

ALTERNATIVE PATHWAY CONTRIBUTIONS TO ANTIOXIDANT ACCUMULATION INTO PLANT RESPONSE TO DIFFERENT STRESSES

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Health-beneficial properties of many secondary plant metabolites have created much interest into the control of their biosynthesis in crop species. Phenolic compounds, L-ascorbic acid (AsA or vitamin C) and other antioxidant molecules make up an important group of such phytonutrients which could be responsible, at last in part, for the protective effect against some chronic degenerative diseases.

Despite the well supported and nearly complete establishment of both many AsA and phenolics pathways and the involvement of genes encoding key activities and transcription factors the understanding of the genetic control of antioxidant accumulation remains still elusive.

However, it is well established that plants modulate antioxidant biosynthesis in response to stress stimuli. As a result, stressed plants may represent a proper environment to study genetic control mechanisms of antioxidant accumulation.

This study is aimed at investigating the overall transcriptional regulation process controlling AsA and phenolics accumulation in response to oxidative and salt stresses. Two *Arabidopsis* populations were deepened into H₂O₂ (5 and 50 mM) in order to apply an oxidative stress. Similarly, another population was floated with a 300 mM NaCl solution to apply a saline stress. Harvested leaves were used to extract and quantify AsA and phenols, as well as to purify mRNA, at different time points after the application of the stress. The oxidative stress resulted in a significant reduction of the AsA accumulation and the reduction was consistent with the intensity of the stress. By contrast, no change in phenol concentration was observed as a consequence of the oxidative treatment. Conversely, the saline stress application showed a significant leaf enrichment of phenol compounds. The same saline stress did not result in significant changes in AsA concentration. This finding suggests that the response of plant antioxidant metabolism depends on the stress applied.

Finally, putatively involved gene families were identified in GeneBank and sequence-specific primers for the relative quantification by qPCR of each transcript were designed. Further efforts will focus on the identification of single transcript modulation and co-regulation mechanisms comprehensively integrating AsA and phenols metabolisms, alternative pathways and specific stress responses.