

The complete chloroplast genome sequence of *Rhus potaninii*

Yunjia Pan^a, Jinglu Feng^a, Liping Nie^{a,b}, Yingxian Cui^{a,b}, Chuhong Yang^a, Yulin Lin^a and Hui Yao^{a,b}

^aInstitute of Medicinal Plant Development, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China;

^bEngineering Research Center of Chinese Medicine Resource, Ministry of Education, Beijing, China

ABSTRACT

We reported the complete chloroplast genome sequences of *Rhus potaninii* which was characterized by *de novo* assembly with Illumina sequencing data. The size of *R. potaninii* complete chloroplast genome is 159,620 bp in length and includes a large single copy region of 87,722 bp, a small single copy region of 18,948 bp, and a pair of inverted repeats of 26,475 bp. Its GC content is 37.9%. A total of 133 genes were predicted, including 86 protein-coding genes, 8 rRNA genes, 37 tRNA genes, and 2 pseudogenes. Maximum-likelihood (ML) phylogenetic tree indicates that *R. potaninii* is sister to *R. chinensis*.

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Rhus potaninii; chloroplast; genome sequence

The deciduous tree *Rhus potaninii* is 5–8 m tall. It grows on the hill or mountain forests at an altitude of 900–2500 m. The *R. potaninii* belongs to Anacardiaceae family of Sapindales order. The *Galla chinensis*, induced by infection with Gallnut Aphid on *R. chinensis*, *R. potaninii*, and *R. punjabensis*, is a traditional Chinese medicine (National

Pharmacopoeia Committee 2010). It is known to have analgesic and anti-inflammatory effects (Sun et al. 2018). In recent years, *Galla chinensis* has attracted the attention of drug researchers at home and abroad because of its unique advantages such as strong pharmacological effect, extensive sources, and strong selectivity (Karimi-Khouzani et al. 2017).

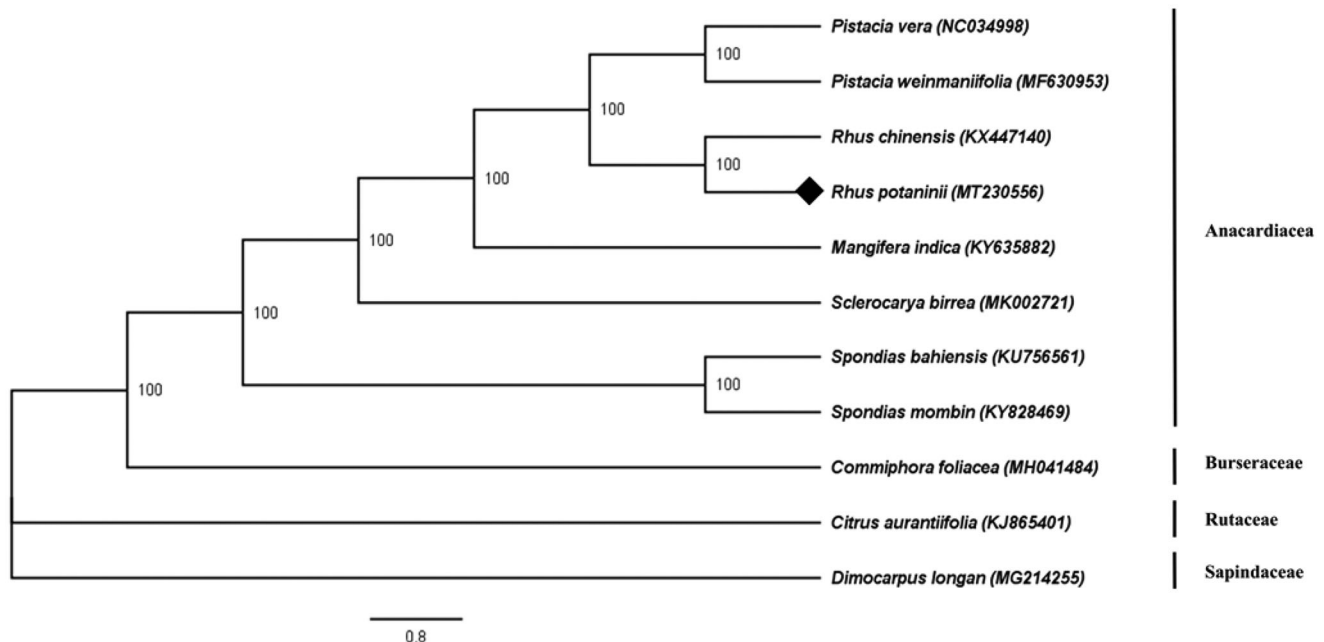


Figure 1. Phylogenetic tree of *Rhus potaninii* and 10 species in order Sapindales using maximum likelihood (ML) analyses based on complete chloroplast genome sequences. The numbers at nodes of phylogenetic tree show the bootstrap support values.

CONTACT Yulin Lin  linyulin@hotmail.com  Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China; Hui Yao  scauyaoh@sina.com  Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China

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Although there are many pharmacology related research of it, there are few researches on its genome. Therefore, our research provides a basis for the study of the coevolution of Gallnut Aphid and host tree and the further study on phylogenetic evolution of *R. potaninii*.

Fresh leaves of *R. potaninii* were collected from Danfeng County, Shaanxi Province (33°36′33.52″N, 110°14′04.89″E). The specimen was saved in Herbarium of Institute of Medicinal Plant Development (voucher: Pan0101). Its total genomic DNA was extracted using QIAGEN DNeasy Plant Mini Kit and the whole genome was sequenced on Illumina HiSeq 2000 platform. Using SOAPdenovo 2 (Luo et al. 2012) and SSPACE (Boetzer et al. 2011) to assemble clean data into a complete chloroplast genome.

The total length of chloroplast genome of *R. potaninii* was 159,620 bp (Genbank accession number: MT230556) with 37.9% GC content. The genome consists of four distinct parts, including a large single copy region of 87,722 bp, a small single copy region of 18,948 bp, and a pair of inverted repeats of 26,475 bp. In the genome, 86 protein-coding genes, 8 rRNA genes, and 2 pseudogenes were identified by CPGAVAS (Liu et al. 2012), DOGMA (<http://dogma.cccb.utexas.edu/>) (Wyman et al. 2004) and BLAST search (Cui et al. 2019), and 37 tRNA genes were annotated by tRNAscan-SE (Schattner et al. 2005).

Phylogenetic analysis of the complete chloroplast genome sequence of *R. potaninii* and 10 species was performed through a maximum likelihood (ML) analyses with 1000 bootstrap replicates (Figure 1), 10 species of which belonging to Sapindales order. The ML tree showed that *R. potaninii* was sister to *R. chinensis* with 100% support value, belonging to the Anacardiaceae family.

Disclosure statement

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

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Data availability statement

The data that support the findings of this study are openly available in NCBI at <https://www.ncbi.nlm.nih.gov/nuccore/MT230556>, accession number MT230556.

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