

MOLECULAR RESPONSES OF THE ANTARCTIC VASCULAR PLANT *DESCHAMPSIA ANTARCTICA* TO ENVIRONMENTAL CHANGES

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ABSTRACT

Antarctic hairgrass (*Deschampsia antarctica* Desv.) is the only natural grass species in the maritime Antarctic. It has been researched as an important ecological marker and as an extremophile plant for studies on stress tolerance. Despite its importance, little genomic information is available for *D. antarctica*. Hence, we present the first *de novo* assembly of its transcriptome by massive parallel sequencing using *D. antarctica* plants grown under various environmental conditions. Total sequence reads generated by pyrosequencing were assembled into 60,765 unigenes, and 29,173 unique protein-coding genes were identified based on sequence similarities to known proteins. The combined results from all three environmental conditions indicated differential expression of 2,353 genes. As quantitative polymerase chain reaction showed that several genes were induced dramatically, they were subjected to functional research. Also, we report the complete chloroplast genome, transcriptome profiles of the coding/noncoding genes, and the posttranscriptional processing by RNA editing in the chloroplast system. The chloroplast genome of *D. antarctica* is 135,362 bp in length with a typical quadripartite structure. Sequence divergence analysis with other plastomes from the BEP clade of the grass family suggests a sister relationship between *D. antarctica*, *Festuca arundinacea* and *Lolium perenne* of the Poeae tribe, based on the whole plastome. In addition, we created an expression profile for 81 protein-coding genes and identified *ndhC*, *psbJ*, *rps19*, *psaJ*, and *psbA* as the most highly expressed chloroplast genes. We also found >30 RNA-editing sites in the *D. antarctica* chloroplast genome, with a dominance of C-to-U conversions. This dataset is the most comprehensive molecular resource currently available for Antarctic plant species and is therefore expected to contribute to a better understanding of the evolution of *D. antarctica* for use in molecular phylogenetic studies and may also help researchers understand the molecular responses of polar organisms to Antarctic environments.