

## Transcriptional changes of rice plant (*Oryza sativa* L.) in response to cold stress during ripening stage

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### [Introduction]

Cold stress induces reduction in yield and quality of rice. Although many studies have investigated the impact of cold stress on rice, researches on physiological changes of rice plants under low temperature during ripening stage are insufficient. Transcriptomic information about the impact of cold stress on rice plant during ripening stage could help us understand the biological mechanism of rice plant. Thus, the objective of this study was to determine transcriptional changes in rice plant in response to cold stress during ripening stage using RNA-Seq

### [Materials and Methods]

Four Korean cultivars (Jinbu, Junamjosang, Hwawang, Kumyeong) of rice (*Oryza sativa* L.) were used as plant materials. At two days after heading, pots were moved into phyto-tron which was controlled at two different temperature conditions (means temperature 18°C-13/23°C and means temperature 22°C-17/27°C) under natural light condition. Total RNA was extracted then 1 µg of total RNA was reverse-transcribed to cDNA using PrimeScrip RT reagent Kit. The quality of cDNA library sequence data was checked using FastQC v0.11.3. Raw sequence reads were trimmed using Trimmomatic v0.33 (Bolger et al., 2014) to remove adapter contamination. Trimmed data in each sample were mapped using Hisat2. IRGSP-1.0 CDS was used as reference. The number of mapped readings for CDS from mapping result file for each sample was obtained using SAMtool. Transcripts with significant differences in expression between 18°C and 22°C were selected by comparing their expression levels to the reference using DESeq2

### [Results and Discussions]

Flag leaves of four rice cultivars after cold stress treatment and untreated rice leaves were harvested at 20 days after heading. Results obtained from differential gene expression (DEG) analysis of cold stress treated library vs. untreated library revealed that 1,253 DEGs were up-regulated, 1,158 DEGs were down-regulated, and 201 DEGs were differentially regulated in rice cultivars. Gene ontology analysis revealed that most of these DEGs were mapped to possess binding and catalytic activities. These DEGs were mostly involved in purine/thiamine metabolism and biosynthesis of antibiotics pathway. In addition, 16 and 31 DEGs were commonly up- and down-regulated in all rice cultivars. Some up-regulated DEGs were associated with plant stabilization and plant defense while some down-regulated DEGs were associated with nutrient transport. These results suggest that cold resistant rice during ripening stage need stress tolerance with active nutrient absorbing traits.

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