

GREEN UNDER SNOW: ADAPTIVE GENETIC CHARACTERISTICS OF PLANT SPECIES LIVING IN THE POLAR REGIONS

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ABSTRACT

Polar regions have environmental factors such as low temperature, high UV radiation, dryness, extreme diurnal cycles, which are very disadvantageous to life. To understand the molecular and physiological adaptation of living organisms to harsh environmental stress, we have developed transcriptome and genome databases of plant species, including green algae, lichen symbiotic photobionts and flowering plants, inhabiting the polar region, and studied the molecular and biochemical functions of the genes associated with the specific environments. As a part of such efforts, (I) we have identified low temperature-specific expressed genes in cultures of psychrophilic *Chloromonas* strain (KCCPM, KNF32) in order to investigate the transcriptome response of *Chloromonas* species under low temperature environment, and many of them were identified as Type II IBPs. The IBPs we found were found in all psychrophilic Arctic/Antarctic *Chloromonas* strains, and the levels of expression were greatly increased by low temperature. They have a genotype of the multi-exon structure and can be found to exist as many homologous genes in the genome. Their promoters have binding sites for transcription factors that play a major role in the cold signaling transduction of the flowering plants. Overexpression of *Chloromonas* IBPs improves the freezing resistance of transgenic *Arabidopsis* plants, which can infer their function in plant cells. (II) Second, we focused on the physiological and developmental differences of flowering plants in extreme natural habitats. *Colobanthus quitensis*, one of two flowering plants in Antarctica, grows in the form of a moss carpet. We performed comparative RNA-seq analysis on the transcriptome of the naturally grown plants in the Antarctic field in growing season, and on the transcriptome of the stress-free growth chamber plants. In this session, the characteristics of gene groups expressed in natural habitat environment and how these gene groups induce physiological and developmental differences in the plant, will be discussed.