

Metabolic genome-wide-association unravels trait architecture and natural variation in tomato primary and secondary metabolisms

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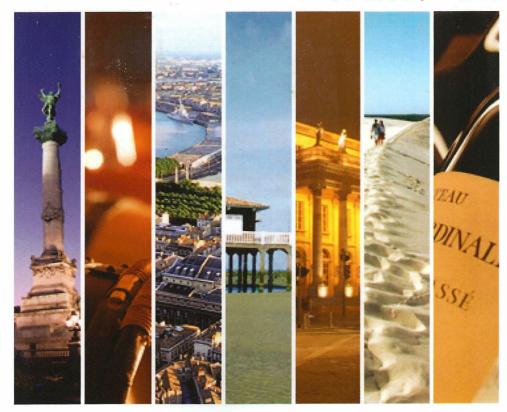
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Metabolic genome-wide-association unravels trait architecture and natural variation in tomato primary and secondary metabolisms

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Modern breeding has impacted fruit quality and volatile content, modifying the organolepticquality of tomato crop varieties. To decipher quality trait inheritance and improve it in moderntomato breeding programs, we characterized an association panel including 70 wild relativeaccessions (S. pimpinellifolium), 170 admixed accessions (S.I. cerasiforme) and 50 elitecultivars (S. lycopersicum). GWAS analysis was conducted using 12,000 SNP markers and aset of primary metabolism traits (sugars, organic and amino acids) as well as a broad range ofvolatiles compounds. This study is the first in tomato reporting associations for a large set ofvolatiles at the genome scale. Metabolite content and genetic inheritance varied in a broadrange over different genetic groups. Four genomic regions were detected highlighting clusters associations for several metabolites. We found significant associations for 84 loci with atotal of 17 traits including glucose, malate or phenylacetaldehyde. Some associations wereconsistent with previously published quantitative trait loci (sugars, guaiacol), while new lociwere identified (phenylacetaldehyde). Local linkage disequilibrium analysis and allele miningallowed the identification of candidate genes to be functionally investigated. These resultsprovide (1) a list of candidate loci and (2) a fast and efficient analytical approach for findinggenetic variants that can be directly used for fruit quality improvement and deciphering thegenetic architecture of complex traits.