Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights

With the support by the National Natural Science Foundation of China and the Ministry of Science and Technology of China, Prof. Luo Jie, Jianbing Yan and their colleagues from the National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University published their achievements in an article "Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights" in *Nature Communications* (2014, 5: 3438—3447).

Plants produce a variety of metabolites that have critical roles in their growth and development. In addition, metabolites provide essential resources for human nutrition, bioenergy, medicine, flavorings, and so on. Understanding plant biochemistry is thus of fundamental importance for sustainable agriculture and resource conservation, especially under changing climate conditions.

Perceived as the end products of cellular regulatory and metabolic processes, the metabolite spectrum and quantities making up the metabolic composition of the plants may be viewed as the metabolic phenotype. The metabolic phenotype provides a link between gene sequence and visible phenotype and metabolites can be used as biomarkers for trait prediction.

A comprehensive study of maize metabolism that combined combining genomics, metabolite and expression profiling methodologies was presented to dissect the genetic basis of metabolic diversity in maize kernels. 983 metabolite features were quantified and 1,459 significant locus-trait associations ($P \leqslant 1.8 \times 10^{-6}$) across three environments through metabolite-based genome-wide association mapping (GWAS) were identified. In addition, most (58.5%) of the identified loci were supported by expression QTLs, and some (14.7%) were validated through linkage mapping. Novel metabolites, genes and metabolic pathways were validated by re-sequencing and transgenic analysis.
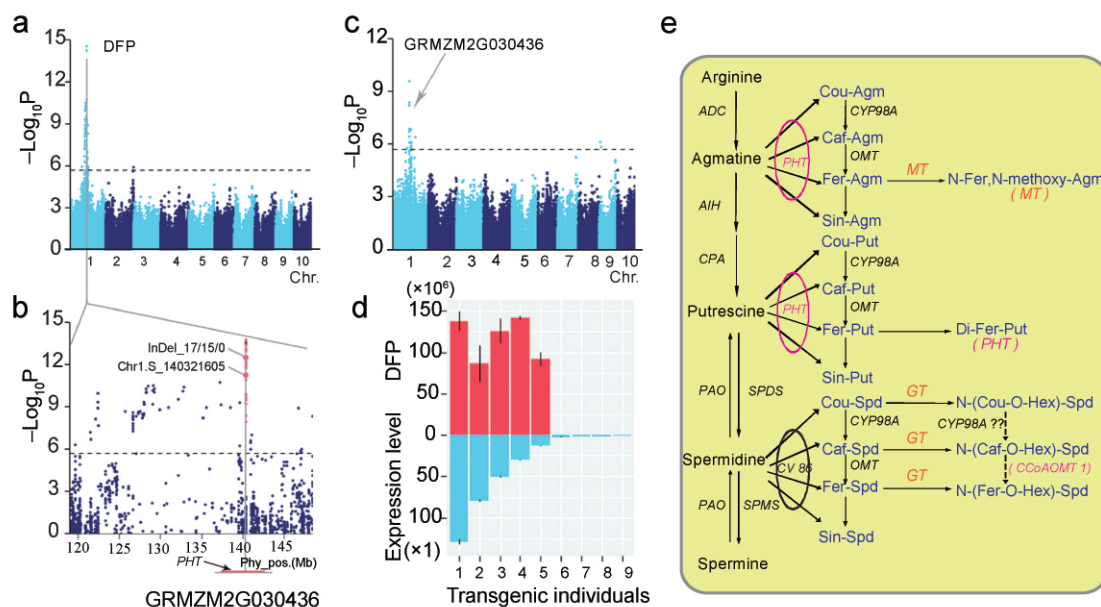

Figure (a) Manhattan plot displaying the GWAS result of the content of DFP (MLM, N＝339). (b) Regional association plot for locus *PHT*. (c) Manhattan plot shows the association between expression level of *PHT* and genome-wide SNPs. (d) Bar plot for DFP content and *PHT* expression level in rice transgenic individuals. (e) Proposed pathway of polyamine conjugates biosynthesis.