

## Complete chloroplast genome sequence of a Chinese traditional cultivar in *Chrysanthemum*, *Chrysanthemum morifolium* ‘Anhuishiliuye’

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### ABSTRACT

The complete plastid genome of *Chrysanthemum morifolium* ‘Anhuishiliuye’, a Chinese traditional cultivar, was determined and analyzed in this work. It had a circular-mapping molecular with the length of 151,059 bp. The LSC and SSC of 82,857 bp and 18,294 bp were separated by two IRs of 24,954 bp. The chloroplast genome of *C. morifolium* ‘Anhuishiliuye’ contains 125 genes, including 83 protein-coding genes, 34 ribosomal RNA genes and 8 transfer RNA genes. Phylogenetic analysis showed that *C. morifolium* ‘Anhuishiliuye’ clustered together with other *Chrysanthemum* species. The data provided would be useful for elucidation of phylogenetics and evolution in *Chrysanthemum* cultivars.

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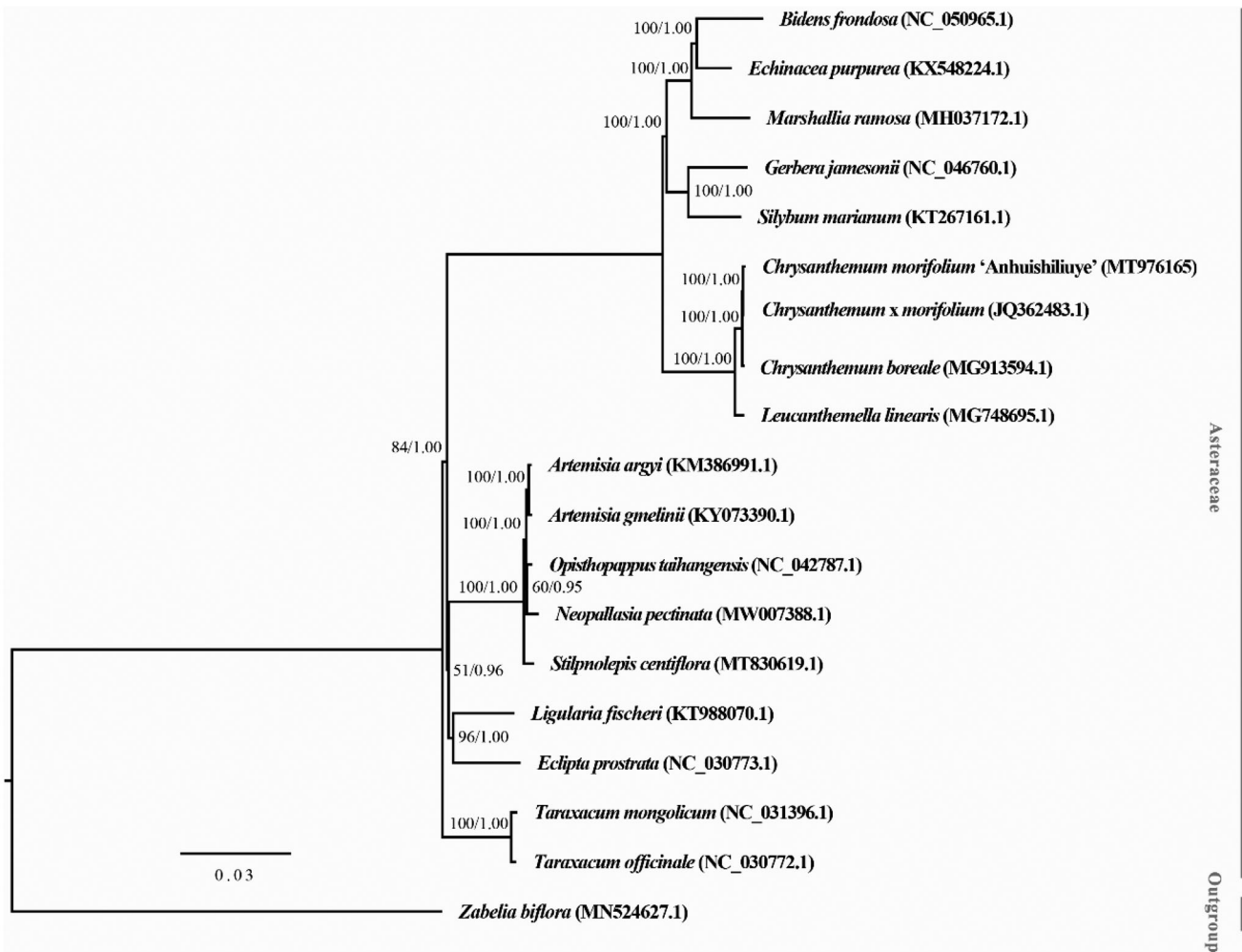
*Chrysanthemum* (*Chrysanthemum morifolium*), in family Asteraceae, is one of the most popular and economically important floricultural crops all over the world, noted for ornamental, edible, tea and medicinal uses. It has approximately 1600 years of cultivation history, which was first cultivated in China and then successively introduced to Japan, Europe, and North American. So that cultivated chrysanthemums are highly heterozygous, whose genetic background are very complicated and coming from multiple species (Su et al. 2019). Understanding the plant chloroplast genetics is essential for identification of commercial cultivars and the determination of their purity. In this study, we reported and characterized the chloroplast genomes of a Chinese ancient cultivar, *Chrysanthemum morifolium* ‘Anhuishiliuye’, which is a big flower (disbud) potted variety. It is short daylight plant and the flowering period is from mid-November to early December in southern China. It is radial inflorescence, with tubular petals and light pink double flower.

