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► To cite this version:

Christopher Sauvage, Benoit Nabholz, S. Gautier, M. Ruiz, Mathilde M. Causse, et al.. The study of domestication reveals a loss of diversity, signature of selection and transcriptional modifications in tomato (*Solanum lycopersicum*). XVIIIth Eucarpia Meeting, Vegetable section, Tomato Working group, Apr 2014, Avignon, France. 1 p. hal-02794508

HAL Id: hal-02794508

<https://hal.inrae.fr/hal-02794508>

Submitted on 5 Jun 2020

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T004 - Christopher Sauvage

The study of domestication reveals a loss of diversity, signature of selection and transcriptional modifications in tomato (*Solanum lycopersicum*)

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Over the last 13,000 years, plant domestication has led to considerable phenotypic modifications through selective breeding. Though changes in key traits such as fruit morphology have been well documented, little is known about the underlying molecular consequences. The comparative study of cultivated and current wild type crop populations should measure the effects of domestication, as this phenomenon is intense, recent and accompanied by selective signatures. Up to now, there have been a limited number of large-scale screens to detect selection in crops using high-throughput Sequencing (HTS). Using the autogamous crop *Solanum lycopersicum* (tomato) and its wild relative (*S. pimpinellifolium*), we investigated the genome-wide signature of domestication at the molecular level.

The HTS of 10 wild and 10 cultivated transcriptomes revealed that 12168/34727 (35%) of the genes experienced a 33% averaged loss of nucleotide diversity following domestication. Regions associated to a loss of diversity, representing candidate regions selected during domestication, were identified across the genome. Tajima's D statistic supported these observations and revealed that 4.4% of the genes were under positive or balancing selection. Average π_N / π_S ratios were estimated to 0.252 and 0.291 in cultivated and wild types, respectively. Moreover, 1.87% and 3.01% of the genes showed ratios over 1, suggesting a signature of positive selection. The analysis of site frequency spectrum across the genome revealed at least two regions showing hard selective sweep. At the transcriptional level, domestication significantly affected 3.39% of the genes with fold changes ranging from -8.99× to +7.85×.

Overall, we evidenced that domestication in tomato has led to loss of nucleotide diversity detectable at the scale of the genome. Moreover, high deviations from neutrality and transcriptional modifications were identified, providing new insights into the domestication process of tomato as well as valuable markers for breeding.

Keywords: genomic, domestication, tomato, diversity