

The complete chloroplast genome sequence of *Ormosia boluoensis*

Yun Guo^{a,b}, Zheng-Feng Wang^{a,c,d} and Hong-Lin Cao^{a,c,d}

^aKey Laboratory of Vegetation Restoration and Management of Degraded Ecosystems, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, Guangdong, China; ^bUniversity of Chinese Academy of Sciences, Beijing, China; ^cCenter for Plant Ecology, Core Botanical Gardens, Chinese Academy of Sciences, Guangzhou, Guangdong, China; ^dSouthern Marine Science and Engineering Guangdong Laboratory, Guangzhou, China

ABSTRACT

Ormosia boluoensis is a critically Endangered species that is exclusively distributed in Xiangtoushan National Nature Reserve in Guangdong province, China. At present, the population of the species is made up of less than 100 adult individuals. Here, we are the first to report the complete chloroplast genome sequence of *O. boluoensis*. The chloroplast genome of *O. boluoensis* is 175,760 bp long and includes a large single-copy region that is 74,613 bp, a small, 18,719 bp single copy region and a pair of inverted repeat regions that are 40,771 bp and 41,657 bp in length, respectively. The overall GC content of the *O. boluoensis* chloroplast genome is 35.58% and contains a total of 134 genes, including 89 protein-coding genes, 8 ribosomal RNA genes, and 37 transfer RNA genes. Phylogenetic analysis revealed that *O. boluoensis* is genetically similar to *O. xylocarpa* and *O. emarginata* genera.

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Ormosia boluoensis belongs to the genus *Ormosia* in Papilionoideae. It has a limited distribution, which is confined to the Xiangtoushan National Nature Reserve (23°16'44"N, 114°22'26"E) in Guangdong province, China. In the field, the size of the population of the species is very small, comprised of less than 100 adults and the risk of extinction for the species is high. Until now, there have been no genomic studies of *O. boluoensis* and the complete genomic sequence of its chloroplast (cp) has not previously been reported. Complete cp genomes are useful tools that provide information regarding phylogenetic relationships, species identification and germplasm diversity (Wang et al. 2019). Therefore, in this study, we reported the complete genomic sequence of the cp from *O. boluoensis* using high-throughput sequencing approaches. The cp genome will provide a reference that may be used to protect *O. boluoensis* in the future.

Plant materials were sampled from Xiangtoushan National Nature Reserve and a voucher specimen was deposited in Herbarium of South China Botanical Garden with IBSC0000922. We used both Illumina- and PacBio-based shotgun sequencing methods to assemble the complete cp genome for *O. boluoensis*. Illumina shotgun sequencing required use of a 150-bp, paired-end library that was generated using the Illumina HiSeq X Ten platform and PacBio shotgun sequencing used the PacBio Sequel system. We obtained about 100G of Illumina reads and about 67G of PacBio reads. Then, software from NOVOPlasty 3.7 (Dierckxsens et al. 2017) and Organelle_PBA 1.0.8 (Soorni et al. 2017) were

employed to assemble the complete cp genome using Illumina reads and PacBio reads, respectively. The two assembled results were finally combined to produce the final complete cp genome of *O. boluoensis*. The complete cp genome was subsequently annotated using PGA (Qu et al. 2019) and the annotated sequences were submitted to GenBank with the accession number MN886968. A phylogenetic inference was carried out using genome_comparator

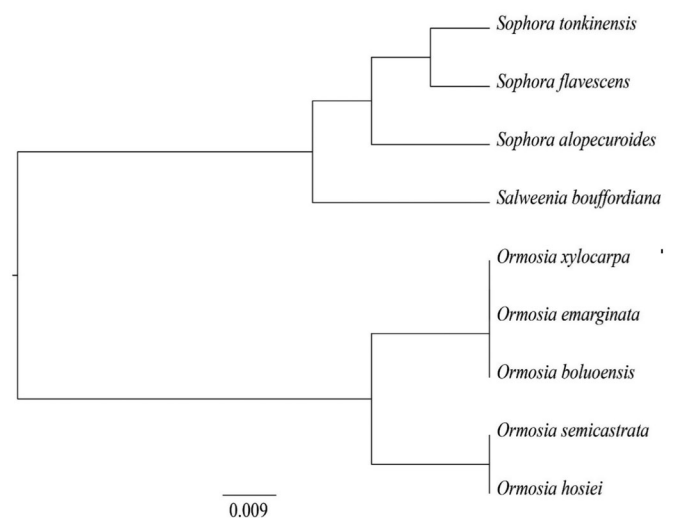


Figure 1. Phylogenetic tree based on the complete chloroplast genome sequences of *O. boluoensis* and eight other species within the Papilionoideae.

(https://github.com/duceppemo/genome_comparator), which is based on genome pairwise distance calculated with Mash (Ondov et al. 2016) between the cp genome of *O. boluoensis* and eight other complete cp genomes of Papilionoideae downloaded from GenBank. The eight cp genomes used for the comparison were *O. semicastrata* (accession No. MK105450.1), *O. hosiei* (accession No. MG813874.1), *O. xylocarpa* (accession No. MK105449.1), *O. emarginata* (accession No. MK105448.1), *Salweenia bouffordiana* (accession No. MF449303.1), *Sophora alopecuroides* (accession No. NC036102.1) and *S. tonkinensis* (accession No. NC042688.1), and *S. flaccescens* (accession No. MH748034.1).

The complete cp genome of *O. boluoensis* consists of a circular molecule containing 175,760 bp. The sequence consists of a large, single-copy (LSC, 74613 bp), a small, single-copy (SSC, 18719 bp), and two inverted repeats (IRA and IRB, 40,771 bp and 41,657 bp, respectively). The percentages of the total genome sequence corresponding to LSC, SSC, and IR regions were 42.45, 10.65, and 46.90%, respectively. The GC content of the chloroplast genome was 35.58%. A total of 134 genes were annotated, including 89 protein-coding, 8 rRNA, and 37 tRNA genes. Phylogenetic analysis revealed that *O. boluoensis* clustered with *O. xylocarpa* and *O. emarginata* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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