

Phenylalanine biosynthesis: the role and evolution of arogenate dehydratase gene family in conifers.

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In plants, arogenate dehydratase activity (ADT, EC 4.2.1.91) is responsible for the last step in the main pathway for phenylalanine biosynthesis, known as the arogenate pathway, which consist in two steps: the conversion of prephenate to arogenate in a reaction catalyzed by the enzyme prephenate aminotransferase (PAT, EC 2.6.1.78) and the decarboxylation of arogenate to render phenylalanine catalyzed by ADT. The arogenate pathway results of particular interest according to the important role of phenylalanine in plant metabolism, acting as the main gate of entry to phenylpropanoids biosynthesis, that constitute up to 30 to 45% of plant organic matter (Razal et al., 1996). This is particularly relevant in perennial woody plants, in which lignification process and resultant biomass acumulation through plant life cycle are notably important.

Despite of the high importance of phenylalanine biosynthesis and derived phenylpropanoids in plants biology, the arogenate pathway still remains poorly characterized, particularly in woody plants. Very recently, two independent publications reported physiological evidences suggesting an alternative arogenate-independent pathway for phenylalanine biosynthesis in plants (Yoo et al., 2013; De la Torre et al., 2014), as described previously in fungi and bacteria. This pathway is dependent of a prephenate dehydratase enzyme (PDT, EC 4.2.1.51) catalyzing the conversion of prephenate to phenylpyruvate, being subsequently converted into phenylalanine through a transamination reaction. It has been reported that ADT and PDT activities are housed in the same proteins in plants (Cho et al., 2007).

Here we present preliminary results focused on the characterization of the ADT/PDT gene family in maritime pine (*Pinus pinaster* Ait.), a conifer tree of ecological and commercial interest. Our results demonstrate the existence of at least 9 ADT-like genes in the *P. pinaster* transcriptome, showing organ- and development-specific mRNA and protein expression profiles. Moreover, 3 of those 9 candidate genes present a distinctive phylogenetic clustering, forming a conifer-characteristic group of ADT-like genes differenced from the remaining ADT sequences. These findings highlights the potential importance of ADT/PDT activities in conifer metabolism, suggesting the existence of a singular and highly-specialized prephenate-related metabolism in conifers.

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