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Global Transcriptome-Wide Association Studies (TWAS) Reveal a Gene Regulation Network of Eating and Cooking Quality Traits in Rice

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[Abstract]

Eating and cooking quality (ECQ) is one of the most complex quantitative traits in rice. The understanding of genetic regulation of transcript expression levels attributing to phenotypic variation in ECQ traits is limited. We integrated whole-genome resequencing, transcriptome, and phenotypic variation data from 84 *Japonica* accessions to build a transcriptome-wide association study (TWAS) based regulatory network. All ECQ traits showed a large phenotypic variation and significant phenotypic correlations among the traits. TWAS analysis identified a total of 285 transcripts significantly associated with six ECQ traits. Genome-wide mapping of ECQ-associated transcripts revealed 66,905 quantitative expression traits (eQTLs), including 21,747 local eQTLs, and 45,158 *trans*-eQTLs, regulating the expression of 43 genes. The starch synthesis-related genes (SSRGs), *starch synthase IV-1 (SSIV-1)*, *starch branching enzyme 1 (SBE1)*, *granule-bound starch synthase 2 (GBSS2)*, and *ADP-glucose pyrophosphorylase small subunit 2a (OsAGPS2a)* were found to have eQTLs regulating the expression of ECQ associated transcripts. Further, in co-expression analysis, 130 genes produced at least one network with 22 master regulators. In addition, we developed CRISPR/Cas9-edited *glb1* mutant lines that confirmed the role of alpha-globulin (*glb1*) in starch synthesis to validate the co-expression analysis. This study provided novel insights into the genetic regulation of ECQ traits, and transcripts associated with these traits were discovered that could be used in further rice breeding.

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