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Post-translational modifications and pathogenicity of the human pathogenic fungus *Aspergillus fumigatus*

Aspergillus nidulans, as other filamentous fungi, was found capable to produce a vast range of secondary metabolites, such as penicillin and sterigmatocystin. Many secondary metabolites are important not only for their impact on industry but also for their clinical relevance. However, most of the gene clusters involved in their production remain silent under standard cultivation conditions. Therefore a major aim of our studies is to unveil under which conditions those secondary metabolite clusters are activated.

Recent studies showed that chromatin remodelling is important for regulating secondary metabolite biosynthesis gene clusters. In our laboratories it had been found that SAGA/ADA, a histone acetyltransferase complex, is mediating the response of the fungus *A. nidulans* to the bacterium *Streptomyces rapamycinicus* and thereby is activating the biosynthesis of secondary metabolites.

In this study we are going to further investigate the role of SAGA/ADA in the activation of the cluster. And furthermore explore the direct impact of modifications on histones on the transcription of secondary metabolite gene clusters.

Publications

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Nützmann HW, Fischer J, Scherlach K, Hertweck C, Brakhage AA (2013) Distinct amino acids of histone H3 control secondary metabolism in *Aspergillus nidulans*. *Appl Environ Microbiol* 79(19), 6102-6109. [Details PubMed](#)

Supervisor

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Start of PhD

March 1, 2012

Doctoral Disputation

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