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Plastome Announcement




# The complete plastome sequence of *Monstera deliciosa* (Araceae), an ornamental foliage plant

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## Abstract

In the current study, we sequenced the complete plastome of *Monstera deliciosa* Liebm. (1849), an attractive foliage plant. The total length of the plastome of *M. deliciosa* is 163,499 bp and it consists of three distinct regions: a large single-copy (90,092 bp), a small single-copy (21,737 bp), and a pair of inverted repeats (IRs, 25,835 bp). The overall GC content is 36.2%, and the genome contains 110 functional genes, excluding pseudogenes. These functional genes encompass 77 protein-coding genes, 29 transfer RNA genes, and four ribosomal RNA genes. Notably, both the *infA* and *rpl23* genes have been identified as pseudogenes. Phylogenetic analysis based on 14 representative plastomes from seven subfamilies indicates that Monsteroideae is monophyletic and sister to Pothoideae. Furthermore, *M. deliciosa* and *M. adansonii* were shown to share a recent common ancestor, the finding for which is supported by a strong bootstrap value. The sequenced plastome of *M. deliciosa* can serve as a valuable resource for establishing phylogenetic relationships and enhancing species identification within the genus *Monstera*. In addition, it

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**Q Keywords:** [Plastome](#) [Monstera deliciosa](#) [ornamental plant](#) [pseudogene](#)

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## Introduction

The genus *Monstera* Adans. (Araceae) is classified under the subfamily Monsteroideae and tribe Monstereae (Cabrera et al. [2008](#)). Comprising over 60 species, the *Monstera* species is native to tropical America and grows in the regions between Mexico and Southern Brazil (Mayo et al. [1998](#); World Plants [2023](#), [www.worldplants.de](http://www.worldplants.de)). New species of *Monstera* are continuously being reported, as evidenced by studies from Zuluaga and Cameron ([2018](#)), Cedeño-Fonseca et al. ([2020](#)), and Cedeño-Fonseca et al. ([2021](#)). Despite ongoing research, the taxonomy and phylogeny of this genus remain relatively understudied. This is primarily due to the wide infraspecific variation observed within the genus, which presents challenges in species identification using traditionally diagnostic morphological features (Madison [1977](#)). Consequently, further investigation and the development of alternative approaches to address these challenges are needed. One promising approach is the use of plastome sequences, which provides genetic insights for species delimitation and the determination of phylogenetic relationships within *Monstera*.

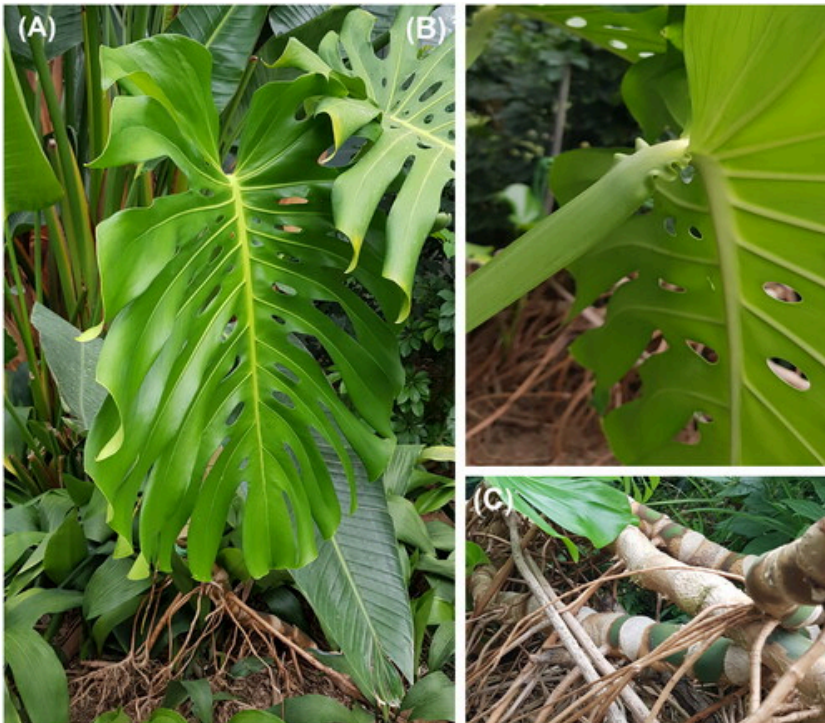
*Monstera deliciosa* Liebm. (1849), which originated in Central America between Mexico and Guatemala, has gained popularity as an ornamental foliage plant and has been introduced to many countries, including South Korea, Japan, and China for the same purpose (Lee and Kim [1980](#); Long et al. [2017](#); Sakamoto et al. [2022](#)). Recently, there has been growing interest in the chimeric forms of *M. deliciosa*, characterized by the presence of both green and albino tissues (Li et al. [2021](#)). This intriguing phenomenon has sparked increased attention and research in horticultural genetic research (Park et al. [2023](#)). Despite the significance of *M. deliciosa* in horticulture, there has been a lack of research utilizing the whole plastome of *M. deliciosa* as a molecular genetic resource. Therefore, the objective of this paper is to bridge this gap by providing the complete plastome sequence of *M. deliciosa*, which allows for further investigations into the genetic traits of this plant.

