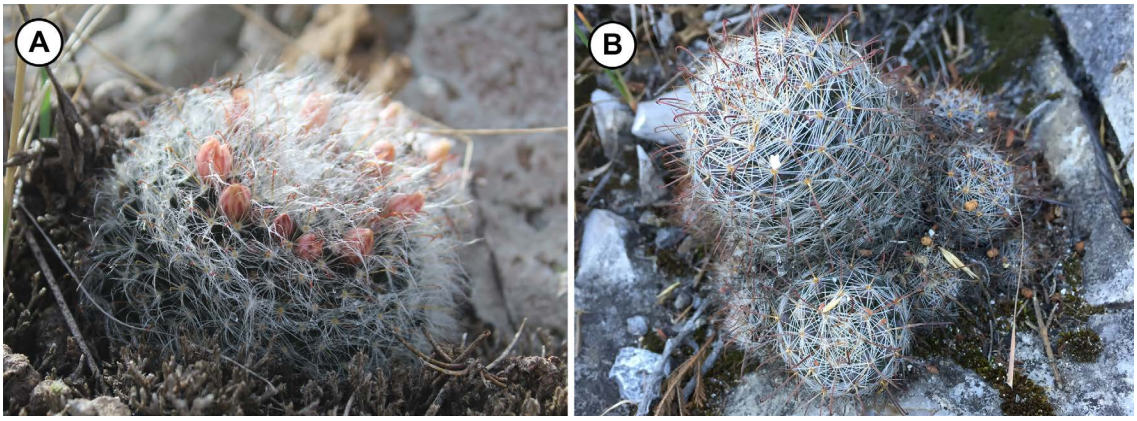

Figure 1. Studied species in their habitat. A) *Mammillaria bocasana*, B) *M. erythrosperma*.

DNA extraction and sequencing. Using freshly collected tissue from the tubercles of only one individual per species, chloroplasts were isolated and cpDNA extracted as described in Shi *et al*. (2012), with slight modifications. The cpDNA quantity and quality were evaluated with a Qubit 3.0 and NanoDrop 2000 (Thermo Fisher Scientific, Waltham, Massachusetts), respectively. We prepared the libraries using the Ion Plus Fragment Library Kit (Thermo Fisher Scientific) and selected DNA fragments of approximately 250 bp using an E-Gel Sizeselect Agarose Gel (Thermo Fisher Scientific). Sequencing of single-end reads of 250 bp was performed on a Personal Genome Machine (Thermo Fisher Scientific) in the Laboratorio Nacional de Identificación y Caracterización Vegetal (LaniVeg) at the University of Guadalajara.

Chloroplast genome assembly. Raw reads quality was assessed in the FastQC v. 0.11.7 program (Andrews 2010). Then, we used the Trimmomatic tool (Bolger *et al.* 2014) to discard reads with low quality (PHRED quality score < 15) using the leading, trailing and avgqual tools. The resulting reads were *de novo* assembled into contigs following the Fast-Plast pipeline (McKain 2017) with slight modifications. Reads were mapped against the genome of *Mammillaria pectinifera* F.A.C. Weber as a reference using Bowtie2 v. 2.5.1 (Langmead & Salzberg 2012) under the very-sensitive-local parameter set to filter for chloroplast-like sequences. These filtered reads were *de novo* assembled using SPAdes 3.15.0 (Bankevich *et al.* 2012) using k-mer sizes of 21, 35, 57, and 89 with the "only-assembler" option. The assembled contigs were merged and extended using the "afin" script available from the Fast-Plast program using default parameters with 50 extension loops and the chloroplast-mapped reads. Once a single contig was reached, the sequence_based_ir.pl script packaged with Fast-Plast was used to find putative IR regions. We used Sequencher v. 4.1.4 (Gene Codes) to verify the IRs. A final coverage analysis to verify the accuracy of our assemblies was conducted using scripts from Fast-Plast and supported by Jellyfish 2 (Marçais & Kingsford 2011). Gene annotation was performed in the GeSeq platform (Tillich *et al.* 2017) and every annotation was manually confirmed. The chloroplast genome circular representation was produced with OGDraw v. 1.3.1 (Greiner *et al.* 2019).

