

Characterization of the Complete Chloroplast Genome of *Rhus chinensis* (Anacardiaceae), An Important Medicinal and Economic Plant from China

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ABSTRACT

Rhus chinensis is a common deciduous tree in the warm temperate zone of eastern Asia, on which Chinese sumac aphids live to form gallnuts with rich tannins. Here, we assembled the complete chloroplast genome of *R. chinensis* with the shot-gun genome skimming method on an Illumina HiSeq4000 platform. The complete chloroplast genome of *R. chinensis* was 149,083 bp in length and had a standard quadripartite structure with the large (LSC, 97,271 bp) and small (SSC, 18,524 bp) single copy regions separated by a pair of inverted repeats (IRs, 16,644 bp each). We successfully annotated 126 genes, including 82 protein-coding genes, 36 tRNAs genes and eight rRNAs genes. Among these genes, 29 genes located in IR regions. The overall GC content of the complete chloroplast genome highly reaches 45.5%.

INTRODUCTION

Rhus chinensis belongs to the Family Anacardiaceae, which is a common deciduous tree that mainly distributed in the warm temperate zone of eastern Asia^[1,2]. This species is an important medicinal plant, whose stem, leaf, flower and fruit can be used in medicine^[3]. Recently, the studies on *R. chinensis* has indicated promising health benefits, such as anticancer, antiviral, antimicrobial, antidiarrheal and anti-inflammatory properties^[4-7]. More importantly, *R. chinensis* is the primary host plant of several Chinese sumac aphids, which live on this species to form galls with high tannins^[8]. The galls are economically important for traditional Chinese medicine and the tannins from the galls have been utilized in the rubber industry and improving leather quality^[9,10]. The previous studies on *R. chinensis* mainly focused on traditional medicinal uses, seed propagation, genetic diversification, genetic diversity and evolutionary history, and other photosynthetic and eco-physiological characteristics^[11-17]. However, it has never been reported about the complete chloroplast genome of *R. chinensis*. Furthermore, with the intensification of excessive deforestation, overgrazing and other anthropogenic activities, the natural resources of *R. chinensis* are declining, which makes its protective effects significantly reduced and seriously affects the sustainable development of ecological environment in the warm temperate zone of eastern Asia. Therefore, we here performed the complete chloroplast genome of *R. chinensis* with Illumina HiSeq4000 platform for the purpose of better understanding the genome structure and function and providing more significant genetic information for the germplasm protection and reasonable development of the traditional medicinal plant.

MATERIALS AND METHODS

We sampled fresh leaf blades of *Rhus chinensis* (**Figure 1**) from Wufeng county, Hubei, China (36°53'6.37"N, 101°51'45.7"E; alt. 1824 m) and preserved them in silica gel until total DNA was extracted. Meanwhile, we recorded the latitude, longitude, and altitude of its sampling locality using an Etrex GIS (Garmin, Taiwan, China). We deposited voucher specimens at the School of Life

Science, Shanxi University, Taiyuan, Shanxi, China.

We extracted total genomic DNA with the Plant Genomic DNA kit (Tiangen Biotech, Beijing, China), and obtained the complete chloroplast genome sequence of *R. chinensis* through the shot-gun genome skimming method on an Illumina HiSeq4000 platform [18]. We performed *de novo* assembly of the complete chloroplast genome sequence of *R. chinensis* in Velvet and annotated it within Geneious 11.0.3 by comparing our sequences to the complete chloroplast genome sequence of *R. chinensis* (KX447140) and other species in Anacardiaceae from GenBank [19]. We circularized a gene map of the complete chloroplast genome using the online program OrganellarGenome DRAW (OGDRAW) based on the above annotated GenBank file [20]. We submitted the complete chloroplast genome to GenBank (Accession number*).

RESULTS AND DISCUSSION

The complete chloroplast genome of *Rhus chinensis* is a typical quadripartite structure with 149,083 bp in length (Figure 1), and consists of 27.8% A, 26.7% T, 21.3% C and 24.2% G. The A + T content (54.5%) is higher than that of G + C (45.5%), which is similar to the complete chloroplast genome of the reported *R. chinensis* [21]. The genome contains two inverted repeat regions (IRA and IRB, 16,644 bp each) separated by the large (LSC, 97,271 bp) and small (SSC, 18,524 bp) single copy regions (Figure 2). We successfully annotated a total of 126 genes, which included 82 protein-coding genes (PCGs), 36 tRNAs genes and eight rRNAs genes (Figure 2).



Figure 1. *Rhus chinensis* species with fruits (A) and galls (B).

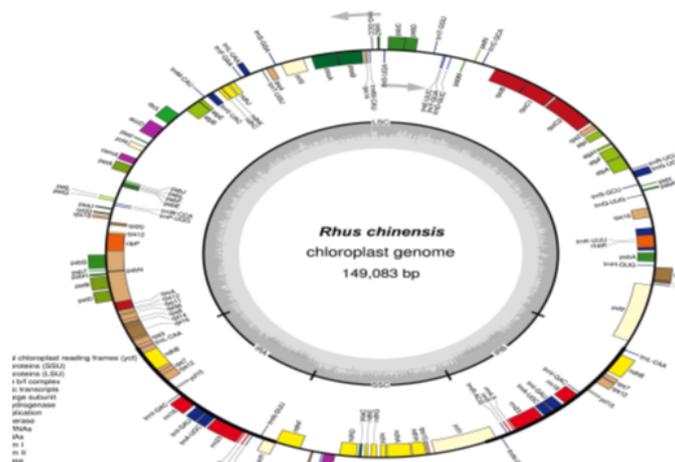


Figure 2. Gene map of the complete chloroplast genome of *Rhus chinensis*. Genes lying inside of the outer circle are transcribed in clockwise direction, whereas those outside are in counterclockwise direction. Thicker lines in the outer circle represent IR regions, which separate the chloroplast genome into LSC and SSC regions. The darker gray in the inner circle corresponds to GC content, while the lighter corresponds to AT content.