## Materials and methods

*Monstera deliciosa* was obtained from the Gangwon Provincial Arboretum, South Korea (37°55'22.0"N, 127°43'32.0"E, voucher number PCGE-KHR2023001, [Figure 1](#)) and grown in a growth room at Kangwon National University until needed for analysis (contact to Hyeran Kim, [ranny@kangwon.ac.kr](mailto:ranny@kangwon.ac.kr)). Genomic DNA was extracted from 100 mg of fresh leaf using the Exgene Plant SV mini kit (GenAll Biotechnology, Seoul,

using a spectrophotometer, while the integrity was confirmed through electrophoresis using a 1% agarose gel.

Figure 1. *Monstera deliciosa* Liebm. (A) Leaves with natural holes; (B) wrinkled geniculum at the petiole; (C) roots with aerial adventitious roots. All photos were taken by Yun at the Gangwon Provincial Arboretum, South Korea.



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Sequencing was performed on the Illumina NovaSeq 6000 platform (Macrogen, Seoul, South Korea). Following this, *de novo* assembly of the plastome was conducted with NOVOplasty ver. 4.3 (Dierckxsens et al. [2017](#)), using a 39 k-mer length as well as a fragment of the *rbcl* gene from *Monstera adansonii* as the seed sequence. The coverage depth of completely sequenced *M. deliciosa* was determined by performing read mapping ([Figure S1](#)). The plastome genes to be annotated were identified using CPGAVAS2 (Shi et al. [2019](#)) and tRNAscan-SE 2.0 software with the default settings (Schattner et al. [2005](#)). The annotation of protein-coding regions was further validated by searching for homologous genes using the NCBI Conserved Domain Database (CDD) (Marchler-Bauer et al. [2011](#)). The circular plastome map of *M. deliciosa* was generated using the OGDRAW ver. 1.3.1 program (Greiner et al. [2019](#)).

