The complete chloroplast genome sequence of *Sargentodoxa cuneata*: genome structure and genomics resources

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The size of the chloroplast genome of *S. cuneata* is 158,094 bp. The cp genome exhibits a quadripartite structure, which includes a pair of inverted repeats (IRa and IRb: 26,132 bp), and separated large single-copy (86,508 bp) and small single-copy (19,322 bp) regions. The GC content of the chloroplast DNA is 38.2%. The chloroplast genome of *S. cuneata* encodes 113 different genes, including 79 protein-coding genes, 30 transfer RNAs, and 4 ribosomal RNAs. A total of 84 perfect chloroplast microsatellites were analyzed in the *S. cuneata*. The majority of the SSRs in this chloroplast genome were mononucleotides (66.67%). The reconstructed phylogeny revealed that *S. cuneata* was sister to the remaining Lardizabalaceae.

**ABSTRACT**

*Sargentodoxa cuneata* is used as traditional Chinese medicine. In this study, we report its complete chloroplast genome by Illumina pair-end sequencing. The total chloroplast (cp) genome size was 158,094 bp in length, containing a pair of inverted repeats of 26,132 bp, separated by large single-copy and small single-copy regions of 86,508 bp and 19,322 bp, respectively. The chloroplast genome of *S. cuneata* encodes 113 different genes, including 79 protein-coding genes, 30 transfer RNAs, and 4 ribosomal RNAs. A total of 84 perfect chloroplast microsatellites were analyzed in the *S. cuneata*. The majority of the SSRs in this chloroplast genome were mononucleotides (66.67%). The reconstructed phylogeny revealed that *S. cuneata* was sister to the remaining Lardizabalaceae.
To estimate phylogenetic relationships of *S. cuneata* with other Lardizabalaceae species. Phylogenetic analysis was performed using the whole chloroplast genome sequence. The chloroplast genome sequences were aligned using MAFFT v7 (Katoh and Standley 2013). Ambiguous alignment regions were trimmed by Gblocks 0.91 b (Castresana 2002). The maximum-likelihood (ML) analyses were performed in RAxML v.8.1.24 (Stamatakis 2014). The statistical support for the branches was calculated by rapid bootstrap analyses with 1000 replicates. The reconstructed phylogeny revealed that *S. cuneata* was sister to the remaining Lardizabalaceae (Figure 1). The whole chloroplast genome sequences provided sufficient genetic information for species identification, phylogeny analysis, and conservation genetics.

**Disclosure statement**

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

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**Data availability statement**

The chloroplast genome sequence of the *S. cuneata* was submitted to GenBank of NCBI (https://www.ncbi.nlm.nih.gov). The accession number from GenBank is MT898426. The raw data have been deposited in SRA under accession no. PRJNA662211 (https://www.ncbi.nlm.nih.gov/sra/PRJNA662211).

![Figure 1. Maximum-likelihood tree of Ranunculales based on the complete chloroplast genome sequences. Bootstrap support values >50% are given at the nodes.](image)

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