Data-based reconstruction of gene regulatory networks of fungal pathogens.

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Abstract

In the emerging field of systems biology of fungal infection, one of the central roles belongs to the modeling of gene regulatory networks (GRNs). Utilizing omics-data, GRNs can be predicted by mathematical modeling. Here, we review current advances of data-based reconstruction of both small-scale and large-scale GRNs for human pathogenic fungi. The advantage of large-scale genome-wide modeling is the possibility to predict central (hub) genes and thereby indicate potential biomarkers and drug targets. In contrast, small-scale GRN models provide hypotheses on the mode of gene regulatory interactions, which have to be validated experimentally. Due to the lack of sufficient quantity and quality of both experimental data and prior knowledge about regulator–target gene relations, the genome-wide modeling still remains problematic for fungal pathogens. While a first genome-wide GRN model has already been published for Candida albicans, the feasibility of such modeling for Aspergillus fumigatus is evaluated

in the present article. Based on this evaluation, opinions are drawn on future directions of GRN modeling of fungal pathogens. The crucial point of genome-wide GRN modeling is the experimental evidence, both used for inferring the networks (omics ‘first-hand’ data as well as literature data used as prior knowledge) and for validation and evaluation of the inferred network models.

Involved units

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Topics

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