The complete chloroplast genome of *Rubus lambertianus* var. *paykouangensis*, an edible wild plant

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**ABSTRACT**

*Rubus lambertianus* Ser. var. *paykouangensis* (Levl.) Hand.-Mazz. is great important in the phylogeny and evolution of the genus *Rubus* L. in the family Rosaceae. The chloroplast genome of *R. lambertianus* var. *paykouangensis* reported in this study is 156177 bp in length, and it has an average GC content of 37.18%. The complete chloroplast genome showed a typical quadripartite structure, comprising a small single copy (SSC) region (18,730 bp) and a large single copy (LSC) region (85,883 bp), both of which were separated by a pair of inverted repeats (IRs, 25,782 bp). This plastome was discovered to contain 129 different genes (112 unique), including 85 protein-coding genes (79 unique), 36 tRNA genes (29 unique), and 8 rRNA genes (4 unique). The published chloroplast genome of *R. lambertianus* var. *paykouangensis* will provide a significant insight into elucidating the phylogenetic relationship of taxa within the genus *Rubus* of the family Rosaceae.
large single-copy (LSC) region of 85,883 bp separated by a pair of identical inverted repeat regions (IRs) of 25,782 bp each. The chloroplast genome is found to contain 129 genes (112 unique), including 85 protein-coding genes (79 unique), 36 tRNA genes (29 unique), and 8 rRNA genes (4 unique).

The ML phylogenetic tree shows that *R. lambertianus* var. *paykouangensis* is mostly related to *R. lambertianus* var. *glaber* in the genus *Rubus*, with bootstrap support values of 100% (Figure 1). All species of the other two genera (*Rosa* and *Fragaria*) from the family Rosaceae have been formed into an independent monophyly. The monophyly of three genera of the family Rosaceae was well-supported by using the complete chloroplast genome sequences. This research lays the foundation for further understanding of the chloroplast genome information of the genus *Rubus*, and sets a new insight into clarifying the phylogeny and genomics of the family Rosaceae.

**Author contributions**

Ying-an Zhu, Shaojie Yuan, and Xuehu Yang were involved in the conception and design, Shiyu Wang and Mingwei Hong...
analyzed and interpreted the data; Ying-an Zhu drafted the paper, Shaojie Yuan and Xuehu Yang revised it critically for intellectual content; all authors approved the final version to be published; and agreed to be accountable for all aspects of the work.

Disclosure statement

The authors have no potential or actual conflicts of interest to report. All authors promise that we have no any unethical behaviors for the study, the field studies were complied with local legislation, and the collections of plant materials were carried out in accordance with guidelines provided by the authors’ institution(s) and national or international regulations. If we have any unethical and illegal behaviors, we will take all responsibilities.

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Data availability statement

The complete chloroplast genome generated for this study has been deposited in GenBank under accession number MZ352082, which is openly available in GenBank through the NCBI at website (https://www.ncbi.nlm.nih.gov/). All high-throughput sequencing data files are available from the GenBank Sequence Read Archive (SRA) under accession number SRR14757447. The associated BioProject and Bio-Sample numbers are PRJNA735803 and SAMN19602745, respectively.

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