A Novel Hybrid Iron Regulation Network Combines Features from Pathogenic and Nonpathogenic Yeasts.

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Projects

Intracellular survival of *Candida glabrata* in phagocytes
Details

Abstract

Iron is an essential micronutrient for both pathogens and their hosts, which restrict iron availability during infections in an effort to prevent microbial growth. Successful human pathogens like the yeast *Candida glabrata* have thus developed effective iron acquisition strategies. Their regulation has been investigated well for some pathogenic fungi and in the model organism *Saccharomyces cerevisiae*, which employs an evolutionarily derived system. Here, we show that *C. glabrata* uses a regulation network largely consisting of components of the *S. cerevisiae* regulon but also of elements of other pathogenic fungi. Specifically, similarly to baker's yeast, Aft1 is the main positive regulator under iron starvation conditions, while Cth2 degrades mRNAs encoding iron-requiring enzymes. However, unlike the case with *S. cerevisiae*, a Sef1 ortholog is required for full growth under iron limitation conditions, making *C. glabrata* an evolutionary intermediate to SEF1-dependent fungal pathogens. Therefore, *C. glabrata* has evolved an iron homeostasis system which seems to be unique within the pathogenic fungi.

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