Characterization of the complete chloroplast genome of *Rosa laevigata* var. *leiocarpus* in China and phylogenetic relationships

Zhiqian Sun\(^{a,b,c}\), Shi Shi\(^{a,b,c}\), Xingchen Pang\(^{a,b,c}\), Jingfeng Chen\(^{a,b,c}\) and Yongbin Wu\(^{a,b,c}\)

\(^{a}\)Guangdong Key Laboratory for Innovative Development and Utilization of Forest Plant Germplasm, South China Agricultural University, Guangzhou, China; \(^{b}\)South China Historical Trail Plant Resources Center of South, China Agricultural University, Guangzhou, China; \(^{c}\)South China Agricultural University, Guangzhou, China

**ABSTRACT**

*Rosa laevigata* var. *leiocarpus* has excellent edible, ornamental and medicinal value in China. In this study, we presented the complete chloroplast genome of *R. laevigata* var. *leiocarpus*. The whole chloroplast genome is 156,373 bp in size, consisting of a pair of inverted repeats (IR 26,047 bp), a large single-copy region (LSC 85,494 bp) and a small single-copy region (SSC 18,785 bp). The *R. laevigata* var. *leiocarpus* chloroplast genome encodes 139 annotated known unique genes including 92 protein-coding genes, 39 tRNA genes, and 8 rRNA genes. Phylogenetic analysis based on chloroplast genomes of 18 plant species reveals that *R. laevigata* var. *leiocarpus* was clustered and closest with *Rosa roxburghii* and also closer to other Rosa species in the evolutionary relationship.

*R. laevigata* var. *leiocarpus* is a variant of *R. laevigata* found in Boluo county, Guangdong province, China, was firstly reported by Wang and Chen in 1995 (Wang and Chen 1995) (Yingqiang W, Pangyu C). *Rosa laevigata* var. *leiocarpus* and *R. laevigata* have good edible, ornamental and medicinal value. The most significant different variation of *R. laevigata* var. *leiocarpus* is that the leaves are thinner and the fruit is smooth and spiny, andnd this particular morphological feature makes it easier to be collected and prepared (Hua et al. 2010). Therefore, we reported the complete chloroplast genome of *R. laevigata* var. *leiocarpus* and explored the phylogenetic relationship with other plant species in Rosaceae family, which would be helpful for its evolution and genetics research.

A wild individual of *R. laevigata* var. *leiocarpus* was sampled from Xia lin, Dongyuan village, Heyuan City, Guangdong province, China (N23° 97'6.65", E114° 71'1.47""). The voucher specimen was deposited in the Herbarium of South China Agricultural University (CANT) under the accession number of CDDB: LLS0006-2. A genome library was constructed using TruSeq DNA sample preparation kit (Illumina, USA) with insertion size of 300 bp and sequenced on Illumina HiSeq Nova platform (guangzhou gerui biotechnology). The output data was a 6GB raw data, 150 bp double-ended read. Clean data were obtained by quality filtering of the raw data, and then the chloroplast genome assembly of plants was carried out by the software GetOrganelle (Jin et al. 2018). The assembled cp genome was annotated with Geseq (Tillich et al. 2017) and compared manually with the complete cp genome for *R. laevigata* var. *leiocarpus* (Genbank accession number: MT150578).

The complete cp genome of *R. laevigata* var. *leiocarpus* was determined. The whole chloroplast genome is 156,373 bp in size, consisting of a pair of inverted repeats (IR 26,047 bp), a large single-copy region (LSC 85,494 bp) and a small single-copy region (SSC 18,785 bp). The *R. laevigata* var. *leiocarpus* chloroplast genome encodes 139 annotated known unique genes including 92 protein-coding genes, 39 tRNA genes, and 8 rRNA genes. This structure is identical to those of other species in Rosaceae family.

We selected other 17 plants species chloroplast genomes from GenBank to assess the relationship of *R. laevigata* var. *leiocarpus*. The phylogenetic tree was reconstructed using maximum-likelihood (ML) methods and performed using IQ-TREE (Nguyen et al., 2015), with the bootstrap value calculated using 1000 replicates to assess node support. The final tree was edited using the iTOL v4 (Ivica and Peer 2019). As shown in the phylogenetic tree result (Figure 1), the chloroplast genome of *R. laevigata* var. *leiocarpus* was clustered and closest with *R. roxburghii*, the genus *Laevigatae* was monophyletic and clustered as the sister group to *R. Sect. Banksianae*. As the data of *R. laevigata* were not released.

**CONTACT** Yongbin Wu  361661041@qq.com  Guangdong Key Laboratory for Innovative Development and Utilization of Forest Plant Germplasm, South China Agricultural University, Guangzhou, 510642, China

© 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.
online, no comparison was conducted. Further study in the future will give a better understanding of its system status. This discovery provides valuable genomic resources for the future development of medicinal plants and phylogeny of Rosaceae.

**Disclosure statement**

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

**Funding**

This work was supported by National traditional Chinese medicine resources survey of the state administration of traditional Chinese medicine, under Grant [GZY-KJS-2018-004]; Central finance forestry reform and development fund (forestry science and technology promotion demonstration subsidy) project, under Grant [(2019) GDTK-06].

**References**

Hua L, Hong P, Fen C, Hua H. 2010. Comparative study on the quality of *Rosa laevigata* var. *leiocarpus* and *Rosa laevigata* Michx. J Guangdong Pharm Coll. 26(04):345–347.

Ivica L, Peer B. 2019. Interactive Tree Of Life (iTOL) v4: recent updates and new developments. Nucleic Acids Res. 47(W1):W256-w259.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. BioRxiv. 256479.

Nguyen L-T, Schmidt H A, Von Haeseler A, Minh B Q. 2015. IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. Molecular Biology and Evolution. 32(1):268–274. doi:10.1093/molbev/msu300.

Tillich M, Lehwerk P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11.

Yingqiang W, Pangyu C. 1995. New Taxa of Guangdong Plants. Journal of Tropical and Subtropical Botany. 3(1):29–33.