



The complete chloroplast genome sequence of *Populus deltoides* 'Siyang-2'

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ABSTRACT

Populus deltoides 'Siyang-2' is an improved variety of forest trees that have been identified recently. It shows superior growth performance compared to other local cultivars in the region of Yangtze-Huaihe in China. In this study, the whole chloroplast (cp) genome sequence of 'Siyang-2' was assembled and characterized by high-throughput sequencing data. The complete cp genome was 156,957 bp in length, containing a large single-copy region (LSC) of 85,096 bp, and a small single-copy region (SSC) of 16,563 bp, which were separated by a pair of 27,649 bp inverted repeat regions (IRs). The cp genome contained 131 genes, including 86 protein-coding genes, 37 tRNA genes, and 8 ribosomal RNA genes. Most of the gene species occur as a single copy, while 20 gene species occur in double copies. The overall GC content of 'Siyang-2' cp genome is 34.6%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.6%, 41.9%, respectively. The complete cp genome provides valuable phylogenetic and cp genetic engineering studies of this important improved poplar species *P. deltoides* 'Siyang-2'.

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Populus deltoides 'Siyang-2' is a selection breeding variety of *Populus*, developed by Dr. huixin Pan from the Poplar Research and Development Center in Nanlin (Nanjing Forestry University). This variety was authorized to be an improved variety of forest trees (Identifier: Su S-SC-PD-002-2018, http://lyj.jiangsu.gov.cn/art/2018/12/12/art_48797_7951901.html) by national forestry and grassland administration in China (Wang et al. 2019). 'Siyang-2' showed superior growth performance in comparison with 'Nanlin 895', an elite hybrid poplar clone in south China being widely planted for agricultural industry and scientific research (Fang and Yang 2003; Fang et al. 2006; Chai et al. 2014; Wang et al. 2016; Chao et al. 2019; Zhu et al. 2018). Although it showed great potential in the economy and ecosystem construction in south China, as a new variety, 'Siyang-2' has not been intensively studied yet. The genetic information and the phylogenetic relationship of 'Siyang-2' remained elusive. In this study, the complete chloroplast (cp) genome sequence of 'Siyang-2' was initially assembled and characterized.

The fresh leaves of *P. deltoides* 'Siyang-2' were sampled from the clonal trials in Baguazhou Farm, Nanjing, China (32°09'N, 118°49'E), and used for DNA extraction by DNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA). The whole genome sequencing was implemented by Hefei Biodata Biotechnologies Inc. (Hefei, China) on the BGISEQ-500 platform. In total, about 34 MB high-quality clean reads were

obtained. The filtered sequences were assembled using the program SPAdes assembler 3.10.0 (Bankevich et al. 2012). The resulting contigs were linked based on overlapping regions using *P. trichocarpa* (EF489041) (Tuskan et al. 2006) as reference. Annotation was performed using the DOGMA (Wyman et al. 2004) and BLAST searches.

The complete chloroplast/plastid genome sequence together with gene annotations was submitted to GenBank under the accession numbers of MN417118 for *P. deltoides* 'Siyang-2'. The cp genome was determined to comprise double-stranded, circular DNA of 156,957 bp, including two inverted repeat (IR) regions of 27,649 bp each, separated by a large single-copy (LSC) and a small single-copy (SSC) region of 85,096 and 16,563 bp, respectively. The genome contained 131 genes, including 86 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. One rps12 gene was divided into two independent transcription units. Most of the genes occurred as a single-copy, while eight protein-coding genes, four rRNA genes, and eight tRNA genes had two copies, respectively. In addition, three protein-coding genes had three exons each. Eight protein-coding genes and six tRNA genes contained two exons. The overall GC content is 34.6%, and the corresponding values in LSC, SSC, and IR regions are 34.5, 30.6, 41.9%, respectively.

