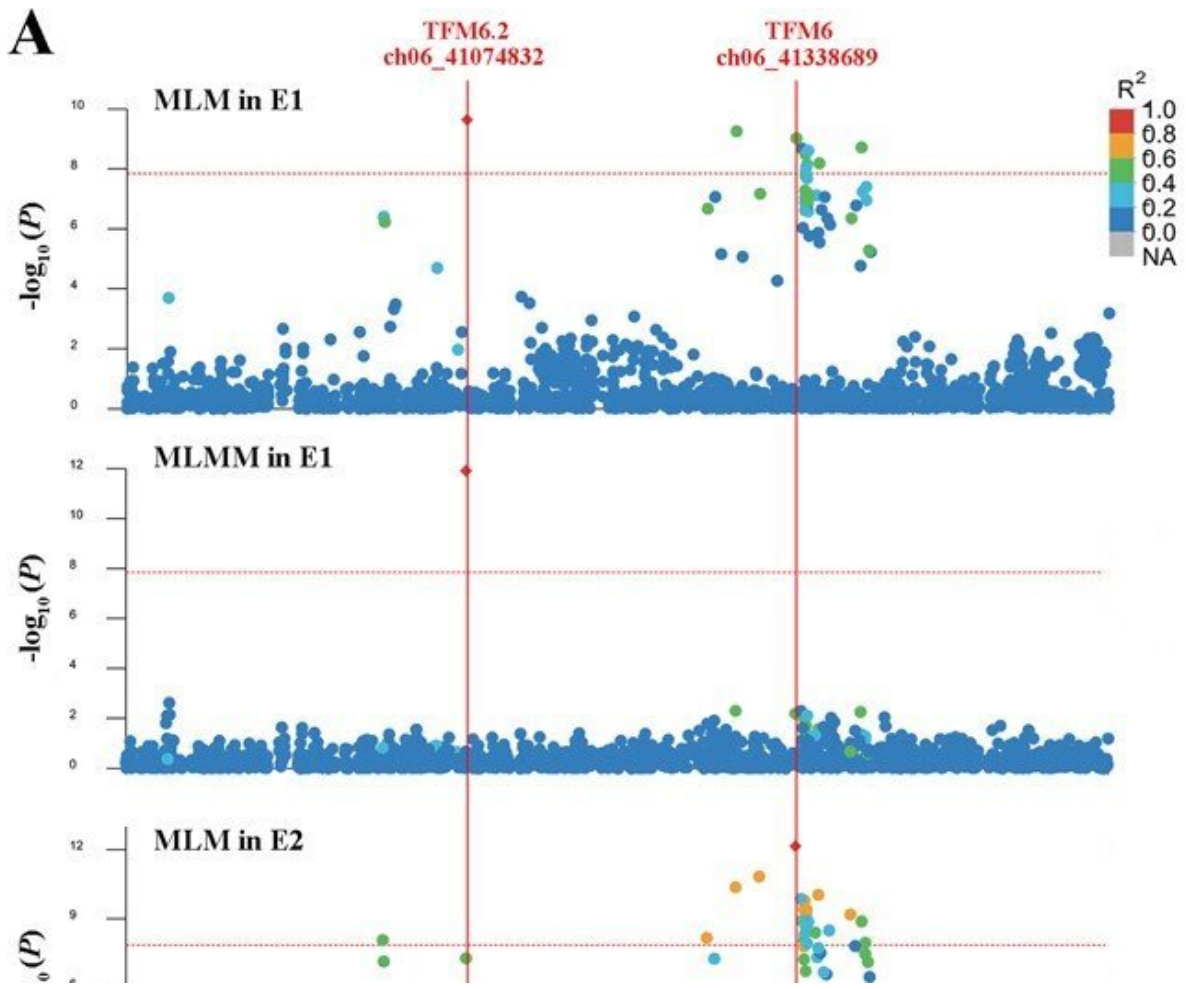
Multiple-model GWAS identifies optimal allelic combinations of quantitative trait loci for malic acid in tomato

April 24 2023



The dotted red lines through the figure denote the SNPs ch06_41074832 and ch06_41338689. (A) Detailed plots selected from representative GWAS results in region 40.8–41.59 Mb on chromosome 6 (x-axis). Lead SNPs in each plot are

