



# The use of a multi-locus mixed model approach for GWAS reveals associations for metabolic traits in the tomato, *Solanum lycopersicum*

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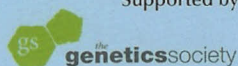
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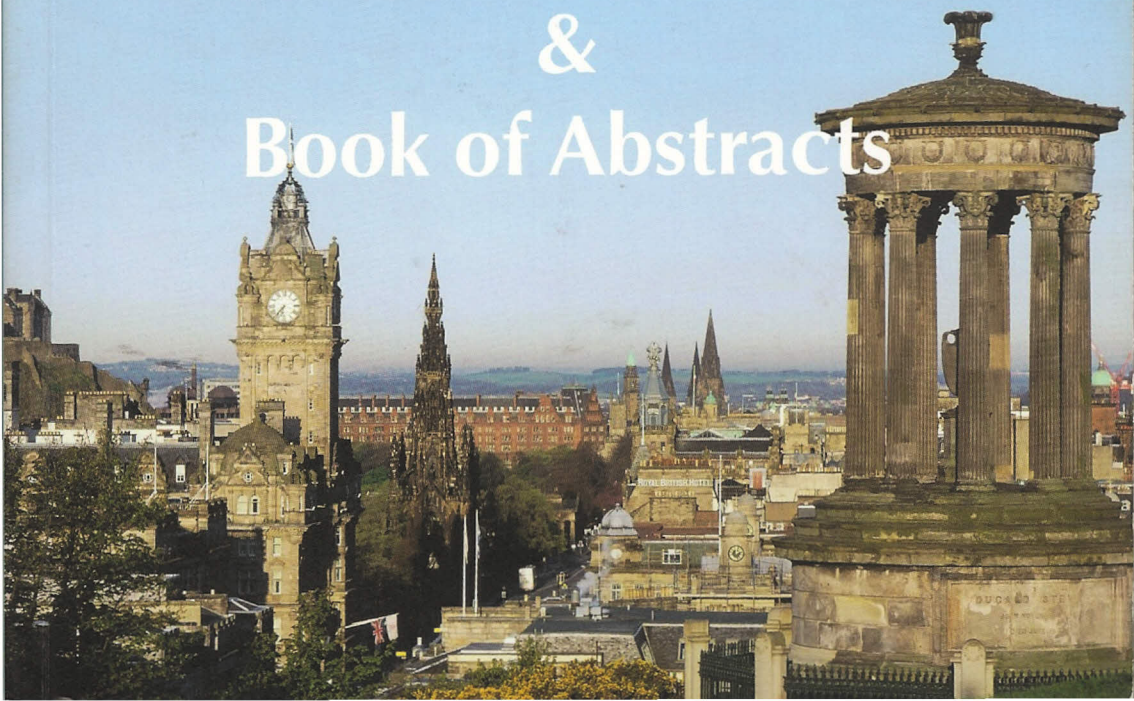
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**THE USE OF A MULTI-LOCUS MIXED MODEL APPROACH FOR GWAS REVEALS ASSOCIATIONS FOR METABOLIC TRAITS IN THE TOMATO, SOLANUM LYCOPERSICUM**

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Genome-wide association studies have been successful in identifying genes involved in polygenic traits notably in crops, towards their improvement. We propose to apply in a major crop, such as tomato, a recently developed multi-locus mixed model as a general method for mapping complex traits in structured populations (Segura et al., 2012). Among major crops, tomato (*Solanum lycopersicum*), is an highly valuable vegetable in the world for its health value (Causse et al. 2010). SNP beadchip (Hamilton et al., 2012) are available and enable GWAS for traits of interest. Recently, a pilot study defined the optimal conditions for GWAS by using cherry tomato accessions (Ranc et al., 2012).

In our study, we examined a core collection of 180 tomato varieties composed of 20 wild accessions (*S. pimpinellifolium*), 130 admixed accessions (*S. cerasiforme*) and 30 domesticated accessions (*S. lycopersicum*). Multi-locus GWAS analysis was conducted using the MLM package (Segura et al., 2012) with 7700 SNP markers and a set of sugar-related, Vitamin C-related and morphological traits as well as a broad range of metabolites related to central carbon metabolism.

The present study is the first one in tomato reporting associations for a large set of traits at the genome scale. We found significant associations for 89 loci with a total of 19 traits including fresh weight, sucrose, ascorbate dehydrogenase, malate or citrate, notably. Identified loci were also concordant with published quantitative trait loci (i.e. Malate), while new loci were identified (for Tocopherol). Moreover, several related metabolites, such as citrate and malate (both involved in Krebs cycle) displayed two identical associations.

These results (1) provide a list of candidate loci to be functionally validated and (2) provide a powerful analytical approach for finding genetic variants that can be directly used for crop improvement and deciphering the genetic architecture of complex trait.