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Transcriptome and Small RNAome Analyses Reveal the Association of pre-harvest Sprouting and Heat Stress Response in Rice (*Oryza sativa* L.)

Minsu Park^{1,2}, Woochang Choi¹, Sang-Yoon Shin^{1,3}, Yujin Kweon¹, Jihyun Eom^{1,3}, Minsun Oh^{1,3}, Chanseok Shin^{1,2,3,4}

¹Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea

²Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

³Research Center for Plant Plasticity, Seoul National University, Seoul 08826, Republic of Korea

⁴Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

[Abstract]

Pre-harvest sprouting (PHS) in rice (*Oryza sativa* L.) is one of the main problems associated with seed dormancy. PHS causes yield loss and reduction of grain quality under unpredictable humid conditions at the ripening stage, thus affecting the economic value of the rice crop. To resolve this issue, it is important to understand the molecular mechanism underlying seed dormancy in rice. Recent studies have shown that seed dormancy is affected by a large number of genes associated with plant hormones. However, the effect of heat stress on seed dormancy and plant hormones is not well understood. In this study, we compared the PHS rate as well as the transcriptome and small RNAome of the seed embryo and endosperm of two different accessions of rice, PHS-susceptible rice (low dormancy) and PHS-resistant rice (high dormancy) under three different maturation stages. We identified and verified the candidate genes associated with seed dormancy and heat stress-related responses in rice using quantitative real-time PCR. We newly discovered hormone-related genes, heat shock protein-related genes, and miRNAs potentially involved in PHS. These findings provide a foundation for understanding the dynamics of transcriptome and small RNAome of hormone- and heat stress-related genes, which affect PHS during seed maturation.

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*Corresponding author: E-mail, cshin@snu.ac.kr Tel. +82-2-880-4653