Transient gene silencing - a step forward in identifying novel pathogenicity factors in the late blight pathogen, Phytophthora infestans

Anna Avrova Petra Boevink Laura Grenville-Briggs Pieter van West Paul Birch and Stephen Whisson 1 Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA, UK.

2 University of Aberdeen, Institute of Medical Sciences, Foresterhill, Aberdeen AB25 2ZD.







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

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

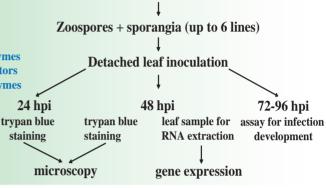
1 PAMP 2 cell wall degrading enzymes 3 cysteine protease inhibitors

2 ROS detoxification enzymes

structural proteins:

2 membrane proteins 3 transporters

2 enzymes affecting development



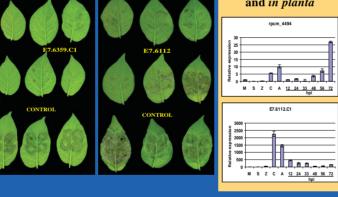
Protoplasts + dsRNA

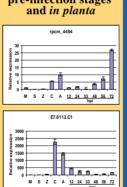
Regenerate

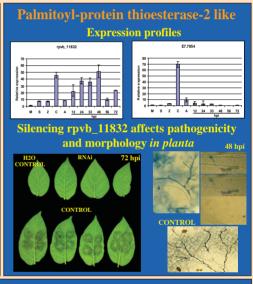


Results

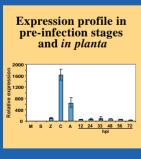
Novel secreted proteins and RxLR effector proteins Silencing these genes affects pathogenicity Secreted protein gene RxLR effector gene expression profiles in expression profiles in pre-infection stages pre-infection stages and in planta and in planta rpcm_4494 للقميم S Z C A <u>12 24 33 48 56 72</u> hpi S Z C A <u>12 24 33 48 56 72</u>









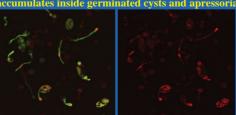


PiHMP1-mRFP fusion

Silencing PiHMP1 affects pathogenicity



accumulates inside germinated cysts and apressoria



Relative expression levels of PiHMP1 in control and silenced lines

localised to haustorial membrane during infection



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.

Both formation of functional pre-infection structures and pathogenicity require the action of many genes.



Future work



Acknowledgements

Localisation of structural proteins by translational fusion to fluorescent proteins, and subsequent observation by confocal microscopy.

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