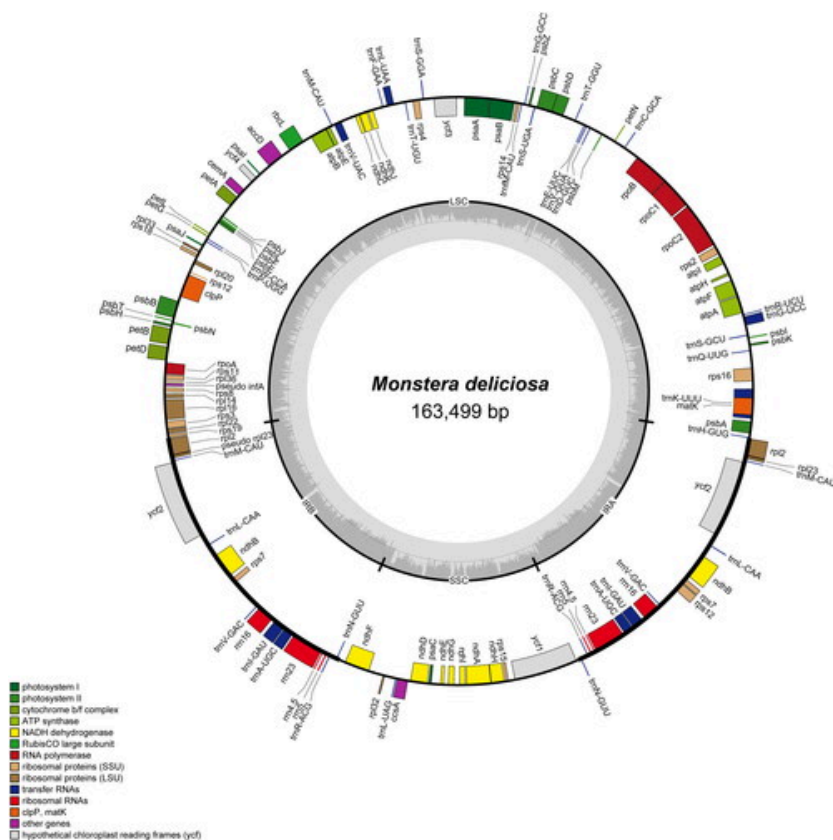
For phylogenetic analysis, 14 species were included, representing seven subfamilies within the Araceae family. However, the subfamily Gymnostachydoideae was excluded from the analysis due to the unavailability of plastome data. Additionally, *Alisma plantago-aquatica* from the Alismataceae family was used as an outgroup. The alignment of whole plastome sequences was carried out using MAFFT ver. 7

(Castresana [2000](#)). Lastly, the phylogenetic tree was constructed using the maximum-likelihood method implemented in IQ-TREE v.1.6.7 (Nguyen et al. [2015](#)), with 1000 bootstrap replicates. The plastome sequence of *M. deliciosa* was deposited in GenBank under the accession number OR260879.

## Results

The plastome of *M. deliciosa* is 163,499 bp in size and exhibits a circular quadripartite structure consisting of a large single-copy (LSC, 90,092 bp), a small single-copy (SSC, 21,737 bp), and a pair of inverted repeat regions (IRs, each 25,835 bp) ([Figure 2](#)). The overall GC content is 36.2%, with variation observed among the different regions: 34.6% in the LSC region, 28.9% in the SSC region, and 42.0% in the IR region.

Figure 2. The plastome map of *Monstera deliciosa*. Genes positioned outside the circle are transcribed in a counterclockwise direction, while genes within the inner circle are transcribed clockwise. The GC content is depicted by the dark grey inner circle.



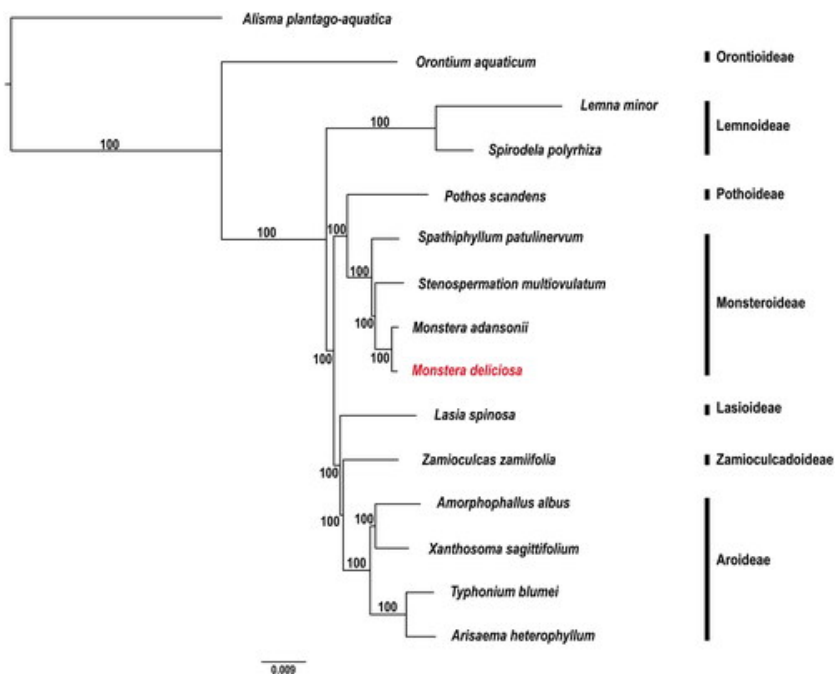
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It was found that *M. deliciosa* has a total of 110 functional genes, excluding pseudogenes. These genes include 77 protein-coding genes, 29 tRNA genes, and four rRNA genes. Among these, 12 protein-coding genes and six tRNA genes possess multiple exons ([Figure S2](#)). Notably, the *infA* gene in the LSC region as

are nonfunctional. The loss of the *infA* gene has been observed in all subfamilies other than basal group Orontioideae.

