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Genome-wide association study of cold stress in rice at early young microspore stage (*Oryza sativa* L.).

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Abstract

Cold stress is one of the most influenced factors to rice yield. In order to identify genes related to cold stress in fertility stage, genome-wide association study (GWAS) was conducted. Cultivated 129 rice germplasm were moved in the growth chamber under the condition of 12°C/RH70%(12h day/12h night when the rice plant was grown in 10 DBH(days before heading). Also, rice plant as control was moved in the green house under condition of 28°C/RH70%(12h day/12h night). After 4 days the plants were moved in a greenhouse. The fertility of rice plant were monitored after the grain were fully grown. The most tolerant rice germplasm to cold stress were Cheongdo-Hwayang-12 and IR38 as 63.1 and 61.8 of fertility and the most recessive rice germplasm were Danyang38 and 8 rice germplasm as 0. As a result of GWAS with re-sequencing data and fertility after cold treatment germplasm using genome association and prediction integrated tool (GAPIT), 99 single-nucleotide polymorphisms (SNPs) were observed by applying a significance threshold of $-\log P > 4.5$ determined by QQ plot. With SNPs region, 14 candidate genes responded to cold stress in fertility stage were identified

Keywords: rice, early young microspore stage, GWAS, cold temperature

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