

IDENTIFICATION OF KEY GENES INVOLVED IN PEROXISOME-DEPENDENT SIGNALLING IN PLANT RESPONSE TO STRESS

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Reactive oxygen species (ROS) act as secondary messengers that can be sensed by specific redox sensitive proteins responsible for the activation of signal transduction culminating in altered gene expression. The subcellular site, in which modifications in ROS/oxidation state occur, can also act as a specific cellular redox network signal. The chemical identity of ROS and their subcellular origin actually is a specific imprint on the transcriptome response. In recent years, a number of transcriptomic studies related to altered ROS metabolism in plant peroxisomes have been carried out. In this study, we made a meta-analysis of these transcriptomic findings to identify common transcriptional footprints for plant peroxisomal-dependent signalling at early and later time points. These footprints highlight the regulation of various metabolic pathways and gene families, which are also found in plant responses to several abiotic stresses. Major peroxisomal-dependent genes are associated with protein and endoplasmic reticulum (ER) protection at later stages of stress while, at earlier stages, these genes are related to hormone biosynthesis and signalling regulation. Further identification of peroxisome-dependent transcription factors has been carried out, involving key TF families such as NAC, WRKY, bHLH and ERF.

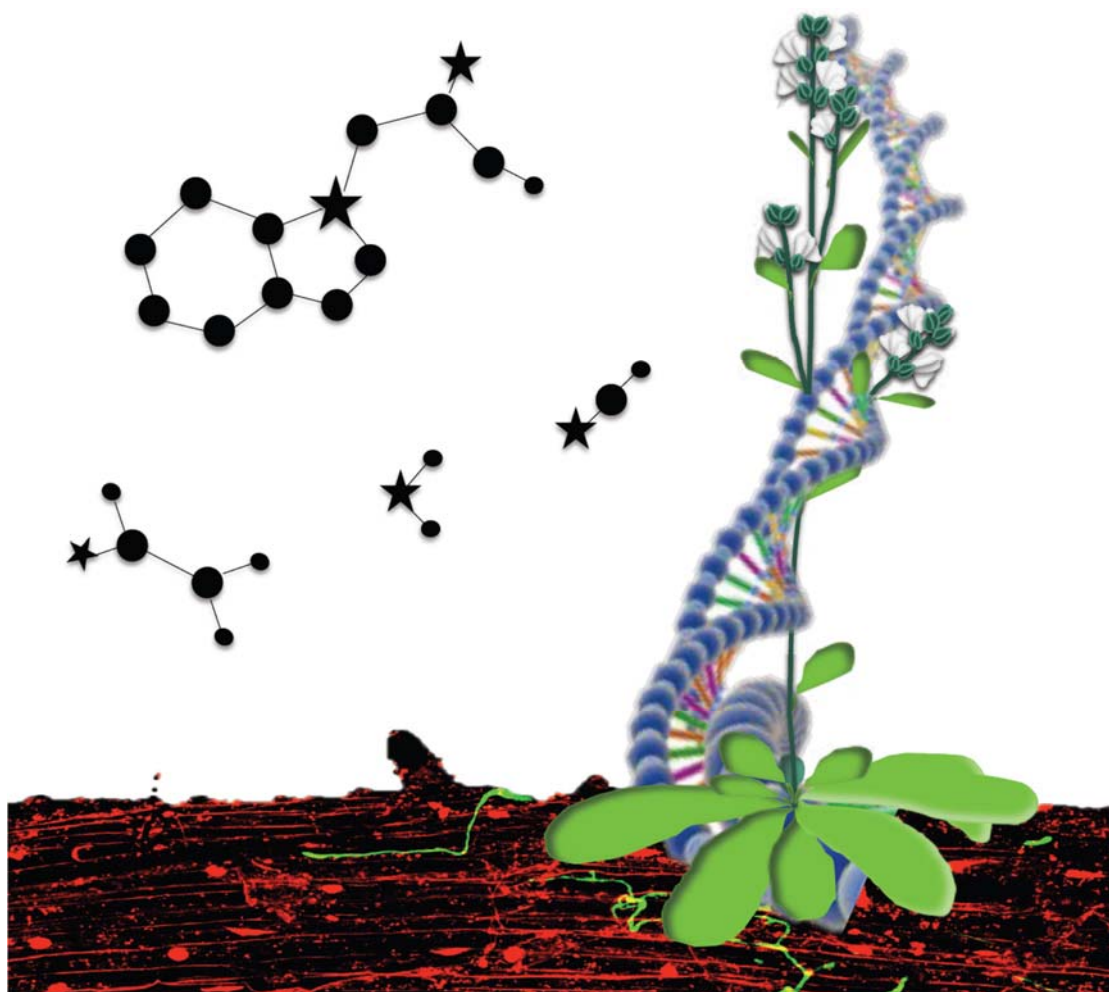
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ABSTRACT BOOK



FUNCTIONAL CHARACTERIZATION OF α/β -HYDROLASE DLK2 AS A REGULATORY ELEMENT IN THE ARBUSCULAR MYCORRHIZAL SYMBIOSIS IN TOMATO PLANTS

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The Arbuscular Mycorrhizal (AM) association is a symbiotic association that occurs between plant roots and a group of AM forming fungi from the *Glomeromycota* phylum. The relationship favours the plant by providing it with a greater amount of nutrients, improving its development, as well as its ability to withstand environmental stresses. All this means that this interaction has a high ecological importance and makes it interesting for study and biotechnological improvement.

It is known that mycorrhization stimulates the metabolism of apocarotenoids in the root and that at least one group of them, specific to mycorrhizal roots, have a regulatory role in the life cycle of the arbuscules, the symbiotic structures of nutrient exchange, accelerating the senescence of the mature ones and enabling the replacement by younger ones. It is not well known how the process works, but it is known that Phosphate deficiency stimulates the expression of genes for the metabolism of apocarotenoids (including strigolactones) that code for enzymes that cut and split carotenoids (CCDs) responsible for the generation of these compounds.

In our laboratory, we have identified a gene that codes for an α/β -hydrolase protein, called DLK2, which has structural characteristics conducive to acting as an apocarotenoid receptor. In addition, through gene silencing experiments, an increase in mycorrhization capacity associated with the induction of genes that promote it (such as RAM1) and the decrease of specific protease genes related to the degradation of the arbuscule are observed. Conversely, defective arbuscules have been seen to develop in overexpression experiments. All this leads us to the hypothesis that DLK2 participates in the regulation of these processes (Ho-Plágaro *et al.*, 2021)

In this communication, we present the results of the characterization of DLK2 overexpressing plants, the analysis of their altered symbiotic phenotype and the study of the transcriptional alteration of the expression of apocarotenoid metabolism genes in the root of these overexpressing plants.

Ho-Plagaro, T., Morcillo, R. J. L., Tamayo-Navarrete, M. I., Huertas, R., Molinero-Rosales, N., Lopez-Raez, J. A., *et al.* (2021). DLK2 regulates arbuscule hyphal branching during arbuscular mycorrhizal symbiosis. *New Phytol.* 229, 548–562. doi: 10.1111/nph.16938

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