Chloroplast genome structure comparison. We selected one sequence for each known chloroplast genome structure in *Mammillaria* (Solórzano *et al*. 2019) for comparison to our new assemblies. *Mammillaria pectinifera* represented the structure 1 (S1), *M. crucigera* Mart. characterized the structure 2 (S2), and *M. zephyranthoides* Scheidw. corresponded to the structure 3 (S3) (Solórzano *et al*. 2019). These representative chloroplast genomes were converted into linear genomes and then aligned to our *M. bocasana* and *M. erythrosperma* plastomes. All genomes were aligned using the plastome of *M. bocasana* as the reference in MAUVE v. 2.4.0 (Darling *et al.* 2004) with the Progressive Mauve Tool using the default parameters. GenBank accession numbers are indicated in Table 1.

Table 1. List of the species used in the analyses.

Species	GenBank accession number	Infrageneric classification *sensu* Hunt *et al.* (2006)
Carnegiea gigantea	NC_027618.1	
Mammillaria albiflora	MN517610.1	Subgenus *Krainzia*, series *Herrerae-Pectiniferae*
M. bocasana	OR863748	Subgenus *Mammillaria*, series *Stylothelae*
M. crucigera	MN517613.1	Subgenus *Mammillaria*, series *Supertextae*
M. erythrosperma	OR863749	Subgenus *Mammillaria*, series *Stylothelae*
M. huitzilopochtli	MN517612.1	Subgenus *Mammillaria*, series *Supertextae*
M. pectinifera	MN519716.1	Subgenus *Krainzia*, series *Herrerae-Pectiniferae*
M. solisioides	MN518341.1	Subgenus *Krainzia*, series *Herrerae-Pectiniferae*
M. supertexta	MN508963.1	Subgenus *Mammillaria*, series *Supertextae*
M. zephyranthoides	MN517611.1	Subgenus *Phellosperma*

Phylogenetic analysis. We downloaded seven chloroplast genome sequences of *Mammillaria* from GenBank published by Solórzano *et al.* (2019). These sequences represented the three different chloroplast genome structures within the genus. The plastome of *Carnegiea gigantea* (Sanderson *et al.* 2015) was included as an outgroup. Detailed GenBank accession numbers for all sequences used in the analysis are listed in Table 1. We aligned the ten complete plastome sequences using MAFFT v. 7.52 (Katoh *et al.* 2019) with default parameters. A maximum likelihood (ML) search was executed in MEGA v. 11 (Tamura *et al.* 2021), employing the GTR + G + I model. Supporting branch values were obtained through 1,000 bootstrap replications. To discard a possible influence of the chloroplast structures in the results, we performed two additional phylogenetic analyses with the same parameters but different datasets. The first analysis used a matrix in which the 21 kb inversion block was reverted for *M. bocasana* and *M. erythrosperma*. In the second one, we filtered for 54 CDS regions shared among all taxa (Table S1). All phylogenetic analyses were performed with the same parameters.

Results

Chloroplast genome structure comparison. The chloroplast genomes of *Mammillaria bocasana* and *M. erythrosperma* exhibited a quadripartite structure, including an LSC, an SSC, and two small IRs. The chloroplast genome of *M. bocasana* was 107,368 bp long with an LSC of 75,290 bp, an SSC of 28,896 bp, and two IRs of 1,591 bp. *Mammillaria erythrosperma* chloroplast genome was 108,069 bp long, from which 76,393 bp conformed the LSC, the SSC was of 28,402 bp, and two IRs of 1,637 bp (Figure 2). The Guanine-Cytosine (GC) content was 37 % in *M. bocasana* and 36.6 % in *M. erythrosperma*.

