

## Characterization of the whole plastome of *Dipentodon Sinicus* (Dipentodontaceae)

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### ABSTRACT

In this study, we sequenced and assembled the whole plastome of *Dipentodon sinicus*. The plastome was 158,020 bp in length and consisted of a pair of inverted repeat regions (IRs, 26,551 bp), a large single-copy region (LSC, 86,624 bp) and a small single-copy region (SSC, 18,294 bp). It encoded 114 unique genes (80 protein-coding genes, 30 tRNA genes and 4 rRNA genes). Phylogenetic analysis showed that *Dipentodon sinicus* was sister to *Tapiscia sinensis*.

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Dipentodontaceae Merrill is a small family in the malvids (Angiosperm Phylogeny Group 2016), which only includes two genera, namely, *Dipentodon* Dunn and *Perrottetia* Kunth (Ma and Bartholomew 2008). However, its phylogenetic position has long been contentious. Dipentodontaceae was placed in Rosales between Hamamelidaceae and Rosaceae by Merrill (1941) when it established. Hutchinson (1959) then transferred the family into Olacales based on the free basal placentation. Cronquist (1981) included the family Dipentodontaceae in Santalales, while Takhtajan (1997) defined it as a member of Violales. Recently, establishing the order Huerteales to accommodate the family was supported by molecular evidence (Angiosperm Phylogeny Group 2009; Worberg et al. 2009; Angiosperm Phylogeny Group 2016).

Although lots of studies have been performed, available genomic resources of Dipentodontaceae are still limited, which severely hinders our understanding for the evolution of the family. Here, we presented the whole plastome of *Dipentodon sinicus* Dunn, the only member of the genus *Dipentodon*. Samples of *Dipentodon sinicus* were collected from Gongshan county (27°44'49"N, 98°40'20"E), Yunnan province, China. Specimen (jyh33135) was deposited in the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN). Total DNA was extracted from the silica-gel-dried leaf using the modified CTAB method (Yang et al. 2014). Ensuing, purified DNA was fragmented into ~500 bp to construct paired-end library. We then prepared Illumina library according to the manufacturer's protocol.

The library was sequenced on the Illumina HiSeq 2000 system. Assembly for the whole plastome of *Dipentodon sinicus* was performed using the method described by Jin et al. (2018) with the plastome of *Tapiscia sinensis* (MF926267) as the reference. We then annotated the plastome in Geneious 10.2 (Kearse et al. 2012), and manually checked for start and stop codons and intron/exon boundaries. Validated complete plastome of *Dipentodon sinicus* was deposited in GenBank under accession number MN275517.

Overall size of the *Dipentodon sinicus* plastome was 158,020 bp, and it presented a typical quadripartite structure, including a pair of inverted repeat regions (IRs, 26,551 bp) divided by a large single-copy region (LSC, 86,624 bp) and a small single-copy region (SSC, 18,294 bp). The plastome of *Dipentodon sinicus* possessed 114 unique genes, including 80 protein-coding genes, 30 tRNA genes, and four rRNA genes. Among them, twelve protein-coding genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl16*, *rpl2*, *rpoC1*, *rps12*, *rps16*, *clpP* and *ycf3*) and six tRNAs (*trnA*-UGC, *trnG*-UCC, *trnI*-GAU, *trnK*-UUU, *trnL*-UAA and *trnV*-UAC) contained at least one intron.

To investigate the phylogeny of *Dipentodon sinicus*, we reconstructed the maximum likelihood tree based on twenty whole plastomes using the software RAxML version 8.2.11 (Stamatakis 2014) with 1,000 bootstrap replicates. *Larrea tridentata* was used as outgroup. The result strongly supported that *Dipentodon sinicus* was sister to *Tapiscia sinensis* (Figure 1).