The phylogenetic relationships of 'Siyang-2' with other 61 species in the Salicaceae family were analyzed by using

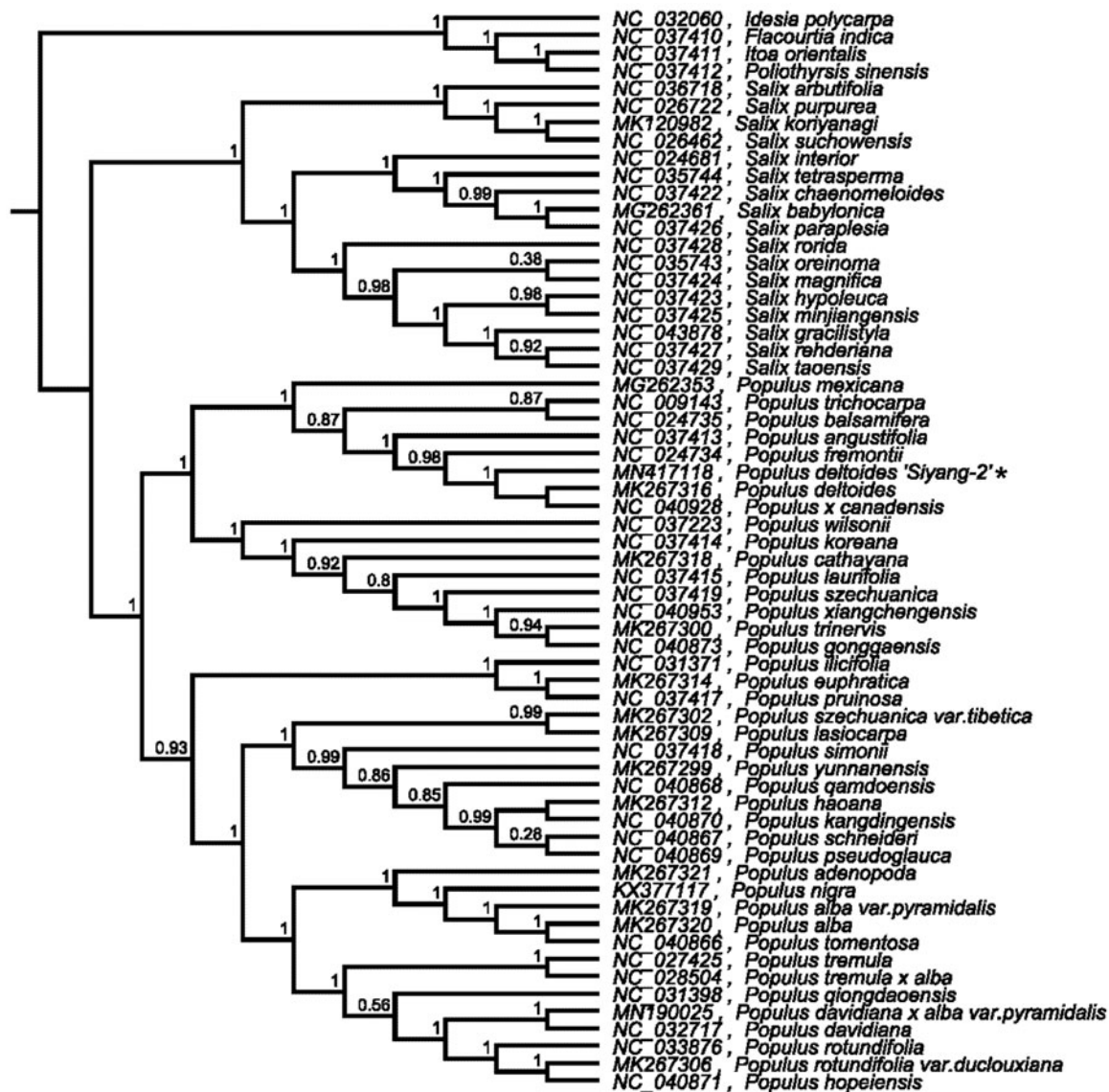


Figure 1. Phylogenetic tree inferred by maximum likelihood (ML) method based on the complete chloroplast genome of *P. deltoides* 'Siyang-2' and other 61 species in the *salicaceae* family, bootstrap values are shown on the branch.

MAFFT v7.307 (Kato and Standley 2013). The ML phylogenetic tree (constructed by FastTree version 2.1.10 (Price et al. 2010)) showed that 'Siyang-2' was closely related to *P. deltoides* and *P. x Canadensis* (Figure 1). The cp genome provides valuable information for further population, phylogenetic, physiological, cp genetic engineering studies of this important improved poplar species *P. deltoides* 'Siyang-2'.

Disclosure statement

No potential conflict of interest was reported by the authors.

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