Antioxidant Gene Network of *Arabidopsis* thaliana and its response towards heat stress

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INTRODUCTION. Most living beings have oxidative phosphorylation mechanism, which generates reactive oxygen species (ROS). Therefore, cells tend to develop antioxidant mechanism to balance ROS production and avoid oxidative damage. Plants have wide (enzymatic and non-enzymatic) antioxidant defenses which can also protect against stress agents. Several antioxidant genes are described and recent works have classified them following some criteria: antioxidant enzymatic function, participation in redox reactions and molecular interactions directly related to antioxidant activity. Based on those, a *Homo sapiens* antioxidant gene network was built to characterize interactions existing among different antioxidant gene products and their substrates. This opened a new panorama to observe antioxidant defense as one system. **OBJECTIVE:** Since there is no similar research for plants, this work builds the antioxidant gene network from *Arabidopsis thaliana* and assess its responses facing heat stress. **MATERIAL AND METHODS:** *A. thaliana* antioxidant genes were retrieved from Gene Ontology term GO:0072593 and TAIR database. Genes were manually curated to minimize redundancy. PPI networks were built using STITCHv4.0 (experimental, database, predicted data, confidence score 0.700). Heat stress was assessed using *limma* R package for differentially expressed genes (DEG) on public dataset GSE63128, retrieved from GEO database. **RESULTS AND DISCUSSION:** We found 212 annotated antioxidant genes, divided in: peroxidase (97), thiol-redox (105), and superoxide-dismutase (SOD,10) from *A. thaliana* and set to interaction network. Two functional clusters were evident: class III peroxidase and mixing peroxidases/SOD. Most thiol-redox surrounds the clusters, suggesting a key interactive role of this protein class on the antioxidant system. Most DEGs from GSE63128 were thiol-redox and were mostly downregulated both on recovery and direct heat situations, while most peroxidases were upregulated. **CONCLUSION:** The inferred antioxidant network was shown responsive and representative. Most network genes were differentially expressed and belong to different functional clusters, which corroborate with the interactive role of thiol-redox hypothesis.

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