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The complete mitochondrial genome of *Salix paraflabellaris*, an endemic alpine plant of Yunnan province of China

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ABSTRACT

Salix paraflabellaris is a procumbent alpine plant endemic to Hengduan Mountain in Yunnan Province, China. The complete mitochondrial genome sequence of this species is a circular molecule of 637,893 bp in size, encoding 34 protein-coding genes, 22 tRNA genes, and 3 rRNA genes. Moreover, two large inverted repeat regions with length of 9557 bp and 3524 bp were identified in the genome. Phylogenetic analysis confirmed the membership of *S. paraflabellaris* in genus *Salix* L., as well as monophyly of both *Populus* and *Salix*.

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Salix paraflabellaris S.D. Chao is a *Salix* L. (Salicaceae) species endemic to Yunnan Province of China. It is an alpine plant distributed in alpine scree slope habitat with elevations around 3500–4500 m in the Hengduan Mountain (Southeast of Qinghai-Tibetan Plateau). *Salix paraflabellaris* is distinct in morphology compared with other *Salix* species: it is a procumbent plant with stems and branches buried in soil and usually ca. 3 cm in height (Fang et al. 1999).

In this study, we sequenced and assembled the complete mitochondrial genome of *S. paraflabellaris*. The leaf sample was collected from an individual of this species from Shangri-La County, Yunnan Province, China (N 28.151, E 99.903). The voucher specimen was deposited in the Herbarium of Kunming Institute of Botany (accession number: CJH1709). Genomic DNA was isolated using a modified CTAB method (Porebski et al. 1997) and then fragmented and used to construct short-insert libraries (300 bp) following the manufacturer's protocol (Illumina Inc., USA), and then paired-end sequenced (150 bp) on an Illumina HiSeq X Ten sequencer. A total of ca. 31.2 million reads were generated. Assembly was performed using NOVOPlasty v2.7.2 (Dierckx et al. 2017) with a *k*-mer of 39.

The mitochondrial genome of *S. paraflabellaris* was assembled as a closed-circular molecule of 637,893 bp in length (GenBank accession No.: MK575518) and annotated by GeSeq (Tillich et al. 2017). The genome contains 59 annotated genes, including 34 protein-coding genes (CDS), 22 tRNA genes, and 3 rRNA genes. All five categories of

mitochondrial protein-coding genes that are typically conserved among plants (Chen et al. 2017) are present in our assembled genome. Interestingly, we identified two large repeats with a length of more than 500 bp using Repeat Finder implemented in Geneious v9.1.4 (Kearse et al. 2012). Both repeats have a frequency of 2 and are presented as inverted repeats with 9557 bp and 3524 bp in length, respectively, and no genes or protein-coding sequences harbored in these two repeats. This kind of large repeats was not found in the other four species of Salicaceae with complete mitochondrial genome available in GenBank.

To confirm the phylogenetic position of *S. paraflabellaris*, we downloaded four Salicaceae species with mitochondrial complete genome from GenBank, and 31 mitochondrial CDS shared by all these five species were aligned using MUSCLE (Edgar 2004) and maximum likelihood (ML) tree was constructed using IQ-TREE v1.6.10 (Nguyen et al. 2015), best-fitted model according to Bayesian information criterion is k3Pu + F using ModelFinder (Kalyaanamoorthy et al. 2017), branch supports were tested by ultrafast bootstrap (UFBoot) (Hoang et al. 2018) and SH-like approximate likelihood ratio test (SH-aLRT) (Guindon et al. 2010) with 10,000 replicates. The ML tree showed that both *Populus* and *Salix* are robust monophyletic clade and sister to each other. This relationship is consistent with former studies (Huang et al. 2017). *Salix paraflabellaris* is nested in the *Salix* clade and sister to *S. purpurea* (Figure 1).

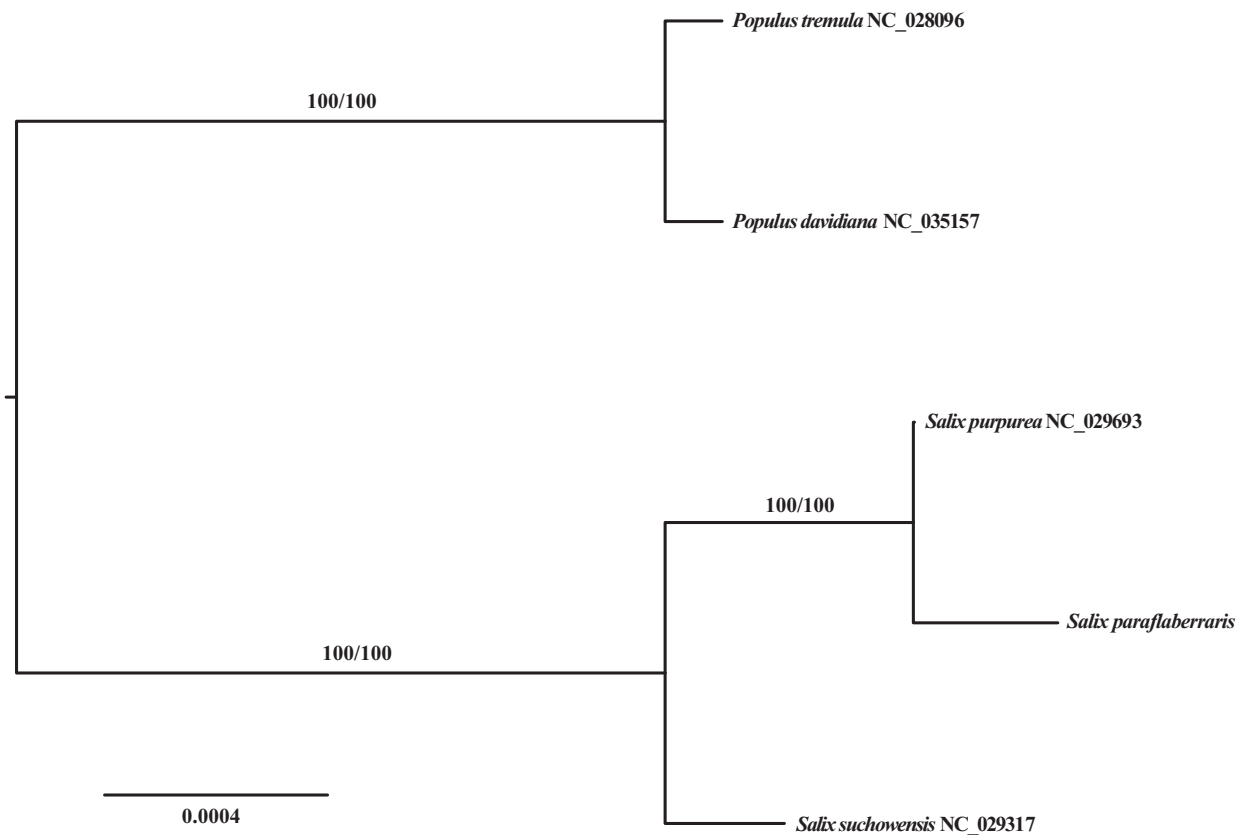


Figure 1. ML phylogenetic tree of *S. paraflabellaris* and four Salicaceae species based on 31 mitochondrial CDS (*atp-1, 4, 6, 8, 9; ccm-B, C, Fc, Fn; cob; cox-1, 2, 3; matR; mttB; nad-1, 2, 3, 4, 4L, 5, 6, 7, 9; rpl-2, 10; rps-3, 4, 7, 12; sdh4*) shared by the five Salicaceae species, branch supports values were reported as SH-aLRT/UFBoot.

Disclosure statement

No potential conflict of interest was reported by the authors.

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