

## The complete chloroplast genome sequence of *Crepidomanes latealatum* (Bosch) Copel

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### ABSTRACT

The complete chloroplast genome sequence of *Crepidomanes latealatum* (Bosch) Copel. was determined in the present study. The genome is 145,943 base pairs (bp) in length and comprised two inverted repeats (32,990 bp) between a large single copy (92,170 bp) and a small single copy (20,783 bp). It contains 88 coding genes, 8 rRNA genes, 34 tRNA genes, and 1 pseudogene of *trnL-UAA*, and the GC content is 37.6%. Molecular phylogenetic analysis based on the plastid genome sequences of related taxa strongly supported the monophyly of the family Hymenophyllaceae, and the genus *Vandenboschia* was a sister group of *Crepidomanes*. In addition, compared to *C. minutum*, two large deletions of 453 bp and 878 bp were found in the IGS regions of *petA-psbI* and *rrn16-trnV-GAC* of *C. latealatum* cp genome, respectively.

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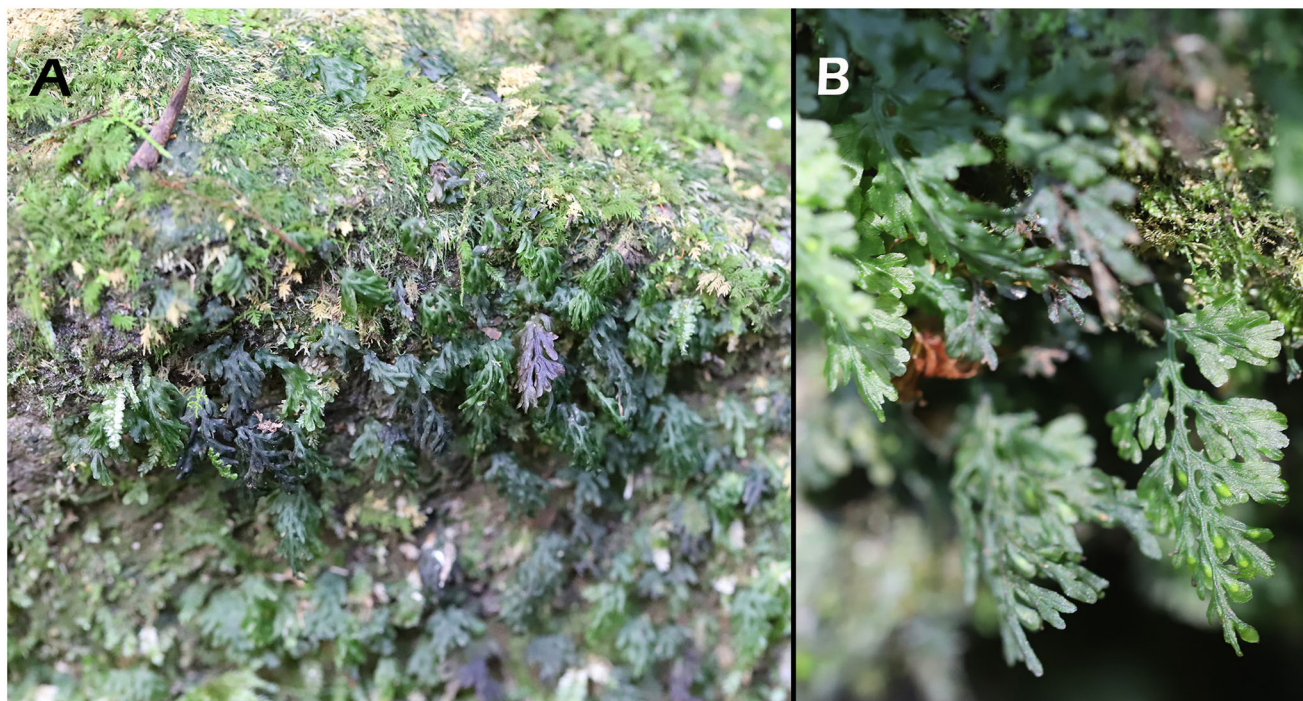
### KEYWORDS

*Crepidomanes latealatum*;  
chloroplast genome; fern;  
hymenophyllaceae





### Introduction


The genus *Crepidomanes*, which belongs to the family Hymenophyllaceae, comprises 30 species (PPG I, 2016). In the

genus, *Crepidomanes latealatum* (Bosch) Copel. was described and published by Copeland (1938) with a synonym *Trichomanes latealatum* Bosch and it has been treated as an accepted name in the present classification (Hassler et al. 2021). It is



**Figure 1.** Photographs of *Crepidomanes latealatum* taken by S. H. Park at the sample collection site: (A) *C. latealatum* growing on a shady rock near a humid valley. (B) Winged rachis and tubular involucre with dilated lips of *C. latealatum*.

