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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 organoleptic quality of tomato crop varieties. To decipher quality trait inheritance and improve it in modern tomato breeding programs, we characterized an association panel including 70 wild relative accessions (*S. pimpinellifolium*), 170 admixed accessions (*S.l. cerasiforme*) and 50 elite cultivars (*S. lycopersicum*). GWAS analysis was conducted using 12,000 SNP markers and a set of primary metabolism traits (sugars, organic and amino acids) as well as a broad range of volatile compounds. This study is the first in tomato reporting associations for a large set of volatiles at the genome scale. Metabolite content and genetic inheritance varied in a broad range over different genetic groups. Four genomic regions were detected highlighting clusters of associations for several metabolites. We found significant associations for 84 loci with a total of 17 traits including glucose, malate or phenylacetaldehyde. Some associations were consistent with previously published quantitative trait loci (sugars, guaiacol), while new loci were identified (phenylacetaldehyde). Local linkage disequilibrium analysis and allele mining allowed the identification of candidate genes to be functionally investigated. These results provide (1) a list of candidate loci and (2) a fast and efficient analytical approach for finding genetic variants that can be directly used for fruit quality improvement and deciphering the genetic architecture of complex traits.