Both plastomes shared identical gene content and order with 108 protein coding genes, tRNAs, and rRNAs (Figure 2, Table 2). Ten of those genes were pseudogenized in *Mammillaria bocasana* and 11 in *M. erythrosperma*. The latter exhibited pseudogenization of the *rps*16 gene, resulting from a partial loss of the first exon. The IRs of both species contained *rpl*2, pseudogene *rpl*23, and *trn*I-CAU with IR lengths of 1,591 bp in *M. bocasana* and 1,637 in *M. erythrosperma*. In both plastomes, the IRa was delimited by the *rps*19 and the *ycf*2 genes and the IRb by the *ndh*B (pseudogene) and *trn*H-GUG genes. Both plastomes lacked functional NADH dehydrogenase-like (NDH) complex (*ndh*) genes, though we detected only pseudogenes of *ndh*B, *ndh*D, and *ndh*F.

When compared to other *Mammillaria* plastome structures, the progressive MAUVE alignment identified a new chloroplast genome structure (S4) characterized by a unique inversion within the LSC region in both species of *Mammillaria* series *Stylothelae* (Figure 3). This inversion was 21,248 bp long in *M. bocasana* and 21,469 bp in *M. erythrosperma* and encompassed 21 coding regions, extending from *pet*G to *atp*E genes (Figure 2). The majority of these inverted genes are associated with photosynthetic functions (Table 2). The analyzed species, that correspond to

