



The complete chloroplast genome sequence of *Ostrya chisosensis*

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Abstract

Ostrya chisosensis (Betulaceae) is a critically endangered species endemic to Texas. In this study, the complete chloroplast (cp) genome of *O. chisosensis* was assembled based on next generation sequencing. The cp genome was 159,107 bp in length, including a large single copy (LSC) region of 88,458 bp, a small single copy (SSC) region of 18,792 bp and a pair of inverted repeats (IRs) of 51,857 bp. The genome contained 124 genes, including 85 protein-coding genes, 30 tRNA genes and 8 ribosomal RNA genes. The majority of these gene species occurred as a single copy and 13 gene species occurred in two copies. The overall GC content of the chloroplast genome was 36.5%, whereas the corresponding values of the LSC, SSC, and IR regions were 34.3, 30.1 and 42.5%, respectively. A phylogenetic analysis demonstrated a close relationship between *O. chisosensis* and *O. rehderiana*.

Keywords *Ostrya chisosensis* · Chloroplast genome · Phylogenetic analysis

Ostrya chisosensis, common name Big Bend hop-hornbeam or Chisos hop-hornbeam, is a kind of tall deciduous tree species endemic to Texas. It is known only from the Chisos Mountains inside Big Bend National Park, in Brewster County, although related populations in northern Chihuahua have not been studied in detail and may be the same species (F.o.N.A.E Committee 1997). This species is reported only 639 mature individuals in the wild and listed as critically endangered species in the IUCN red list (Shaw et al. 2014; <http://www.iucnredlist.org/details/194284/0>). Due to small population and limited habitat, it is more susceptible to stochastic events. Therefore, measures of conservation and restoration are urgently needed. In this case, its genomics information is definitely fundamental to formulate a comprehensive conservation strategy. Here, we presented the complete chloroplast genome of *O. chisosensis* (GenBank: MG584735) based on the next-generation sequencing data.

A fresh leaf was collected from a mature individual of *O. chisosensis* in Big Bend National Park (Texas, USA,

29.33°N, 103.25°W), then it was dried using silica gel. Genomic DNA was isolated using the modified CTAB method (Doyle 1987). The whole-genome sequencing was conducted with 150 bp pair-end reads on the Illumina HiSeq Platform (Illumina, San Diego, CA). In total, 174 million high quality base pairs of sequence data were obtained and used for the cp genome assembly using the Fast-Plast pipeline (<https://github.com/mrmckain/Fast-Plast>; McKain and Wilson, unpublished). Annotation was performed with a newly developed command-line application called Plann (Plastome Annotator), which is suitable for plastomes annotation with a well-annotated sequenced relative (Huang and Cronk 2015). Then, we corrected the annotation with Geneious (Kearse et al. 2012). The plastid genome map was generated with OGDRAW (<http://ogdraw.mpimp-golm.mpg.de/>) (Lohse et al. 2013). We also constructed the phylogenetic trees with the maximum likelihood (ML, RaxML version 8, Stamatakis 2014) and bayesian analysis (BI, MrBayes version 3, Ronquist and Huelsenbeck 2003) methods based on the alignments created by the MAFFT (Katoh and Standley 2013) within the nine species plastid genomes.