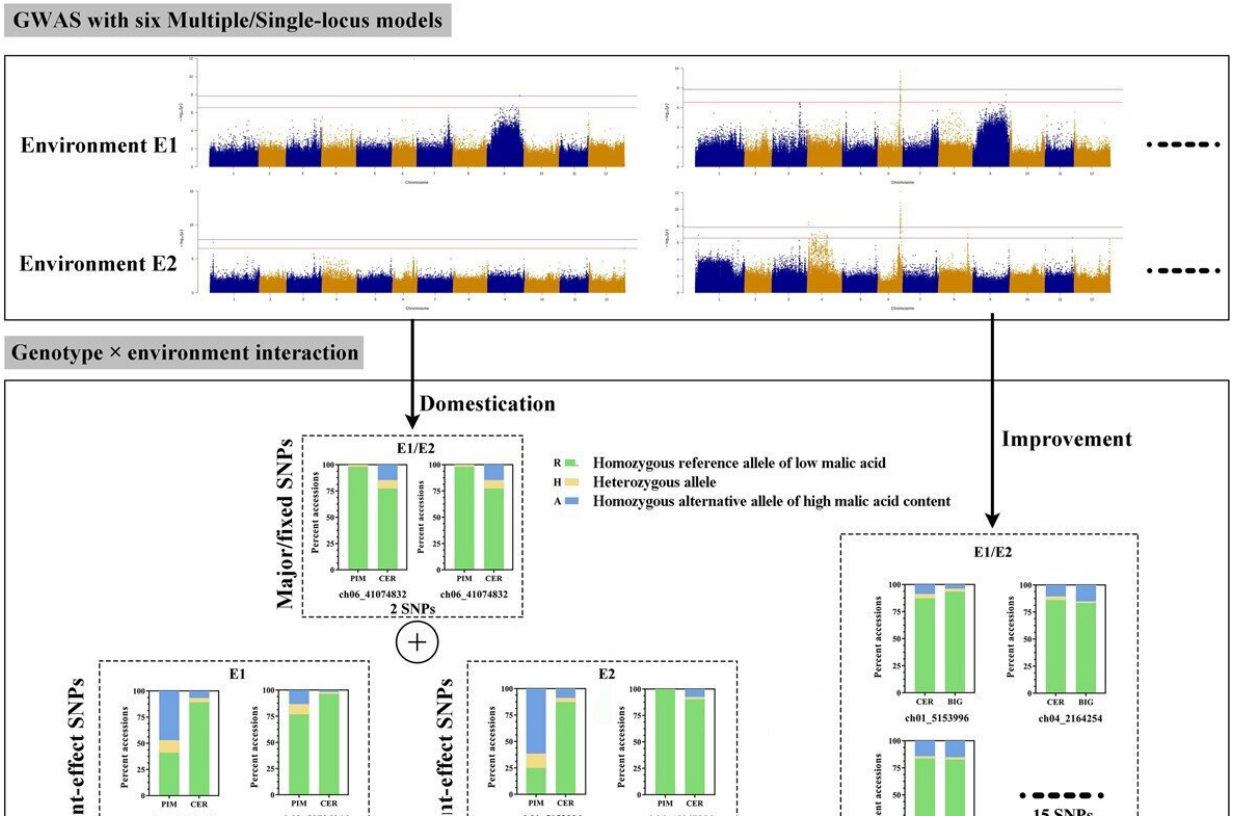
indicated in red. The pairwise R2 values among all SNPs are given in the color scale. The solid red lines indicate the significance threshold of the P-value (1.41 × 10−8). (B) Heat map depicting the LD block in the 0.79 M genomic region corresponding to (A). The LD blocks within this region are indicated with a black border. The R2 values are indicated in the color scale. Magenta and green vertical lines represent SNPs located in LD blocks and orange vertical lines represent no SNP. The green slashes indicate the position of the SNPs in the LD blocks. (C) Candidate gene models. For each gene model, blue boxes represent untranslated regions, yellow boxes represent coding sequences, thin black lines between boxes represent introns, and thick black arrows indicate gene orientation. The T to A change in the forward strand DNA converts an AAG codon (Gln) to a TAG in the reverse strand (coding DNA strand), causing premature termination of translation. A previous study has proved that Solyc06g072910 and Solyc06g072920 are a single gene. Credit: *Horticulture Research* (2023). DOI: 10.1093/hr/uhad021

A study published in the journal *Horticulture Research* sought to identify loci and decipher the polygenic architecture of malic acid content in tomato fruit. The authors carried out a GWAS using six milestone models with two-environment repeats. A series of associated SNP variations were identified from GWAS, and 15 high-confidence annotated genes were obtained based on the lead SNPs and the malic acid accumulation.

The optimal allelic combination of the 15 loci was presented for tastier tomato. The genetic parameters of population-differentiation were employed to identify potential selective sweep signals on malic acid during domestication and improvement.

The authors identified natural variations underlying malic acid in tomato with multiple-model GWAS. This study will provide new genetic insights into how tomato malic acid content evolved during breeding and

optional QTL combinations for higher malic acid in tomato.



Workflow of the genome-based selection of loci for MA accumulation. Credit: *Horticulture Research* (2023). DOI: 10.1093/hr/uhad021

More information: Wenxian Gai et al, Multiple-model GWAS identifies optimal allelic combinations of quantitative trait loci for malic acid in tomato, *Horticulture Research* (2023). DOI: 10.1093/hr/uhad021

Provided by NanJing Agricultural University

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