The whole chloroplast genome of *Neomartinella yungshunensis* (Brassicaceae), an unusual wild plant

Weiguo Chai, Huimin Li, Xiang Chen, Jieren Qiu and Pengguo Xia

Institute of Biotechnology, Hangzhou Academy of Agricultural Sciences, Hangzhou, PR China; Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou, PR China

**ABSTRACT**

*Neomartinella yungshunensis* (W. T. Wang) Al-Shehbaz 2000 is a kind of perennial herb usually distributed in Yongshun County, Xiangxi Tujia Miao Autonomous Prefecture, Hunan Province. It was the first time to report the complete chloroplast genome sequence of *N. yungshunensis*. The complete chloroplast genome was 152,597 bp in size, including a large single-copy (LSC) region of 83,145 bp, a small single copy region (SSC) of 17,400 bp, and a pair of reverse repeats (IR) of 26,026 bp. It contained 133 genes in the chloroplast genome, including 87 protein-coding genes (PCGs), 37 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The GC content of the chloroplast genome was 36.4%. The phylogenetic analysis showed that *N. yungshunensis* is closely related to *Eutrema integrifolium* (NC_049636).

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**CONTACT**
Pengguo Xia (xpg_xpg@zstu.edu.cn) College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou 310018, PR China

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relationship among *N. yungshunensis* and other species (Figure 1). The complete chloroplast genome sequence of *N. yungshunensis* can provide necessary data for phylogenetic studies of Brassicaceae. It is hoped that this study will help resolve the intrageneric and interspecific phylogeny of Cruciferae.

**Ethical approval**

Research and collection of plant material was conducted according to the guidelines provided by Xi’an Botanical Garden. Permission was granted by Hangzhou Academy of Agricultural Sciences to carry out research on the species.

**Author contributions**

W.C., J.Q and P.X. conceived and designed this study. X. C. and H. L. conducted analysis. J.Q, P.X. and X.C. contributed the analytical methods. W.C. wrote the manuscript. P.X. edited the manuscript. All authors have read and agreed to the published version of the manuscript.

**Disclosure statement**

The authors report no conflicts of interest.

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**ORCID**

Pengguo Xia [http://orcid.org/0000-0003-3572-7616](http://orcid.org/0000-0003-3572-7616)

**Data availability statement**

The data that support the findings of this study are openly available in NCBI (https://www.ncbi.nlm.nih.gov) GenBank with the accession number (MW981639). The associated BioProject, SRA, and BioSample numbers of the funding are PRJNA723133, SRR14278903, and SAMN18805689 respectively.

**Figure 1.** A phylogenetic tree of *Neomartinella yungshunensis*, 25 related species and an outgroup was constructed based on the complete chloroplast genome using the maximum likelihood (ML) method. Numbers in each node indicated the bootstrap support values.
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