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## Exploring the metabolic diversity in major crops

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Application of a newly developed widely-targeted metabolomics strategy simultaneously detected hundreds of both primary and secondary metabolites in rice and disclosed several subspecies-specific metabolites that may reflect, as well as affect the subspecies differentiation of rice. Distinct and overlapped accumulation was observed and complex genetic regulation of metabolism was revealed in two different tissues by subsequent metabolic QTL (mQTL) mapping and metabolic genome-wide association study (mGWAS). Hundreds of loci with high resolution and large effects were uncovered. Interactive gene/metabolite identification/annotation was facilitated for both functional genomics and metabolomics. Data mining revealed a large number of candidate genes underlying metabolites that are of physiological and agronomical importance, and also be applied to the bulk identification of tailing enzymes contributing most to metabolic diversity. Similar approaches were also applied to the understanding of maize kernel metabolome. Furthermore, comparative mGWAS between rice and maize resulted in greatly increased power and resolution in both species. Exploring the modification of phytochemicals has also identified flavone-O-glucosyltransferases that determine the natural variation of rice flavones and their allelic variation contributes to UV-B tolerance in nature. Finally, a multi-omics study revealed the rewiring of fruit metabolome during tomato breeding including the selection of five major loci reduced the accumulation of anti-nutritional steroidal glycoalkaloids in ripened fruits and the breeding for pink tomatoes modified the content of over one hundred metabolites. Our studies revealed novel biochemical and genetic insights of important aspects of plant metabolism and provided a powerful tool for large-scale gene identification, pathway elucidation, and for knowledge-based crop genetic improvement.

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