On the way toward systems biology of *Aspergillus fumigatus* infection.

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Abstract

Pathogenicity of *Aspergillus fumigatus* is multifactorial. Thus, global studies are essential for the understanding of the infection process. Therefore, a data warehouse was established where genome sequence, transcriptome and proteome data are stored. These data are analyzed for the elucidation of virulence determinants. The data analysis workflow starts with pre-processing including imputing of missing values and normalization. Last step is the identification of differentially expressed genes/proteins as interesting candidates for further analysis, in particular for functional categorization and correlation studies. Sequence data and other prior knowledge extracted from databases are integrated to support the inference of gene regulatory networks associated with pathogenicity. This knowledge-assisted data analysis aims at establishing mathematical models with predictive strength to assist further experimental work. Recently, first steps were done to extend the integrative data analysis and computational modeling by evaluating spatio-temporal data (movies) that monitor interactions of *A. fumigatus* morphotypes (e.g. conidia) with host immune cells.

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