The complete chloroplast genome sequence of *Rhaponticum uniflorum*, the first of the genus *Rhaponticum*

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**ABSTRACT**

*Rhaponticum uniflorum* is commonly used as a source for traditional medicines with the main effect of clearing heat. Here, we sequenced the complete chloroplast (cp) genome of *R. uniflorum* to develop molecular markers for taxonomic classification and species determination of *R. uniflorum*. It was 152,760 bp in size and had a typical circular structure, including a pair of inverted repeats with 25,205 bp, a large single-copy region with 83,687 bp, and a small single-copy region with 18,663 bp. The genome encodes 110 unique genes, including 80 protein-coding, four rRNA and 26 tRNA genes. Phylogenomic analysis shows that *R. uniflorum* is closely related to the *Saussurea*. The study is useful for phylogenetic and population genetic studies of *Rhaponticum* plants.
Figure 1. Molecular phylogenetic tree showing the position of *Rhaponticum uniflorum* in the family Asteraceae based on the complete chloroplast genomes among 29 species. The tree was constructed using maximum likelihood (ML) algorithm. Numerical value beside each node shows the bootstrap value obtained from 1000 replications. The branch lengths are scaled with a scale bar. The GenBank accession number for the corresponding sequences is shown to the right of the Latin name.

**Ethics approval and consent to participate**

The research, including the collection of plant materials, was carried out in accordance with guidelines provided by the authors’ institutions and national or international regulations.

**Authors’ contributions**

The article was designed and conceived by Chang Liu and Chengxi Wei; it was Liqiang Wang, HuBoqin, Qiang Zhou, Mei Jiang and Guohua Gong who got involved in the analysis and interpretation of the data; HuBoqin and Qiang Zhou drafted the article; Chang Liu 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**

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

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Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession NO. MW683229. The associated BioProject, BioSample, and SRA number are PRJNA722731 and SAMN18790581, and SRR14270266 respectively.

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