Yeast two-hybrid screening reveals a dual function for the histone acetyltransferase GcnE by controlling glutamine synthesis and development in *Aspergillus fumigatus*.

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Projects

Oxidative inactivation of primary metabolism pathways in the human pathogenic fungus *Aspergillus fumigatus*
Details

Molekularbiologische Untersuchungen zur funktionellen Genomanalyse des humanpathogenen Pilzes *Aspergillus fumigatus*
Details

Abstract

The acetyltransferase GcnE is part of the SAGA complex which regulates fungal gene expression through acetylation of chromatin. Target genes of the histone acetyltransferase GcnE include those involved in secondary metabolism and asexual development. Here, we show that the absence of GcnE not only abrogated conidiation, but also strongly impeded vegetative growth of hyphae in the human pathogenic fungus *Aspergillus fumigatus*. A yeast two-hybrid screen using a *Saccharomyces cerevisiae* strain whose tRNA molecules were specifically adapted to express *A. fumigatus* proteins identified two unprecedented proteins that directly interact with GcnE. Glutamine synthetase GlnA as well as a hypothetical protein located on chromosome 8 (GbpA) were identified as binding partners of GcnE and their interaction was confirmed in vivo via bimolecular fluorescence complementation. Phenotypic characterization of gbpA and glnA deletion mutants revealed a role for GbpA during conidiogenesis and confirmed the central role of GlnA in glutamine biosynthesis. The increase of glutamine synthetase activity in the absence of GcnE indicated that GcnE silences GlnA through binding. This finding suggests an expansion of the regulatory role of GcnE in *A. fumigatus*.

Identifier

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