Regulatory networks controlling nitrogen sensing and uptake in *Candida albicans*.

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Abstract

Nitrogen is one of the key nutrients for microbial growth. During infection, pathogenic fungi like *C. albicans* need to acquire nitrogen from a broad range of different and changing sources inside the host. Detecting the available nitrogen sources and adjusting the expression of genes for their uptake and degradation is therefore crucial for survival and growth as well as for establishing an infection. Here, we analyzed the transcriptional response of *C. albicans* to nitrogen starvation and feeding with the infection-relevant nitrogen sources arginine and bovine serum albumin (BSA), representing amino acids and proteins, respectively. The response to nitrogen starvation was marked by an immediate repression of protein synthesis and an up-regulation of general amino acid permeases, as well as an up-regulation of autophagal processes in its later stages. Feeding with arginine led to a fast reduction in expression of general permeases for amino acids and to resumption of protein synthesis. The response to BSA feeding was generally slower, and was additionally characterized by an up-regulation of oligopeptide transporter genes. From time-series data, we inferred network interaction models for genes relevant in nitrogen detection and uptake. Each individual network was found to be largely specific for the experimental condition (starvation or feeding with arginine or BSA). In addition, we detected several novel connections between regulator and effector genes, with putative roles in nitrogen uptake. We conclude that *C. albicans* adopts a particular nitrogen response network, defined by sets of specific gene-gene connections for each environmental condition. All together, they form a grid of possible gene regulatory networks, increasing the transcriptional flexibility of *C. albicans*.

Identifier

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