Introduction

The so-called pediatric anesthesia refers to the anesthesia from the neonate to the age of 12 years, but the main target is children under 6 years old, especially the physiological characteristics of children under 3 years old have obvious differences with adults. Many special problems encountered in pediatric anesthesia and their use in the special measures are also based on this age. Pediatrics are not the epitome of adults. The physiological functions of newborns and infants are very different from those of adults. Therefore, children’s anesthesia must be familiar with the anatomical and physiological characteristics of children, and the anesthesia techniques and methods applied to adults must be properly adjusted, improved or processed and calculated accurately before they can be applied to children of different ages and can ensure children with the safety of anesthesia. In our previous study, we have proved that the bud fat of the *Populus szechuanica* C.K. Schneid. has important application values on the cenesthesia, which could significantly reduce the occurrence of hypotension after anesthesia. The complete chloroplast genome sequence of *P. szechuanica* was characterized from Illumina pair-end sequencing. The chloroplast genome of *P. szechuanica* was 156,717 bp in length, containing a large single-copy region (LSC) of 84,900 bp, a small single-copy region (SSC) of 16,527 bp, and two inverted repeat (IR) regions of 27,645 bp. The overall GC content is 36.70%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.7%, and 41.9%, respectively. The genome contains 131 complete genes, including 86 protein-coding genes (68 protein-coding gene species), 37 tRNA genes (29 tRNA species) and 8 rRNA genes (4 rRNA species). The Maximum Likelihood phylogenetic analysis showed that *P. szechuanica* and *P. koreana* clustered together as sisters to other *Populus* species.

The complete chloroplast genome sequence of *Populus szechuanica*, a medicinal plant for child anesthesia application

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ABSTRACT

*Populus szechuanica* C.K. Schneid. is used for wind and sand fixation, farmland protection, soil and water conservation. And some varieties bud fat and inflorescence are available for medicinal use; poplar bark contains tannin and can be used as tanning material. It is also widely used in afforestation and greening in cities across China. In addition, the *P. szechuanica* also showed vital important application values on the child anesthesia, which could significantly reduce the occurrence of hypotension after anesthesia. The complete chloroplast genome sequence of *P. szechuanica* characterized from Illumina pair-end sequencing. The chloroplast genome of *P. szechuanica* was 156,717 bp in length, containing a large single-copy region (LSC) of 84,900 bp, a small single-copy region (SSC) of 16,527 bp, and two inverted repeat (IR) regions of 27,645 bp. The overall GC content is 36.70%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.7%, and 41.9%, respectively. The genome contains 131 complete genes, including 86 protein-coding genes (68 protein-coding gene species), 37 tRNA genes (29 tRNA species) and 8 rRNA genes (4 rRNA species). The Maximum Likelihood phylogenetic analysis showed that *P. szechuanica* and *P. koreana* clustered together as sisters to other *Populus* species.

KEYWORDS

Complete chloroplast genome; phylogenetic analysis; child anesthesia application

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The fresh leaves of *P. szechuanica* were collected from Xizang (91°10'E; 29°41'N). Fresh leaves were silica-dried and taken to the laboratory until DNA extraction. The voucher specimen (ZCY001) was laid in the Herbarium of the Affiliated Hospital of Southwest Medical University and the extracted DNA was stored in the −80°C refrigerator of the Key Laboratory of Department of Pain Management. 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) for assembling and finishing the genome. The genome sequences of *P. szechuanica* were deposited in GenBank under the accession number MT593369.1.

Figure 1. Maximum Likelihood (ML) analysis of *Populus szechuanica* and other related species based on the complete chloroplast genome sequence.
to assemble chloroplast genomes. We used *Populus qamdoensis* (GenBank: NC040868) 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. szechuanica* (GenBank accession number MT593369) was characterized from Illumina pair-end sequencing. The chloroplast genome of *Populus szechuanica* was 156,717 bp in length, containing a large single-copy region (LSC) of 84,900 bp, a small single-copy region (SSC) of 16,527 bp, and two inverted repeat (IR) regions of 27,645 bp. The overall GC content is 36.70%, while the corresponding values of the LSC, SSC, and IR regions are 34.5%, 30.7%, and 41.9%, respectively. The genome contains 131 complete genes, including 86 protein-coding genes (68 protein-coding gene species), 37 tRNA genes (29 tRNA species) and 8 rRNA genes (4 rRNA species).

We used the complete chloroplast genomes sequence of *P. szechuanica* and 33 other related species to construct phylogenetic tree. The 34 chloroplast genome sequences were aligned with MAFFT (Katoh and Standley 2013), and then the Maximum Likelihood (ML) tree was constructed by MEGA 7.0 (Kumar et al. 2016). The ML phylogenetic analysis showed that *P. szechuanica* and *P. gonggaensis* have the closest genetic relationship (Figure 1).

**Disclosure statement**

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

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MT593369. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA682691, SRR13203218, and SAMN17005496 respectively.

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