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TECHNICAL NOTE

Characterization of the complete chloroplast genome of *Populus qiongdaoensis* T. Hong et P. Luo

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Abstract We report the complete chloroplast DNA (cpDNA) of *Populus qiongdaoensis* T. Hong et P. Luo, which is an endangered tree species, by employing next-generation sequencing reads and de novo assembly. The chloroplast genome of *P. qiongdaoensis* is 1,56,074 bp in length, with 36.70 % GC content. It contains a pair of inverted repeats (27,548 bp) which were separated by a large single copy (84,467 bp) and a small single copy region (16,512 bp). A total of 131 genes were annotated, which included 86 protein-coding genes, 37 tRNA genes and eight rRNA genes. A neighbor joining tree based on the reported chloroplast genomes of *Populus* showed that the chloroplast of the *P. qiongdaoensis* is most closely related to the *P. tremula* and *P. rotundifolia*.

Keywords Chloroplast genome · Endangered species · Salicaceae · Phylogenetic analysis

Populus qiongdaoensis, belongs to the genus of *Populus*, family of salicaceae, is deciduous arbor. It is an endangered tree species only found on mountainous regions in Bawangling and Zhizailing, Hainan (Liang and Fang 2012; Luo and Hong 1987). At present, *Populus* has ten previously reported chloroplast genomes, and more sequences would be necessary to assess phylogenetic relationships and to reconstruct reticulate evolution. However, the complete chloroplast genome sequence is not available for this plant species. In this study, we characterized the complete chloroplast genome sequence of *P. qiongdaoensis* to contribute to further physiological, molecular and phylogenetical studies of this tree species.

Total genomic DNA was extracted from leaves of *P. qiongdaoensis* collected from Changjiang (Hainan, China; coordinates: 109°05′0.57″ E, 19°07′24.6″ N), and were used for the total genomic DNA extraction with a modified CTAB method (Doyle and Doyle 1987). An Illumina paired-end (PE) genomic library was constructed and sequenced using an Illumina HiSeq platform (Illumina, San Diego, CA). Firstly, we obtained 40 million high quality reads and assembled using Velvet software (Zerbino and Birney 2008). The representative chloroplast contigs were retrieved, ordered and combined into a single draft sequence, through comparison with the chloroplast sequence of *P. tremula* W52 (KP861984) (Kersten et al. 2016) as a guidance and corrected the annotation with Geneious (Kearse et al. 2012). The genome map was drawn by an internet tool–OGDRAW v1.2 (Lohse et al. 2013) (http://ogdraw.mpimp-golm.mpg.de/). To analyze the phylogenetic relationships between *P. qiongdaoensis* and related species in *Populus*, the chloroplast genome sequences of a total of 12 species in Salicaceae were aligned by MAFFT (http://mafft.cbrc.jp/alignment/software/) (Katoh et al.2002) and then used MEGA6 (Tamura et al. 2013) software to construct a neighbor-joining (NJ) tree (with 1000 bootstrap replicates). *Ricinus communis* derived from Euphorbiaceae was used as outgroup for tree rooting. The cpDNA sequence with complete annotation information was deposited at GenBank database under the accession number KX534066.

As shown in Fig. 1, the chloroplast genome of *P. qiongdaoensis* was 1,56,074 bp in length, with 36.7 % GC content and consisted of four distinct regions, such as large single-

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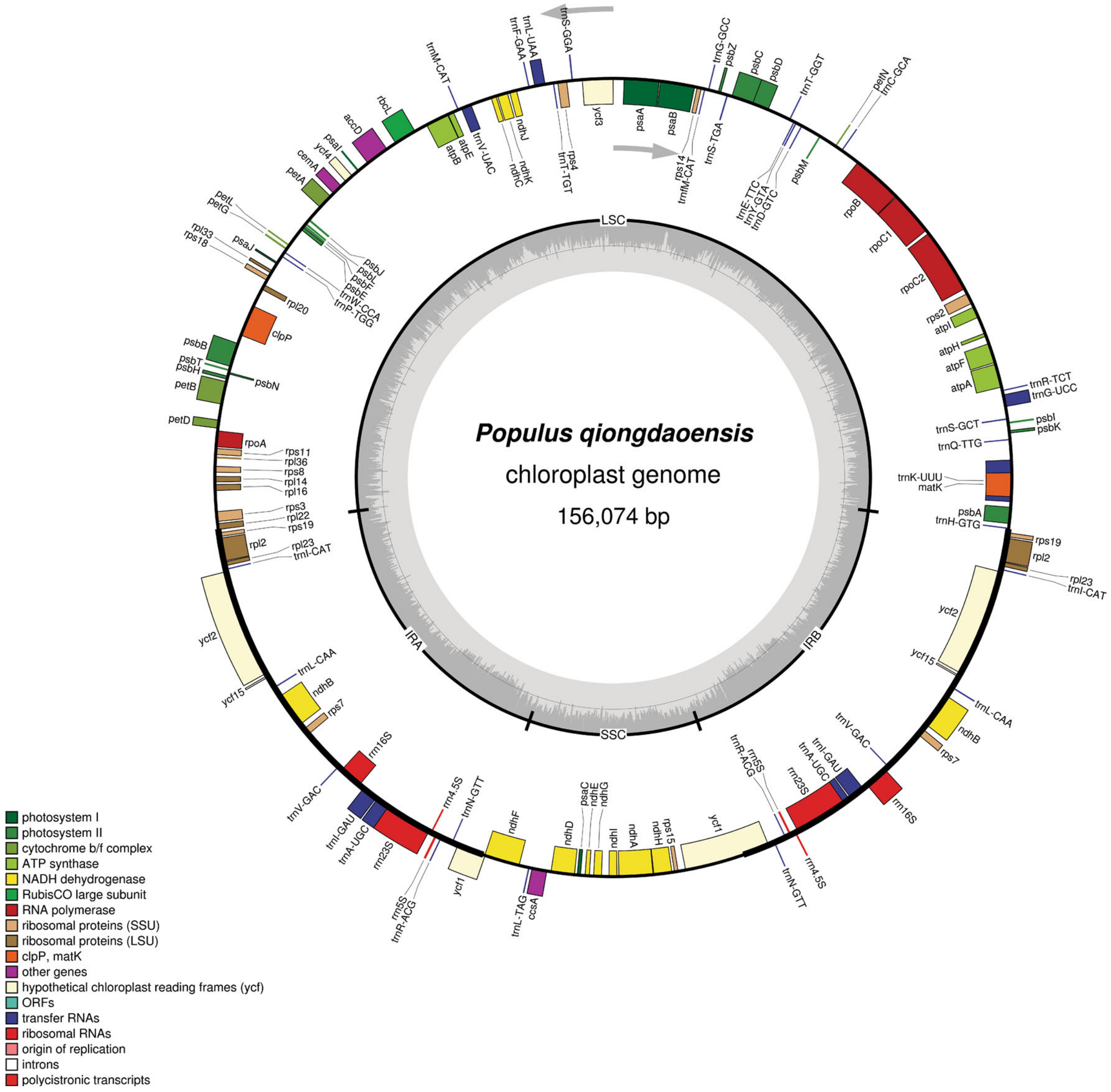

