

The complete chloroplast genome of ‘Yulinglong’ (*Narcissus tazetta* var. *chinensis*) with double-petaled in southeast of China

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ABSTRACT

In this study, the complete chloroplast (cp) genome of *Narcissus tazetta* var. *chinensis* cv ‘Yulinglong’ was sequenced and assembled by next-generation sequencing. The complete cp genome is 159,376 in length and contained 137 genes, consisting of 91 protein-coding genes, eight ribosomal RNA genes, and 38 transfer RNA genes. Phylogenetic analyses based on chloroplast genomes highly supported that ‘Yulinglong’ was evolutionarily close to *Narcissus tazetta* subsp. *chinensis*, which may provide more desirable information for the phylogenetic relationship between *Narcissus tazetta* var. *chinensis* and its relative species.

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Narcissus tazetta var. *chinensis* is the only variant of *Narcissus L.*, belonging to the Amaryllidaceae (Chen et al. 2013). The genus originated from Late Oligocene to early Miocene, about 29.3–18.1 Ma (Santos-Gally et al. 2012). Chinese narcissus (*Narcissus tazetta* var. *chinensis*) is one of the ten traditional flowers in China and has high ornamental and economic values (Morikawa et al. 2016). It is widely distributed Fujian, Zhejiang and other southeast coastal areas in China. At present, there is the major cultivated species of Chinese narcissus called ‘Jinzhangyintai’ with six petal-like tepals surmounted by a cup-shaped corona. Recently, a variant of Chinese Narcissus named ‘Yulinglong’ with double-petaled appeared in Fujian Province of China (Ren et al. 2017). Cytogenetics, hybridization (Marques et al. 2017), and the evolution of polymorphic sexual systems (Zonneveld 2008) of *Narcissus tazetta* were widely studied. But, a detailed phylogenetic framework is still lacking. Here, the complete chloroplast (cp) genome of ‘Yulinglong’ was assembled, and it could facilitate to the study of the phylogeny, and breeding of *Narcissus tazetta*.

The plant material of fresh leaves tissue were obtained from Caiban Village, Jiuhu Town, Zhangzhou (Fujian, China, 117°59′56″E, 24°48′40″N), and were stored in Fujian Agriculture and Forestry University (No. FAFUYSJ01). Total genomic DNA was extracted using the optimized CTAB method (Li et al. 2013) and used to construct to build an Illumina pair-end library. The library was performed on an

Illumina Hiseq 2000 platform (Illumina, San Diego, CA, USA) at Beijing Genomics Institute (BGI, Shenzhen, China) and generating approximately 3.4 G of raw data. Illumina sequencing data was filtered using the FastQC program (Andrews 2014). High-quality clean reads of around 2.6 G were applied for genome assembly by using SPAdes v 3.9.0 (<http://bioinf.spbau.ru/spades>) (Bankevich et al. 2012) and the cp genome annotation was used with the online program GeSeq (Tillich et al. 2017). The genome sequence of ‘Yulinglong’ has been deposited in GenBank with accession number MW322827.

The complete circular cp genome of ‘Yulinglong’ is 159,376 bp in length, with overall GC content of 37.6%, which comprises a large single-copy region of 85,941 bp, a small single-copy region of 16,451 bp, and a pair of inverted repeat regions of 28,492 bp. A total of 137 genes were predicted, including 91 protein-coding genes, 38 transfer RNA genes (tRNA), and 8 ribosomal RNA genes (rRNA). Among all unique genes, 15 genes tRNA (*trnK-UUU*, *rps16*, *trnG-UCC*, *atpF*, *rpoC1*, *trnL-UAA*, *trnV-UAC*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *trnI-GAU*, *trnA-UGC*, *ndhA*) contained one intron, whereas two genes (*clpP*, *ycf3*) contained two introns. The maximum likelihood (ML) analysis was performed using RaxML software v 8.2.9, of which the bootstrap values were calculated using 1000 replicates under the GTRGAMMAI substitution model in CIPRES (Stamatakis 2014). The complete chloroplast sequence of 26 species was illustrated as the phylogenetic dendrogram (Figure 1). The result showed that ‘Yulinglong’ is clustered with

