

FUNCTIONAL CHARACTERIZATION OF A TOMATO GST GENE UNDER DIFFERENT ABIOTIC STRESSES

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Glutathione S-transferases, Solanum lycopersicum, Nicotiana tabacum, salt stress, drought stress

Climate change poses a formidable obstacle in addressing the exponential growth of the global population and the escalating demand for food. Abiotic stresses, such as drought and salinity, exert negative impacts on stomatal conductance, crop growth, and yield. Furthermore, these abiotic stresses trigger the accumulation of reactive oxygen species (ROS) within plant cells, leading to detrimental physiological damage and provoking oxidative stress responses.

To mitigate ROS accumulation, plant cells deploy several antioxidants and antioxidant enzymes. A significant group in this context includes the glutathione S-transferase (GST) superfamily encoded at genomic level by a complex gene family involved in stress tolerance and xenobiotic detoxification. Depending on their gene organization, sequence similarity and functions, plant GSTs could be grouped into several classes. Previous results proved the pivotal role of Tau class members in abiotic stress response and highlighted their contribution in enhancing plant tolerance.

Our goal was to investigate the role of the tomato gene Solyc07g056420, encoding for a Tau GST, in controlling the plant response to two key abiotic stresses, i. e. drought and salinity.

Three months-old T3 offspring tobacco transgenic plants over-expressing the tomato Solyc07g056420 (0E_gst) were treated with a 50% rate of

reintegration of lost water (half water restitution – HWR) and showed a significantly higher levels in leaf chlorophyll A, chlorophyll B, flavonoids and antioxidant capacity compared to wild type plants. Conversely, OE_{gst} plants supplied with salinized water responded with a significant lower increase in antioxidants capacity and a lower decrease in the flavonoids contents than wild type plants.

Results underlined the role of Solyc07g056420 in mediating abiotic stress response and the control of the cell redox. These findings pave the way for development of new plants more tolerant to environmental stresses.

Ongoing transcriptomic analysis will further investigate the role of the tomato Solyc07g056420 in controlling the expression of genes involve in the Foyer-Halliwel–Asada cycle.