colonization and for generation of simple sugars used for nutritional purposes. Thus xylanases are thought to play an important role in fungal pathogenesis. The gene XPP1 – Xylanase promoter binding protein 1 – was first described as a xylanase regulator in the filamentous ascomycete Trichoderma reesei, acting not only as a regulator of xylanase gene expression, but also as a repressor of secondary metabolism. We identified a XPP1 homologue in the maize anthracnose pathogen C. graminicola (CgXPP1) and obtained deletion mutants. By comparing these mutants with the wild type strain, we aim to investigate the role of XPP1 in the maize pathogenesis. Interestingly, first results show that in XPP1-deficient mutants a shift in transcript abundance of the xylanase transcription factor XLR1 occurs. We are currently studying the role of XPP1 and XLR1 in growth of vegetative hyphae on simple and polymeric carbohydrates, as well as in virulence.

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30-6 - Die Bedeutung von CRE1 und SNF1 für die Synthese Zellwand abbauender Enzyme und Virulenz des Mais Anthraknose Pathogens *Colletotrichum graminicola*

Roles of CRE1 and SNF1 in production of cell wall-degrading enzymes (CWDE) and full virulence of the maize anthracnose pathogen Colletotrichum graminicola

Alan de Oliveira Silva[1], Chirlei Glienke[2], Holger B. Deising[1]

[1]Martin-Luther-University Halle-Wittenberg, Faculty of Natural Sciences III, Phytopathology and Plant Protection
[2]Federal University of Paraná, Center of Biological and Health Sciences, Department of Genetics

Colletotrichum graminicola causes leaf anthracnose and stalk rot in maize. The pathogen differentiates an infection cell called an appressorium in order to invade the epidermal maize cell in a turgor pressure-driven fashion, possibly supported by secreted cell wall-degrading enzymes (CWDEs), which have previously been associated with virulence in different filamentous fungi. However, due to their enormous number and functional redundancy, targeted deletion of individual CWDE genes rarely caused virulence defects, and their role in fungal infection remains poorly understood. As an alternative to deletions of individual CWDE genes, targeted mutagenesis of genes controlling the expression of many genes encoding CWDEs may improve understanding the function of these enzymes during pathogenesis. The *CRE1* gene codes for a transcriptional repressor recognizing a conserved motif in the promoter region of many CWDEs genes. With opposite effect, the *SNF1* gene encodes a serine-threonine protein kinase required for phosphorylation of Cre1 and de-repression of genes subject to catabolite repression.

In this study we identified and functionally characterized *CRE1* and *SNF1* of *C. graminicola*. In comparison to the wild-type strain (WT), deletion mutants for both genes showed impaired vegetative growth and asexual sporulation, as well as penetration rates in maize leaves, as the mutants were significantly affected in their ability to cause anthracnose symptoms. In Δ*snf1* mutants, reduced growth rates only occurred on polymeric carbon sources, but not on simple sugars such as glucose and sucrose. The homologue of the xylanase transcription factor *XLNR* of *Aspergillus oryzae*, harboring a Cre1 binding site, was repressed in Δ*snf1* mutants and overexpressed in Δ*cre1* mutants even even in the presence of simple sugars. The fact that both Δ*cre1* and Δ*snf1* mutants exhibit strongly reduced virulence highlights the role of catabolite repression and de-repression in the hemibiotroph *C. graminicola*.

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