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Development of Wheat breeding Resources for improving Metabolic Disorders and Replacing Imported Wheat

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[Abstract]

The increasing number of Westernized eating patterns based on wheat flour in Korea has led to an increase in the rate of diseases such as obesity and diabetes, which has become a social problem. Wheat consumption is increasing due to changes in eating habits, but domestic wheat has low price competitiveness and has stagnated recently, so it is necessary to secure new resources to differentiate from imported wheat. Resistant starch, a newly created resource in domestic wheat, can act as a prebiotic similar to dietary fiber in the body, inducing microbial changes in the gut and having beneficial effects on metabolic syndrome. Wheat research on resistant starch was carried out based on the breeding of high amylose. A genome-wide association study (GWAS) was used to perform SNP identification and expression analysis related to wheat amylose through phenotype and genotype. 561 wheat core collection gene sources were investigated for amylose content in wheat, and related genes were extracted and analyzed. In the GWAS analysis, the model formulas BLIMK, FarmCPU, GLM, MLM, and MLMM were used to derive results such as QQ plots and Manhattan plots through phenotypic data. Among these models, BLAST was conducted to find the association between the SNPs identified using FarmCPU and genes related to starch, and 15 were found. Using the identified markers, it becomes easier to develop and browse related wheat cultivars according to their amylose content.

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