

Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism

With the support by the National Natural Science Foundation of China and the Ministry of Science and Technology of China, Prof. Luo Jie and his colleagues from the National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, published their research findings in an article “Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism” in *Nature Genetics* (2014, 46(7): 714–721).

Plants metabolites are important to world food security in terms of maintaining sustainable yield and providing food with enriched phytonutrients. Here they reported a comprehensive profiling for 840 metabolites and a further metabolic genome-wide association study (mGWAS) based on ~6.4 million SNPs obtained from 529 diverse accessions of *Oryza sativa*. Hundreds of common variants were identified influencing numerous secondary metabolites with large effects at high resolution. Data mining revealed 36 candidate genes modulating levels of metabolites that are of potential physiological and nutritional importance. As a proof-of-concept, five candidate genes were functionally identified or annotated. The study provides insights into genetic and biochemical bases of rice metabolome and can be used as a powerful complementary tool to classical phenotypic traits mapping for rice improvement.

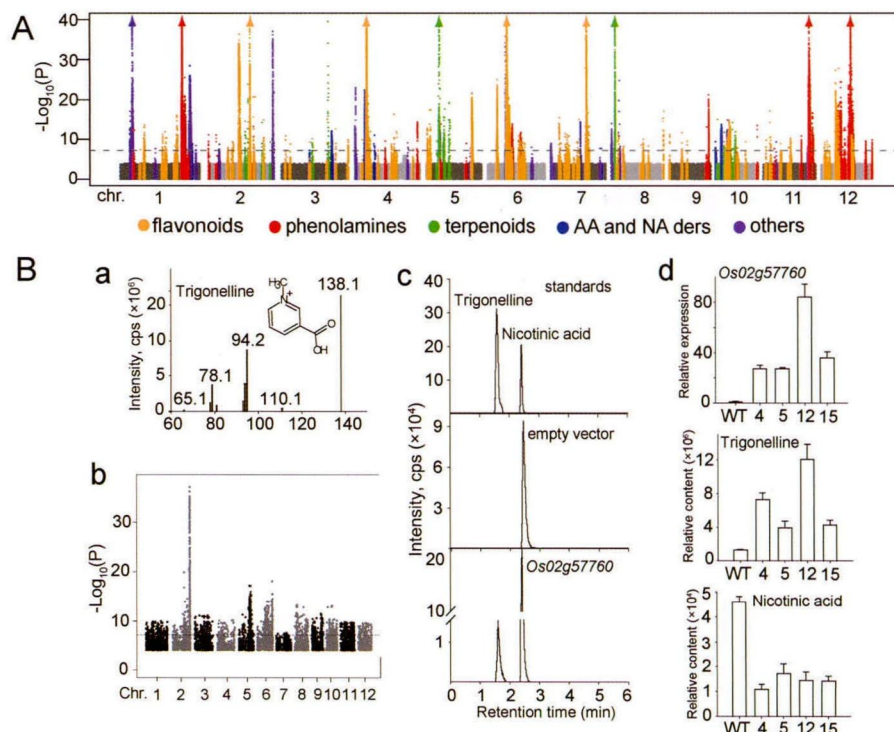


Figure A, Manhattan plots of mGWAS results with genetic association. B, Functional identification of *Os02g57760* (*O*-methyltransferase); a, structure and LC-MS/MS fragmentation of trigonelline; b, Manhattan plot displaying the GWAS result of the content of trigonelline; c, LC-MS chromatograms of *in vitro* enzyme assay showing the enzyme activity of recombinant *Os02g57760*; d, *in vivo* function of *Os02g57760*.