Secretomics identifies Fusarium graminearum proteins involved in the interaction with barley and wheat - DTU Orbit (07/02/2019)

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Fusarium graminearum is a phytopathogenic fungus primarily infecting small grain cereals, including barley and wheat. Secreted enzymes play important roles in the pathogenicity of many fungi. In order to access the secretome of F. graminearum, the fungus was grown in liquid culture with barley or wheat flour as the sole nutrient source to mimic the host–pathogen interaction. A gel-based proteomics approach was employed to identify the proteins secreted into the culture medium. Sixty-nine unique fungal proteins were identified in 154 protein spots, including enzymes involved in the degradation of cell walls, starch and proteins. Of these proteins, 35% had not been identified in previous in planta or in vitro studies, 70% were predicted to contain signal peptides and a further 16% may be secreted in a nonclassical manner. Proteins identified in the 72 spots showing differential appearance between wheat and barley flour medium were mainly involved in fungal cell wall remodelling and the degradation of plant cell walls, starch and proteins. The in planta expression of corresponding F. graminearum genes was confirmed by quantitative reverse transcriptase-polymerase chain reaction in barley and wheat spikelets harvested at 2–6 days after inoculation. In addition, a clear difference in the accumulation of fungal biomass and the extent of fungal-induced proteolysis of plant β-amylase was observed in barley and wheat. The present study considerably expands the current database of F. graminearum secreted proteins which may be involved in Fusarium head blight.

**General information**
State: Published
Organisations: Department of Systems Biology, Enzyme and Protein Chemistry, University of Copenhagen
Pages: 445-453
Publication date: 2012
Peer-reviewed: Yes

**Publication information**
Journal: Molecular Plant Pathology
Volume: 13
Issue number: 5
ISSN (Print): 1464-6722
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.2 SJR 1.932 SNIP 1.537
Web of Science (2017): Impact factor 4.188
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.45 SJR 1.942 SNIP 1.57
Web of Science (2016): Impact factor 4.697
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.68 SJR 2.167 SNIP 1.633
Web of Science (2015): Impact factor 4.335
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.48 SJR 2.065 SNIP 1.688
Web of Science (2014): Impact factor 4.724
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.7 SJR 2.096 SNIP 1.631
Web of Science (2013): Impact factor 4.485
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.09 SJR 1.766 SNIP 1.587
Web of Science (2012): Impact factor 3.877
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2