Tropentag, September 11-13, 2024, hybrid conference

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Multi-omics unraveled genes and pathways responsible for the low glycemic index and high protein rice

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Abstract

To address the growing incidences of increased diabetes and to meet the daily protein requirements, we developed low glycemic index (GI) rice varieties with a protein yield exceeding 14 %. In the development of recombinant inbred lines using Samba Mahsuri and IR^{3}6 amylose extender as parental lines, we identified quantitative trait loci (QTLs) and genes associated with low GI, high amylose content (AC), and high protein content (PC). By integrating genetic techniques with classification models, this comprehensive approach identified candidate genes on chromosome 2 (qGI2.1/qAC2.1 spanning the region from 18.62 Mb to 19.95 Mb), exerting influence on low GI and high amylose. Notably, the phenotypic variant with high value was associated with the recessive allele of the starch branching enzyme 2b (sbeIIb). The genome-edited sbeIIb line confirmed low GI phenotype in milled rice grains. Further, combinations of alleles from the highly significant SNPs from the targeted associations and epistatically interacting 2 genes showed ultra-low GI phenotypes with high amylose and high protein. Metabolomics analysis of rice with varying AC, PC, and GI revealed that the superior lines of high AC and PC, and low GI were preferentially enriched in glycolytic and amino acid metabolism, whereas the inferior lines of low AC and PC and high GI were enriched with fatty acid metabolism. The high amylose and high protein RIL (HAHP_101) were enriched in essential amino acids like lysine. Besides amino acids, pathway analysis unveiled phenolic compounds such as tricin, caffeoylquinic acid, feruloylglucoside, p-coumaroyglucoside, luteolin-6-glucoside, hydroxygallic acid derivative, caffeoyl hexoside, and sinapoyl glucoside were found to significantly accumulate in the low and ultra-low GI rice lines. Such lines may be highly relevant for food product development to address diabetes and malnutrition.

Keywords: Glycemic index, metabolomics, protein, QTLs, starch

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