CONCLUSION

Furthermore, all other genes of the complete chloroplast genome appeared in the single copy region except that five protein-coding genes (*ndhB*, *rps7*, *rps12*, *ycf1*, *ycf15*), six tRNA genes (*trnA-UGC*, *trnI-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, *trnV-GAC*) and four rRNA genes (*rrn4.5*, *rrn5*, *rrn16*, *rrn23*) were duplicated within the IRs. Additionally, the GC content of the complete chloroplast genome, LSC, SSR and IR regions were 36.2%, 36.9%, 32.6% and 45.5%, respectively.

Such information is very crucial not only to develop and screen *Rhus* genus-specific cpDNA barcodes, but also to provide a lot of useful genetic resources for the analysis of species delimitation and speciation, characterization of population genetic structure and genetic diversity, and more effective protection of the genus.

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REFERENCES

1. Miller AJ, et al. Phylogeny and biogeography of *Rhus* (Anacardiaceae) based on ITS sequences data. *International Journal of Plant Sciences*. 2001;162:1401-1407.
2. Yi TS, et al. Phylogenetic and biogeographic diversification of *Rhus* (Anacardiaceae) in the Northern Hemisphere. *Mol Phylogenet Evol*. 2004;33:861-879.
3. Gu Q, et al. A new benzofuranone and anti-HIV constituents from the stems of *Rhus chinensis*. *Planta Med*. 2007;73:279-282.
4. Ahn YJ, et al. Growth inhibitory effects of *Galla Rhois*-derived tannins on intestinal bacteria. *J Appl Microbiol*. 1998;84:439-443.
5. Kim SH, et al. The anti-anaphylactic effect of the gall of *Rhus javanica* is mediated through inhibition of histamine release and inflammatory cytokine secretion. *Int J Immunopharmacol*. 2005;5:1820-1829.
6. Yang H, et al. Screening the active constituents of Chinese medicinal herbs as potent inhibitors of Cdc25 tyrosine phosphatase, an activator of the mitosis-inducing p34cdc2 kinase. *J Zhejiang Univ Sci*. 2005;6B:656-663.
7. Chen JC, et al. Identification of *Escherichia coli* enterotoxin inhibitors from traditional medicinal herbs by *in silico*, *in vitro*, and *in vivo* analyses. *J Ethnopharmacol*. 2009;121:372-378.
8. Zhang GX, et al. *Fauna Sinica Insecta*, vol. 14. Homoptera: Mindaridae and Pemphigidae. Beijing: Science Press. 1999.
9. Chu JP, et al. Effect of compounds of *Galla chinensis* on remineralisation of initial enamel carious lesions *in vitro*. *Int J Dent*. 2007;35:383-387.
10. Yang ZX, et al. Phylogeny of *Rhus* gall aphids (Hemiptera: Pemphigidae) based on combined molecular analysis of nuclear *EF1 α* and mitochondrial *COII* genes. *Entomological Science*. 2010;13:351-357.
11. Ouyang MA, et al. New phenol glycosides from the roots of *Rhus javanica* var. *roxburghiana*. *J Chin Chem Soc*. 2008;55:223-227.
12. Abbasi AM, et al. Medicinal plants used for the treatment of jaundice and hepatitis based on socio-economic documentation. *Afr J Biotechnol*. 2009;8:1643-1650.
13. Huang J and Qiu F. A study on propagation of *Rhus chinensis* by seeds. *Guihaia*. 1994;14:85-89.
14. Javadi F, et al. Molecular phylogeny of the subgenus *Ceratotropis* (genus *Vigna*, Leguminosae) reveals three eco-geographical groups and late Pliocene-Pleistocene diversification: Evidence from four plastid DNA region sequences. *Ann Bot*. 2011;108:367-380.
15. Zhang Y, et al. Evolutionary history of *Rhus chinensis* (Anacardiaceae) from the temperate and subtropical zones of China based on cpDNA and nuclear DNA sequences and ecological niche modeling. *Front Genet*. 2018.
16. Li Y, et al. Effects of Chinese gallnut on photosynthetic characteristics and total nitrogen content of *Rhus chinensis*. *Acta Ecologica Sinica*. 2013;33:6876-6884.
17. Bu Q, et al. Eco-physiological characteristics of the exotic plant *Rhus typhina* in comparison with its indigenous congeners

Rhus chinensis. Scientia Silvae Sinicae. 2017.

18. Zimmer EA and Wen J. Using nuclear gene data for plant phylogenetics: progress and prospects II. Next-gen approaches. J Syst Evol. 2015;53:371-379.
19. Zerbino DR and Birney E. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res. 2008;18:821-829.
20. Lohse M, et al. Organellar genome DRAW-a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. Nucleic Acids Res. 2013;41:W575-W581.
21. Lee YS, et al. The complete chloroplast genome sequence of *Rhus chinensis* Mill (Anacardiaceae). Mitochondrial DNA B Resour. 2016;1:696-697.