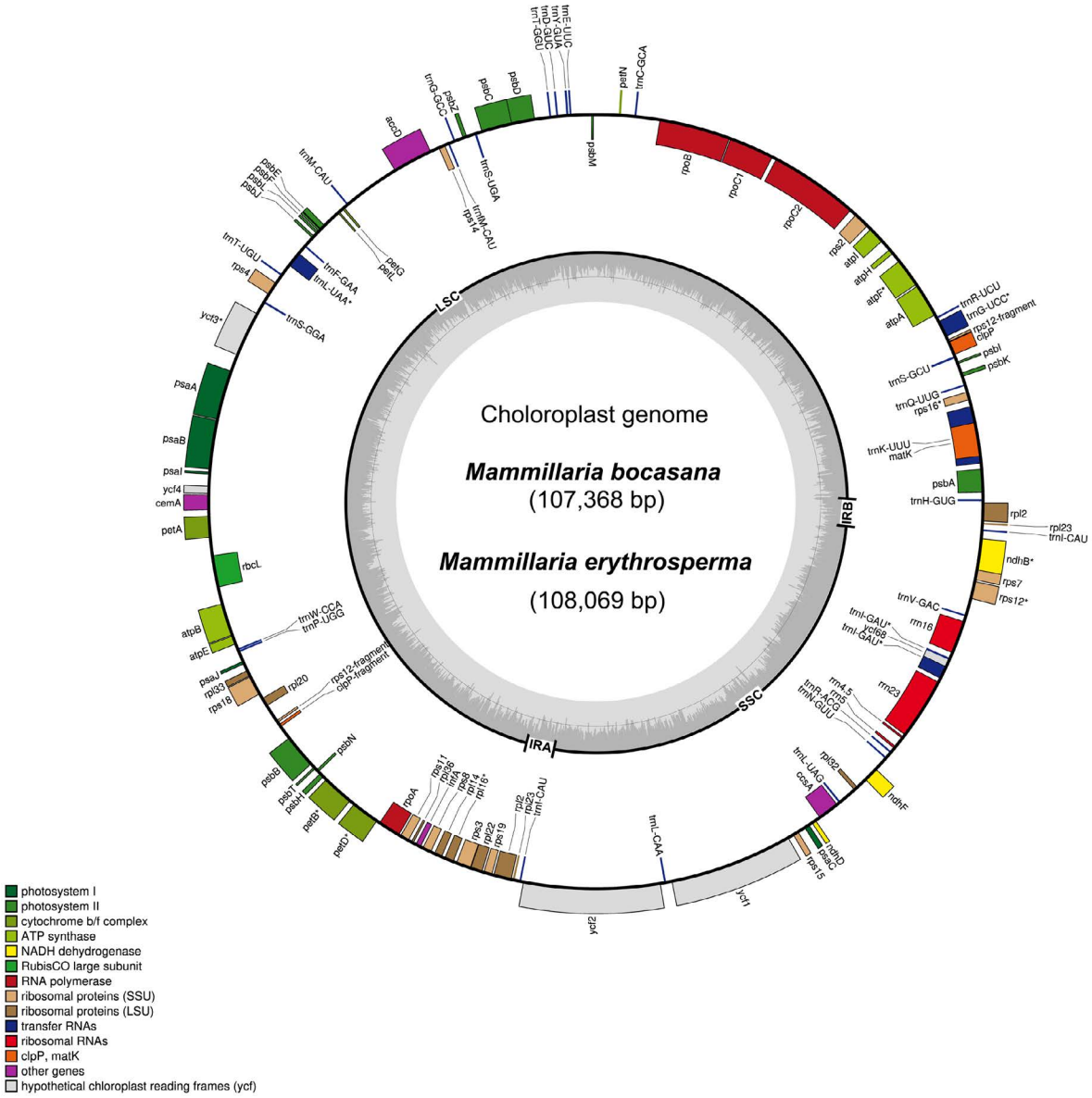

Figure 2. Chloroplast genome structure of *Mammillaria bocasana* and *M. erythrosperma*.

the S1, S2, and S4, had all the other gene blocks in the same order and arrangement. However, the alignment showed remarkable reductions and inversions in the S3, compared with all the other structures.

Phylogenetic analysis. The chloroplast genome recovered robust phylogenetic relationships, with bootstrap support values (BS) exceeding 95 % for all tree branches (Figure 4). The analyses with the complete plastomes, the complete plastomes with the 21 kb reverted block, and the shared CDS, recovered mostly the same topology. These differed in the placement of *Mammillaria albiflora* and *M. zephyranthoides*, and the relationships within *M.* series *Supertextae* (Figures 4, S1, S2). Here, we used the phylogeny inferred with the complete plastomes to describe and discuss our results (Figure 4). The resulting phylogeny placed our two plastome sequences in a monophyletic group within all other *Mammillaria* species (BS = 100 %). Interestingly, species with the same chloroplast structure were dispersed across different clades (Figure 4), except for *Mammillaria bocasana* and *M. erythrosperma*, which had a sister spe-

Table 2. Gene content of the chloroplast genome of *M. bocasana* and *M. erythrosperma*. *Ψ* indicates a pseudogene in both species; *Complete gene in *M. bocasana*, pseudogene in *M. erythrosperma*; **One copy functional and the other a pseudogene in both species.

