

# The Partial Chloroplast Genome of *Hypericum monogynum* L. (Guttiferae)

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## Abstract

*Hypericum monogynum* L. is an important medicinal and ornamental plant which belongs to the genus *Hypericum* in the Guttiferae family. The partial chloroplast genome sequence of *H. monogynum* has been presented in this study. The assembled partial chloroplast genome (cpDNA) was 120,005 bp in size, with an overall 36.96% GC content. It is 70 genes that are included in the chloroplast genome of *Hypericum monogynum* in this study, which are consisted of 33 protein-coding genes, 30 transfer RNA genes, as well as 7 ribosomal RNA genes. Phylogenetic analysis with the reported chloroplast genomes revealed that *Hypericum monogynum* is separated to other species in Guttiferae family, and it might well function as an external group of Guttiferae family.

## Keywords

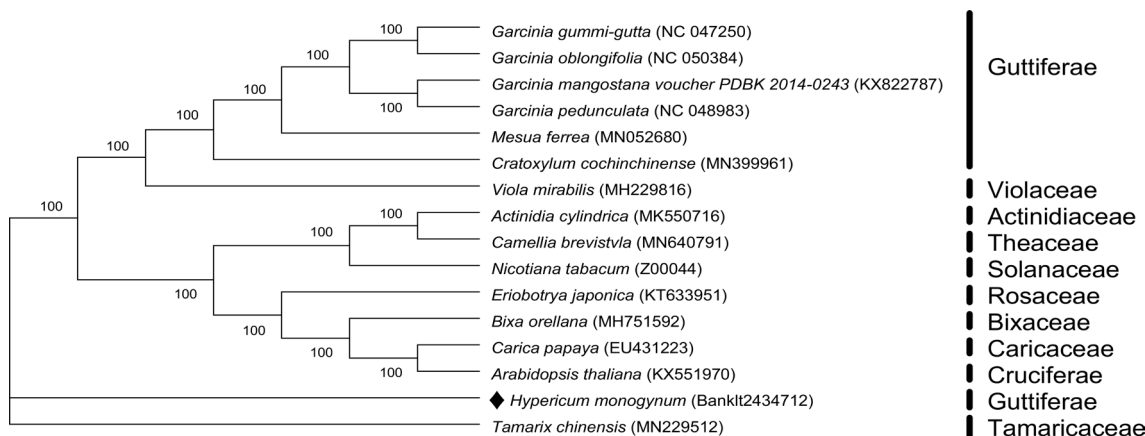
Genus *Hypericum*, Phylogenetic Analysis, Genome Sequencing

*Hypericum monogynum* L. is a representative species belonging to the genus *Hypericum* that includes 500 species approximately [1] [2]. Widely distributed in the tropical and subtropical areas of China, *H. monogynum* has gained a highly reputation for its neuroprotective [3] and anti-oxidant [2] effects, besides it has been applied to treat mild-to-moderate depressions in European countries [4]. Not only does *H. monogynum* play a vital role in modern medical health cause but also it has obvious ornamental values as a shrub. It is reported that extracts and isolated compounds from various genus *Hypericum* exhibit extensive bioactivities in modern pharmacology, such as anti-oxidation, anti-bacteria and

anti-virus [5] [6]. Based on these, there is no denying that replenishing information about genomes of species in the Hypericum family is urgent, which can help protect and make most of the resources. Although a few studies related to transcriptome sequencing and small RNA sequencing of *H. monogynum* has been reported [7], the chloroplast genome sequence of it has not been available till now, even no any chloroplast genome of the genus Hypericum. Here, we perform the partial chloroplast genome sequence of *H. monogynum* to provide a genomic resource and to clarify the phylogenetic relationship of this plant with other species in the Guttiferae family and other common plants.

Total genomic DNA was extracted from the fresh and healthy leaves of a single individual of *H. monogynum*, which was sampled from Anhui University of Traditional Chinese Medicine Anhui, China. DNA was obtained by CTAB method, then operated by Genewiz Biotechnology Co. Ltd. (Suzhou, China). DNA libraries with different indices were multiplexed and loaded on an Illumina HiSeq instrument according to manufacturer's instructions (Illumina, San Diego, CA, USA). Sequencing was carried out using a 2 × 150 paired-end configuration, image analysis and base calling were conducted by the HiSeq control software (HCS) + OLB + GAPipeline-1.6 (Illumina) on the HiSeq instrument. The reads with controlled quality assembled using Velvet (version 1.2.10) [8], and gaps filled with SSPACE (version 3.0) [9] and GapFiller (version 1-10) [10]. Based on the clean data, the coding gene, tRNA, rRNA and other ncRNAs were predicted by software Prodigal (version 2.6.3) [11], and then Rfam database (version 12.0) [12] was used to align genome sequence to Rfam library. The chloroplast genome of *H. monogynum* was assembled *de novo*.

The partial chloroplast genome of *H. monogynum* was obtained which has a total length of 120,005 bp in this study. The overall GC content is 36.96%. There are 70 protein coding genes, 33 tRNA genes, and 7 rRNA genes typical for the chloroplast genome of *H. monogynum*. By phylogenetic analysis with 15 complete chloroplast genomes of related plants, though *H. monogynum* is a representative



Note: Numbers on the nodes are bootstrap values from 1000 replicates.

**Figure 1.** Phylogenetic tree of *H. monogynum* with 15 previously reported species was constructed by partial chloroplast genome sequences.

species belonging to the Guttiferae family. However, according to **Figure 1**, it does not group with any other species in the Guttiferae family analyzed, it could well function as an external group.

### 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 BankIt2434712.

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### Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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