GWAS reveals candidate regions for metabolic traits in tomato, Solanum lycopersicum

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GWAS reveals candidate regions for metabolic traits in tomato, Solanum lycopersicum

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Modern breeding can impact crop cultivars volatile fruit content, inducing low volatile profile and therefore low organoleptic quality (Klee and Tieman 2013). Genome-wide association studies have been successful in identifying genes involved in polygenic traits notably in tomato, and can be a useful way towards fruit quality improvement. Genotyping arrays (Sim, Durstewitz et al. 2012; Viquez-Zamora, Vosman et al. 2013) are available and enable GWAS for traits of interest. We present an association panel including 70 wild relative accessions (*S. pimpinellifollium*), 170 admixed accessions (*S.l. cerasiforme*) and 50 domesticated accessions (*S. lycopersicum*). GWAS analysis was conducted using single and multi-locus analysis (Yu et al., 2006; Segura et al., 2012) with 12000 SNP markers and a set of sugar-related, amino-acids as well as a broad range of volatiles. The present study is the first one in tomato reporting associations for a large set of volatiles at the genome scale. We found significant associations for 84 loci with a total of 17 traits including glucose, malate or phenylacetaldehyde. Identified loci were also concordant with previously published quantitative trait loci (guaiacol), while new loci were identified (phenylacetaldehyde). These results (1) provide a list of candidate loci to be functionally validated and (2) provide a powerful approach for finding genetic variants that can be directly used for fruit quality improvement and deciphering the genetic architecture of complex traits.

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