Genes group		Name	Number
Photosynthesis	Photosystem I	*psa*A, *psa*B, *psa*C, *psa*I, *psa*J	5
	Photosystem II	*psb*A, *psb*B, *psb*C, *psb*D, *psb*E, *psb*F, *psb*H, *psb*I, *psb*J, *psb*K, *psb*L, *psb*M, *psb*N, *psb*T, *psb*Z	15
	ATP synthase	*atp*A, *atp*B, *atp*E, *atp*F, *atp*H, *atp*I	6
	NADH dehydrogenase	*ndh*BΨ, *ndh*DΨ, *ndh*FΨ,	3
	Cytochrome complex	*pet*A, *pet*B, *pet*D, *pet*G, *pet*L, *pet*N	6
	Rubisco Large Subunit	*rbc*L	1
	Acetyl-CoA carboxylase beta subunit	*acc*DΨ	1
Genetic expression control	Ribosomal large subunit proteins	*rpl*2 (2), *rpl*14, *rpl*16, *rpl*20, *rpl*22, *rpl*23 (2)Ψ, *rpl*32, *rpl*33Ψ, *rpl*36	11
	RNA polymerase subunits	*rpo*A, *rpo*B, *rpo*C1, *rpo*C2	4
	Ribosomal small subunit proteins	*rps*2, *rps*3, *rps*4, *rps*7, *rps*8, *rps*11, *rps*12, *rps*14, *rps*15, *rps*16*, *rps*18, *rps*19	12
	Ribosomal RNA	*rrn*16, *rrn*23, *rrn*4.5, *rrn*5	4
	Transfer RNA	*trn*C-GCA, *trn*D-GUC, *trn*E-UUC, *trn*F-GAA, *trn*fM-CAU, *trn*G-GCC, *trn*G-UCC, *trn*H-GUG, *trn*I-CAU (2), *trn*I-GAU, *trn*K-UUU, *trn*L-CAA, *trn*L-UAA, *trn*L-UAG, *trn*M-CAU, *trn*N-GUU, *trn*P-UGG, *trn*Q-UUG, *trn*R-ACG, *trn*R-UCU, *trn*S-GCU, *trn*S-GGA, *trn*S-UGA, *trn*T-GGU, *trn*T-UGU, *trn*V-GAC, *trn*W-CCA, *trn*Y-GUA	29
Other	Conserved Open Reading Frames (ORF)	*ycf*1, *ycf*2, *ycf*3, *ycf*4Ψ, *ycf*68Ψ	5
	Cytochrome C synthesis	*ccs*A	1
	Chloroplast envelope membrane protein	*cem*A	1
	Maturase	*clp*P (2**), *mat*K	3
	Translation initiation factor	*inf*A	1
Total			108

cies relationship with strong support (BS = 100 %). Further, this clade was sister to a group that included species from *M*. subg. *Mammillaria* series *Supertextae* (*M. supertexta*, *M. crucigera* and *M. huitzilopochtli*) and *M*. subg. *Krainzia* (*M. pectinifera* and *M. solisioides*). The phylogeny did not support the monophyly of *Mammillaria* subg. *Mammillaria* nor *M*. subg. *Krainzia* (Figure 4, Table 1). While *M*. subg. *Mammillaria* appeared to be paraphyletic, *M.* series *Supertextae* (BS = 100 %) and *M.* series *Stylothelae* (BS = 100 %) formed two monophyletic groups.

Discussion

Chloroplast genome structure comparison. The chloroplast genome sequences of *Mammillaria bocasana* and *M. erythrosperma* (*Mammillara* series *Stylothelae*) exhibit an undescribed plastome structure (S4) (Figure 2). This new

structure shares similar gene content and arrangement with the S1, represented by *M. pectinifera* (Solórzano *et al.* 2019). It differs, however, by a ~ 21 kb inversion within the LSC that had not been reported in other *Mammillaria* species (Figure 3). The inversion contains mainly protein coding genes related to photosynthesis. On the other hand, the IRs of *M. bocasana* and *M. erythrosperma* (S4) were similar in length and gene content to those of *M. albiflora* and *M. pectinifera* (S1) (Solórzano *et al.* 2019). The distinctive features of this new structure are the inversion within the LSC and the presence of the *rpl*2 gene in the IRs instead of a partial sequence of the *ycf*2 gene (Table 3). Our results support the idea that *trn*I-CAU is involved in reconfiguring of IRs in *Mammillaria* (Solórzano *et al*. 2019). Boundary shifts seem to result from gene rearrangements, but further research is needed.