As evidenced by the phylogenetic tree, Monsteroideae forms a monophyletic group and presents as the sister clade to Pothoideae (Figure 3). Furthermore, within the Monsteroideae clade, it can be noted that *M. deliciosa* and *M. adansonii* share a recent common ancestor. All relationships among species in the tree are strongly supported by high bootstrap values (BS = 100).

Figure 3. Phylogenetic tree generated using the maximum-likelihood method implemented in IQ-TREE v.1.6.7, based on complete plastome sequences. The species sequenced in this study is indicated in red and the accession numbers of species used for phylogenetic analysis are as follows: *Alisma plantago-aquatica* (MK090659), *Orontium aquaticum* (MT226773), *Lemna minor* (DQ400350), *Spirodela polyrhiza* (MN419335), *Pothos scandens* (MN046891), *Spathiphyllum patulinervum* (MN477425), *Stenospermation multiovulatum* (MN046893), *Monstera adansonii* (MN046888), *Monstera deliciosa* (OR260879), *Lasia spinosa* (MT226772), *Zamioculcas zamiifolia* (MT226775), *Amorphophallus albus* (OP531918), *Xanthosoma sagittifolium* (MW628970), *Typhonium blumei* (MT872311), and *Arisaema heterophyllum* (ON060885).



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## Discussion and conclusions

This study reports the first complete plastome sequence of *M. deliciosa*. It was found that *M. deliciosa* displays the conserved quadripartite structure that has been observed in previous reports on plastome

demonstrated a high level of similarity in terms of gene composition, gene order, and the number of genes (Henriquez et al. [2020a](#)). However, in line with previous studies on Monsteroideae (Henriquez et al. [2020a](#), [2020b](#)), a nonfunctional *infA* gene was identified as characterized by the presence of an internal stop codon in the LSC region. The loss of the *infA* gene, observed in all subfamilies other than Orontioideae, serves as a synapomorphy for the clade consisting of six subfamilies: Lemnoideae to Aroideae. Conversely, the *rpl23* gene in *M. deliciosa* was also shown to exhibit one internal stop codon, which consequently distinguishes it from other Monsteroideae species. Our phylogenetic tree is consistent with a previous study conducted by Henriquez et al. ([2014](#)), providing further support for the monophyly of Monsteroideae and its sister relationship with Pothoideae.

Given the advantages of uniparental inheritance and the highly conserved nature of plastomes, which still provide sufficient information to capture evolutionary events (Raubeson and Jansen [2005](#)), the complete plastome sequence of *M. deliciosa* will prove to be of considerable value in various research areas. For example, it can serve as a resource for the establishment of phylogenetic relationships within the Monsteroideae subfamily and facilitate elucidation of its evolutionary history. In addition, the plastome sequence can aid in the development of molecular markers capable of distinguishing between different *Monstera* species. In turn, these markers can contribute to more accurate species identification and subsequent classification. Ultimately, the plastome of *M. deliciosa* can facilitate investigations into its own horticultural value and genetic characteristics.

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## Author contributions

H.K. conceived this study and collected the sample. H.K. and S.Y. performed the experiments. S.Y. analyzed the data and wrote the manuscript. H.K. and S.Y. revised the manuscript.

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## Supplemental material

## The complete plastome sequence of *Monstera deliciosa* (Araceae), an ornamental foliage plant

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### The complete plastome sequence of *Monstera deliciosa* (Araceae), an ornamental foliage plant

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## Acknowledgements

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## Disclosure statement

The authors declare that there is no conflict of interest regarding the publication of this article.

## Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank on the

BioProject, SRA, and Bio-Sample numbers are PRJNA992674, SRR25232409, and SAMN36379614, respectively.

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## Additional information

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