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, anti-diarrheal 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 gallnuts with rich tannins [8]. The gallnuts are economically important for traditional Chinese medicine and the tannins from the gallnuts 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
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 shotgun 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 outsides 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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