A novel hybrid iron regulation network combines features from pathogenic and non-pathogenic yeasts.

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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 is well-investigated for some pathogenic fungi and in the model organism, *Saccharomyces cerevisiae*, which employs an evolutionary derived system. Here, we show that *C. glabrata* uses a regulation network largely consisting of components of the *S. cerevisiae* regulon, but also elements of other pathogenic fungi. Specifically, similar to baker's yeast, Aft1 is the main positive regulator under iron starvation, while Cth2 degrades mRNAs encoding iron-requiring enzymes. However, unlike *S. cerevisiae*, a Sef1 ortholog is required for full growth under iron limitation, 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.

Involved units

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Nutrient acquisition in infections

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