Chromatin mapping identifies BasR, a key regulator of bacteria-triggered production of fungal secondary metabolites.

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Projects

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

Integrated genome-wide data analysis by ensemble learning methods to understand infection processes
Details

Heterologous expression of silent gene clusters in fungi
Details

Abstract

The eukaryotic epigenetic machinery can be modified by bacteria to reprogram the response of eukaryotes during their interaction with microorganisms. We discovered that the bacterium *Streptomyces rapamycinicus* triggered increased chromatin acetylation and thus activation of the silent secondary metabolism ors gene cluster in the fungus *Aspergillus nidulans*. Using this model we aim at understanding mechanisms of microbial communication based on bacteria-triggered chromatin modification. By genome-wide ChIP-seq analysis of acetylated histone H3 we uncovered the unique chromatin landscape in *A. nidulans* upon co-cultivation with *S. rapamycinicus* and relate changes in the acetylation to that in the fungal transcriptome. Differentially acetylated histones were detected in genes involved in secondary metabolism, amino acid and nitrogen metabolism, signaling, and encoding transcription factors. Further molecular analyses identified the Myb-like transcription factor BasR as the regulatory node for transduction of the bacterial signal in the fungus and show its function is conserved in other Aspergillus species.

Identifier

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