


The complete chloroplast genome of *Rubus pinfaensis*, an edible and medicinal dual-purpose plant

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ABSTRACT

Rubus pinfaensis H. Lév. & Vaniot is of great importance in the phylogeny and evolution amongst Rosaceae, genus *Rubus* L. plants. The chloroplast genome of *R. pinfaensis* was reported in this study, which is 155,523 bp in size, with an average GC content of 37.13%. The complete chloroplast genome has a typical quadripartite structure, including a large single copy (LSC) region (85,211 bp) and a small single copy (SSC) region (18,718 bp), which were separated a pair of inverted repeats (IRs, 25,797 bp). This plastome contained 129 different genes (112 unique), including 85 protein-coding genes (79 unique), 36 tRNA genes (29 unique), and 8 rRNA genes (4 unique). The chloroplast genome of *R. pinfaensis* has completed that will be based on the phylogeny and genomic studies in the family Rosaceae, genus *Rubus* L.

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Rubus pinfaensis H. Lév. & Vaniot belong to genus *Rubus* L. section *Idaeobatus* Focke, Subsection *Pungentes* (Focke) Yu et Lu in the family Rosaceae, widely distributed in Hubei, Hunan, Taiwan, Guangxi, Sichuan, Yunnan and Guizhou province in China (Robertson 1974; Yu and Lu 1985; Thompson 1995; Lu and Boufford 2003). The fresh golden or orange fruits can be used for food, vinting (making wine) and medicine, and the roots and leaves can also be used for medicine. For the reasons of inter- and intraspecific hybridization, polyploidization and apomixis, it is extremely difficult in species delimitation in genus *Rubus* L. because of the complexity of their morphological variations (Alice and Campbell 1999), especially with *R. ellipticus* Smith. Therefore, it is essential to reconstructing phylogeny based on sufficient molecular markers if the relationship between species want to be well understood, for the sake of efficiently utilizing these wild *Rubus* germplasm resources in raspberry hybrid breeding. In this study, we reported the complete chloroplast genome of *R. pinfaensis*, a wild species widespread in temperate zone, subtropical and tropical China, with elevation between 500 and 2200 m, as a resource for future studies on the taxonomy of *Rubus* L.

The complete sequence of chloroplast genome of *R. pinfaensis* was reported in this study. The fresh leaves of *R. pinfaensis* were collected from Cuihua Town, Dagan County, Zhaotong City, Yunnan Province of China (27°45'14" N, 103°53'51" E). The sheets of vouchered specimen, Zhu-20201014R04, are stored at the herbaria HHP-YNAU (Herbarium

of Horticultural plants, College of Landscape and Horticulture, Yunnan Agricultural University). Total genomic DNA was extracted from fresh leaves by using DNA Plantzol Reagent (Invitrogen, Carlsbad, CA, USA) to construct chloroplast DNA libraries. The extracted DNA was sequenced by Illumina HiSeq Sequencing System (Illumina, San Diego, CA) and shotgun library was constructed. About 2.42 Gb pair-end (150 bp) raw reads were obtained and the low-quality sequences were filtered using CLC Genomics Workbench v8.0 (CLC Bio, Aarhus, Denmark) to get high-quality clean reads. NOVOPlasty software (Dierckxsens et al. 2017) was used to align and assemble cp genome with *R. niveus* Thunb (MT576936) served as the reference. The complete chloroplast genome of *R. pinfaensis* was automatically annotated using CpGAVAS (Liu et al. 2012) and then adjusted and confirmed with Geneious 9.1 (Kearse et al. 2012). The sequence data was deposited into GenBank. Then the complete chloroplast genome was submitted to the GenBank under the accession number of MZ352081.

The size of chloroplast genome of *R. pinfaensis* is 155,523 bp, with an average GC content of 37.13%, which exhibited a typical quadripartite structure comprising a large single-copy (LSC) region of 85,211 bp and a small single-copy (SSC) region of 18,718 bp separated by a pair identical inverted repeat regions (IRs) of 25,797 bp each. The chloroplast genome contains 129 genes (112 unique), including 85 protein-coding genes (79 unique), 36 tRNA genes (29 unique), and 8 rRNA genes (4 unique).