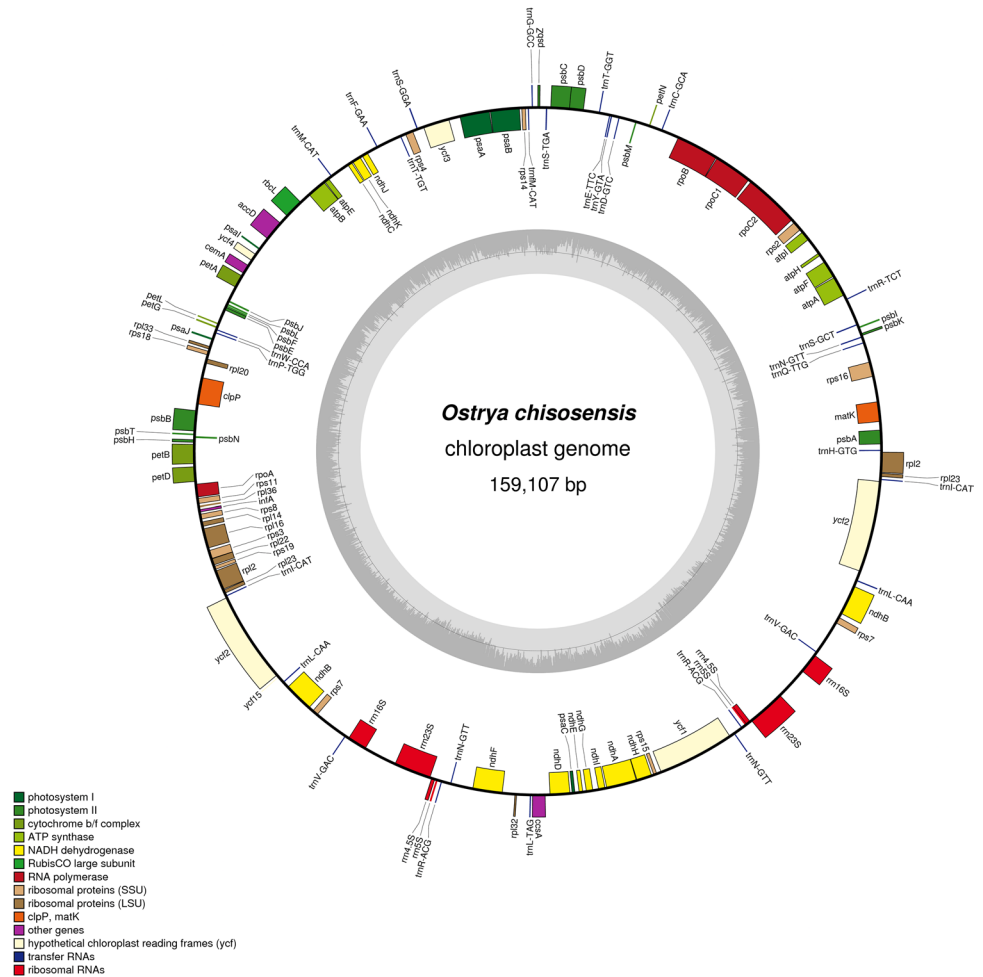
The complete chloroplast genome of *O. chisosensis* was a quadripartite circular and 159,107 bp in length, comprising a large single copy (LSC) of 88,458 bp and a small single copy (SSC) of 18,792 bp, separated by two inverted repeat (IR) regions of 51,857 bp (Fig. 1). It contained 123 genes, included 85 protein-coding, 8 ribosomal RNA, and

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Fig. 1 Gene map of the *Ostrya chisosensis* chloroplast genome



30 tRNA genes. The plastome contained 95 unique genes, 14 genes duplicated in the IR regions. Among annotated genes, 10 genes contained a single intron, and four genes had two introns (i.e., *clpP*, *ycf3*, *rps12* and *rp12*). The base compositions of the whole chloroplast genome were uneven (31.4% A, 18.6% C, 18.6% G, 32.17% T), with an overall GC content of 36.5%, and the corresponding values of the LSC, SSC and IR regions reaching 34.3, 30.1 and 42.5%, respectively.

To ascertain the phylogenetic position of *O. chisosensi*, we conducted a phylogenetic analysis using nine complete chloroplast genomes including *O. rehderiana*, *O. trichocarpa*, *Carpinus putoensis*, *Carpinus tientaiensis*, *Corylus chinensis* and *Corylus fargesii* representatives in Fagales and two outgroups (Fig. 2). The results indicated that all three species from the *Ostrya* were clustered together and *O. chisosensis* was most closely related to *Ostrya rehderiana*. This complete chloroplast genome can be readily used for population genomic studies of *O. chisosensis*, and such information would be fundamental to formulate potential new conservation and management strategies for this endangered species.

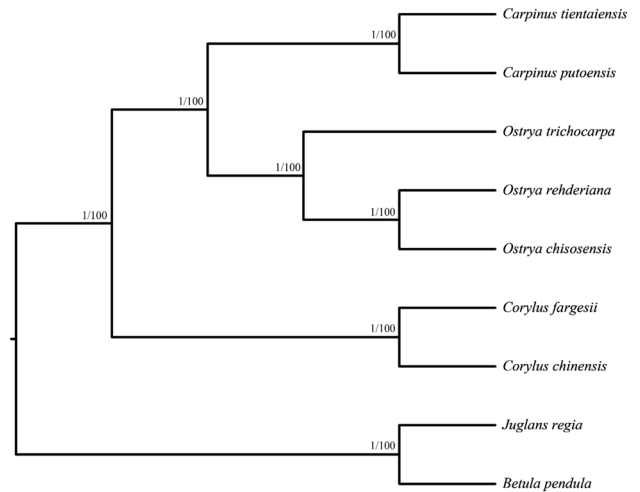


Fig. 2 The phylogenetic tree based on the 9 complete chloroplast genome sequences. Bayesian posterior probabilities/ML bootstrap values are shown at nodes. Accession numbers: *Carpinus tientaiensis* KY117036, *Carpinus putoensis* KX695124, *Corylus chinensis* NC_032351, *Corylus fargesii* NC_031854, *Juglans regia* NC_028617, *Ostrya chisosensis* MG584735, *Ostrya rehderiana* KT454094, *Ostrya trichocarpa* KY088271, *Betula pendula* LT855378

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