

The complete chloroplast genome sequences of *Delavaya toxocarpa* and *Harpullia cupanioides* (Dodonaeeidae, Sapindaceae)

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Abstract

The complete chloroplast (cp) genomes of *Delavaya toxocarpa* and *Harpullia cupanioides* were reported here. In *D. toxocarpa*, the total genome size was 161,325 bp in length, consisting of two IRs (26, 698 bp) separated by the LSC (88, 698 bp) and SSC (19, 231 bp) regions. The genome contained 131 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes respectively. The GC-content of the complete chloroplast genome was 37.5%. As to *H. cupanioides*, the complete chloroplast genome was 159, 776 bp in length, consisting of two IRs (26, 938 bp) separated by the LSC (87, 804 bp) and SSC (18, 096 bp) regions. The genome contained 131 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes respectively. The GC-content of the complete chloroplast genome was 37.8%. A phylogenetic analysis indicated that *D. toxocarpa* was closely related to *Koelreuteria*, and *H. cupanioides* was close with *Dodonaea viscosa*. This study will be useful for the phylogenetic position determination as well as future phylogenetic study of *Delavaya toxocarpa* and *H. cupanioides*.

Full Text

Delavaya toxocarpa Franch. is the only species of the monotypic genus *Delavaya* Franch. (Sapindaceae) mainly distributed in southwestern China and northern Vietnam (Xia and Gadek 2007). It has economic value in the oil industry (Luo and Chen, 1985; Long and Song, 2012). *Harpullia cupanioides* Roxburgh (Sapindaceae) is a tall tree and is usually used for its timber (Luo & Chen, 1985). In plants, the chloroplast genome is helpful for population genetics study, species-level identification, and phylogenetic analysis (Lyu et al., 2020).

Previously, the studies regarding *Delavaya toxocarpa* mainly focused on its cultivation, chemical constituents and morphology (Lyu et al. 2015; Qin et al. 2001; Cao et al. 2014), and studies of *Harpullia cupanioides* mainly focused on its chemical constituents (Gohary and Hamida, 2005). There is no datum currently available about their complete chloroplast genome). In this study, we assembled the complete chloroplast genome of *D. toxocarpa* and *H. cupanioides* for the first time and analyzed the reasonably relationships among these species and other allies.

Fresh silica-dried leaves of *Delavaya toxocarpa* (accession number: Li, 20210801) were collected from Kunming (25.141676°N, 102.751317°E), Yunnan Province, China, and those of *Harpullia cupanioides* (accession number: Caizhi 20210704) were collected from Jinuo Township (22.042443°N, 101.011163°E), Jinghong City, Yunnan Province, China. The voucher specimens were deposited in HYNH (Hengyang Normal University Herbarium). The total genomic DNA was extracted for the following operation. Sequencing was conducted on the Illumina NovaSeq system (Illumina, San Diego, CA, USA). After comparing with all existing chloroplast genomes of Sapindaceae in GenBank, chloroplast genome-related reads of *D. toxocarpa* were obtained. The raw reads of *D. toxocarpa* were assembled using NOVOPlasty 3.7 (Dierckxsens et al. 2017) with ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcL*) gene from *Sapindus mukorossi* (GenBank accession number: KM454982) as seed, while the raw reads of *H. cupanioides* were assembled using GetOrganelle (Jin et al. 2020). After that, the complete genome

sequence was annotated using online annotation tool GeSeq (<https://chlorobox.mpimp-golm.mpg.de/geseq.html>) (Tillich et al. 2017) and adjusted manually if necessary.

Like other Sapindaceae members, *Delavaya toxocarpa* and *Harpullia cupanioides* also had two large inverted repeats (IRs), separated by large single-copy (LSC) and small single-copy (SSC) regions. In *D. toxocarpa*, the complete chloroplast genome (GenBank accession number: ON098017) was 161,325 bp in length, consisting of two IRs (26,698 bp) separated by the LSC (88,698 bp) and SSC (19,231 bp) regions. The genome contained 131 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes respectively. The GC-content of the complete chloroplast genome was 37.5%. As to *H. cupanioides*, the complete chloroplast genome (GenBank accession number: ON098016) was 159,776 bp in length, consisting of two IRs (26,938 bp) separated by the LSC (87,804 bp) and SSC (18,096 bp) regions. The genome contained 131 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes respectively. The GC-content of the complete chloroplast genome was 37.8%.

To ascertain the phylogenetic position of *Delavaya toxocarpa* and *Harpullia cupanioides*, phylogenetic analysis was conducted. Phylogenetic tree was constructed using the chloroplast genome sequences of these two species and 13 representative Sapindaceae species whose cp genome sequences were achieved from the NCBI. Multiple sequence alignments were completed with MAFFT (Katoh et al. 2005). Phylogenetic analysis was conducted by Maximum likelihood (ML) method using raxmlGUI (Silvestro and Michalak 2012) with rapid bootstrap (1000 replicates) and GTRGAMMA model selected. It was shown that *D. toxocarpa* and *H. cupanioides* were close with each other. Moreover, *D. toxocarpa* was closely related to *Koelreuteria* species and *H. cupanioides* was close with *Dodonaea viscosa* (Figure 1). It is reasonable to place *Delavaya toxocarpa* and *H. cupanioides* in the subfamily Dodonaeoideae. The result will be useful for the phylogenetic position determination as well as future phylogenetic study of *Delavaya toxocarpa* and *H. cupanioides*, and even Sapindaceae.

