

Characterization of the complete chloroplast genome of an aquatic plant, *Sparganium stoloniferum* subsp. *choui* (Typhaceae)

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ABSTRACT

Sparganium stoloniferum subsp. *choui* is an aquatic perennial herb distributed in Northeast China. It was published as a new species in 1992 and recognized as a subspecies of *S. stoloniferum* in Flora of China in 2010. The complete chloroplast genome of *S. stoloniferum* subsp. *choui* was sequenced and assembled. The genome size was 161,865 bp in length with 36.8% GC content. Its quadripartite structure consisted of the large single copy (LSC, 88,953 bp) and small single copy (SSC, 19,098 bp) regions, separated by a pair of inverted repeats (IRs) of 26,907 bp. The genome contained 114 distinct genes, including 80 protein-coding genes, 30 tRNA genes, and four rRNA genes. The phylogenetic analysis including four *Sparganium* species showed that two subspecies of *S. stoloniferum* were not monophyletic, supporting the resurrection of *S. choui* as a species.

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Sparganium L. is an aquatic perennial genus including approximately 14–19 species and occurs mainly in temperate and cool regions (Cook and Nicholls 1986, 1987; Kaul 2000; Sun and Simpson 2010). *Sparganium stoloniferum* (Buch.-Ham. ex Graebn.) Buch.-Ham. ex Juz. is a widespread species in Asia and of ecological and economic importance. The dried tuberous rhizome of *S. stoloniferum* is a widely used gynecological drug in traditional Chinese medicine (Jia et al. 2021). Two subspecies of *S. stoloniferum*, subspecies *stoloniferum* and *Sparganium stoloniferum* subsp. *choui* (D.Yu) K.Sun, were recorded in Flora of China (Sun and Simpson 2010). The latter was recognized from a new species *S. choui* published by Yu (1992), which differs from *S. stoloniferum* among panicle length, male head number, anther length, and fruit size (Yu 1992; Sun and Simpson 2010). The complete chloroplast (cp) genome of *S. stoloniferum* has been reported (Su et al. 2019). Here, we reported complete cp genome of *S. stoloniferum* subsp. *choui* and constructed phylogenetic tree to test the monophyly of two subspecies of *S. stoloniferum*.

The sample of *S. stoloniferum* subsp. *choui* was collected from Arong Banner, Inner Mongolia, China (48.13°N, 123.46°E). A specimen was deposited at the herbarium of Wuhan University (www.whu.edu.cn, Xinwei Xu, xuxw@whu.edu.cn) under the voucher number Xu568. Total genomic DNA was extracted by using the DNA Secure Plant Kit (Tiangen Biotech, Beijing, China). Library preparation and genome sequencing were conducted on the Illumina HiSeq

2500 platform (Benagen Inc., Wuhan, China). SPAdes v.3.9.0 (Nurk et al. 2017) was used to assemble the obtained paired-end reads. With the reference cp genome of *Typha latifolia* L. (Guisinger et al. 2010; NC_013823.1), the assembled sequence was annotated in GeSeq (<https://chlorobox.mpimp-golm.mpg.de/geseq.html>) (Tillich et al. 2017). The obtained complete cp genome of *S. stoloniferum* subsp. *choui* was then submitted to GenBank (accession no. MW829765).

The complete cp genome of *S. stoloniferum* subsp. *choui* is 161,865 bp in length, including a large single copy (LSC) region of 88,953 bp, a small single copy (SSC) region of 19,098 bp, and two inverted repeat (IR) regions of 26,907 bp. The GC contents of LSC, SSC, IR and whole genome are 34.8%, 30.4%, 42.4%, and 36.8%, respectively. There are 114 distinct genes annotated, including 80 protein coding genes, 30 tRNA genes, and four rRNA genes. A total of 18 genes contain introns, and three of them have two introns (*ycf3*, *clpP*, and *rps12*). Bayesian inference of phylogeny was conducted based on eight cp genomes of Typhaceae and Bromeliaceae species using MrBayes v.3.2.7a (Ronquist et al. 2012). The phylogenetic tree showed that two subspecies of *S. stoloniferum* was not monophyletic, and subspecies *stoloniferum* was most closely related to *S. eurycarpum* rather than subspecies *choui* (Figure 1), supporting the resurrection of *S. choui* as a species.

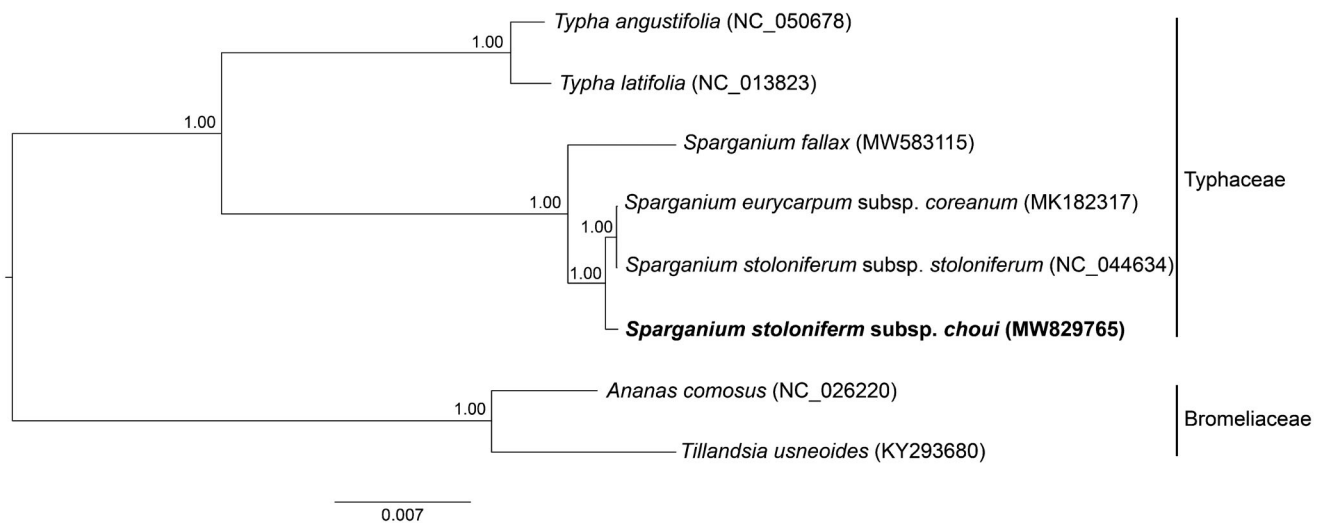


Figure 1. Phylogenetic relationships of eight Typhaceae and Bromeliaceae species based on Bayesian inference of chloroplast genomes. The position of *Sparganium stoloniferum* subsp. *choui* is highlighted in bold and numbers above each node are Bayesian posterior probabilities.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov/> under the accession no. MW829765. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA718700, SRR14126901, and SAMN1855935, respectively.

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