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The grain yield regulator NOG1 plays a dual role in latitudinal adaptation and cold tolerance during rice domestication

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Abstract

Rice originated in tropical and subtropical regions and is distributed worldwide. Low temperature is one of the most critical abiotic stresses affecting grain yield and geographical distribution of rice. It is vital to elucidate the molecular mechanism of chilling tolerance in rice for ensuring cereals production. Previously we isolated the domestication-related gene NOG1 which affects rice grain number and yield. In this study, we specified that rice varieties harboring high-yielding *NOG1* allele are more distributed in low-latitude regions. Additionally, we observed *NOG1* influences the chilling tolerance of rice. Through genome-wide transcriptional analysis after cold treatment at 10°C, there were 717 differentially expressed genes (DEGs) in *nog1* near-isogenic lines compared with the control Guichao 2, including 432 up-regulated DEGs and 284 down-regulated DEGs. Gene ontology annotations and KEGG enrichment analysis of DEGs showed that various biological processes and signaling pathways were related to cold stress, such as lipid metabolism and genetic information processing. These results provide new insights into the mechanism of chilling tolerance in rice and the molecular basis of environmental adaptation during rice domestication.

Keywords: *NOG1*, cold stress, domestication, differentially expressed genes, RNA-seq

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