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# The complete chloroplast genome of *Aralia atropurpurea* (Araliaceae, the ginseng family) from the Sino-Himalayan region, China

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**ABSTRACT**

*Aralia atropurpurea* (Araliaceae) is a perennial medicinal herb endemic to southwest China. In this study, the complete chloroplast (cp) genome of *A. atropurpurea* was reported and phylogenetic analysis was conducted. The cp genome of *A. atropurpurea* is 156,272 bp in length, consisting two inverted repeats (IRs, 25,963 bp), a small single copy (SSC, 18,080 bp), and a large single copy (LSC, 86,266 bp) region. It encodes 133 genes including 88 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The maximum-likelihood tree shows *A. atropurpurea* grouping with the other two *Aralia* sect. *Aralia* species, and a close relationship between *Aralia* and *Panax*.

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*Aralia atropurpurea* (Araliaceae, the ginseng family) is a perennial herb with strong rhizomes, and it has been used as a traditional medicinal herb in China. *Aralia atropurpurea* is endemic to the Sino–Himalayan region, southwest China, growing in forests at 1800–3300 m altitudes (Wen 2011). The sample in this study was collected by J. Liu (2018) from Panzhihua city, Sichuan province, with the geographic coordinate: 26°17′18″N, 101°48′58″E. The voucher specimen (*JLiu 729*) was deposited at the Sichuan Agricultural University Herbarium (SAU).

Genomic DNA was extracted from silica-gel dried leaves using the SDS buffer. DNA sample was randomly fragmented into 400–600 bp in size by an ultrasonicator. An Illumina paired-end DNA library with 500-bp insert size was constructed using a NEBNext UltraIIDNA Library Prep Kit (New England Biolabs Inc., Ipswich, MA). A total of 1.1 Gb paired-end reads (2 × 150 bp) were obtained with the Illumina HiSeq2500 platform (Illumina, San Diego, CA). Trimmomatic (Bolger et al. 2014) was used to remove the adapters without filtering or quality trim. NOVOPlasty (Dierckxsens et al. 2017) was applied for the chloroplast (cp) genome *de novo* assembly, with the sequence of the Rubisco-bis-phosphate oxygenase (RuBP) subunit used as the seed sequence. One circularized assembly was obtained. The cp genome was annotated using Geneious Prime (https://www.geneious.com).

The cp genome of *A. atropurpurea* (GenBank Accession No. MH809524) is 156,272 bp in length, with a typical quadripartite structure, including a large single-copy (LSC, 86,266 bp), a small single copy (SSC, 18,080 bp) and a pair of inverted repeats (IRs, 25,963 bp). Genome annotation reveals 133 functional genes including 88 protein-coding genes, 37 tRNA genes, and 8 rRNA genes, in which 16 genes (5 tRNA, 4 rRNA, and 7 protein-coding genes) are duplicated in the IR regions. Among these genes, 15 genes (6 tRNA genes and 9 protein-coding genes) each contain one intron while 3 protein-coding genes (*clpP*, *rps12*, and *ycf3*) have two introns each. The gene *rps12* was found to be a typical trans-spliced gene with three exons, as previously reported in *Panax ginseng* (Zhao et al. 2014). The *A. atropurpurea* cp genome consists of 50.4% coding regions, and the overall G/C content is 38.1%.

