

## The complete chloroplast genome sequence of *Brasenia schreberi* (Cabombaceae)

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### ABSTRACT

*Brasenia schreberi* is a perennial aquatic herb. We determined the complete chloroplast genome sequence for *B. schreberi* using Illumina sequencing data. The complete chloroplast sequence is 158,993 bp, include large single-copy (LSC) region of 88,779 bp, small single-copy (SSC) region of 21,665 bp, a pair of invert repeats (IR) regions of 21,078 bp. Plastid genome contains 132 genes, 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis base on 12 chloroplast genomes indicates that *B. schreberi* is sister to *Cabomba* spp. in Cabombaceae.

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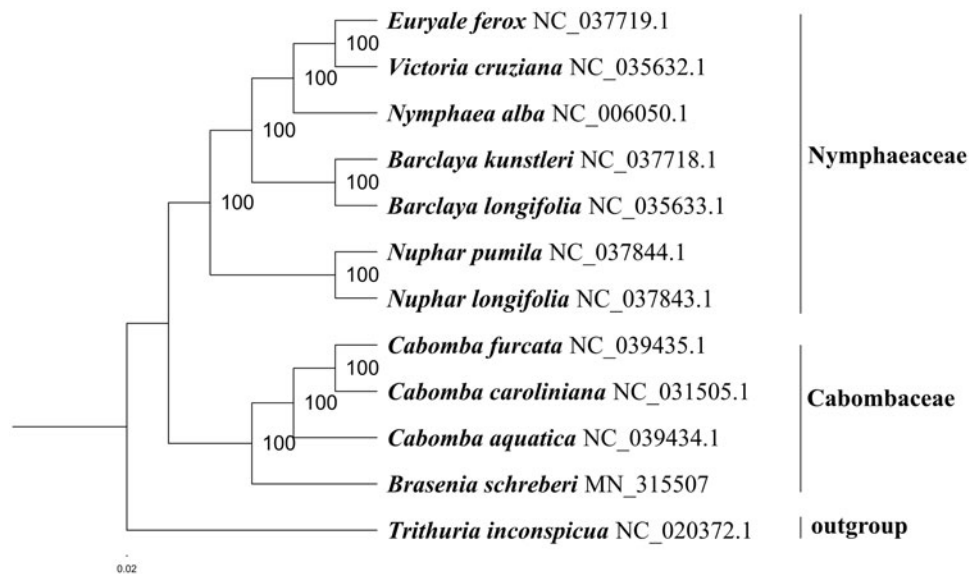
*Brasenia schreberi* belongs to Cabombaceae and is a perennial herbaceous aquatic plant widely but sporadically distributed in freshwater ponds and lakes in temperate and tropical regions of eastern Asia, Australia, Africa, West Indies, and the Americas (Raymond and Dansereau 1953; Aston 1977; Choi 2007). *Brasenia schreberi* is an important aquatic cash crop with medicinal and edible functions for health care. Its tender leaves are rich in gelatine, carbohydrates, fats, vitamins, and minerals and are considered as one of the most valuable vegetables with extremely nutritional value. The growth of *B. schreberi* requires higher environmental conditions. While in recent years, frequent interference of human activities and habitat fragmentation results in a dramatic decline in its population size, which makes it an Endangered status. In 1999, it was listed as National I level Key Protecting Endangered Wild Species in China (Yu 1999). In this study, we report the complete chloroplast genome (cp) of *B. schreberi* based on Illumina pair-end sequencing data.

The plant material of *B. schreberi* was collected from Fujian province, China (Changle, Fuzhou: 119°51'19uzhou: Fu25°96'69uzhou:Fu. The voucher specimen is kept at the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (specimen code FAFU07033).

DNA extraction from fresh leaf tissue, with 500 bp randomly interrupted by the Covaris ultrasonic breaker for library construction. The constructed library was sequenced PE150 by Illumina HiseqXtenplatform, approximately 2GB data generated. Illumina data were filtered by script in the

cluster (default parameter: -L 5, -p 0.5, -N 0.1). Complete plastid genome of *Cabomba aquatica* (GeneBank accession: NC\_039434.1) as reference, plastid genome of *B. schreberi* was assembled by GetOrganelle pipe-line (<https://github.com/Kinggerm/GetOrganelle>), it can get the plastid-like reads, and the reads were viewed and edited by Bandage (Wick et al. 2015). Assembled chloroplast genome annotation base on comparison with *C. aquatica* by Geneious v 11.1.5 (Biomatters Ltd., Auckland, New Zealand) (Kearse et al. 2012). The annotation result was drawn with the online tool OGDRAW (<http://ogdraw.mpimp-golm.mpg.de/>) (Lohse et al. 2013).

The complete plastid genome sequence of *B. schreberi* (GenBank accession: MN315507) was 158,993 bp in length, with a large single-copy (LSC) region of 88,779 bp, a small single-copy (SSC) region of 21,665 bp, and a pair of inverted repeats (IR) regions of 21,078 bp. Complete chloroplastid genome contains 132 genes, there were 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The complete genome GC content was 39%. In order to reveal the phylogenetic position of *B. schreberi* with other members of Cabombaceae, a phylogenetic analysis was performed based on 11 complete chloroplast genomes, and one taxon, *Trithuria inconspicua* as an outgroup. They all downloaded from NCBI GenBank. The sequences were aligned by MAFFT v7.307 (Katoh and Standley 2013), and phylogenetic tree constructed by RAxML (Stamatakis 2014) The phylogenetic tree showed that *B. schreberi* is sister to *Cabomba* spp. of Cabombaceae with strong support (Figure 1).



**Figure 1.** Phylogenetic analysis of 11 species and one taxa (*Trithuria inconspicua*) as an outgroup based on plastid genome sequences by RAxML, bootstrap support value near the branch.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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