

WELCOME WORD	
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SOCIAL EVENTS & SIDE MEETINGS	
PROGRAM AT A GLANCE	<p style="text-align: center;">A COMPARATIVE TRANSCRIPTOME ANALYSIS OF ANTARCTIC FIELD- AND CHAMBER SAMPLES OF COLOBANTHUS QUITENSIS REVEALS THAT LOW TEMPERATURE HAS REACTED AS A PREFERENTIAL FACTOR</p> <p style="text-align: center;"><i>Sung Mi Cho, Hyoungseok Lee, Hyun Park and Jungeun Lee*</i></p> <p style="text-align: center;"><i>Korea Polar Research Institute, Incheon 21990, Korea</i></p> <p style="text-align: center;"><i>smcho@kopri.re.kr</i></p>
DETAILED PROGRAM	<p style="text-align: center;">ABSTRACT</p>
LIST OF POSTERS	<p>Environmental stimuli given during the life of a plant can change the metabolism in the cell by regulating the gene expression by the signal transduction process in the plant cell and affect the whole plant development. <i>C. quitensis</i> has emerged as an important plant species that implies a mechanism of abiotic stress resistance in plants because it has naturally adapted to harsh environments in Antarctic Peninsula. In this study, we were able to obtain the snapshots of transcriptome of plants acclimated to harsh natural environments and in plants acclimated in stress-free growth chambers. Through the de novo assembly analysis via high-throughput sequencing, we obtained 26,347 annotated genes and classified them into the functional categories and determined a group of genes showing differences in expression depending on the habitat environment. Through the ortholog analysis with the genes of model plants, we found that the core environmental stress response genes were abundantly expressed in plants grown in natural habitat with various environmental stress factors. Also, we suggest that the differential expression of the transcription factors might affect the morphological differences according to the habitat to adapt the harsh environment.</p>
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