

The complete chloroplast genome sequence of *Populus rotundifolia*, and a comparative analysis with other *Populus* species

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ABSTRACT:

Populus rotundifolia, which is an endemic of the Himalayas and adjacent regions, is the species that occupy the highest habitat in the *Populus* genus. The complete chloroplast genome sequence of *Populus rotundifolia* was characterized from Illumina pair-end sequencing. The chloroplast genome of *P. rotundifolia* was 155,212 bp in length, containing a large single-copy region (LSC) of 84,545 bp, a small single-copy region (SSC) of 16,859 bp, and two inverted repeat (IR) regions of 26,904 bp. The overall GC content is 36.80%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.5%, and 42.3%, respectively. The genome contains 131 complete genes, including 86 protein-coding genes (62 protein-coding gene species), 37 tRNA genes (29 tRNA species) and 8 rRNA genes (4 rRNA species). The Neighbour-joining phylogenetic analysis showed that *P. rotundifolia* and *Populus davidiana* clustered together as sisters to other *Populus* species.

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Introduction

Populus rotundifolia, whose habitat is of the highest elevation among all *Populus* species (Salicaceae), occurs in the mountainous areas between 2300 m and 4500 a.s.l. in the Himalaya and adjacent areas. This aspen is an ideal model in ecological and evolutionary studies, since it is a dominant species in high mountain ecosystem. However, largely due to anthropogenic cutting and climatic environment's change, its natural habitats have been fragmented, yet none is known concerning its genetic background (Zheng et al. 2017; Hou et al. 2018). *P. rotundifolia* plays an important ecological role in boreal and temperate forests, serving as wildlife habitats and watersheds; they can dominate riparian forests, but are ecologically adaptable. *P. rotundifolia* has wide geographic distribution, high intraspecific polymorphism, adaptability to different environments, combined with a relatively small genome size. Consequently, *P. rotundifolia* represents an excellent model for understanding how different evolutionary forces have sculpted the variation patterns in the genome during the process of population differentiation and ecological speciation (Neale and Antoine 2011). Moreover, we can develop conservation strategies easily when we understand the genetic information of *P. rotundifolia*. In the present research, we constructed the whole chloroplast genome of *P. rotundifolia* and understood many genome variation information about the species, which will provide beneficial help for population genetics studies of *P. rotundifolia*.

The fresh leaves of *P. rotundifolia* were collected from Xizang (29°30'N, 92°15'E). Fresh leaves were silica-dried and

taken to the laboratory until DNA extraction. The voucher specimen (YYY001) was laid in the Herbarium of Chongqing University of Arts and Sciences and the extracted DNA was stored in the –80 °C refrigerator of the Key Laboratory of College of Landscape Architecture and Life Science. We extracted total genomic DNA from 25 mg silica-gel-dried leaf using a modified CTAB method (Doyle 1987). The whole-genome sequencing was then conducted by Biodata Biotechnologies Inc. (Hefei, China) with Illumina HiSeq platform. The Illumina HiSeq 2000 platform (Illumina, San Diego, CA) was used to perform the genome sequence. We used the software MITObim 1.8 (Hahn et al. 2013) and metaSPAdes (Nurk et al. 2017) to assemble chloroplast genomes. We used *P. tremula* (GenBank: NC_027425) as a reference genome. We annotated the chloroplast genome with the software DOGMA (Wyman et al. 2004), and then corrected the results using Geneious 8.0.2 (Campos et al. 2016) and Sequin 15.50 (<http://www.ncbi.nlm.nih.gov/Sequin/>).

The complete chloroplast genome of *P. rotundifolia* (GenBank accession number MT482542) was characterized from Illumina pair-end sequencing. The complete chloroplast genome sequence of *Populus rotundifolia* was characterized from Illumina pair-end sequencing. The chloroplast genome of *P. rotundifolia* was 155,212 bp in length, containing a large single-copy region (LSC) of 84,545 bp, a small single-copy region (SSC) of 16,859 bp, and two inverted repeat (IR) regions of 26,904 bp. The overall GC content is 36.80%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.5%, and 42.3%, respectively. The genome

