

The Death Is Red: Analysis of the Predicted Secretome of *Aspergillus welwitschiae*, with Emphasis in Pathogenicity and Carbohydrate Metabolism

Gabriel Quintanilha Peixoto, Daniel Silva Araújo, Rodrigo Bentes Kato, Paula Luíze Camargos Fonseca, Luiz Marcelo Ribeiro Tomé, Fábio Malcher Miranda, Rommel Thiago Jucá Ramos, Bertram Brenig, Vasco A de C Azevedo, Fernanda Badotti, Eric Roberto Guimarães Rocha Aguiar, Aristóteles Góes Neto

University Göttingen

Abstract

In 2018 *Aspergillus welwitschiae* was described as the causing agent of the bole rot disease of sisal (*Agave sisalana*) rather than *Aspergillus niger* as previously thought. *A. welwitschiae* is a cryptic species of the *A. niger*/*welwitschiae* clade. Since then, we have sought to understand the mechanisms of pathogenicity of this fungus by sequencing the genome of two strains isolated from infected stem tissues of *A. sisalana*, and subsequent analysis of the gene content of these fungi. The genomes, sequenced in Illumina HiSeq 2500 platform, were assembled de novo and annotated. Obtained genome size in CCMB663 was 34.8 Mbp containing 12,549 protein-coding genes, while CCMB674 genome is 32.2 Mbp long, containing 11,809 protein-coding genes. The resulting gene prediction models were used for analyzing secretomes, in which different software was applied as filters to select the putative secreted proteins that were subsequently associated with Gene Ontology (GO) terms. Our results show that most of the associated terms describe functions associated with the degradation of proteins, lipids, and especially carbohydrates and that the relative abundance of these terms is similar between different isolates. From this set of proteins predicted to be secreted, possible effector proteins were identified, which are involved in the invasion and colonization of the infected plant. Most of the identified putative effector proteins have no similarity with known effectors, and in those in which was possible to identify conserved domains, essential and very important genes associated to virulence in plants are included, including genes that act to silence the immune response or to stimulate it, causing cell death in plant tissues. Secretory and cytosolic plant cell wall degrading enzymes were also analyzed, describing a great diversity of genes encoding for carbohydrate-active enzymes, some of which specialized in the degradation of carbohydrates present in large amounts in the tissues of sisal stem. Altogether, our results improved the understanding of the *Aspergillus welwitschiae* x *Agave sisalana* pathosystem, and also identified new effectors of interest in the fungus-plant interaction.

Funding: