

Mitochondrial DNA Part B Resources

ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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To cite this article: Chuan Peng, Chih-Chieh Yu & Yao-Wu Xing (2021) The complete chloroplast genome of *Androsace erecta* (Primulaceae) and its phylogenetic implication, Mitochondrial DNA Part B, 6:7, 1987-1989, DOI: [10.1080/23802359.2021.1938723](https://doi.org/10.1080/23802359.2021.1938723)

To link to this article: <https://doi.org/10.1080/23802359.2021.1938723>



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Published online: 14 Jun 2021.



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MITOGENOME ANNOUNCEMENT



The complete chloroplast genome of *Androsace erecta* (Primulaceae) and its phylogenetic implication

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ABSTRACT

With about 153 species, the genus *Androsace* (Primulaceae) is known for its horticultural and economic importance. In this study, we report the complete chloroplast genome of *Androsace erecta* Maximowicz, a morphologically distinct species of Sect. *Orthocaulon* native to the Western China. The plastome of *A. erecta* is highly conserved in genome size, structure, and content when compared to all previously published plastomes of the genus. The phylogenomic analysis strongly supported *A. erecta* as sister to a clade comprising species of Sections *Aizoidea* and *Chamaejasme*. Lastly, we selected the four most variable regions across the *Androsace* species plastomes (*trnK^{UUU}-rps16*, *trnS^{GCU}-trnG^{UCC}*, *psbE-petL*, and *infA-rps8*), which were considered to be suitable candidate DNA barcodes for *Androsace*.

ARTICLE HISTORY

Received 8 March 2021

Accepted 29 May 2021

KEYWORDS

Androsace Sect.
Orthocaulon; molecular
systematics; whole
plastome sequence

Plants of the genus *Androsace* are highly prized for their ornamental and pharmaceutical values (Smith et al. 1997). The genus is commonly found in northern temperate regions, yet occupying a wide range of elevational gradients, from 800 to 6350 m a.s.l. (Hu and Kelso 1996; Dentant 2018). The genus is known for its morphological diversity, comprising seven highly variable sections (Hu 1994; Hu and Kelso 1996). In particular, the monotypic Section *Orthocaulon* contains only one species, *Androsace erecta* Maximowicz, whose peculiar morphology (a densely leafy stem and lack of a basal rosette) has attracted significant attention for over a century (Knuth and Pax 1905; Hu and Kelso 1996; Schneeweiss et al. 2004). In this study, we sequenced the complete chloroplast genome of *A. erecta* for the first time. To investigate its phylogenetic position, we selected another five species (see Figure 1), which altogether represent the four major sections of *Androsace*, including Sect. *Chaemajasma*, the sister clade of Sect. *Orthocaulon*. Subsequent phylogenomic analyses were conducted based on plastome data available in GenBank and the newly generated plastome built by us. The sample of *A. erecta* was collected from a wild population found in Deqin County, near the National Highway G214 (28.451833°N, 98.858769°E). The voucher was deposited at the Herbarium of Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences (V000018, HITBC, <http://hitbc.xtbg.ac.cn/>, ljw@xtbg.org.cn).

Total genomic DNA was extracted from leaves dried with silica gel, using a modified CTAB procedure (Doyle and Doyle 1987). About 8 Gb of genomic data were generated by an

Illumina NovaSeq 6000 platform with a reading length of 150 bp. More than 28 million clean reads were *de novo* assembled and annotated by the GetOrganelle toolkit (Jin et al. 2020) and CPGAVAS2 (Shi et al. 2019), and then manually adjusted in Geneious (Kearse et al. 2012). The complete chloroplast genome (over 133× coverage) was aligned by MAFFT (Katoh and Standley 2013). The resulting genome matrix was subsequently used to reconstruct the maximum likelihood tree through RAXML under a GTRGAMMA + I model with 1000 bootstraps (Stamatakis 2014) on the CIPRES online portal (<https://www.phylo.org/>). The tree was visualized with FigTree version 1.4.4 (Rambaut 2010). The nucleotide diversity (π) of the five *Androsace* plastomes were calculated by DnaSP with 500 bp window size and 200 bp step size respectively (Rozas et al. 2017).

With a GC content of 37.2%, the plastome of *A. erecta* was a circular DNA molecule of 153,547 bp (MW450886), with a typical quadripartite structure including two IRs of 26,008 bp separating the LSC of 83,745 bp and the SSC of 17,786 bp. We identified 111 unique genes, 80 CDS (coding sequences), 34 transfer RNAs (*tRNAs*), and four ribosomal RNAs (*rRNAs*), which are all consistent with previously published *Androsace* plastomes. Unlike its unique morphology, the plastome of *A. erecta* is highly conserved in genome size, structure, and gene content, similar to most Primulaceae taxa.

