Rubus rosifolius Sm. 2010 belongs to the genus Rubus in the family Rosaceae and is widely distributed globally. This species is native to the Solomon Islands, New Caledonia, Vanuatu (eastern coastal Australia), and Mauritius (southern Indonesia), Indonesia, and China (Quadros et al. 2020). R. Rosifolius produces beautiful ornamental white flowers and red fruit. R. rosifolius is used in traditional medicine to treat diarrhea and stomach diseases and has analgesic, antimicrobial, antihypertensive, and other pharmacological properties (Quadros et al. 2020). Thus, genetic and genomic information on R. rosifolius is vital for systematic research and conservation. However, the complete chloroplast (cp) genome of Rubus rosifolius remains unclear. In this study, we sequenced the complete cp genome of R. rosifolius to promote further study and conservation.

Samples of R. rosifolius were collected from the Guizhou Botanical Garden, Guiyang, Guizhou Province, China (26°37′20″N, 106°43′29″E). The College of Agriculture approved this study, which was performed under the National Wild Plant Protective Regulations. The voucher specimen (KXP20210701X) was deposited at the Laboratory of the College of Agriculture at Guizhou University, Guiyang (contact person: Xuelian Yang, email: yxl1299927812@outlook.com). Total genomic DNA was extracted from 300 mg of fresh leaves using the CTAB method. Libraries with an average length of 350 bp were constructed using a NexteraXT DNA library preparation kit. The Illumina NovaSeq 6000 platform was used to sequence these libraries and create raw sequence data. After editing using the NGS QC Tool Kit v2.3.3 (Patel and Jain 2012), we assembled the complete cp genome from 3.82 G of high-quality data using the de novo assembler SPAdes v3.11.0 (Bankevich et al. 2012). Finally, the complete cp genome was annotated using the PGA software (Qu et al. 2019).

The complete cp genome of R. rosifolius (GenBank accession no. OL435124) had a typical quadripartite structure and a size of 155,650 bp. Fifteen genes (trnK-UUU, rps16, trnG-UCC, atpF, rpoC1, trnL-UAA, trnV-UAC, petB, petD, rpl16, rpl2, ndhB, trnL-GAU, trnA-UGC, and ndhA) contained an intron, and two genes (cplP and ycf3) contained two introns. The gene rps12 showed trans-splicing. Phylogenetic analysis showed that R. rosifolius was closely related to Rubus taiwanicola, Rubus rubroangustifolius, and Rubus glandulosopunctatus.
was constructed using the RAxML var 8.2.9 software (Stamatakis 2014) and 1000 bootstrap replicates, based on the maximum likelihood method. The results showed that *R. rosifolius* is closely related to *Rubus taiwanicola* (NC_057631.1), *Rubus glandulosopunctatus* (NC_057624.1), and *Rubus rubroangustifolius* (NC_057629.1), with high bootstrap values (>90) (Figure 1).

**Author contributions**

Xue-Lian Yang and Xia Wang conceived of and designed the research. Xue-Lian Yang, Xia Wang, Wanping Zhang, and Li Yan collected the samples and performed the experiments. Xue-Lian Yang, Xia Wang, Wanping Zhang, Yong-Fei Wu, Xiang-Jing Hu, and Li Yan analyzed the data. Wanping Zhang and Xiang-Jing Hu drafted and revised the manuscript. All authors approved the final manuscript and agreed to be accountable for all aspects of this work.
Disclosure statement

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

Data availability statement

The genome sequence data supporting the findings of this study are available in the NCBI GenBank (https://www.ncbi.nlm.nih.gov/) under accession no. OL435124. The associated BioProject, SRA, and Bio-Sample numbers were PRJNA786327, SRR17183907, and SAMN23667426, respectively.

Funding

This work was supported by the National Fund under [Grant 31860225]; the Qian Kehe Foundation (2019) under [Grant 1408]; and the Qian Kehe Platform Personnel (2018) under [Grant 5781].

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