In planta proteomics and proteogenomics of the biotrophic barley fungal pathogen 
blumeria f.sp. hordei

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**In Planta Proteomics and Proteogenomics of the Biotrophic Barley Fungal Pathogen Blumeria graminis f.sp. hordei**

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### Overview

**Introduction**

Whilst there is increasing evidence that the outcome of the interaction between a pathogen and a host is dependent on protein-protein interactions, very little information is available on plant proteomes of biotrophic plant pathogens. Here a proteogenomic approach has been employed to supplement the annotation of the recently sequenced genome (www.Blugen.org) and to cast light on the biology of the infection process of the economically important barley powdery mildew pathogen, Blumeria graminis f.sp. hordei.

**Strategy**

Proteins from three different Blumeria tissues were isolated from infected barley leaves: 1) conidia (vegetative spores), 2) hyphae (which grow on the leaf surface), and 3) barley leaf epidermis containing haustoria (the 'feeding' organs). A gel-LC-MS/MS approach was used: Proteins were separated by SDS-PAGE prior to in-gel tryptic digestion. Peptides were separated by RPlC coupled to a 3D ion trap or an orbitrap mass spectrometer. A Blumeria genomic database was used to identify and align peptides onto DNA contigs. Validated ORFs were annotated using the SwissProt database for Blast similarity searches and recovering gene ontology information.

**Results**

- **Proteins identified exclusively in haustoria are smaller, secreted and predominately unknown (7/9).**
- **Conclusions**
  - Successful proteogenomic approach to annotate the genome
  - Helps genome assembly
  - Reveals gene functionality and novel ORFs
  - Characteristics of proteins exclusively detected in haustoria
  - Mostly unknown, small and secreted proteins
  - Discovery of putative new fungal effectors secreted in the host
  - The haustorium is involved in stress, immunity and defence, nutrient uptake and metabolism (monosaccharides).

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**Outline**

1. **Introduction: Barley powdery mildew.**
2. **Methods**
   - Experimental
   - Bioinformatics
3. **Results**
   - Blumeria proteomes analysed by gel-LC MS/MS.
4. **Conclusions**