Systems biology of fungal infection.

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Projects

Prediction of gene regulatory networks involved in the differentiation, secondary metabolism and cross talk of *Aspergillus nidulans*
Details

Abstract

Elucidation of pathogenicity mechanisms of the most important human-pathogenic fungi, Aspergillus fumigatus and Candida albicans, has gained great interest in the light of the steadily increasing number of cases of invasive fungal infections. A key feature of these infections is the interaction of the different fungal morphotypes with epithelial and immune effector cells in the human host. Because of the high level of complexity, it is necessary to describe and understand invasive fungal infection by taking a systems biological approach, i.e., by a comprehensive quantitative analysis of the non-linear and selective interactions of a large number of functionally diverse, and frequently multifunctional, sets of elements, e.g., genes, proteins, metabolites, which produce coherent and emergent behaviors in time and space. The recent advances in systems biology will now make it possible to uncover the structure and dynamics of molecular and cellular cause-effect relationships within these pathogenic interactions. We review current efforts to integrate omics and image-based data of host-pathogen interactions into network and spatio-temporal models. The modeling will help to elucidate pathogenicity mechanisms and to identify diagnostic biomarkers and potential drug targets for therapy and could thus pave the way for novel intervention strategies based on novel antifungal drugs and cell therapy.

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