Exploration of Key Genes and Molecular Makers for Differences in Sugar Accumulation in Litchi fruits based on Genome-wide Association Analysis

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Abstract

Litchi(*Litchi chinensis* Sonn.) is the most important subtropical economic fruit tree in southern China. The edible part of litchi is aril, and an important factor in determining fruit quality is the type and content of sugar in litchi aril. The form of sucrose, glucose and fructose was mainly existed in the soluble sugar of aril, which were differences among accessions. But the molecular genetic mechanism of sugar accumulation in different varieties was not clear and related molecular markers had not been developed.

In this study, a core collection comprising of 276 accessions as the research materials. we detected the content of sucrose, glucose and fructose from mature aril in two seasons (2019 and2020) using HPLC system. A total of 2442670 high-quality identified from the previously re-sequenced studies were used for GWAS analysis. To rapidly identify candidate genes, we adopted a method combing peak SNPs in GWAS with transcriptome data and annotation of the orthologs in *Arabidopsis*. Finally, a significantly associated SNP and candidate gene(*Lc009111*,G/A) was obtained on chromosome 7. *Lc009111* encodes invertase (Beta-fructofuranosidase soluble) enzyme and was designated *LcVIN*. In most of plants, VIN play a role in hydrolyzing sucrose into glucose and fructose. The genomic full-length sequence of the *LcVIN* is 5536bp, including 7 exons and 6 introns. the accessions carry GA genotype had significantly lower sucrose and higher reducing sugar (include glucose and fructose) than did those with AA genotype. Therefore, we performed qRT–PCR with two types of varieties and used transgenic methods to validate the function of *LcVIN*. The gene was more highly expressed in reducing sugar accumulation varieties than in sucrose accumulation varieties. Overexpression of *LcVIN* in tomato (Micro Tom) fruits resulted in the content of sucrose was

lower treble than those in wild type, and the content of glucose and fructose were significantly higher than wild type.

A 500bp deletion located in the first intron of sucrose accumulation accessions by alignment of re-sequencing datas of two type varieties for *LcVIN* sequence. Then a molecular marker was designed, which could clearly distinguish sucrose, reducing sugar and intermediate accumulation. In summary, this study identified a key candidate genes and linkage markers for sugar metabolites for improvement of litchi quality.

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