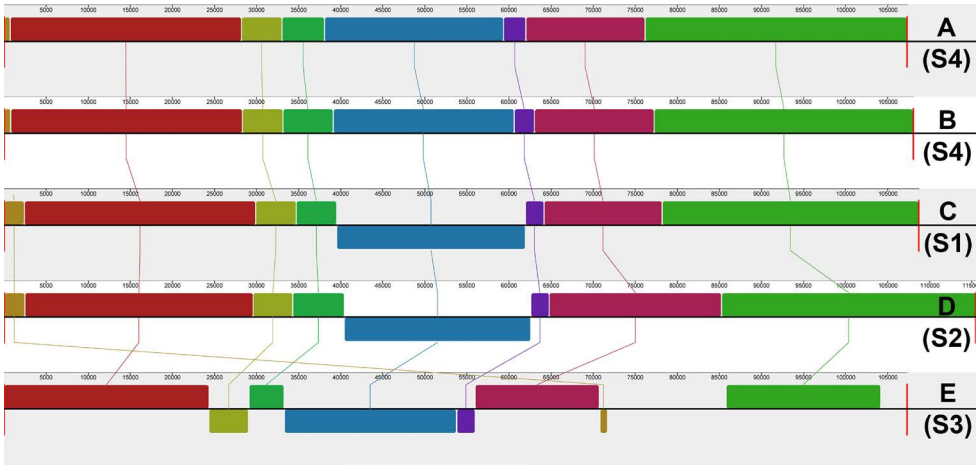

Figure 3. MAUVE alignment. A) *Mammillaria bocasana*, B) *M. erythrosperma*, C) *M. pectinifera*, D) *M. crucigera*, E) *M. zephyranthoides*. The codes S1, S2, and S3 represent the chloroplast genome structures found by Solórzano *et al*. (2019) and S4 indicates the new structure found in this work.

Compared with other Cactaceae, the *Mammillaria* plastomes display high variation associated with gene translocations and inversions (Solórzano *et al*. 2019, Yu *et al*. 2023). Plastome variation is common in Cactaceae and typically involves changes within the IRs. This variation is given by gene rearrangements, expansion and contraction of coding and non-coding regions, and changes in the boundaries of the IRs (Yu *et al*. 2023). Palmer (1986) and Walker *et al*. (2015) suggested that the IR could induce isomers, particularly within the SSC. This phenomenon is common in Cupressaceae (Guo *et al*. 2014, Qu *et al*. 2017) and was recently discovered within the LSC in Cactaceae (Yu *et al*. 2023). In cacti, the frequence of isomers is estimated around 1 % (Yu *et al*. 2023). Another source of plastome variation is the high presence of short repeat sequences that promote chloroplast structure differentiation mediated by intramolecular recombination (Ruhlman *et al.* 2017, Qu *et al*. 2017). When comparing the plastomes in the MAUVE alignment, we found short sequence repeats near the boundaries of the 21 kb inverted block of genes within the LSC of *M. bocasana* and *M. erythrosperma*. High short repetitive regions are common within the LSC of *Mammillaria* plastomes (Chincoya *et al*. 2020). It is possible that repetitive sequences in *Mammillaria* may serve as recombination points and cause the rearrangements. As stated and demonstrated by Yu *et al*. (2023) more studies are needed to confirm this or to discard the presence of plastome isomers. Given this, it is possible that some *Mammillaria* plastome structures are merely isomers, but further evaluation is needed.

In Cactaceae, the length of chloroplast genomes exhibits high variability due to gene losses, gene duplications, pseudogenization, and expansions/contractions of the IRs (Solórzano *et al.* 2019, Köhler *et al.* 2023, Yu *et al.* 2023). *Mammillaria* is known for having some of the shortest plastomes within the family, and our findings were consistent with this pattern. In the plastome of *M. bocasana* and *M. erythrosperma*, we observed the pseudogenization of the following genes: *acc*D, *ndh*B, *ndh*D, *ndh*F, *rpl*23 (both copies), *rpl*33, *rps*16, *ycf*4, *ycf*68, and *clp*P (one copy) (Table 2). All these pseudogenes have been previously found in other species of the genus (Solórzano *et al.* 2019) and are common within Cactaceae (Yu *et al.* 2023). The plastomes of *M. bocasana* (S4) and *M. zephyranthoides* (S3) are

Table 3. Length and gene content of the inverted repeat regions of *Mammillaria*. The symbol Ψ indicates a pseudogene. The S1 to S3 structures are those reported by Solórzano *et al*. (2019). S4 denominates the structure found in this work.

