

IMPACT OF STRUCTURAL AND EPIGENETIC VARIATION ON QUANTITATIVE TRAITS DURING TOMATO DOMESTICATION

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structural variation, quantitative traits, epigenetic variation, gene editing, tomato

Structural variation has fueled phenotypic diversification and underlies important domestication and quantitative traits in crop plants. Nevertheless, the genetic drivers of plant structural variation at the population level remain poorly understood. We recently reported long-read sequencing of 100 diverse tomato genomes, which captured the extent and genomic features of structural variants. We demonstrate that SVs are widespread between domesticated and wild tomato genomes and that they underlie a large fraction of phenotypes selected during tomato domestication and breeding. Among the most prominent SVs are TEs and

related repeats, which can impact gene expression and phenotypes in various ways, including coding and cis-regulatory sequence disruption, but also through epigenetic effects such as DNA methylation. To evaluate the contribution of the aforementioned mechanisms to quantitative trait variation, we have selected a gene controlling fruit development, harboring TE-induced SVs overlapping with regulatory sequences, and that was inactivated during tomato domestication. To disentangle the contribution of genetic and epigenetic mechanisms to the loss of gene expression in domesticated tomato, we have harnessed CRISPR-based systems to attempt manipulation of local transcription and epigenetic patterns, to quantitatively modulate fruit traits. This work sheds light on the complexity of molecular causes underlying gene silencing by SVs, and provides a roadmap for engineering changes in gene activity and traits of agronomic value in tomato and other crops.