Fig. 1 Gene map of the *P. qiongdaoensis* chloroplast genome

copy region (84,467 bp), small single-copy region (16,512 bp) and a pair of inverted repeat regions (27,548 bp). A total of 131 genes were annotated, which included 86 protein-coding genes, 37 tRNA genes and eight rRNA genes. According to the phylogenetic tree, *P. qiongdaoensis* was much closely related to *P. tremula* and *P. rotundifolia*, as expected (Fig. 2). The newly characterized *P. qiongdaoensis* complete chloroplast genome will provide essential data for further study on the phylogeny and evolution of the genus *Populus* and of the Salicaceae, and provide valuable insight into conservation and restoration efforts for this endangered species.

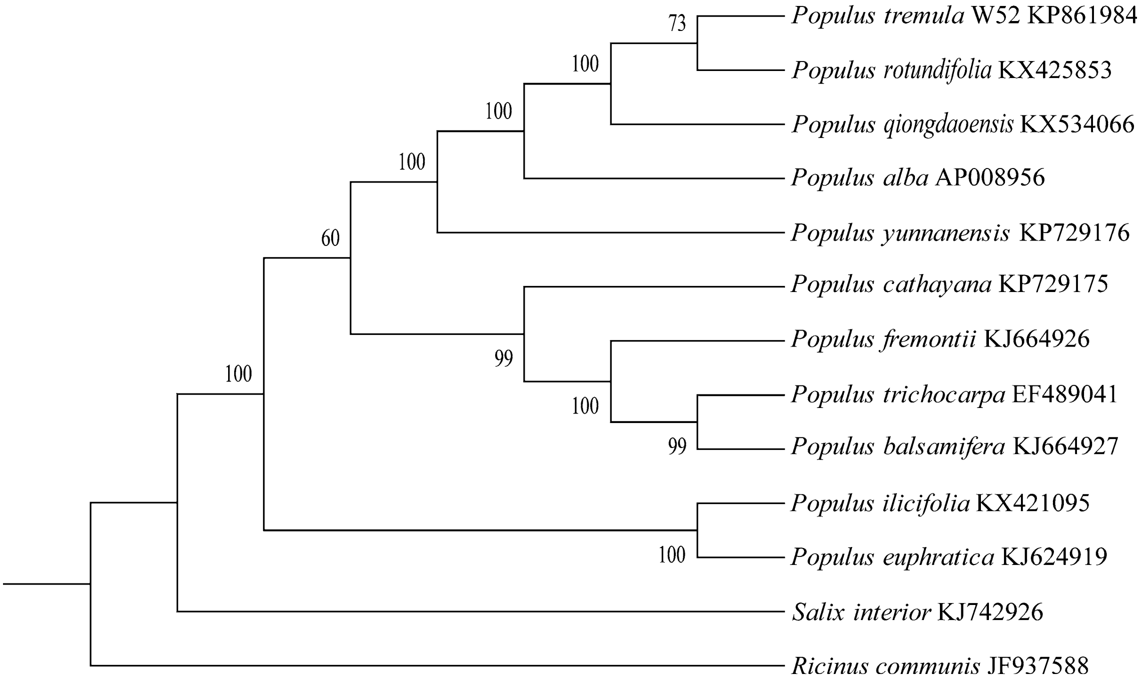

Fig. 2 Phylogenetic tree was built with NJ methods using MEGA 6.0 program (Tamura et al. 2013) based on 13 CP genome sequences, including one species of *Ricinus* as outgroup. Bootstrap support values (%) are indicated in each node. GenBank accession numbers: *P. alba* (AP008956), *P. balsamifera* (KJ664927), *P. cathayana* (KP729175), *P. euphratica* (KJ624919), *P. fremontii* (KJ664926), *P. ilicifolia* (KX421095), *P. qiongdaoensis* (KX534066), *P. rotundifolia* (KX425853), *P. trichocarpa* (EF489041), *P. yunnanensis* (KP729176), *P. tremula* W52 (KP861984), *Salix interior* (KJ742926), *Ricinus communis* (JF937588)

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Compliance with ethical standards

Conflict of interest The authors declare no conflict of interest.

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