

***In silico* GENOME WIDE SEARCH FOR PUTATIVE GENES OF THE ANTIOXIDANT KEY ENZYMES INVOLVED IN THE PHYSIOLOGICAL ELIMINATION OF ROS**

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Biotic and abiotic stresses such as wounding, heavy metals, illumination, temperature extremes, drought or salt stress cause an increase of reactive oxygen species (ROS) which are related with programmed cell death (PCD). Thus, the accumulation of ROS increase activity of catalase (CAT), ascorbate peroxidase (APX) and superoxide dismutase (SOD) which take part of cell defense mechanism against ROS. In grafted plants, vascular elements are regenerated by complex processes and the rootstock can be successful or incompatible. Whereas the biological formation of incompatible and compatible grafts are similar at the early phase of development, it has been reported that oxidative stress change at the point of union in incompatible herbaceous grafts. In this work, we have performed an *in silico* assessment of genes involved in ROS elimination. APX, SOD and CAT were identified by BLAST searches in Peach, Malus and Arabidopsis genomes. Evolutionary relationships were inferred by phylogenetic analysis of aligned amino acid sequences for each gene family showing that they were highly conserved among the Rosaceae family. Additionally, specific gene expression and enzymatic activity were assayed in different kind of pear and quince tissues used for vegetable grafting studies. The results showed that SOD activity was higher than APX and CAT in callus tissue. Work is currently ongoing to determine gen expression and activity of these antioxidant enzymes in different graft combinations at different developmental stages.