**MITOGENOME ANNOUNCEMENT**

**The complete chloroplast genome of *Wurfbainia neoaurantiaca* (Zingiberaceae: Zingiberea) from Yunnan Province, China**

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Abstract

*Wurfbainia neoaurantiaca* is a medicinal plant endemic to Yunnan Province, China. In this study, its complete chloroplast genome was assembled and characterized. The total genome size of *W. neoaurantiaca* was 158,484 bp in length, consisting of a large single-copy region (LSC), a small single-copy region (SSC) and two inverted repeat regions (IRs) with 88,605 bp, 15,285 bp and 29,822 bp, respectively. Its GC content was 36.08%. The chloroplast genome encoded 113 unique genes, including 79 protein-coding, 30 tRNA, and four rRNA genes. The result of the phylogenetic analysis indicated that *W. neoaurantiaca* was related to *W. villosa* var. *xanthioides* and supported de Boer’s classification that *W. compacta*, *W. longiligularis*, *W. neoaurantiaca*, *W. villosa*, *W. villosa* var. *xanthioides* and *Amomum krervanh* belonged to the *Wurfbainia* Clade.

The complete chloroplast genome of *Wurfbainia neoaurantiaca* was collected from Jinghong (100°52′44″E; 21°48′56″N), Yunnan Province, China. Voucher specimen (Y20180726015) and its DNA (DNA-Y20180726015) were deposited in the Herbaria and Medicinal Plant Cultivation Research Center of Yunnan Branch Institute of Medicinal Plant Development, Chinese Academy of Medical Sciences and Peking Union Medical College.

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coding sequences. Except for trnL-CAA encoded by UUG and termination codon UAA, 28 amino acid codons with RSCU value >1 ended with A/U. Simple sequence repeats (SSRs) were mined using MISA-web (https://web-blast.ipk-gatersleben.de/misa/), and up to 153 SSRs were detected in the whole chloroplast genome, including 94 mono-, 32 di-, five tri-, 16 tetra-, four penta-, and two hexa-nucleotide SSRs.

The chloroplast genome sequences of 23 species (including W. neoaurantiaca) from Zingiberaceae and three outgroup taxa from the Musaceae were aligned with MAFFT 7.307 (Katoh and Standley 2013). A phylogenetic tree was constructed using RAxML 8.2.12 (Stamatakis 2014) with 1000 Bootstrap replicates and using the GTR+F+R2 model according to ModelFinder (Kalyaanamoorthy et al. 2017). The result indicated that the selected species from the Zingiberaceae were clustered within a lineage distinct from the outgroup. Five Wurfbainia species and Amomum krvvanh formed a monophyletic clade in the Zingiberaceae. Wurfbainia neaurantiaca was fully resolved in a clade with W. longiligularis, W. villosa var. xanthioides, W. villosa and more closely related to W. villosa var. xanthioides (Figure 1). According to the recircumscription of the genus Amomum, W. compacta, W. longiligularis, W. neaurantiaca, W. villosa, W. villosa var. xanthioides and Amomum krvvanh were classified into the Wurfbainia Clade (de Boer et al. 2018). Our results confirm the classification and further illustrate the relationship among W. neaurantiaca and the other five species.

Disclosure statement

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

Data availability

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. MW145134. The associated BioProject, BioSample and SRA numbers are PRJNA699991, SAMN17817191 and SRP304958, respectively.

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