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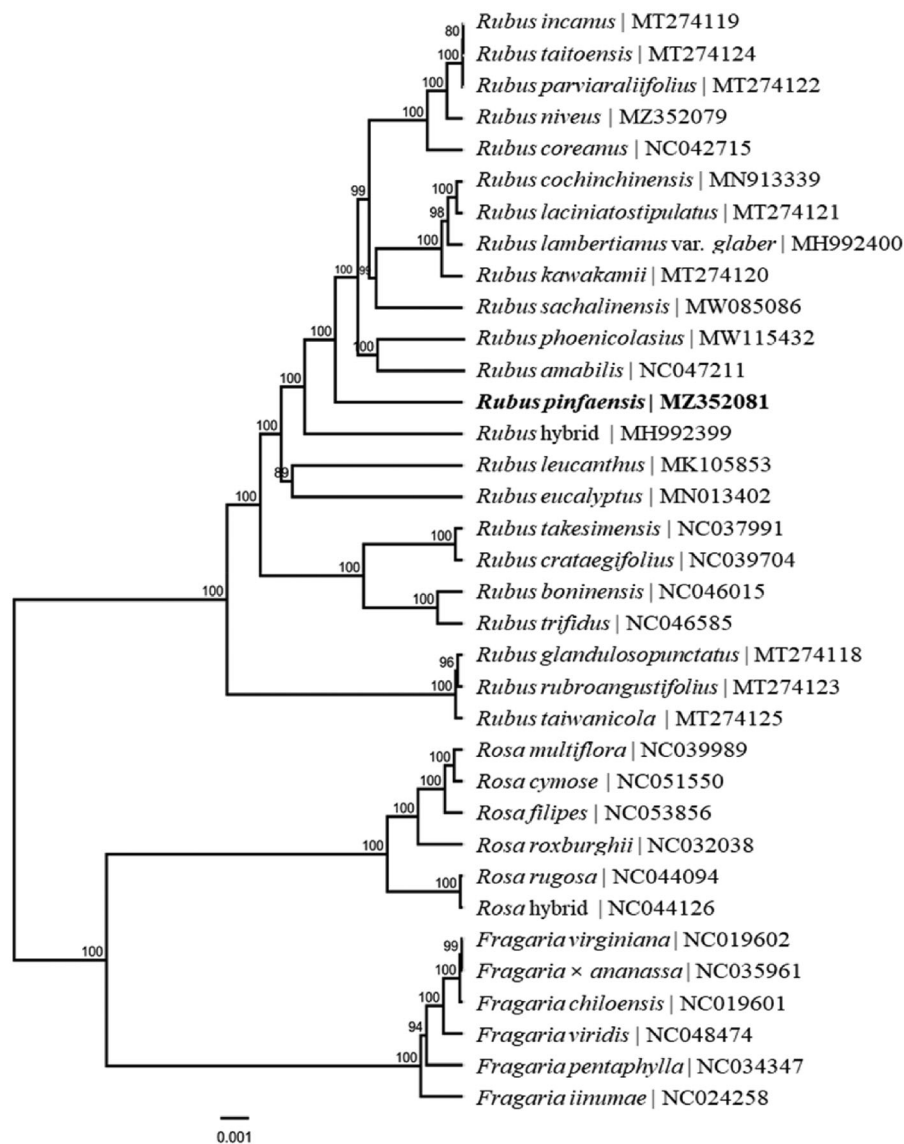


Figure 1. Phylogenetic relationships of 20 species from *Fragaria*, *Rosa* and *Rubus* of Rosaceae based on the complete chloroplast genome sequences. Bootstrap percentages are indicated for each branch.

The ML phylogenetic tree shows that *R. pinfaensis* and other 22 species of genus *Rubus* L. formed a monophyly, with bootstrap support values of over 80% (Figure 1), and all species of the other two genus from Rosaceae have formed an independent monophyly. The monophyly of three genera of Rosaceae is well-supported using complete chloroplast genome sequence. This research lays the foundation for further understanding of the chloroplast genome information of *Rubus* plants, and provides important information for the development and utilization of characteristic plant resources.

Disclosure statement

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

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Data availability statement (DAS)

The complete chloroplast genome generated for this study has been deposited in GenBank with accession number MZ352081, which is openly available in GenBank of NCBI at website (<https://www.ncbi.nlm.nih.gov/>). All high-throughput sequencing data files are available from the GenBank Sequence Read Archive (SRA) accession number: SRR14757448. The associated BioProject and Bio-Sample numbers are PRJNA735803 and SAMN19602744 respectively.

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