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“Characterization of the arogenate dehydratase family in Arabidopsis”

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The aromatic amino acids, phenylalanine (phe), tyrosine and tryptophane are precursors for protein synthesis and many secondary metabolites including flavonoids, lignins, melanins, phenols or tannins. As such they contribute to the plant's structural support, pigment and scent formation, protection from UV light and predators. While essential to all organisms, only plants, fungi and bacteria are able to synthesize aromatic amino acids de novo. The conversion from prephenate to phenylalanine, the last step in phe synthesis, requires the enzymatic activity of a dehydratase and an amino transferase. The Arabidopsis genome encodes six genes which share extensive sequence similarity to bacterial prephenate dehydratases. We have demonstrated that the encoded enzymes act as arogenate dehydratases (ADTs) and that three also act as prephenate dehydratases (PDT). The overall molecular structure of the six AtADTs is conserved all having an N-terminal transit peptide, an internal catalytic domain and a C-terminal ligand binding regulatory domain. However, it is unclear why plant genomes code for several ADTs while the bacterial need for phe is often covered by a single enzyme. We are interested in a detailed molecular analysis of the ADT family in Arabidopsis to understand the diverse roles and contributions of individual family members during plant development and in response to environmental cues.