By the cp genomic data, we reconstruct the phylogenetic tree of Asteraceae family to reveal the relationship and provide useful information for further study of *Chrysanthemum* cultivars. Fresh leaves of *C. morifolium* ‘Anhuishiliuye’ were collected from the mature plant in the green house of Zhongkai university of agriculture and engineering (22°40′18.69″N, 113°15′5.37″E) and stored in South China Botanical Garden, CAS. After DNA extraction, a library with the insertion size of 350 bp was constructed, and high-throughput DNA sequencing (pair-end 150 bp) was performed on an Illumina X10 platform. In total, 10 G raw reads

were obtained for de novo assembly of cp genome in NOVOPlasty (Dierckxsens et al. 2017), and then annotated in Plann (Huang and Cronk 2015) and GeSeq using the default parameters. The complete genome sequence *C. morifolium* ‘Anhuishiliuye’ together with gene annotations were submitted to NCBI GenBank under the accession number MT976165.

The whole cp genome of *C. morifolium* ‘Anhuishiliuye’ was 151,060 bp in length, with two short inverted repeat (IRa and IRb) regions of 24,954 bp, a large single-copy (LSC) region of 82,858 bp, and a small single-copy (SSC) region of 18,294 bp. The overall GC content of cp genome is 37.45%. The cp genome of *C. morifolium* ‘Anhuishiliuye’ contained 125 genes, including 83 protein-coding genes, 34 rRNA genes, and 8 tRNA genes. Most of these genes did not contain intron, 16 genes contained one intron, and two genes (clpP and ycf3) contained two introns. All genes occurred as a single copy, except that 16 genes were duplicated in IR regions.

A phylogenetic analysis was carried out using cp genome sequences of *C. morifolium* ‘Anhuishiliuye’ and other 17 species within family Asteraceae and *Zebelia biflora* as outgroup (Figure 1). The sequences were aligned using MAFFT 7 (Katoh and Standley 2013). A maximum likelihood tree was constructed using RAxML 8.2.12 (Stamatakis 2014), and a Bayesian inference tree was constructed with MrBayes 3.2.7 (Ronquist et al. 2012). Phylogenetic analysis revealed that *C. morifolium* ‘Anhuishiliuye’ was grouped with species of genus *Chrysanthemum*, in consistent with the previous study in *Chrysanthemum* (Tyagi et al. 2019). In conclusion, this complete cp genome would establish a solid foundation for



**Figure 1.** Phylogeny of *Chrysanthemum morifolium* 'Anhuishiliuye', other Asteraceae species and *Zebelia biflora*. Phylogenetic tree was based on complete chloroplast genome with Maximum-likelihood (ML) and Bayesian (BI). Numbers above the branches are ML bootstrap/BI posterior probability.

future genetic studies in *C. morifolium* and its relative species.

### 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 available in NCBI at <https://www.ncbi.nlm.nih.gov/>, reference number [MT976165]. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA682858 SRR13205719 and SAMN17012931, respectively.

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