The first complete chloroplast genome of a mangrove fern, *Acrostichum speciosum*

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**ABSTRACT**

*Acrostichum* genus is the only mangrove fern that distribute in the intertidal zones of tropical and subtropical regions. *A. speciosum* is one rare species occurring in only few locations in Hainan and Guangdong, China. To study the evolutionary history of fern will improve our understanding of the origin of vascular plants. Here, we provide the complete chloroplast genome of *A. speciosum*, which is 156,095 bp in length with a GC content of 38.45%. A pair of identical inverted repeat regions (IRs) of 24,938 bp separate a large single copy (LSC) region of 84,476 and a small single copy (SSC) region of 21,744 bp. A total of 112 genes were annotated, including 72 protein-coding genes, 32 tRNA genes, and 8 rRNA genes. Phylogenetic analysis based on 30 ferns showed that *A. speciosum* and *Ceratopteris richardi*, both are aquatic plants, formed an original base clade in Pteridaceae. Our work reports the complete chloroplast genome of mangrove fern *A. speciosum*, which will help to improve understanding of the evolutionary history of ferns.

Mangroves contain 84 species from about 16 families, which inhabit in the intertidal ecosystems of tropical to subtropical coasts (Nabeelah et al. 2019). There exist three fern species of mangroves, *Acrostichum speciosum*, *Acrostichum aureum* and a hybrid *Acrostichum aureum* $\times$ *Acrostichum speciosum* (Yamamoto et al. 2016). To investigate the evolutionary history of fern plants will greatly improve our understanding of the origin of vascular plants. Plastid genomes display remarkable conservation in sequence and stability in gene organization, making them ideal molecules to study plant phylogeny (Daniell et al. 2016). Unlike the well-studied seed plants, chloroplast genome investigations of ferns are limited (Robison et al. 2018). To the aspect of mangrove ferns, a hybrid of mangroves, *Acrostichum speciosum, Acrostichum aureum* and *Alsophila podophylla* (Yamamoto et al. 2016). However, lack of the chloroplast genome sequence resulted in limited understanding of these mentioned data. Therefore, we reported the chloroplast genome of *A. speciosum*, which is a rare species in south China.

The plant material of *A. speciosum* was collected from the plantation of Dongzhaihang Mangrove Research Institute, Haikou, China (110°34′36.87″E, 19°57′6.77″N), and the voucher specimen is deposited in the herbarium of Hainan Normal University (specimen no. 19HNNU1223). The total genomic DNA was extracted from fresh leaves of *A. speciosum* by CTAB method (Doyle and Doyle 1987). The DNA was then randomly fragmented to 500 bp for library construction, which was sequenced PE-150 using Illumina Hiseq 2000 platform. A total of 5 Gb raw reads were obtained and assembled to generate the complete chloroplast genome using SOAPdenovo2 (Luo et al. 2012). Assembled chloroplast genome was annotated using online tool CPGAVAS (Shi et al. 2019).

The complete chloroplast genome of *A. speciosum* has a circular DNA of 156,095 bp with 38.45% of GC content (GenBank MT026711). A large single copy (LSC) of 84,476 and a small single copy (SSC) of 21,744 bp are separated by a pair of identical inverted repeat regions (IRs) of 24,938 bp each. Totally, 112 genes were annotated, including 72 protein-coding genes, 32 tRNAs, and 8 rRNAs.

A total of 30 representative ferns were selected to construct a phylogenetic tree of Pteridaceae. Maximum-likelihood (ML) approach was performed using the complete chloroplast genome sequences of *A. speciosum*, 27 Pteridaceae species and two outgroups (*Alsophila spinulosa* and *Alsophila podophylla*). All sequences were aligned using MAFFT v7.455 (Katoh and Standley 2013). RAxML software (Stamatakis 2014) was used to build the phylogenetic tree with General Time Reversible $+\Gamma$ Gamma nucleotide substitution model $+$ proportion of invariable sites (GTRGAMMAI) using 1000 bootstrap replicates. The result showed that *A. speciosum* and *Ceratopteris richardi*, both are aquatic plants,
formed an original base clade in Pteridaceae, indicating that water ferns might have chloroplast genome sequence more similar to the ancestors (Figure 1). This study provides a high-quality complete chloroplast genome of mangrove fern *A. speciosum*, which will be useful to better understanding the evolutionary history of ferns.

**Disclosure statement**

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

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