

Regulatory network modelling of iron acquisition by a fungal pathogen in contact with epithelial cells.

Linde J, Wilson D, Hube B, Guthke R (2010) Regulatory network modelling of iron acquisition by a fungal pathogen in contact with epithelial cells. *BMC Syst Biol* 4, 148.

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Abstract

Reverse engineering of gene regulatory networks can be used to predict regulatory interactions of an organism faced with environmental changes, but can prove problematic, especially when focusing on complicated multi-factorial processes. *Candida albicans* is a major human fungal pathogen. During the infection process, this fungus is able to adapt to conditions of very low iron availability. Such adaptation is an important virulence attribute of virtually all pathogenic microbes. Understanding the regulation of iron acquisition genes will extend our knowledge of the complex regulatory changes during the infection process and might identify new potential drug targets. Thus, there is a need for efficient modelling approaches predicting key regulatory events of iron acquisition genes during the infection process.

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Identifizier

doi: 10.1186/1752-0509-4-148

PMID: 21050438