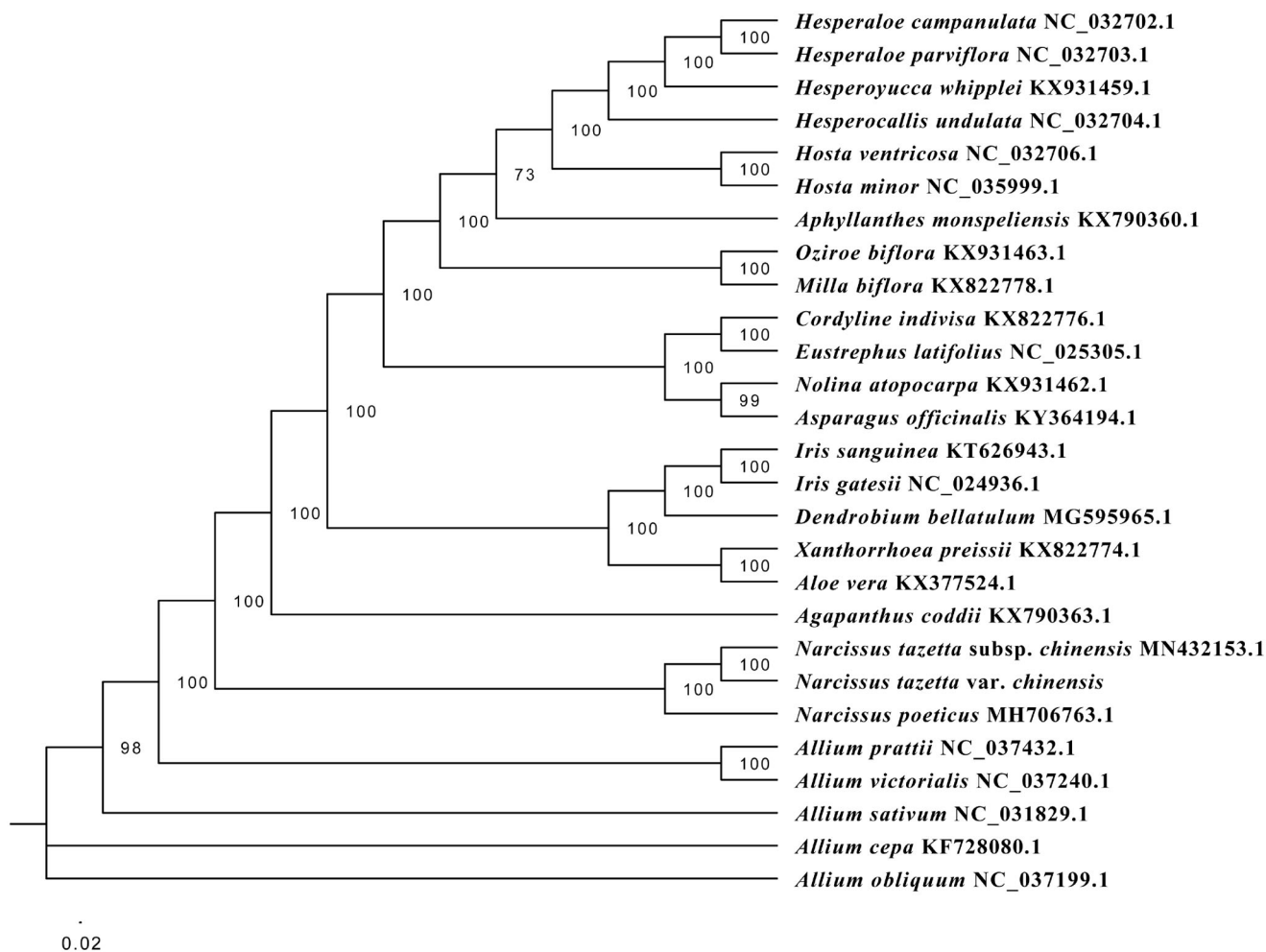


Figure 1. The maximum likelihood (ML) phylogenetic tree was constructed based on the complete chloroplast genomes of 26 species. All sequence data were downloaded from GenBank.

Narcissus tazetta subsp. *Chinensis*, which supplies available reference for *Narcissus tazetta* subsp. *Chinensis* hybridizing.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, reference number MW322827.

The 'Yulinglong' (*Narcissus tazetta* var. *chinensis*) raw data can be found on the website (<https://dataview.ncbi.nlm.nih.gov/object/SRR14141432>).

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