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Maize Downy Mildew Resistance SNP Molecular Marker Development and Verification through HRM Analysis

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[Introduction]

Maize is one of the world's 3 major crops, and it has a high yield per unit area and is easy to cultivate. In addition, it is used for food as well as feed and industrial raw materials, and the world consumption in 2020/21 is 1,158 million tons. Maize Downy Mildew (DM) affects the entire plant growth cycle, leading to death or yield loss due to reduced growth in severe cases. For the control of DM on maize, such as spraying fungicides and incineration, cultivating resistant varieties is attracting attention due to environmental pollution issues. We selected SNP markers for the cultivation of new DM-resistant varieties and confirmed them through a crossbreeding population.

[Materials and Methods]

After downy mildew infection in Ki11, a cultivar resistant to DM, transcriptome analysis was performed to select genes. Genomic DNA was extracted from resistant cultivars Ki11 and Ki3 and susceptible cultivars B73 and selected gene regions were amplified using PCR. SNPs were selected by comparative analysis of the sequence of the amplification site. HRM (High Resolution Melting) analysis of the selected SNP was performed on 200 samples of the F7 population obtained by crossing B73 x Ki11.

[Results and Discussion]

Transcriptome analysis was performed to select transcripts with high expression for infection. 2 specific SNPs were selected from gene regions amplified from DM resistant and susceptible cultivars. By HRM analysis, the genotype and phenotype concordance rates for each SNP marker were 51% and 53%, respectively. This shows a pattern and concordance rate similar to the HRM results for SNPs of other candidate genes, and is expected because the DM resistance gene is not associated with a single SNP. The selected transcript was confirmed to be expressed as SLC35F1 (Solute carrier family 35 member F1), it is classified as Nucleotide-Sugar Transporters. This is a factor that can cause changes in immune response and virulence in various eukaryotes, and is expected to be involved in resistance to diseases caused by microorganisms. The SNP markers selected in this study can perfectly select resistant varieties with an infection rate of 15% or less in the F7 population when performing multiple comparisons.

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