

The complete chloroplast genome of a fern genus *Thelypteris interrupta*

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ABSTRACT

In this study, we report the complete chloroplast (cp) genome of *Thelypteris interrupta*, a fern member, and comparative analysis with its related family members. The cp genome was 155,983 bp long, with a typical quadripartite structure including a pair of inverted repeat regions (25,614 bp) separated by a large (82,769 bp) and small (21,986 bp) single-copy (SC) region. The genome encodes a total of 88 protein-coding genes, 35 tRNA genes, and 8 rRNA genes. Additionally, we identified 86 RNA editing sites in 52 genes; most of the substitution was U to C (52 sites), while C to U conversion occurred in 34 positions. The phylogenetic analysis strongly supported the relationship of *T. interrupta* with *Ampelopteris prolifera* and *Christella appendiculata* of Thelypteridoideae family.

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Introduction

Thelypteris interrupta (Thelypteridaceae), commonly known as *Cyclosorus interruptus*, is a fern species broadly distributed in tropic and sub-tropic regions of all the continents (Sinclair et al. 2012). The leaves of *T. interrupta* are believed to be effective against general sickness, cough, and burns (Quadri-Spinelli et al. 2000). However, in Korea, the natural resources

of *T. interrupta* have been overexploited and included in the list of endangered species. Additionally, genomic information of the species is limited, and there is no clear authentication system to distinguish *T. interrupta* from its relatives.

Here, we report the first complete chloroplast (cp) genome sequence of *T. interrupta*. The samples of *T. interrupta* were collected from its natural habitat in Jeju Island,

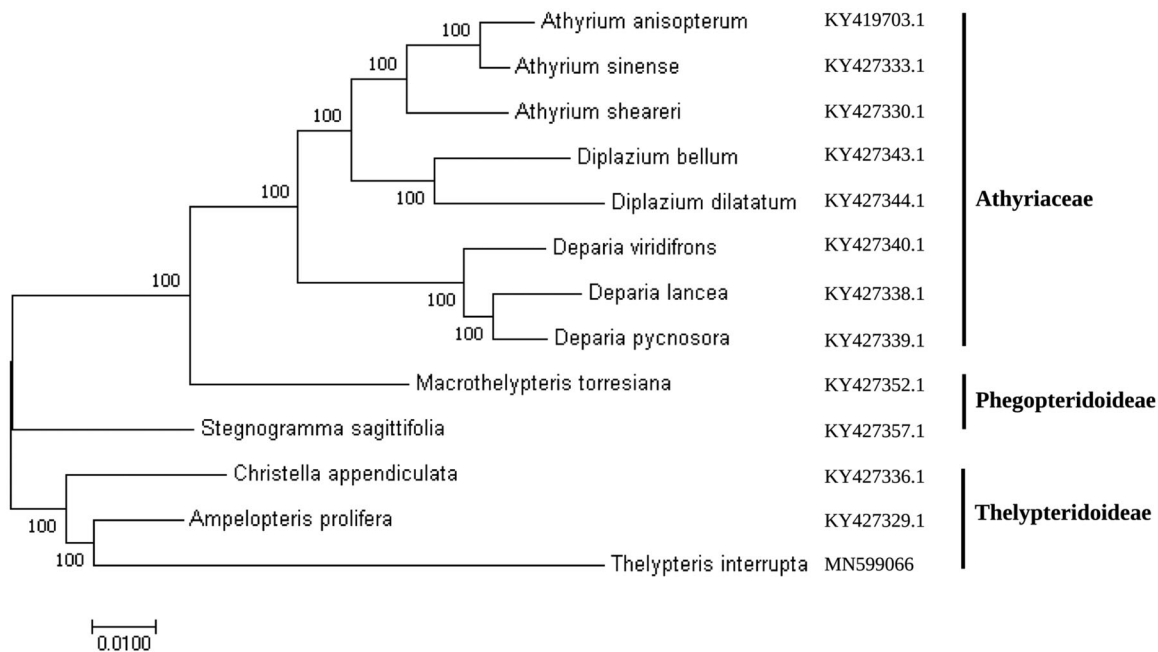





Figure 1. Molecular phylogenetic tree of the fern family Athyriaceae, Phegopteridoideae, and Thelypteridoideae based on the complete cp genome of 13 species.

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South Korea. The specimen is stored in the Herbarium of National Institute of Biological Resources, Incheon, South Korea (Voucher number: NIBRVP0000627878). Genomic DNA was extracted following the modified CTAB method (Doyle 1987). After the pair-end library was constructed, whole-genome sequencing was performed using an Illumina HiSeq 4000 platform (Illumina Inc., San Diego, CA, USA). Trimmomatic v0.32 (Bolger et al. 2014) was used to filter and trim reads and Newbler assembler, v2.9 (454 Life Sciences, Branford, CT) for assembling the high-quality reads. The initial annotation of the cp genome was conducted using the DOGMA program (Wyman et al. 2004), and tRNAscan-SE to predict protein-coding genes, transfer RNA genes, and ribosome RNA genes (Lowe and Eddy 1997). We have submitted the assembled and annotated sequence to GenBank under accession number MN599066.

To investigate the phylogenetic status of *T. interrupta* within the fern family, 12 complete cp genomes belonging to the family Athyriaceae, Phegopteridoideae, and Thelypteridoideae were selected. A neighbor-joining (NJ) tree was constructed with Mega 6.0 using 1000 bootstrap replicates (Tamura et al. 2013). Results clustered the fern species into three groups (Figure 1). All the members of family Athyriaceae (*Athyrium anisopterum*, *Athyrium sinense*, *Athyrium sheareri*, *Diplazium bellum*, *Diplazium dilatatum*, *Deparia lancea*, *Deparia pycnosora*, *Deparia viridifrons*) and one member of Phegopteridoideae family (*Macrothelypteris torresiana*) clustered in one group. *Stegnogramma sagittifolia* (Phegopteridoideae) was placed in distinct clusters while another group comprised members from Thelypteridoideae family (*Christella appendiculata*, *Ampelopteris prolifera*, and *Thelypteris interrupta*). *Thelypteris interrupta*, along with *C. appendiculata* and *A. prolifera* formed a monophyletic clade with a high bootstrap value, indicating a close relationship among these species.

Author contributions

KCP and IYC conceived and designed research. MK and IYC prepared the sample materials and analyzed the data. RVR

and EJC contributed to the data analysis and drafted the manuscript. EJC and KCP edited the manuscript. All authors read and approved the final manuscript.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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