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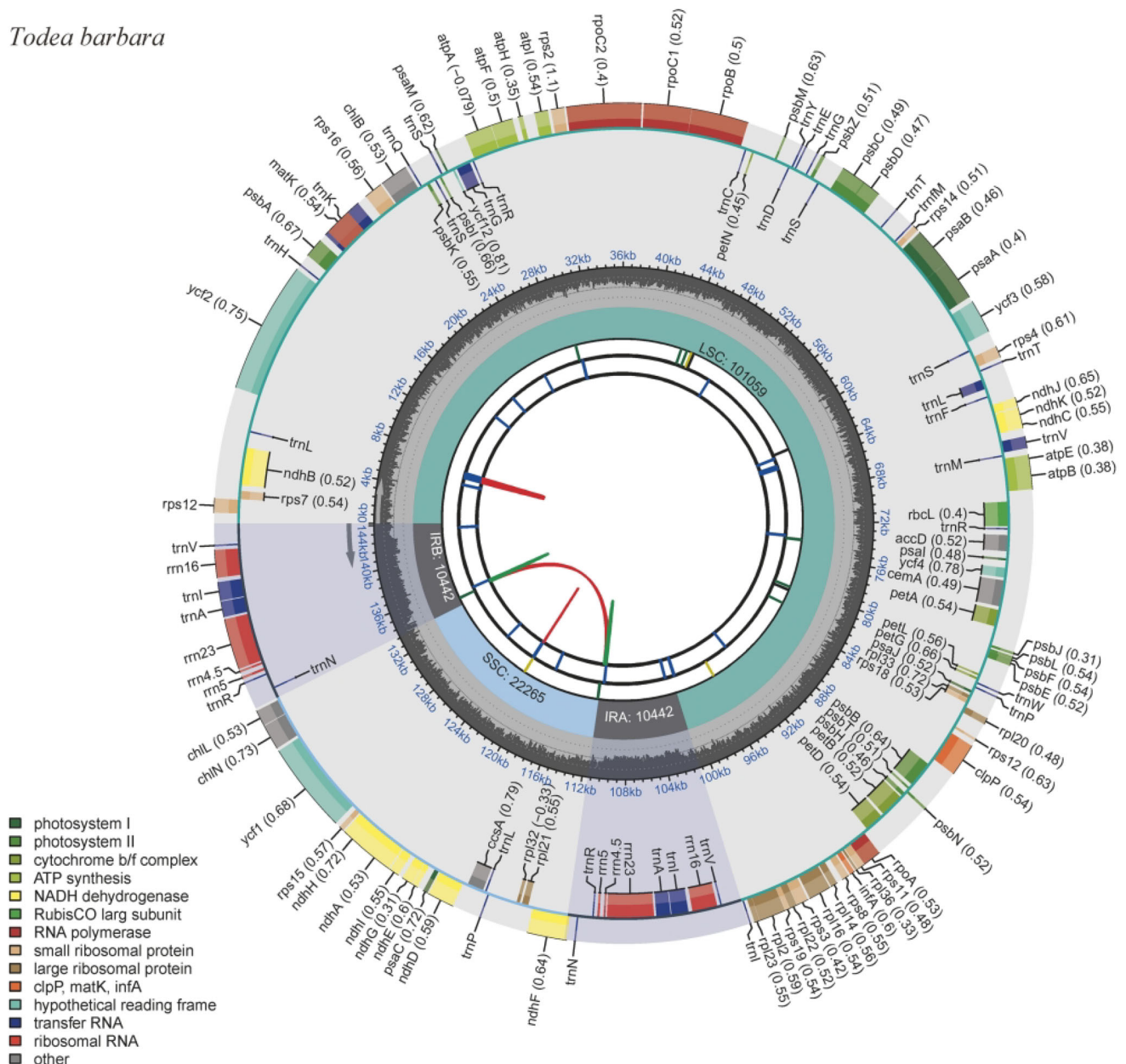
characterized by stipes very narrowly presence, ovate-oblong to oblong-subtriangular laminae, oblong and dark green pinnae, false veinlets presence, and cup-shaped and dilated involucres with campanulate in lower part and bilabiate in upper part (Lee et al. 2014), and is widely distributed from subtropical to tropical regions of Eurasia, such as Malaysia, India, Japan, China, and Korea (Moon 2008; Patil et al. 2014). However, in Korea, it is listed as a member of class V Floristic Target Species, which are distributed only in a very small area or are discontinuously distributed. Therefore, *C. latealatum* is regarded as an indicator of the conservation priority of major domestic species (Kim et al. 2018). Although complete chloroplast (cp) genome data for vascular plants have rapidly accumulated, a lack the information on ferns remains. In the present study, we clarified the cp genome structure of

*C. latealatum* and compared it with related taxa to provide genomic data for understanding the phylogenetic relationships of the family Hymenophyllaceae.

