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Candidate Genes Related to Sugar Content in Sweetpotato using GWAS

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[Abstract]

Sweetpotato is rich in starch, which is converted to sugar during storage due to enzymatic hydrolysis. The sugar content of sweetpotato is a component related to taste and storability. In this study, the sugar content (fructose, glucose, maltose, sucrose and total sugar content) of 94 genotypes was evaluated and the GWAS (Genome-Wide Association Study) was conducted to search for candidate genes for sugar content. The fructose and glucose content were $0.2 \sim 8.8$ and $0.2 \sim 9.4$ g/100g, respectively. The maltose, sucrose and total sugar content were $0.2 \sim 9.1$, $3.2 \sim 30.0$ and $7.9 \sim 40.2$ g/100g, respectively. The fructose and glucose showed a positive correlation (0.98). The 94 genotypes were genotyped with genotyping-by-sequencing (GBS) and aligned against the reference genome sequences of sweetpotato. The GBS libraries from 94 genotypes were sequenced on an Illumina HiSeqXten system, and 1,339,892 SNPs (Single Nucleotide Polymorphism) were generated. Filtering for < 60% missing rate and > 0.05 minor allele frequency resulted in a total of 44,255 SNPs used in GWAS. The GAPIT (Genome Association and Prediction Integrated Tool) was used to conduct based on the mean of sugar content with a Bonferroni-corrected chromosome-wide significance threshold with a $-\log_{10}(P)$ of 5.95. The significant SNPs were obtained with fructose (seven), glucose (six), maltose (four) and sucrose (nine). There were several genes related to sugar content around the significant SNPs such as sugar transport protein 8-like, probable galactose-1-phosphate uridyltransferase-like and beta-amylase. These results will contribute to understanding of sugar content and conversion in sweetpotato.

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