University of Reading

Chemical Analysis Facility

Case study 1

Proteogenomics of an agriculturally important fungus: Powdery mildew, an obligate barley pathogen.

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OVERVIEW

An in-depth proteomics study of the economically important barley pathogen powdery mildew (*Blumeria graminis* f.sp. *hordei*) was undertaken.

The two main goals of this study were:

1. To improve the genome annotation by validating gene models from identified peptides using the FT-LTQ-Orbitrap for nanoLC-tandem mass spectrometry analysis.
2. To discover elicitor proteins which are involved in the interaction between plant host (barley) and the obligate pathogen (Blumeria).

INTRODUCTION

Blumeria graminis f.sp. *hordei* is a biotrophic pathogen, which means that it exclusively infects and grows on barley plants. Thus, it constitutes an example of extreme and specialised parasitism. In a preliminary study (1) we showed that it was possible to detect Blumeria proteins in infected barley leaves, and a more in-depth proteogenomics approach could be undertaken using state-of-the-art liquid chromatography and mass spectrometry available at CAF.

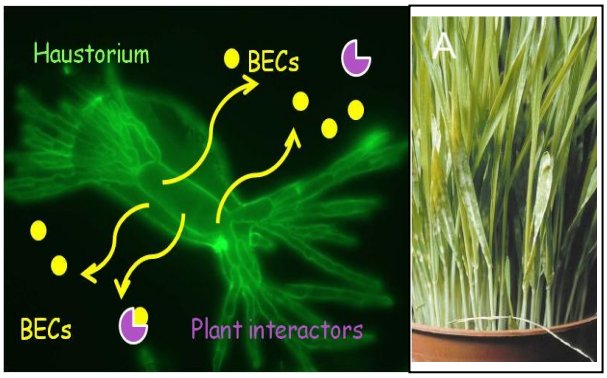
RESULTS

This study allowed the identification of more than *a thousand proteins*. Out of these, about *60* proteins are *Blumeria Effector Candidates (BECs)*, being *small, secreted* proteins and only detectable in *haustoria* cells, which are at the physical interface between barley and Blumeria.

CONCLUSIONS

The two study goals were achieved:

1. The Blumeria genome is now one of the best annotated plant fungal pathogens with almost 6000 manually annotated genes. Previous gene models were substantially improved by the proteomics work (2).
2. So far over 60 proteins have been identified as BECs and are candidates for further elucidation of the crucial interactions between barley and Blumeria.



PERSPECTIVES

The role of BECs as effectors will be further investigated:

1. Bioassays will be performed to identify which BECs are involved in the infection process.
2. Protein-protein interactions between BECs and barley proteins will unravel the molecular mechanisms of the infection process.

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