Structure	Species	IR length (bp)	IR genes content
S1	*Mammillaria albiflora, M. pectinifera*	1,348; 1,544	*rpl*23, *trn*I-CAU, *ycf*2
S2	*Mammillaria crucigera, M. huitzilopochtli, M. solisioides, M. supertexta*	14,522; 14,488; 14,428; 14,490	*trn*Q-UUG, *rps*16, *trn*K-UUU, *mat*K, *psb*A, *trn*H-GUG, *rpl*2, *rpl*23, *trn*I-CAU, *ycf*2
S3	*Mammillaria zephyranthoides*	28,252	*psb*A, *trn*H-GUG, *trn*I-CAU, *ycf*2, *ndh*B, *rps*7, *rps*12, *trn*V-GAC, *rrn*16, *trn*I-GAU, *rrn*23, *rrn*4.5, *rrn*5, *trn*R-ACG, *trn*N-GUU, *ndh*F, *rpl*32
S4	*Mammillaria bocasana, M. erythrosperma*	1,591; 1,637	*rpl*2, *rpl*23Ψ, *trn*I-CAU

the shortest among *Mammillaria* (~ 107 kb), but they differ from each other in their gene content (108 and 130, respectively) and arrangement, suggesting a different evolutionary pathway. According to Chincoya *et al*. (2023), the divergence of most *Mammillaria* clades occurred ~ 4.5 Mya, which implies a recent diversification of chloroplast structures within the genus. It is necessary to assemble more *Mammillaria* plastomes to trace an accurate evolutionary history.

The evolutionary implications of losing *ndh* genes are not fully understood. These genes play a role in the cyclic electron flow of ATP production (Martín *et al.* 2009, Strand *et al.* 2019). The partial or complete loss of the *ndh* genes suite is common in gymnosperms (Braukmann *et al.* 2009, Martín & Sabater 2010) and frequently occurs in angiosperms (Blazier *et al.* 2011, Sun *et al.* 2017, Sun *et al.* 2018, Könyves *et al.* 2021, Mower *et al.* 2021, Cao *et al.* 2022). In Cactaceae, the complete loss or pseudogenization of multiple *ndh* genes is common (Sanderson *et al.* 2015, Solórzano *et al.* 2019, Morais da Silva *et al.* 2021, Köhler *et al.* 2023, Yu *et al.* 2023). In general, it is not yet clear whether these genes have been transferred to the mitochondrial or nuclear genomes or if there are alternative metabolic pathways that compensate for their absence (Lin *et al.* 2015, Ruhlman *et al.* 2015, Sanderson *et al.* 2015, Ranade *et al.* 2016, Strand *et al.* 2019). These genes appear to be dispensable under favorable conditions but become crucial when plants are exposed to abiotic stress conditions (Ruhlman *et al.* 2015, Lin *et al.* 2017, Sabater 2021). All *Mammillaria* species lacking the *ndh* genes inhabit arid or semiarid regions and it remains unknown how they grow in harsh environments and compensate for the absence of some or all of these genes.

The *de novo* assembled plastomes of *Mammillaria bocasana* and *M. erythrosperma* lacked the *rpl*16 intron. However, the gene seems to be completely functional because only the main intron is excised and a complete gene remains (Butterworth *et al.* 2007). The same case has been rarely documented in Amaryllidaceae, Geraniaceae, Goodeniaceae, Papaveraceae, and Plumbaginaceae, but it is infrequent even within them (Campagna & Downie 1998, Zhang *et al*. 2020, Kim *et al*. 2023). Consequently, this feature is considered a robust signal of common ancestry (Campagna & Downie 1998). Up to this point, all the other chloroplast genomes known for *Mammillaria* have the *rpl*16 intron. Therefore, it is highly plausible that the absence of the *rpl*16 intron could be a synapomorphy for *M.* series *Stylothelae*, as suggested by Butterworth *et al.* (2007). To evaluate this, additional taxa sampling is necessary, including recently described species within the series (González-Zamora *et al.* 2022, 2023, Ortiz-Brunel *et al.* 2023).