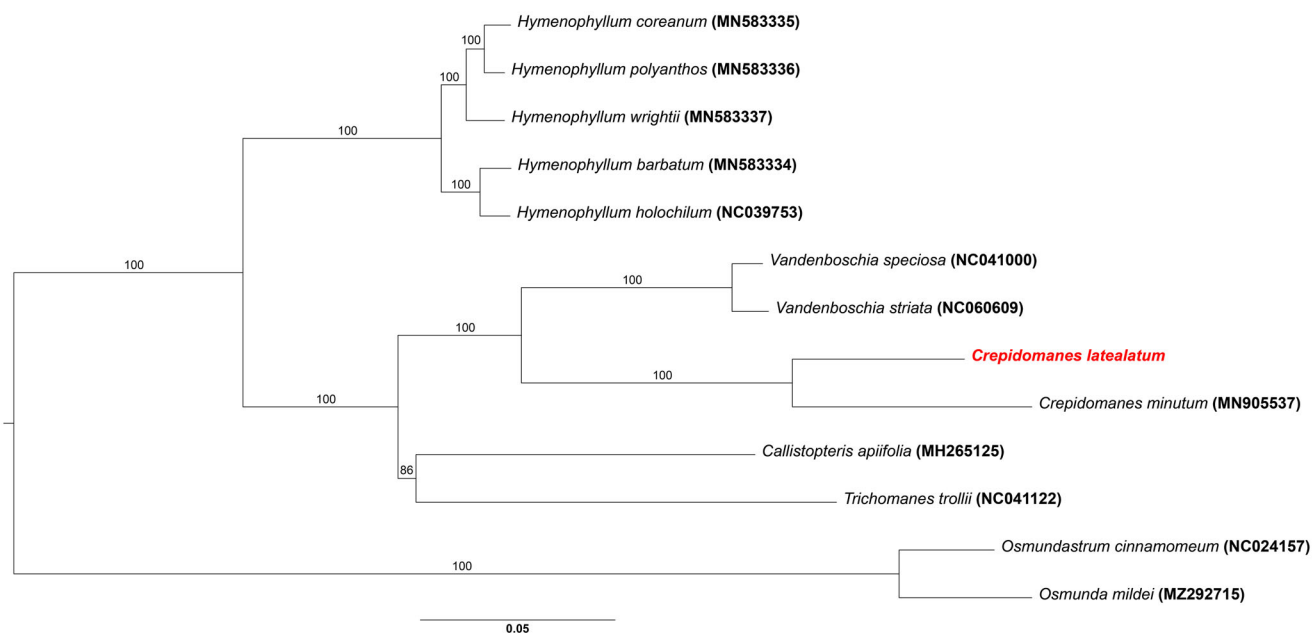
## Materials and methods

The plant material of *C. latealatum* was collected from Youngcheon-dong, Seogwipo-si, Jeju island, Korea (33°17'59.96"N, 126°34'47.31"E, alt. 288 m) (Figure 1). A voucher specimen (CBNU2018-0153, [pleura@naver.com](mailto:pleura@naver.com)) was deposited at the Herbarium of Chungbuk National University (CBNU). Total genomic DNA was extracted from a leaf dehydrated using silica gel, using a DNeasy Plant Mini Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol. Sequencing was conducted using the HiSeq X Ten system

### *Todea barbara*



**Figure 2.** Complete chloroplast genome map of *Crepidomanes latealatum*, containing six tracks. From the center, the first track shows the dispersed repeats, which consist of direct (red) and palindromic (green) repeats. The second and third tracks show the long and short tandem repeats, respectively. The regional composition of the genome, LSC, SSC, and IRs, are identified on the fourth track. The GC content along the genome is plotted in the fifth track. The genes are shown on the outer sixth track.