As rooted by two *Primula* species (Figure 1), our phylogenetic analysis confirmed the previous infrageneric scheme of *Androsace* at the sectional level (Schneeweiss et al. 2004; Wang et al. 2004), and strongly supported that Sect.

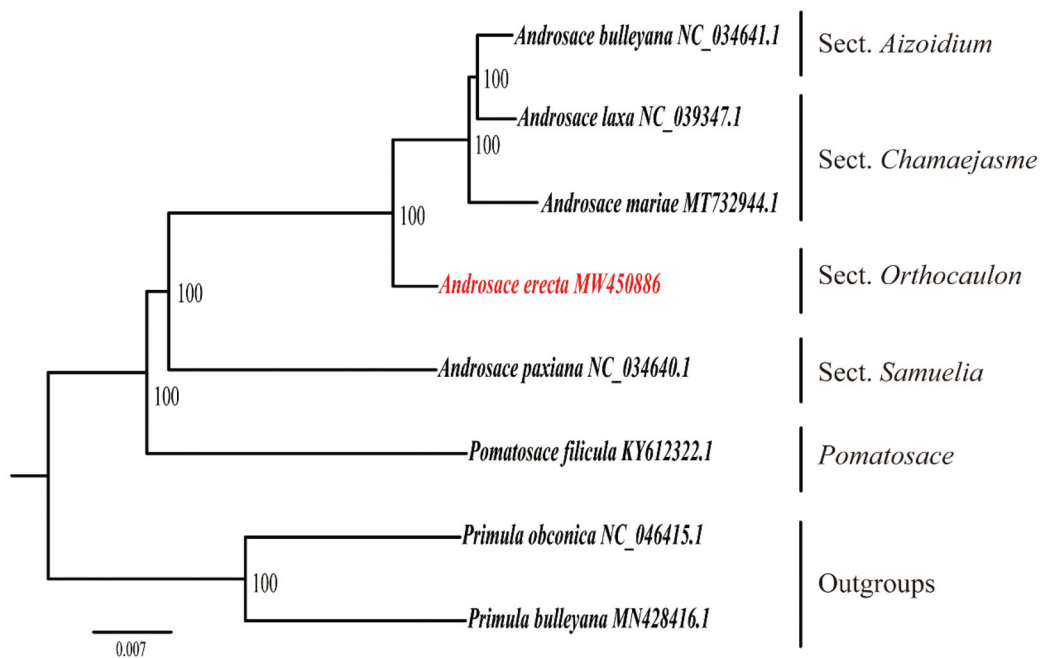


Figure 1. Maximum likelihood tree of 8 species based on the complete chloroplast genome data. The branch statistics are the bootstrap values.

Orthocaulon Hand. - Mazz. (*A. erecta*) is sister to the clade comprising *Sect. Chamaejasme* Koch. (*A. laxa*, *A. mariae*) and *Sect. Aizoidium* Hand.- Mazz. (*A. bulleyana*). However, the genus *Pomatoace*, which is nested in *Androsace* in previous studies (Boucher et al. 2012; Roquet et al. 2013), was found to be the sister clade of the *Androsace* with a high support value (BS: 100). Considering our limited taxon sampling, the result still needs further investigation.

As a popular garden plant (Smith et al. 1997), correct species identification of *Androsace* is important for trading the species (Dixon et al. 2016; Dentant 2018). Therefore, we have evaluated and recognized four highly variable regions (*trnK^{UUU}-rps16*, *trnS^{GCU}-trnG^{UCC}*, *psbE-petL*, *infA-rps8*; $\pi > .08$) by comparing the nucleotide diversity of the plastomes of the five species considered here. They are considered to have a high potential for developing DNA barcodes and as genetic markers for ecological and evolutionary studies of *Androsace* (Shaw et al. 2007; Dong et al. 2012).

Acknowledgments

We are grateful for the support from the HPC Platform of the Public Technology Service Center, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences.

Disclosure statement

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

Funding

This work was supported by a National Natural Science Foundation of China grant [U1802242].

Data availability statement

The genome sequence data that support the finding of this study are openly available in GenBank at <https://www.ncbi.nlm.nih.gov/nucleotide/MW450886> under the accession number MW450886. The associated BioProject, BioSample, and SRA numbers are PRJNA706062, SAMN18115972, and SUB9180715, respectively.

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