From wild relatives to super tomatoes: Unearthing new genetic potential

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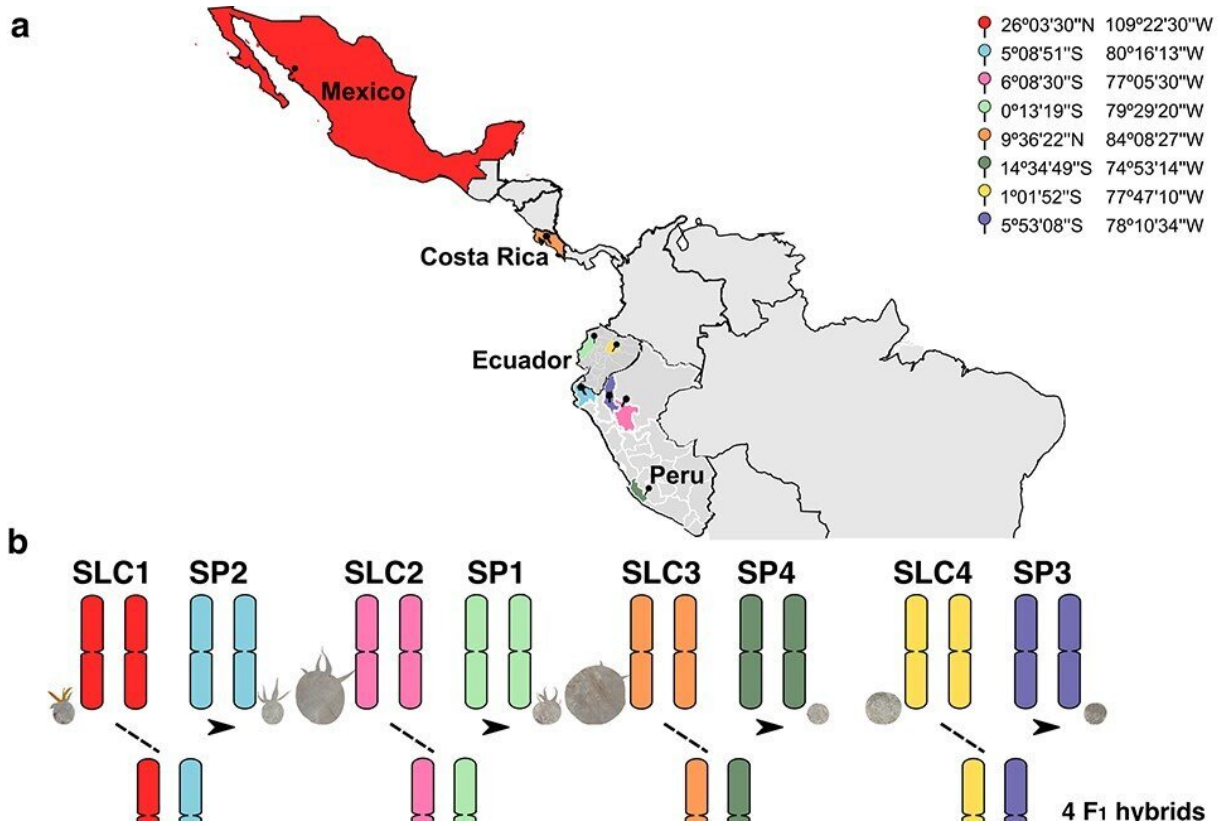

(A) Origin of the different SLC and SP founders selected for the ToMAGIC population development represented with the different colour codes. (B) The funnel breeding design to develop the 354 ToMAGIC lines. The eight founders with a different colour to represent their genomic background are represented at a scale based on the real fruit size. Arrows indicate the direction of the cross. (C) Distribution of the 6488 filtered markers (in red), the Heinz 1706 SL4.0 annotated genes (in light green), and the genes covered by the filtered markers (in dark green) across the 12 tomato chromosomes. Credit: *Horticulture Research*

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Tomato breeding has historically depended on a narrow genetic pool, leading to decreased diversity and loss of valuable traits. Traditional methods and biparental populations fall short in harnessing the full potential of wild relatives, posing challenges in improving traits like fruit size, disease resistance, and adaptability. Addressing these challenges, comprehensive genetic resources that integrate diverse alleles from wild and weedy tomatoes are essential for discovering novel genes and boosting breeding efficiency.

In collaboration with ENEA, researchers from the Universitat Politècnica de València developed an eight-way tomato Multiparental advanced generation intercross (MAGIC) population combining Solanum lycopersicum var. cerasiforme and Solanum pimpinellifolium.

Published in *Horticulture Research* on June 3, 2024, the study highlights how this population aids in identifying genes associated with key traits. By intercrossing eight founders with diverse genetic backgrounds, the team created 354 genotyped lines, bridging the gap between wild and cultivated tomatoes and providing breeders with a powerful tool for crop improvement.

The tomato MAGIC (ToMAGIC) population comprises 354 lines derived from eight diverse founder lines of wild and weedy tomatoes, revealing 6,488 high-quality SNPs. Phenotyping identified associations with traits such as fruit size, leaf morphology, and pigmentation.

Notably, the WUSCHEL gene was linked to locule number, a crucial trait in domestication, while the FW2.2 gene was associated with fruit weight. Dominant wild alleles offer potential for enhancing cultivated

varieties. A novel mutation in the SlMYB-ATV gene was also discovered, influencing anthocyanin production, particularly in cold-adapted founders. These findings underscore ToMAGIC's role in uncovering genetic variations crucial for developing resilient, productive tomatoes.

"The ToMAGIC population marks a major advancement in tomato genetics," stated Dr. Santiago Vilanova, the study's senior researcher from the Universitat Politècnica de València. "By incorporating wild and weedy relatives, we've created a resource that not only taps into uncharted genetic diversity but also enhances our ability to discover and validate genes. This breakthrough enables us to overcome genetic limitations and develop superior tomato cultivars with enhanced traits."

The ToMAGIC population holds significant potential for tomato breeding, offering a pathway to integrate wild genetic diversity into breeding programs. It helps identify novel genes governing key traits, enabling the creation of resilient, high-yielding tomato varieties. Beyond research, ToMAGIC can directly impact the selection of elite lines for commercial breeding, enhancing crop performance across varying environments and meeting the rising demand for better agricultural productivity.

More information: Andrea Arrones et al, A novel tomato interspecific (Solanum lycopersicum var. cerasiforme and Solanum pimpinellifolium) MAGIC population facilitates trait association and candidate gene discovery in untapped exotic germplasm, *Horticulture Research* (2024). DOI: 10.1093/hr/uhae154

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