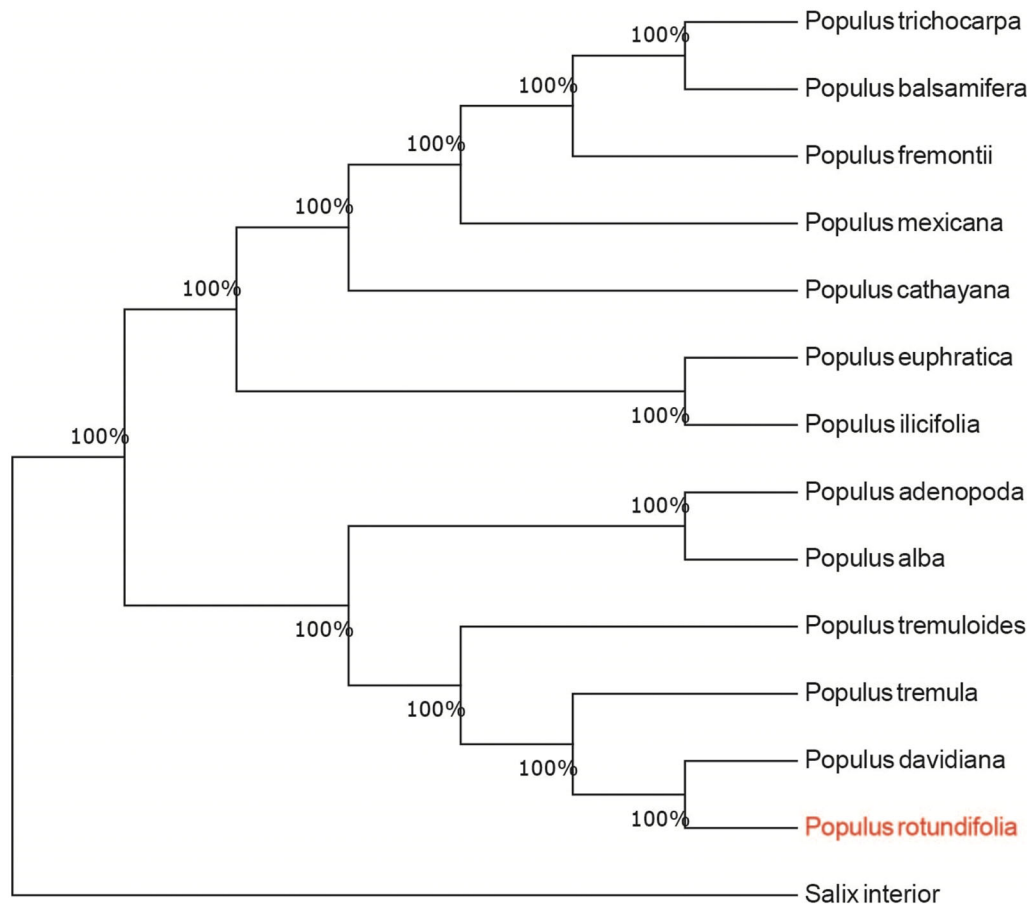


Figure 1. Neighbour-joining (NJ) analysis of *P. rotundifolia* and other related species based on the complete chloroplast genome sequence. Genbank accession numbers: *P. tremula* (KP861984), *P. rotundifolia* (KX306825), *P. yunnanensis* (KP729176), *P. euphratica* (KJ624919), *P. adenopoda* (NC032368), *P. rotundifolia* (MT482542), *P. cathayana* (KP929175), *P. balsamifera* (KJ664927), *P. ilicifolia* (NC031371), *P. trichocarpa* (EF489041), *P. fremontii* (KJ664926), *P. tremuloides* (MN561844) and *Salix interior* (NC024681).

contains 131 complete genes, including 86 protein-coding genes (62 protein-coding gene species), 37 tRNA genes (29 tRNA species) and 8 rRNA genes (4 rRNA species).

To confirm the phylogenetic location of *P. rotundifolia* within the family of *Populus*, we used the complete chloroplast genomes sequence of *P. rotundifolia* and 13 other related species of *Populus* and *Salix interior* as outgroup to construct phylogenetic tree. The 14 chloroplast genome sequences were aligned with MAFFT (Katoh and Standley, 2013), and then the Neighbour-joining tree was constructed by MEGA 7.0 (Kumar et al. 2016). The results confirmed that *P. rotundifolia* was clustered with *P. davidiana* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data that support the findings of this study are openly available in National Center for Biotechnology Information (NCBI) at <https://www.ncbi.nlm.nih.gov>, accession number MT482542.

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