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## **Meta-analysis of GWAS provides new insights into genetic control of tomato flavor**

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Tomato flavor has changed over the course of long-term domestication and intensive breeding. To understand the genetic control of flavor related traits, we performed a meta-analysis of genome-wide association studies (GWAS) for 18 traits, using 775 tomato accessions and 2,316,117 SNPs from three GWAS panels (*Sauvage et al., 2014; Bauchet et al., 2017 and Tieman et al., 2017*). *In a first step, we imputed SNP data to increase genome coverage for two out of three panels and ran EMMAX software for each panel separately. From each run, the genomic inflation factor and standard errors of the beta coefficients were implemented in two meta-GWAS models: the inverse variance-weighted fixed effect and the Han Eskin random-effect model that takes heterogeneity across studies into account. Then, from the meta-GWAS results, we conducted a statistical fine-mapping of the candidate loci following a heuristic linkage disequilibrium (LD) approach.* We discovered 305 significant associations for the contents of sugars, acids, amino acids and flavor-related volatiles. We showed that fruit citrate and malate contents have been impacted by selection during domestication and improvement, while sugar content has undergone less stringent selection. Results suggest that it may be possible to significantly increase volatiles that positively contribute to consumer preferences while reducing unpleasant volatiles, by selection of the relevant allele combinations. Our results provide genetic insights into the influence of human selection on tomato flavor and demonstrate the benefits obtained from meta-analysis.