

PYROSEQUENCE ANALYSIS OF THE ANTARCTIC HAIRGRASS DESCHAMPSIA ANTARCTICA UNDER VARIOUS ABIOTIC STRESSES

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Deschampsia antarctica is the only monocot that thrives in the Antarctic region. Despite it is an invaluable resource for the identification of genes associated with tolerance to various environmental pressures, little transcriptome information is available. In order to get a broad view of genetic responses to various abiotic stresses, we synthesized and sequenced cDNA fragments from RNAs of one control and three plant samples under low temperature, high salt, and PEG treatment. Using massively parallel pyrosequencing, we obtained 370,169 *D. antarctica* expressed sequence tags (ESTs) at an average size of 212 bp per read. A majority of sequences (337,581 reads) could be assembled into 28,177 contigs with an average size of 425 bp. Finally, we could have a total of 60,765 unigenes containing 28,177 singletons. Using similarity searches against several public databases, we constructed a functional classification of the ESTs into categories such as genes related to responses to stimuli, as well as photosynthesis and metabolism. *In silico* analysis using 28,177 contigs revealed that 585, 586, and 774 contigs were specifically up-regulated, and 36, 379, and 217 contigs were specifically down-regulated by low temperature, high salt, and PEG treatment, respectively. Real-time PCR analysis of various stress responsive genes revealed different patterns of regulation in the different environments, suggesting that these genes are involved in responses to specific environmental factors