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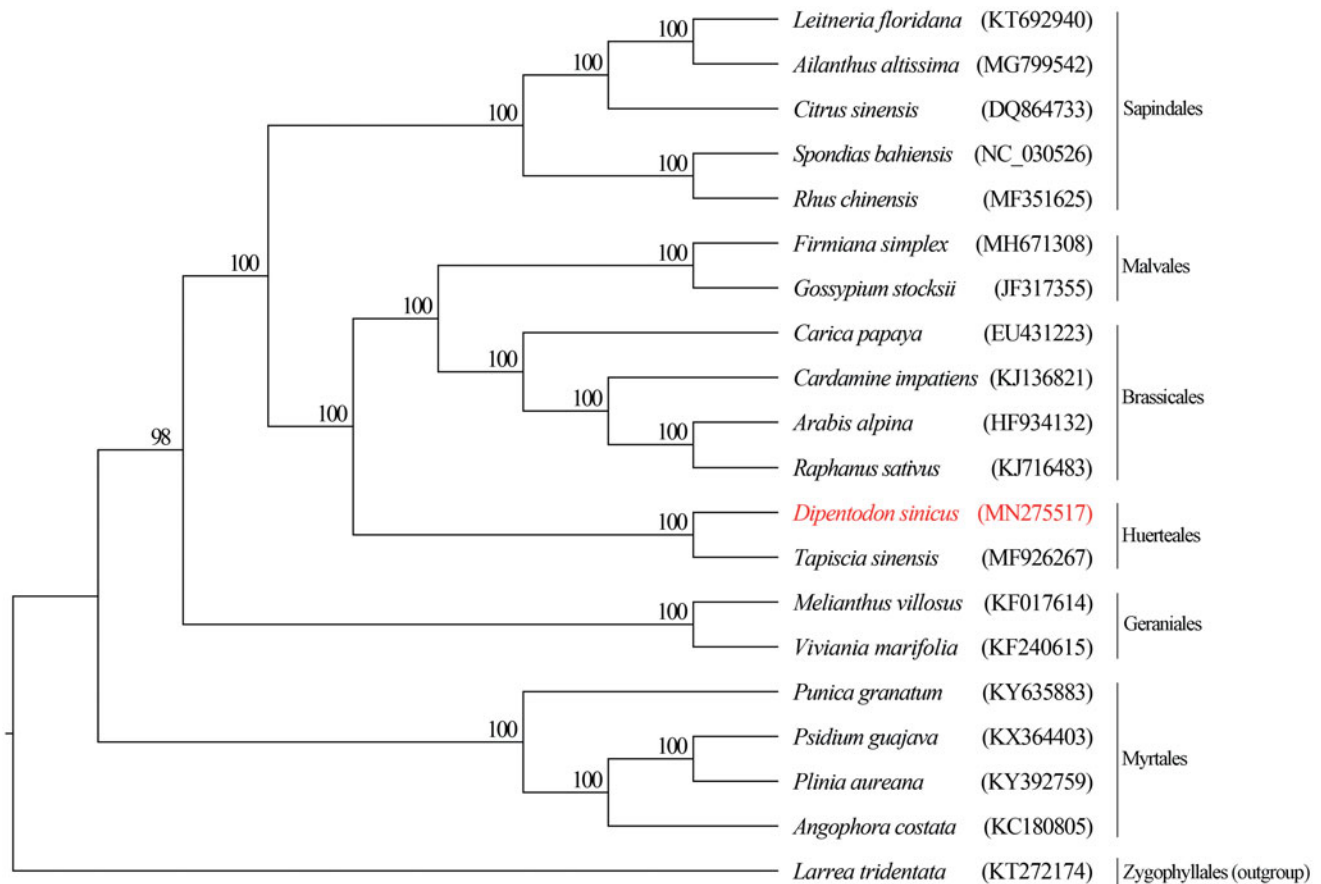


Figure 1. Maximum likelihood (ML) tree was generated with whole plastomes. The bootstrap values are presented above the clade.

## Disclosure statement

The authors declare no potential conflict of interests.

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## References

- Angiosperm Phylogeny Group. 2009. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III. *Bot J Linn Soc.* 161:105–121.
- Angiosperm Phylogeny Group. 2016. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG IV. *Bot J Linn Soc.* 181:1–20.
- Cronquist A. 1981. *An integrated system of classification of flowering plants.* New York: Columbia University Press.
- Hutchinson J. 1959. *The families of flowering plants, vol. 1, Dicotyledons.* Oxford: Clarendon Press.
- Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. *bioRxiv.* 256479. doi:10.1101/256478.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics.* 28: 1647–1649.
- Ma J, Bartholomew B. 2008. Dipentodontaceae. In: Wu ZY, Raven PH, editors. *Flora of China, Vol. 11.* Beijing and St. Louis: Science Press and Missouri Botanical Garden Press; p. 494–495.
- Merrill ED. 1941. The upper Burma plants collected by Captain F. Kingdon Ward on the Vernay-Cutting expedition, 1938–39. *Brittonia.* 4:20–23.
- Stamatakis A. 2014. Raxml version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30:1312–1313.
- Takhtajan AL. 1997. *Diversity and classification of flowering plants.* New York: Columbia University Press.
- Worberg A, Alford MH, Quandt D, Borsch T. 2009. Huerteales sister to Brassicales plus Malvales, and newly circumscribed to include Dipentodon, Gerrardina, Huerteia, Perrottetia, and Tapiscia. *Taxon.* 58: 468–478.
- Yang JB, Li DZ, Li HT. 2014. Highly effective sequencing whole chloroplast genomes of angiosperms by nine novel universal primer pairs. *Mol Ecol Notes.* 14:1024–1031.