

P15

Complete chloroplast genome sequences of an Antarctic moss

Sanionia uncinata

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Organellar genomes for the bryophytes are poorly represented, currently only three mosses, four liverworts, and two hornworts have sequenced, annotated chloroplast genomes. Moreover, while the Antarctic vegetation is dominated by the bryophytes, there is no report on the plastid genomes for the Antarctic bryophytes despite its biological importance. *Sanionia uncinata* is the dominant moss species in the maritime Antarctic. It has been researched as an important marker for ecological studies and as an extremophile plant for studies on stress tolerance. Here, we report the complete chloroplast genome from *S. uncinata*, which can be exploited in comparative studies to identify the lineage-specific divergence across different species. The complete chloroplast genome of *S. uncinata* is 124,374 bp in length with a typical quadripartite structure, including the large (LSC: 86,570 bp) and small (SSC: 18,430 bp) single-copy regions, separated by a pair of identical inverted repeats (IR: 9,687 bp). It contains 114 unique genes, including 82 unique protein-coding genes, 37 tRNA genes, and 4 rRNA genes. Two genes encoding α subunit of RNA polymerase (*rpoA*) and encoding cytochrome b_6/f complex subunit VIII (*petN*) were absent in *S. uncinata* chloroplast genome. We could identify nuclear genes homologous to those genes, which indicate that functional *rpoA* and *petN* have been transferred from the chloroplast to the nucleus. These data may contribute to a better understanding of the evolution of *S. uncinata* within the bryophytes for use in molecular phylogenetic studies.