Declarations

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Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The data that support the findings of this study are openly available in NCBI at <http://www.ncbi.nlm.nih.gov/>, reference number ON098016, ON098017.

References

1. Cao LM, Cao M, Liu JH, Wang ZX, Lin Q, Xia NH (2014) Sporogenesis and gametogenesis of *Delavaya toxocarpa* (Sapindaceae) and their systematic implications. *J Syst Evol* 52(4):533–539
2. Dierckxsens N, Mardulyn P, Smits G (2017) NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res* 45(4):e18
3. Gohary El, Hamida MA (2005) Phytochemical and biological study of seeds of *Harpullia pendula* Planch. and *Harpullia cupanioides* Roxb. cultivated in egypt. *Bull Fac Pharm (Cairo University)* 42(2):95–104
4. Jin JJ, Yu WB, Yang JB et al (2020) GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome Biol* 21(1):241
5. Katoh K, Kuma K-I, Toh H, Miyata T (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Res* 33(2):511–518
6. Long CL, Song HC (2012) Chinese diesel plants. Science Press, Beijing, p 146
7. Luo XR, Chen DZ (1985) Sapindaceae. In: *Flora Reipublicae Popularis Sinicae*. Beijing: Science Press. 47: 4–72
8. Lyu SH, Huang FZ, Zeng DJ, Xu GP, Li XK (2015) The stump sprouting characteristics of the pioneer tree *Delavaya toxocarpa* in rocky desertification region. *J Nanjing Forestry Univ (Natural Sci Edition)* 39(03):65–70
9. Lyu YZ, Dong XY, Sun HN, Huang LB (2020) Characterization of the complete chloroplast genome sequence of *Koelreuteria bipinnata*. *Mitochondrial DNA B* 5(3):3342–3343
10. Qin B, Wang HQ, Zhu DY, Shao ZY, Tu L, Zhou DH (2001) Investigation on the Chemical Constituents of *Delavaya yunnanensis*. *Nat Prod Res Dev* 13(2):16–18
11. Silvestro D, Michalak I (2012) RaxmlGUI: a graphical front-end for RAxML. *Org Divers Evol* 12:335–337
12. Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S (2017) GeSeq - versatile and accurate annotation of organelle genomes. *Nucleic Acids Res* 45:W6–W11
13. Xia NH, Gadek PA (2007) Sapindaceae. In: Wu ZY and Raven PH (eds), *Flora of China*. Vol. 12. Beijing: Science Press and St. Louis: Missouri Botanical Garden Press; p. 10

Figures

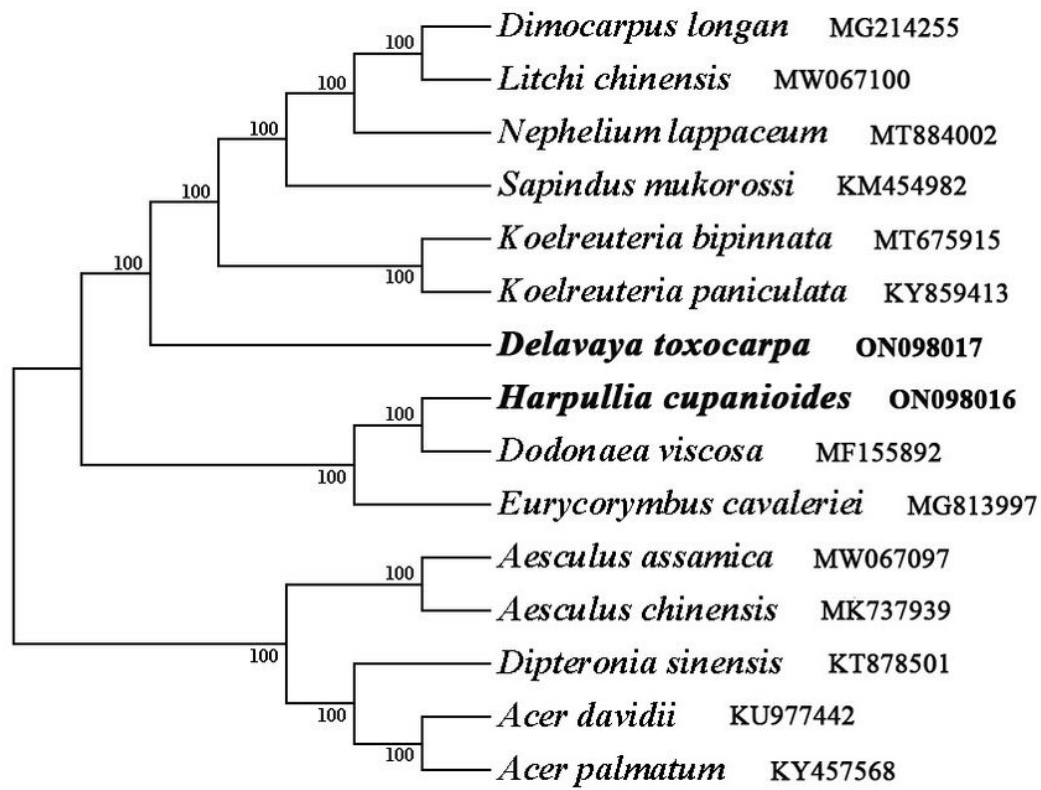


Figure 1

The phylogenetic tree based on the 15 complete chloroplast genome sequences.