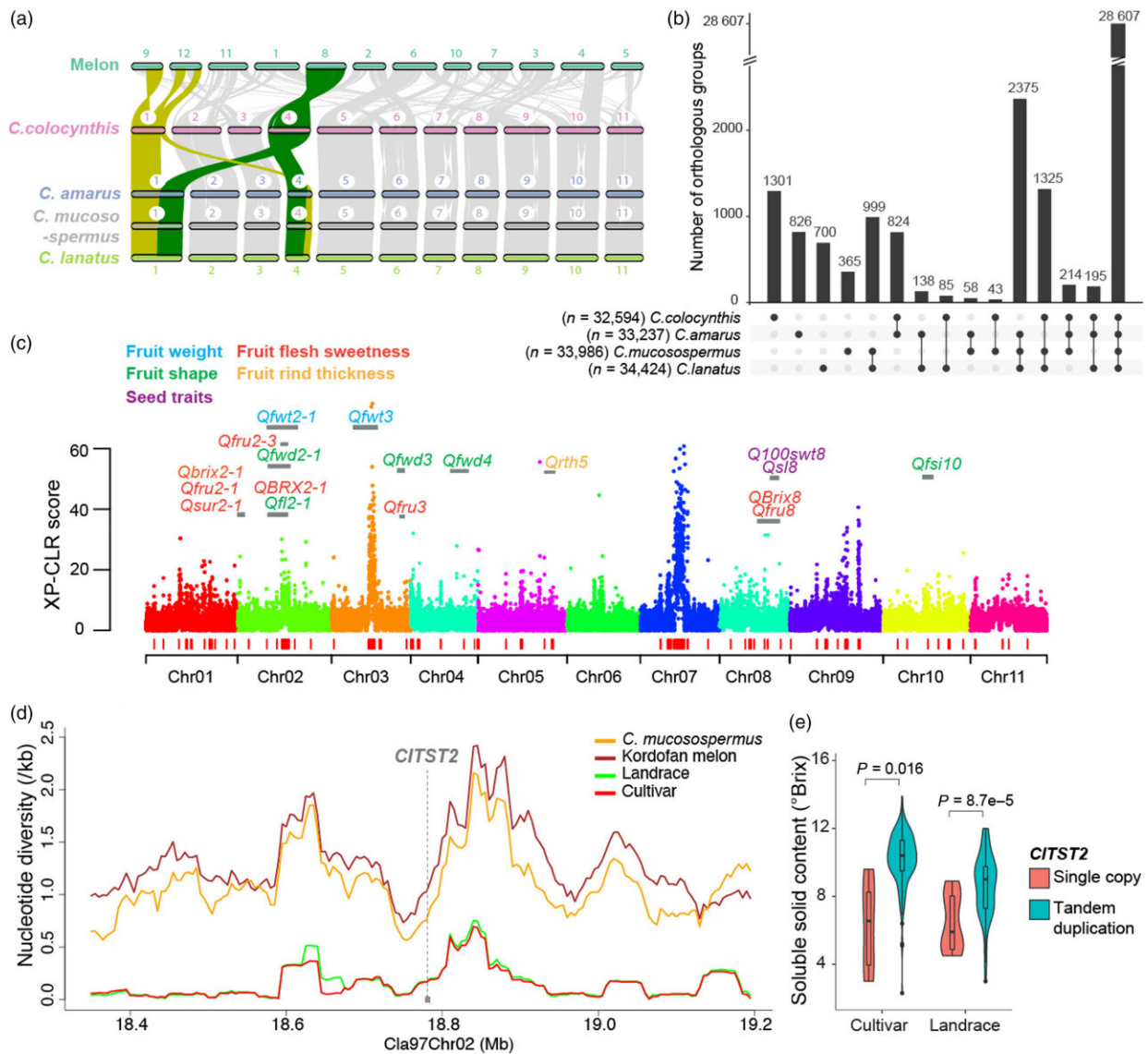


Behind the rind: New genomic insights into watermelon evolution, quality, and resilience

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Citrullus genus super-pangenome reveals variations in wild and cultivated watermelons. (a) Synteny among the genomes of melon and various watermelon

species. Genomic regions syntenic to *C. colocynthis* chromosomes 1 and 4 are highlighted in yellow and green, respectively. (b) Upset diagram of orthologous groups among the four watermelon species. (c) Domestication sweeps detected through comparing landraces to Kordofan melons. Red bars at the bottom indicate genomic regions under selection. (d) Nucleotide diversities in genome regions surrounding the *CITST2* gene in different watermelon populations. (e) Comparison of fruit flesh sweetness between accessions carrying the two different alleles of *CITST2*, using *t*-test with unequal variance. Credit: *Plant Biotechnology Journal* (2023). DOI: 10.1111/pbi.14120

Watermelon is a globally significant agricultural product, both in terms of the total amount produced and the total economic value generated.

Scientists at the Boyce Thompson Institute have constructed a comprehensive "super-pangenome" for [watermelon](#) and its wild relatives, uncovering beneficial genes lost during domestication that could improve [disease resistance](#) and fruit quality of this vital fruit crop.

"We aimed to delve deeper into the genetic variations that make watermelons so diverse and unique," stated Professor Zhangjun Fei, the study's lead author. "Our findings not only provide insights into the evolutionary journey of watermelons but also present significant implications for breeding and disease resistance."

The watermelon super-pangenome was built using reference genome sequences and genome resequencing data from 547 watermelon accessions spanning four species—cultivated watermelon (*Citrullus lanatus*) and its wild relatives *C. mucosospermus*, *C. amarus*, and *C. colocynthis*.

Analyses of the super-pangenome revealed that many disease-resistance genes present in wild species were lost during domestication, as early

farmers selected for fruit quality traits like sweetness, flesh color, and rind thickness. "These beneficial genes could be reintroduced into modern cultivars to breed more resilient watermelon varieties," noted Fei.

A key discovery of the research, recently published in the *Plant Biotechnology Journal*, was the identification of a tandem duplication of the sugar transporter gene CITST2 that enhances sugar accumulation and fruit sweetness in cultivated watermelon. This genetic variant was rare in wild watermelons but was selected during domestication.

"The super-pangenome provides a valuable genetic toolkit for breeders and researchers to improve cultivated watermelon," said Fei. "By understanding the genetic makeup and evolutionary patterns of watermelons, we can develop varieties with enhanced yield, increased disease resistance, and improved adaptability."

More information: Shan Wu et al, A *Citrullus* genus super-pangenome reveals extensive variations in wild and cultivated watermelons and sheds light on watermelon evolution and domestication, *Plant Biotechnology Journal* (2023). [DOI: 10.1111/pbi.14120](https://doi.org/10.1111/pbi.14120)

Provided by Boyce Thompson Institute

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