

From domestication to modern breeding: what have learned from genetic resources in tomato?

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"From Domestication to modern breeding: what have learned from genetic resources in tomato?"

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The tomato is one of the most produced vegetable in the world and this species is also a model in science to the study of fruit development. Over the past 60 years, many sampling campaigns in Central and South America (source area) helped preserving more than 80,000 accessions of this species, including most of its crop wild relatives. In parallel, the contribution of molecular biology through the development of molecular markers was used to map many QTLs for traits of agronomic interest such as fruit quality and resistance to biotic and abiotic stresses. Since 2012, date of publication of the tomato genome, the combination of the rich genetic resources and high-throughput genomic was used to extend the work to a genome-wide scale to better understand its dynamic, to identify large amount of polymorphic sites but also revisiting scientific questions, such as the evolutionary history (i.e. domestication) of this species and the study of the genetic architecture of quantitative traits through new approaches such as genome-wide association study (GWAS) or genomic selection genomics. The genetic resources of this species are essential for fundamental scientific research but also for the genetic improvement of this species.

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