The complete chloroplast genome sequence and phylogenetic analysis of the medicinal plant *Rubus chingii* Hu

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**ABSTRACT**

*Rubus chingii* Hu is an important traditional Chinese medicine with a beneficial effect on the kidney. In this study, we report the complete chloroplast genome sequence of *R. chingii*. The assembled chloroplast genome was 155843 bp in length, containing two inverted repeated (IR) regions of 25372 bp each, a large single copy (LSC) region of 86456 bp and a small single copy (SSC) region of 18643 bp. The genome contained 130 genes, including 86 protein genes, eight rRNA genes, and 36 tRNA genes. The overall GC content of complete chloroplast genome was 37.1%. Phylogenetic analysis demonstrated that *R. chingii* clustered together with the monophyletic group of *R. crataegifolius* and *R. takesimensis*, suggesting a close relationship among the three species from Tribe Rubeae.

The Chinese wild raspberry *Rubus chingii* Hu is a widely distributed economic and medicinal plant belonging to the Rubus genus in the family Rosaceae (Gu et al. 1993). The fruits of *R. chingii* have been employed as a functional food as well as a traditional medicine to treat kidney enuresis and other illnesses in the clinic (He et al. 2018). The fresh leaves of this species were often used as popular beverages in China. The ethanol extract from the fruits of *R. chingii* exhibited protecting activity to the skin against UVB damage, suggesting potential applications in cosmetics (She et al. 2019). Furthermore, Rubus is one large and diverse genus containing plentiful species with similar morphologies, causing complicated arguments on the species identification and classification (Alice and Campbell 1999). Molecular identification is an efficient approach for species-level differentiation via standard DNA barcodes. Here, we report the complete chloroplast genome of *R. chingii* to provide genomic resources for molecular marker development and clarify the phylogenetic position of this plant within others in Rosaceae.

The sample of *Rubus chingii* was collected from the area of Jiulongshan National Nature Reserve in Zhejiang Province (28°41′58.49″N, 119°10′51.01″E). The specimen was deposited in the collection center of Zhejiang Chinese Medical University with the specific identifying number of JSL-1903. Total genomic DNA was extracted and sequenced using the Illumina Hiseq Platform according to the previous report (Ying et al. 2019). The chloroplast genome of *R. chingii* was assembled by metaSPAdes with the chloroplast sequence of *R. crataegifolius* as reference (Nurk et al. 2017). The chloroplast was annotated using GeSqe and further corrected by BLAST (Tillich et al. 2017). The complete cp genome of *R. chingii* was submitted to GenBank with the accession number of MN885523.

The length of the complete chloroplast genome sequence of *R. chingii* was 155843 bp, with a large single copy (LSC) region of 86456 bp, a small single copy (SSC) region of 18643 bp, and two separated inverted repeated (IR) regions of 25372 bp each. A total of 130 genes were identified in the cp of *R. chingii*, including 86 protein-coding genes, 36 tRNA genes and 8 rRNA genes. The overall GC content was 37.1%, and the corresponding contents for LSC, SSC and IR regions were 35.0%, 30.9% and 42.8%, respectively. The genome included 16 duplicated genes in the IR region and exhibited 51.5% protein-coding sequences. Moreover, a total of 57 small single repeats (SSR) are identified in the cp of *R. chingii*, ranging from 10 bp to 18 bp.

The complete genome sequences of *R. chingii* and other 17 representative species from Rosaceae family were analyzed using MEGA 7.0 by maximum-likelihood (ML) method to confirm the phylogenetic position (Kumar et al. 2016).
The result demonstrated a sister relationship between \textit{R. chingii} and the combined group forming by \textit{R. crataegifolius} and \textit{R. takesimensis}, suggesting a close relationship among the three species (Figure 1). In addition, Rubus species clustered in a clade together with high supporting scores, but did not display sister-relationship with the monophyletic group of other species in Rosaceae (Figure 1). These results suggested the unique evolutionary status of Rubus and required further revision on the taxonomy of Family Rosaceae.

**Disclosure statement**

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

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