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Poster Communication Abstract – 2.49

INVESTIGATING THE NUCLEOTIDE DIVERSITY IN THE GLUTATHIONE S-TRANSFERASE GENE FAMILY ACROSS THE TOMATO GENE POOL AND ITS SIGNIFICANCE IN CONTROLLING PLANT RESPONSE TO STRESS

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The agricultural sector faces a significant challenge in dealing with environmental stresses, which greatly reduce crop productivity. Due to global warming and climate change, abiotic stresses are predicted to become more frequent. In this scenario, to meet a growing global demand for food, breeding crops for enhanced tolerance to harsh environments is promising. The cultivated tomato (*Solanum lycopersicum* L.) is one of the most important vegetable crops in the world and the genome of its wild relatives *Solanum pimpinellifolium*, *Solanum lycopersicoides* and *Solanum pennellii* have been sequenced and their effective tolerance to extreme environments well documented. However, knowledge about tomato genetic diversity is limited and its phenotypic significance dramatically unpredictable to make its exploitation proficient. Glutathione S-transferase (GST) genes have been identified in numerous plant species and are involved in various physiological, developmental, and stress modulation pathways. The aim of this study was to provide a comprehensive description of the GST nucleotide diversity in the tomato gene pool and contextual mining of functional significance for plant adaptability to challenging stresses. We identified 83 GST genes in *Solanum lycopersicum* (ITAG 4.1) and their orthologues within the wild relatives. Sequences were analyzed for their exon-intron structures, conserved protein motifs, putative subcellular locations, phylogenetic relationships and duplication events. Interaction networks,

promoter and cis-regulatory elements and gene expression profiles were also identified. Phylogenetic analysis enabled grouping GST genes into ten subclasses. Furthermore, protein–protein interaction networks revealed the central role of GST genes controlling the cell redox state. A reference non-redundant core collection of 75 tomato genotypes was selected from a larger collection of worldwide accessions genotyped by SSR markers. The core collection was screened for drought tolerance at the fruit set stage on the first flower truss. The leaves were assayed for gas exchange and colorimetric variations and profiled for H2O2, ascorbic acid and antioxidant capacity. The most tolerant and sensitive tomato accessions were selected. Plants were grown in lysimeters where the water supply was managed to apply two levels of soil water potential that is 10-20 kPa in the control treatment and 100-120 kPa for the drought treatment, respectively. To deepen our understanding of the regulatory mechanisms that control photo-assimilation, photo-assimilate allocation and fruit yield and quality under limited levels of available water, leaves, stems and fruit at different ripening stages were collected for RNA-seq analysis. Further bioinformatics analysis will allow us to validate the role of specific GSTs and other key genes in controlling the response of tomato plants to drought and modulating photo-assimilate allocation in sensitive and tolerant genomic backgrounds.