To infer the phylogenetic relationships between *A. atropurpurea* and the related species, the whole cp genome sequences of 23 species of Araliaceae were aligned using MAFFT v.7 (Katoh and Standley 2013) and the maximum-likelihood (ML) analysis was conducted using IQ-TREE v.1.4.2 with 1000 bootstrap replicates (Nguyen et al. 2015). The ML tree (Figure 1) shows that *A. atropurpurea* clustered with the other two *Aralia* sect. *Aralia* species, and the genus *Aralia* has a close relationship with *Panax*. The cp genome sequences possess many phylogenetic informative sites and are helpful to clarify the complex phylogenetic relationships and the biogeographic history of *Aralia*.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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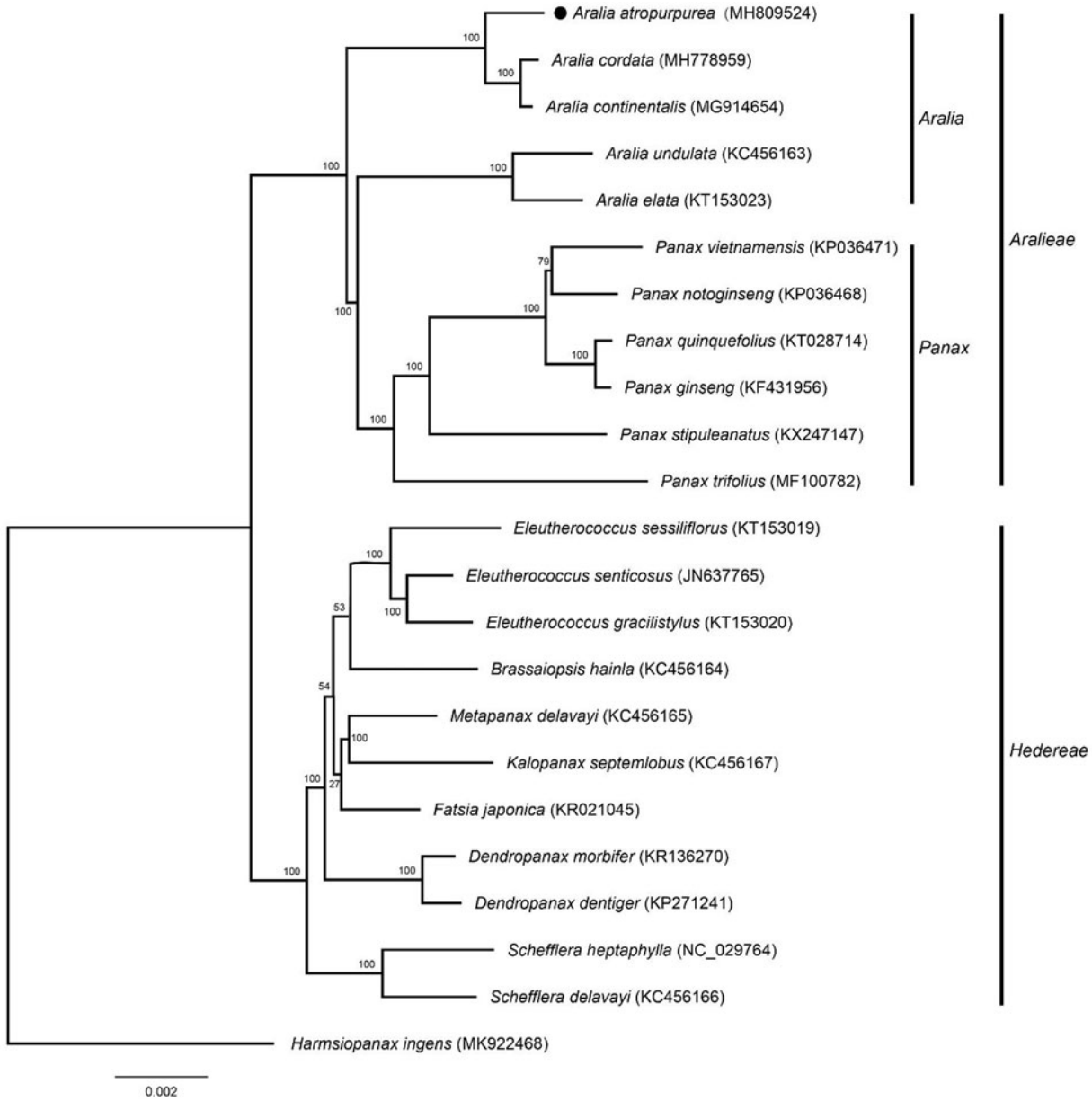


**Figure 1.** Maximum-likelihood phylogenetic tree based on the complete cp genome sequences of 23 species from the family Araliaceae, *Harmsiopanax ingens* is used as the outgroup. Numbers on branches indicate the bootstrap value.

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