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Title:

Navigating rice seedling cold resilience: QTL mapping in three inbred line populations and the search for genes

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Abstract:

We explored natural genetic variation in rice to facilitate the breeding of climate-resilient cultivars. Three inbred line populations developed from crosses between cold-tolerant and cold-sensitive parents were used for quantitative trait locus (QTL) mapping of two traits: degree of membrane damage after 1 week of cold exposure quantified as percent electrolyte leakage (EL) and percent low-temperature seedling survivability (LTSS) after 1 week of recovery growth. This revealed seven EL QTL and 16 LTSS QTL, most of which overlapping with larger QTL regions previously uncovered by genome-wide association study (GWAS) mapping. At least 25 cold-tolerance candidate genes were identified based on genomic differences between the cold-tolerant and cold-sensitive parents. RNA-seq experiments showed that most of the 25 genes were cold temperature regulated and many have deleterious nucleotide variants in the cold-sensitive parents, which might contribute to its cold-sensitive phenotype.