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METABOLIC CHANNELING OF PHE FOR LIGNIN BIOSYNTHESIS IN MARITIME PINE

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The amino acid phenylalanine (Phe) is the main precursor of phenylpropanoids biosynthesis in plants. This vast family of Phe-derived compounds can represent up to 30% of captured photosynthetic carbon, playing essential roles in plants such as cell wall components, defense molecules, pigments and flavors. In addition to its physiological importance, phenylpropanoids and particularly lignin, a component of wood, are targets in plant biotechnology.

The arogenate pathway has been proposed as the main pathway for Phe biosynthesis in plants (Maeda et al., 2010). The final step in Phe biosynthesis, catalyzed by the enzyme arogenate dehydratase (ADT), has been considered as a key regulatory point in Phe biosynthesis, due to its key branch position in the pathway, the multiple isoenzymes identified in plants and the existence of a feedback inhibition mechanism by Phe. So far, the regulatory mechanisms underlying ADT genes expression have been poorly characterized, although a strong regulation of the Phe metabolic flux should be expected depending on its alternative use for protein biosynthesis versus phenylpropanoid biosynthesis. This second fate involves a massive carbon flux compared to the first one.

In this study we report our current research activities in the transcriptional regulation of ADT genes by MYB transcription factors in the conifer Pinus pinaster (maritime pine). The conifers channels massive amounts of photosynthetic carbon for phenylpropanoid biosynthesis during wood formation. We have identified the complete ADT gene family in maritime pine (El-Azaz et al., 2016) and a set of ADT isoforms specifically related with the lignification process. The potential control of transcription factors previously reported as key regulators in pine wood formation (Craven-Bartle et al., 2013) will be presented.

Maeda et al. (2010) Plant Cell 22: 832-849.
El-Azaz et al. (2016) The Plant Jounal. Accepted article, doi: 10.1111/tpj.13195
Craven-Bartle et al. (2013). The Plant Journal 74(5):755-766