



***De novo* transcriptome assembly and detection of stress-responsive genes in the Antarctic flowering plant, *Colobanthus quitensis* (Kunth) Bartl**

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Despite *Colobanthus quitensis* (Kunth) Bartl. (Caryophyllaceae) is the only dicot plant to have been colonized Antarctic regions, little has been reported about the genetic information related to environmental adaptation. Here, we report the results of deep transcriptome sequencing of cDNA library from *C. quitensis*. The library was generated from a pool of transcripts, combining RNAs from the field plants living in King George islands of Maritime Antarctica and the plants grown in a laboratory chamber. A single lane run using an Illumina HiSeq-2000 sequencer produced 160,264,674 reads totalling 16.2 Gb of sequence data. After assembly, we obtained 95,010 contigs with an average length of 1,376bp. Assembled sequences were annotated based on homology to genes in multiple public databases. A full-length cDNA finding analysis expected that 11% of contigs (10,456) are full-length cDNA sequences with complete ORFs and that 47.4% of contigs (45,037) are protein-coding sequences with orthologues in public databases and 12.5% of contigs (11,837) are putative novel genes. Differential expression analysis revealed that 3,901 genes have significant different transcripts levels between field-grown plants and 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 *C. quitensis* exposed to high solar UV-B radiation in Antarctica.