

Fungal model systems and the elucidation of pathogenicity determinants.

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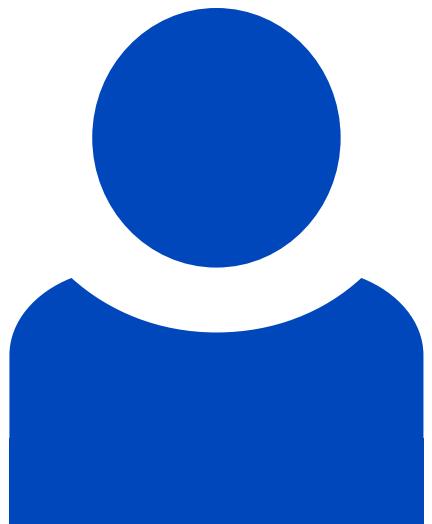
Abstract

Fungi have the capacity to cause devastating diseases of both plants and animals, causing significant harvest losses that threaten food security and human mycoses with high mortality rates. As a consequence, there is a critical need to promote development of new antifungal drugs, which requires a comprehensive molecular knowledge of fungal pathogenesis. In this review, we critically evaluate current knowledge of seven fungal organisms used as major research models for fungal pathogenesis. These include pathogens of both animals and plants; *Ashbya gossypii*, *Aspergillus fumigatus*, *Candida albicans*, *Fusarium oxysporum*, *Magnaporthe oryzae*, *Ustilago maydis* and *Zymoseptoria tritici*. We present key insights into the virulence mechanisms deployed by each species and a comparative overview of key insights obtained from genomic analysis. We then consider current trends and future challenges associated with the study of fungal pathogenicity.

Involved units

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Leibniz-HKI-Authors



Clara Baldin

[Details](#)



Axel A. Brakhage

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