

**Project title:** Gene regulation of the catabolism of aromatics in the saprophytic fungus *Aspergillus nidulans*

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**Duration:** 6 to 9 months

**Summary:**

The aerobic catabolism of aromatic hydrocarbons in fungi occurs ultimately via one of five intermediates, either catechol, protocatechuate, hydroquinone, homogentisate or gentisate. These intermediates and their upper precursors are channelled to the 3-oxoadipate and homogentisate pathways (and their variants). Only recently, the genetic basis of these pathways was disclosed in the Ascomycota fungi *Aspergillus nidulans* and *Penicillium chrysogenum* (Martins et al., 2015). One of the important findings of our previous work is the functional redundancy of the components of different branches and/or pathways owing fungi different tools to achieve degradation of an aromatic hydrocarbon. A comprehensive study of the gene regulation of 3-oxoadipate and homogentisate pathways is currently required to uncover ways to modulate the catabolism of aromatics by Ascomycota fungi.

**This project will focus on:**

Study of the gene regulation in the aromatics pathways in the model fungus *A. nidulans*. This will mostly be accomplished by maintenance and culture of fungi and gene expression analysis by quantitative real time RT-PCR. Simple aromatic hydrocarbons will be tested aiming to provide an in depth understanding of the families of compounds able to elicit strong responses in the transcription of genes assigned to the pathway(s) components. The objective is to identify compounds that act as inducers of the degradation pathways in this saprophytic fungus.

Martins, T.M., Hartmann, D.O., Planchon, S., Martins, I., Renaut, J., Silva Pereira, C., 2015. The old 3-oxoadipate pathway revisited: New insights in the catabolism of aromatics in the saprophytic fungus *Aspergillus nidulans*. *Fungal Genet. Biol.* 74, 32-44.