

GENOME-WIDE IDENTIFICATION AND EXPRESSION ANALYSIS OF THE GLUTAREDOXIN GENE FAMILY IN SOLANACEAE INDICATE A ROLE OF CC-TYPE IN DEFENSE RESPONSES OF PLANTS TO PATHOGENS

ESPOSITO S.*, CAPPETTA E.**, TRANCHIDA-LOMBARDO V.**, TUCCI M.**, DE PALMA M.**

*) Research Centre for Cereal and Industrial Crops, CREA-CI, CREA, Foggia, Italy

**) Institute of Biosciences and BioResources, IBBR, CNR, Portici (NA), Italy

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Glutaredoxins (GRXs) are ubiquitous glutathione-dependent oxidoreductases that catalyze reduction of protein disulfide bridges or the reduction of mixed disulfides bond between glutathione and protein in plant cells. These enzymes play a key role in defense against oxidative stress but there is growing evidence that GRXs are also involved in cell signaling and development.

Despite this gene family has been characterized in model and crop species, information is still lacking for *Solanaceae*, one of the most relevant plant families worldwide. To fill this gap, we performed a genome-wide analysis of the *GRXs* gene family in *Solanum lycopersicum*, *S. tuberosum*, *S. melongena* and *Capsicum annuum* to explore their structure-function and evolution. Using the latest genome release of each species, a total of 283 *GRXs* genes were identified (58 in tomato, 60 in potato, 69 in eggplant and 79 in pepper). Phylogenetic analysis divided our candidates into the four classes CPYC-, CGFS-, GRL- and CC-type, and highlighted a higher diversity in terms of number of candidates belonging to CC-type in the four genomes. The distribution and synteny of these candidates on chromosomes were also determined. An uneven distribution of *GRXs* on the 12 chromosomes was observed among the four species, with the highest number of candidates anchored on chromosomes 2 and 5 in pepper, on chromosome 11 in eggplant and on chromosome 4 in tomato and potato. Interestingly, on this latter chromosome we disclosed a cluster of *GRXs* candidates of the land plants-specific CC-type class, which arose through tandem duplications. To investigate the possible role of these events in the functional evolution of CC-type *GRXs*, an in-depth characterization of duplicated tandem CC-type candidates was carried out in tomato, widely recognized as a model organism for *Solanaceae*. A cis-regulatory elements analysis of putative promoter sequences allowed us to discover different elements within the cluster of *GRXs*, suggesting possible roles in plant development, hormone responses, and biotic and abiotic stress responses. Specific *GRXs*, selected on the basis of differences in the promoter elements, revealed divergent expression profiles during the progression of pathogen infection caused by *Botrytis cinerea*. This study provides new insights into the identification, structure and evolution of the *GRXs* gene family in *Solanaceae* and paves the way for their possible exploitation for crop improvement. The presented data suggest that duplications played a major role in the evolution of plant-specific CC-type *GRXs* and give hints on the potential role of their tandem duplications following biotic stress.