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[GM63]

Functional analysis of AP2 transcription factors in Antarctic moss *Sanionia uncinata*

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Antarctica is one of the most extreme conditions for plant growth and its vegetation is mainly dominated by bryophytes. The mosses in Antarctica grow mostly in coastal areas and are expected to have developed various unique physiological/molecular mechanisms to survive in extreme environments. *Sanionia uncinata* (Hypnales; Amblystegiaceae) is a dominant moss species in the maritime Antarctic and considered as a good target species to investigate genes associated with abiotic stress tolerance of mosses. In this study, we aimed to select and characterize function of a key transcription factor which induces the cold tolerance process in *S. uncinata* at the molecular level. Based on the transcriptome analysis, we could find twenty genes containing AP2 DNA binding domain, showing transcriptional induction in response to cold stress treatment (2jÉ). To characterize their functions related to cold tolerance, we generated transgenic plants which constitutively express *SuAPL* genes using the model moss *Physcomitrella patens*, exhibiting significantly lower cold tolerance than the Antarctic moss. Some of transgenic mosses displayed enhanced freezing tolerance in terms of electrolyte leakage under freezing conditions, compared to wild-type. In addition, their protonemal growth was accelerated below 8jÉ indicating enhanced cold tolerance, while the gametophore development was considerably retarded. These results suggest that *SuAPL* have important functions in cold adaption of *Sanionia uncinata* to extreme Antarctic environments and they can cause multiple effects in abiotic stress tolerance and in stem cell development of mosses as well.

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De novo assembly and transcriptome analysis of the moss *Sanionia uncinata* in response to relative water content reduction in the Antarctic natural habitat

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*Sanionia uncinata* is one of the dominant moss species in the maritime Antarctic. This extremophile plant has been used as an important model organism for studying stress tolerance responses. Plants generally undergo physiological changes in response to drought stress but little is known about dehydration responses of *S. uncinata*. Transcriptomic characterization is necessary for identifying genes involved in stress adaptation of an Antarctic moss, *S. uncinata*, to extreme environment. Total RNA was prepared from the gametophore under three different drying conditions (Wet, Semi-dry, and Dry) and subjected to RNA-Seq analysis. This study demonstrated a number of differentially expressed genes under dry condition compared to Semi-dry and Wet conditions. We have identified differentially expressed genes that showed a significant response to dehydration. The physiological process most affected by water gradient at the molecular level was photosynthesis. This overall survey of transcripts and stress-relevant genes can contribute to understanding the stress-resistance mechanism of Antarctic moss and will accelerate the practical use of the genetic resources for this organism.

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