Phylogenetic analysis. The ML tree confirmed the inclusion of our newly sequenced chloroplast genomes within *Mammillaria* (Figure 4). *Mammillaria* subg. *Mammillaria* is paraphyletic, partly due to the inclusion of *M. pectinifera* and *M. solisioides*, which belong to *M*. subg. *Krainzia*. Similar results have been reported in recent, more comprehensive studies, indicating the need for further research (Chincoya *et al.* 2023). Our results agreed with the monophyly of series *Supertextae*, which was also identified by Cervantes *et al.* (2021). In all three phylogenetic analyses performed with different datasets, *Mammillaria bocasana* and *M. erythrosperma* grouped as sister to the

clade containing the subgenera *Mammillaria* and *Krainzia*. It is possible that *M*. series *Stylothelae* is monophyletic, as well as other series within *M*. subg. *Mammillaria*. Taxon sampling was limited in the present and previous works, and thereby only limited conclusions can be drawn until denser sampling can be done.

Our phylogenetic analyses support that using complete chloroplast genome sequences or only the shared CDS can produce well-supported hypotheses. An independent study based solely on chloroplast protein-coding genes yielded a similar topology (Solórzano *et al.* 2019). In this study, we performed a phylogenetic analysis with the original full plastomes aligned, other with the ~ 21 kb inversion of *M. bocasana* and *M. erythrosperma* reverted, and another only with 54 shared CDS for all taxa. The full original plastomes dataset produced a better resolved phylogeny, but the hypothesis generated with the inverted block reverted retrieved the same topology and support (Figures 4, S1). However, using the CDS dataset, the placement of *M. albiflora* and *M. zephyranthoides* was different (Figures 4, S2). Any of the three approaches is useful in establishing insights into the evolutionary history of the *Mammillaria* chloroplast genomes. However, it is necessary to increase the taxon sampling to test if some structures have a unique origin (Figure 4). Different chloroplast genome structures have been identified in some species-rich groups with significant morphological variation (Cauz-Santos *et al*. 2020, Köhler *et al*. 2020, Lee *et al*. 2021). With the discovery of a fourth structure characterizing until now the *Mammillaria* series *Stylothelae,* it becomes evident that more extensive taxon sampling across *Mammillaria* is required. Other chloroplast structures might exist within the genus.

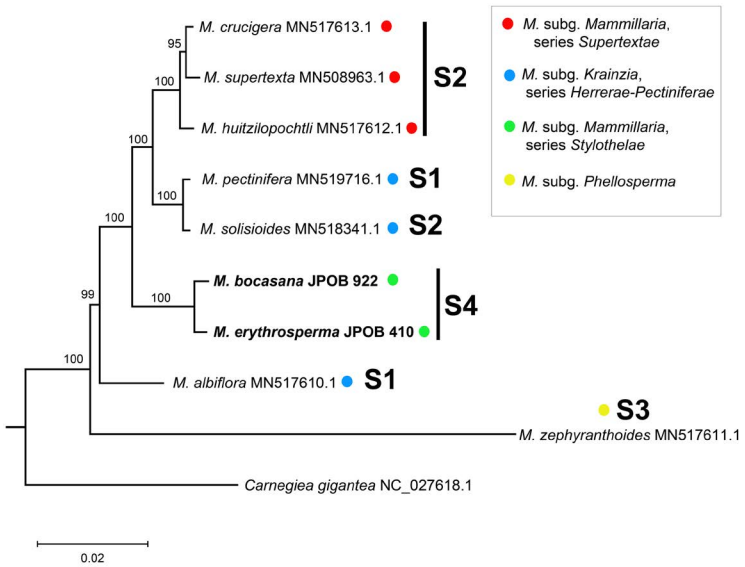

Figure 4. Phylogenetic analysis based on Maximum Likelihood. The numbers above the branches represent the Bootstrap support values. Codes for the structures (S) are the same as in Figure 3.

Supplementary material

Supplemental data for this article can be accessed here: https://doi.org/10.17129/botsci.3446

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