**Figure 3.** Phylogenetic tree of *Crepidomanes latealatum* and related taxa inferred from maximum likelihood analysis based on the 88 coding genes sequences. The outgroup was *Osmundastrum cinnamomeum* (NC 024157; Kim et al. 2014) and 5 genera of the family Hymenophyllaceae were included together with *osmunda mildei* (MZ292715). the bootstrap supporting values are described on the branches. The position of *C. latealatum* is indicated in red. The following sequences were used: MN583336 for *hymenophyllum polyanthos* (Kim and Kim 2020), MN583335 for *H. coreanum* (Kim and Kim 2020), MN583337 for *H. wrightii* (Kim and Kim 2020), MN039753 for *H. holochilum* (Kuo et al. 2018), NC063573 for *Crepidomanes minutum*, NC041000 for *Vandenboschia speciosa* (Ruiz-Ruano et al. 2019), NC060609 for *V. striata* (Wang et al. 2022), MH265125 for *callistopteris apiifolia*, and NC041122 for *Trichomanes trollii* (Lehtonen 2018).

(Illumina, San Diego, CA, USA). In total, 17,554,992' paired-end reads (151 base pairs (bp) in length) were obtained and trimmed using trimmomatic 0.39 (Bolger et al. 2014) with the options LEADING:10, TRAILING:10, SLIDINGWINDOW:4:20, and MINLEN:50. Then, 16,204,252 reads remained, which were assembled into the reference plastome of *C. minutum* (MN 905537), following Kim and Chase (2017). Finally, a circular cp genome sequence was constructed with 330.2 coverage depth.

All genes were annotated based on existing genes in other fern cp genomes using Geneious 22.1.1 (Kearse et al. 2012). A cp genome map was generated using CPGView (Liu et al. 2023; <http://www.1kmpg.cn/cpgview/>). Each coding gene was aligned using MAFFT (Katoh et al. 2002). The concatenated alignment using 85 coding genes was 74,608 bp long. The partition models were selected using ModelFinder with edge-proportional partitions and merge options (Chernomor et al. 2016; Kalyaanamoorthy et al. 2017).

Maximum likelihood analysis was performed using IQ-Tree 2 (Minh et al. 2020) with 1,000 ultrafast bootstraps (Hoang et al. 2018). The IQTREE condition was `iqtree2.exe -s Concatenated.phy -p partition_length.nex -m MFP + MERGE -bb 10000`. *Osmundastrum cinnamomeum* (NC024157) was included in the phylogenetic analysis as an outgroup for related taxa of the family Hymenophyllaceae.

## Results and discussion

The cp genome of *C. latealatum* (NC072291, Figure 2) is 145,943 bp long with two inverted repeats (IRs) (32,990 bp) between a large single copy (LSC) (92,170 bp) and a small single copy (SSC) (20,783 bp). It contains 131 genes, comprising 88 protein-coding genes, 8 ribosomal RNAs, 34 transfer RNAs, and 1 pseudogene of *trnL-UAA*. The GC content of the

genome was 37.6% (Supplementary Figure 1). Compared to the cp genome of the related taxon *C. minutum* (MN 905537), it is 531 bp shorter in length and 0.5% higher in GC content. In addition, two large deletions of 453 bp and 878 bp occurred in the IGS regions of *petA-psbI* and *rrn16-trnV-GAC*, respectively. However, another large deletion of 3,100 bp was observed in the *maK-rps16* region of the *C. minutum* cp genome.

The molecular phylogenetic analysis strongly supported the monophyly of the family Hymenophyllaceae, and a sister relationship between *Crepidomanes* and *Vandenboschia* was also confirmed within the family (Figure 3). It was consistent with previous phylogenetic study of Ebihara et al. (2006).

## Conclusion

The complete cp genome of *Crepidomanes latealatum* is presented for the first time in this study. It has a typical circular form composed of 145,943 bp and 132 genes. Based on molecular phylogenetic analysis using the cp genome sequence data, the phylogenetic position of *Crepidomanes latealatum* was confirmed in the family Hymenophyllaceae, and the genus *Crepidomanes* was shown to be a sister group of *Vandenboschia*.

## Authors' contributions

Conceiving and designing the study, JSK and HTK; collecting the plant material, SHP and HTK; managing the voucher specimen and extracting genomic DNA, SHP; performing and analyzing data, JHH and HTK; writing – original draft preparation, JHH; writing – review and editing, JSK; supervision, JSK and HTK; all authors have read and agreed to the published version of the manuscript.

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## Data availability statement

The genome sequence data supporting the findings of this study are available in the NCBI GenBank under accession no. NC072291 ([https://www.ncbi.nlm.nih.gov/nuccore/NC\\_072291.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_072291.1)). The associated BioProject, SRA, and Bio-Sample numbers are PRJNA951456, SRR24044269, and SAMN34043022, respectively.

## Disclosure statement

The authors have no conflicts of interest in this study.

## Ethical approval

*Crepidomanes latealatum* is not an endangered or protected species; therefore, permission is not required to collect this species. Research on this species, including the collection of plant materials, was conducted following the guidelines provided by the Chungpook National University.

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