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**Construction of transcriptome databases of the Antarctic native angiosperms have adapted to extreme environments**

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Land plants are often exposed to unfavorable conditions for growth. Extreme temperatures, drought, high salinity and high-UV radiance, are typical environmental stress factors that inhibit the growth and development of plant and these environmental stress can alter cellular structures and cause damage to physiological functions. The Antarctic is one of the toughest environment for life to survive. Because of the harsh conditions, an extremely small number of species has been survived and only two native angiosperms are present, *Colobanthus quitensis* (Kunth) Bartl. (Caryophyllaceae) and *Deschampsia antarctica* Desv. (Poaceae). Despite they have been studied as an extremophile that has successfully adapted to marginal land, limited genetic research has focused on these due to the lack of genomic resources. Here, we present the results of deep transcriptome sequencing of *D.antarctica* and *C.quitensis*. Total sequence reads were assembled into 90,446 unigenes (average length: 929bp) for *D.antarctica* and 95,010 unigenes (average length: 1,300 bp) for *C.quitensis*. Assembled sequences were annotated based on homology to genes in multiple public databases. Differential expression analysis revealed that the lists of genes with significant different transcripts levels between in field-grown plants and in laboratory-grown plants. In the differentially expressed gene groups, the gene ontology terms: response to stimulus, response to stress, photosynthesis and carbohydrate metabolic process, were significantly enriched. Through the comparative analysis with the abiotic stress-transcriptomes of other species, we identified that the UV-B responsive gene sets, previous reported in model plants, are highly expressed in the field-grown plants exposed to high solar UV-B radiation in Antarctica.