Identification of novel pathogenicity factors in the late blight pathogen, *Phytophthora infestans*

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**Background**

*Phytophthora infestans* causes late blight of potato and tomato. It produces several different cell types prior to host penetration and during the early stages of infection. Appressoria, structures formed just prior to infection, are likely to contain many transcripts required for successful penetration of the host and establishment of a compatible interaction.

**Strategy**

**High throughput screen for gene function in *P. infestans***

50 genes up-regulated in germinated cysts, appressoria and *in planta* secreted proteins:
- 9 novel secreted proteins
- 21 RxLR class effectors
- 1 adhesion
- 1 PAMP
- 2 cell wall degrading enzymes
- 3 cysteine protease inhibitors
- 2 ROS detoxification enzymes
- structural proteins:
  - 2 membrane proteins
  - 3 transporters
  - 2 enzymes affecting development
  - 4 other

**Protoplasts + dsRNA**

- Regenerate
- Detached leaf inoculation
- 24 hpi trypan blue staining
- 48 hpi leaf sample for RNA extraction
- 72-96 hpi Assay for infection development

**Results**

**Novel secreted proteins and RxLR effector proteins**

| Secreted protein gene expression profiles in pre-infection stages and *in planta* |
|---|---|
| *PiHMP1* fusion |
| Expression profile in pre-infection stages and *in planta* |

**Silencing *PiHMP1* effects pathogenicity**

- Accumulates inside germinated cysts and appressoria
- Localised to haustorial membrane during infection

**RxLR effector gene expression profiles in pre-infection stages and *in planta***

**Future work**

**Acknowledgements**

We thank the Scottish Executive Environment and Rural Affairs Department (SEERAD) and the Biotechnology and Biological Sciences Research Council (BBSRC) for financial support.

**Conclusions**

Transient RNAi is effective for identifying genes with a major role in pathogenicity. RNAi can inform hypotheses for downstream analysis of pathogenicity in *P. infestans*. Both formation of functional pre-infection structures and pathogenicity require the action of many genes.