

The complete chloroplast genome sequence of *Rhus chinensis* Mill (Anacardiaceae)

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ABSTRACT

In this study, complete chloroplast genome sequences of *Rhus chinensis* was characterized by *de novo* assembly using whole genome sequence data. The chloroplast genome of *R. chinensis* were 149,011bp long, which was comprised of a large single copy region of 96,882bp, a small single copy region of 18,647bp, and a pair of inverted repeats of 16,741bp. The genome contained 77 protein-coding genes, four rRNA genes and 30 tRNA genes. Phylogenetic tree revealed that *R. chinensis* was closely grouped with *Spondias* species, *S. tuberosa* and *S. bahiensis*, belonging to the Anacardiaceae family.

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The *Rhus* genus in the Anacardiaceae family consists of 250 species that are mainly distributed in temperate and tropical regions (Rayne & Mazza 2007). *Rhus chinensis* has been used as a traditional medicine in Asia for treatment of cold, fever and malaria (Rayne & Mazza 2007). In particular, extract of the galls, induced by infection with *Schlechtendalia chinensis* (Bell), is known to be effective on bacterial control since galls are rich in gallotannin (50–70%) along with phenolic compounds such as gallic acid (Djakpo & Yao 2010). Previous *R. chinensis* studies have mainly focused on its biological activities, however, there is no report regarding genome of this

plant species until now. In this study, we characterized a chloroplast genome sequence of *R. chinensis* and analyzed its phylogenetic relationship with other species. The genome information can be further applied to genetic and molecular study of this plant species.

Chloroplast genome of the *R. chinensis* was characterized based on the previous studies (Kim et al. 2015a,b). In brief, we isolated total genomic DNA from leaf tissues of *R. chinensis* which were collected from Yanggu, Gangwon Province (38°17'33.2"N, 128°08'37.1"E) in South Korea (Seoul National University voucher No. IM151120-1) and performed whole

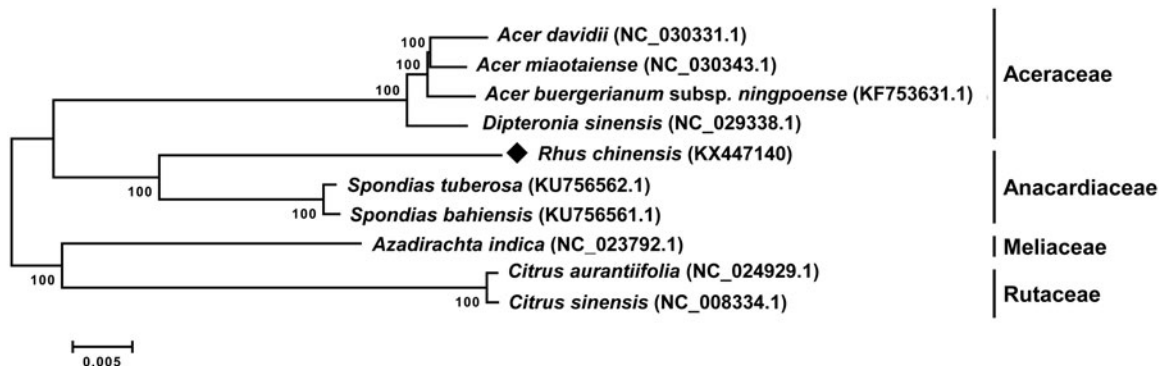




Figure 1. Phylogenetic tree showing relationship between *Rhus chinensis* and nine species belonging to the Sapindales order. The phylogenetic tree was constructed using complete chloroplast genome sequences of the ten species and analyzed neighbour-joining method with 1000 bootstrap values in MEGA 6.0. The numbers in the nodes of phylogenetic tree indicated the bootstrap support values.

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genome sequencing using an Illumina MiSeq platform (Illumina, San Diego, CA). High quality paired end reads of about 0.8Gb were assembled using CLC genome assembler 4.6 (v. beta 4.6, CLC Inc., Aarhus, Denmark). The contigs representing chloroplast sequence were retrieved, ordered and combined into a single sequence by comparing with chloroplast genome of *Azadirachta indica* (NC_023792.1).

Complete chloroplast genome of *R. chinensis* (KX447140) was 149,011 bp in length. The genome consisted of four distinct parts such as a large single copy region of 96,882 bp, a small single copy region of 18,647 bp, and a pair of inverted repeats of 16,741 bp. In the genome, 77 protein-coding genes, four rRNA genes, and 30 tRNA genes were identified through DOGMA annotation (<http://dogma.cccb.utexas.edu/>) and BLAST searches.

Complete chloroplast genome sequence of *R. chinensis* was subjected to phylogenetic analysis with nine species belonging to the Sapindales order by neighbour-joining method with 1000 bootstrap values in the MEGA 6.0 (MEGA Inc., Englewood, NJ) (Figure 1) (Tamura et al. 2013). The phylogenetic analysis revealed that *R. chinensis* was closely located with two *Spondias* species, *S. tuberosa* (KU756562.1) and *S. bahiensis* (KU756561.1), belonging to the Anacardiaceae family.

Disclosure statement

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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