RNAi as a tool to study virulence in the pathogenic yeast *Candida glabrata*.

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Details

Abstract

The yeast Candida glabrata is a major opportunistic pathogen causing mucosal and systemic infections in humans. Systemic infections caused by this yeast have high mortality rates and are difficult to treat due to this yeast's intrinsic and frequently adapting antifungal resistance. To understand and treat C. glabrata infections, it is essential to investigate the molecular basis of C. glabrata virulence and resistance. We established an RNA interference (RNAi) system in C. glabrata by expressing the Dicer and Argonaute genes from Saccharomyces castellii (a budding yeast with natural RNAi). Our experiments with reporter genes and putative virulence genes showed that the introduction of RNAi resulted in 30 and 70% gene-knockdown for the construct-types antisense and hairpin, respectively. The resulting C. glabrata RNAi strain was used for the

screening of a gene library for new virulence-related genes. Phenotypic profiling with a high-resolution quantification of growth identified genes involved in the maintenance of cell integrity, antifungal drugs, and ROS resistance. The genes identified by this approach are promising targets for the treatment of C. glabrata infections.

Involved units

Microbial Pathogenicity Mechanisms Bernhard Hube Read more

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Topics

Interactions with immune cells (MPM)

Pathomechanisms at the mucosal interphase

Evolution & adaptation in pathogenicity

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Identifier

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