

MITOGENOME ANNOUNCEMENT

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The complete chloroplast genome of Cathay Poplar: *Populus cathayana* Rehder

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ABSTRACT

The complete chloroplast genome of *Populus cathayana* was determined in this study. The total length of the chloroplast genome size is 155 449 bp, with 36.95% GC content. A pair of inverted repeats of 27 525 bp are separated by a large single-copy region (LSC, 83 911 bp) and a small single-copy region (SSC, 16 488 bp). About 104 unique genes were annotated, including 76 protein coding genes, 24 tRNA genes and 4 rRNA genes.

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Populus, comprising about 90 species all over the world, is widely distributed from tropical island to subarctic forest in the north hemisphere (Ding 1995). Because of high level of morphological variation within species and extensive interspecies hybridization, the species identification in this genus remains an intricate problem. The chloroplast of angiosperm, mainly maternal inherited, now extensively used to investigate reticulate relationship among species. Comparative phylogenetic analysis based on nuclear DNA and cpDNA sequences has been used to detect recent hybridization (Hamzeh & Dayanandan 2004; Wang et al. 2014). Feng et al. (2013) tested five chloroplast barcodes among 21 *Populus* species from western China, but still failed to discriminate several groups of species, especially from sympatric or parapatric areas.

At present, *Populus* has six previously reported chloroplast genomes, and more sequences would be necessary to assess phylogenetic relationships and to reconstruct the reticulate evolution.

Populus cathayana Rehder (Rehder 1931) is an endemic species of Section *Tacamahaca* distributed in northern and western China, where the genus possesses a great diversity of species and subspecies (Chen et al. 2007). However, little genetic information of this species is available and the cp genome has not been sequenced.

In this study, voucher specimens of *P. cathayana* were deposited at the herbarium of Beijing Forestry University (BJFC), and DNA samples were properly stored at Laboratory of Systematic Evolution and Biogeography of Woody Plants,

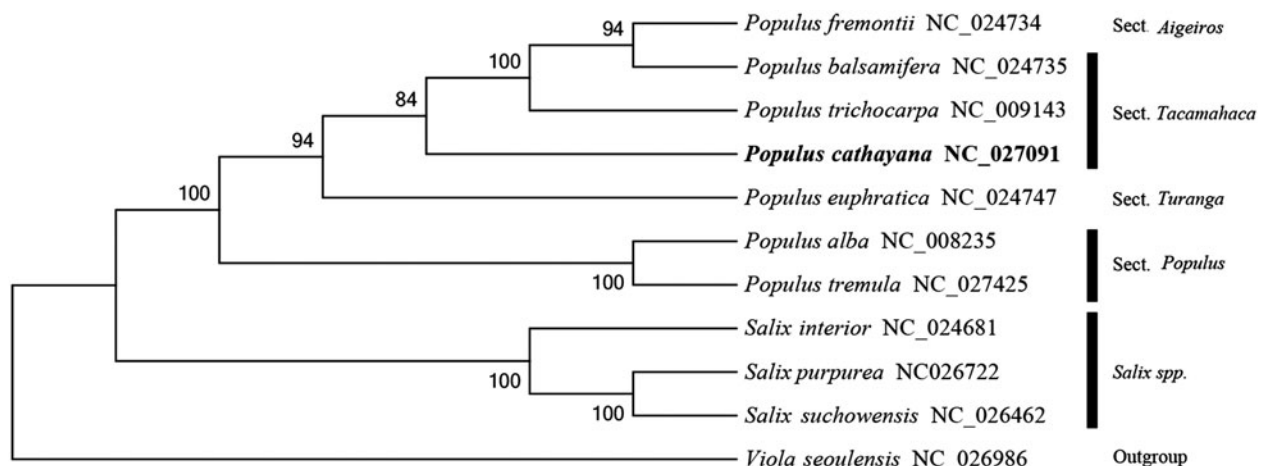


Figure 1. Phylogenetic tree was built with NJ methods using MEGA 6.0 program (Tamura et al. 2013) based on 11 cp genome sequences, including one species of Violaceae as outgroup. NJ bootstrap values are shown above each node, and the NJ bootstrap for 10 000 replicates is indicated in each node.

Beijing Forestry University, Beijing, China. The complete cp genome sequence was determined using a modified whole chloroplast genome sequencing protocol developed by our group (Du et al. 2015) and the GenBank accession number was NC_027091.

The *P. cathayana* chloroplast genome is 155 449 bp in length, with 36.95% overall GC content. It is a typical circular structure, including a large single-copy region (LSC, 83 911 bp) and a small single-copy region (SSC, 16 488 bp) separated by a pair of inverted repeats (IRs, 27 525 bp). There are 84 protein-coding genes, 29 tRNA genes and eight rRNA genes. About 104 of them are unique, and 17 genes are duplicated in the IR regions. In the 155 449 bp genome, protein-coding genes, tRNA genes and rRNA genes occupy 52.74%, 1.41% and 5.82%, respectively. Ten genes contained one or two introns, including *atpF*, *ndhA*, *ndhB*, *rpl16*, *rpl2*, *rpoC1*, *rpoC2*, *clpP*, *ycf3* and *rps12*.

The phylogenetic tree was constructed using neighbor-joining (NJ) methods based on the whole cp genome of 10 species within the family Salicaceae and *Viola seoulensis* as out-group (Figure 1). The phylogenetic analysis revealed that the genus *Populus* was strongly supported as monophyletic.

Disclosure statement

The authors report no conflict of interest. The authors alone are responsible for the content and writing of this article.

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