1. Introduction
Food security is becoming a crucial issue, with crop yields being decreased by plant pathogens. One of the major pathogens is the grey mould, *Botrytis cinerea*. The key to developing resistant plants is to gain a better understanding of the molecular mechanisms that take place when a plant is infected.

The PRESTA (Plant Responses to Environmental Stresses in Arabidopsis) project seeks to determine the gene networks in Arabidopsis that mediate the responses to abiotic and biotic stresses, using high definition time series microarrays. Several genes with multiple up- and downstream interactions (“hub” genes) were identified in network reconstruction modelling, and in this project, three were selected for further investigation.

2. Downstream targets of CIR1
Performed microarrays
- CATMA v4 arrays
- 2 timepoints - 26 and 36 hpi
- 4 pooled biological replicates
- 4 technical replicates
- Slide hybridisations shown on right

Data analysis using limma - linear models
FDR corrected p-value cutoff of 0.01

The number of common genes between the different datasets are shown on the left. Of most interest were those circled in red.

These genes are potentially downstream of CIR1, as well as being induced in response to *B. cinerea* infection.

Interesting genes (from 36 hour data) included:
- § AT3G22235 - similar to a gene that is circadian and pathogen controlled
- § EBF2 - an ethylene regulator

3. Yeast one-hybrid
Yeast one-hybrid works by allowing a transcription factor (TF) from a library, to interact with a promoter of interest. If a positive interaction occurs, the production of the *HIS3* reporter gene is induced, allowing the yeast cells to grow on media lacking histidine.

4. Upstream targets of TGA3
Performed yeast one-hybrid
- - Promoter fragment shown on right

Interesting TFs that bound:
- § MYB family TFs
- § ATbZIPs
- § CBF family

5. Upstream targets of ARF2
Performed yeast one-hybrid
- - Three overlapping promoter fragments screened

- Shown on right

Interesting TFs that bound:
- § ORA59
- § NF-YC
- § ATERFs & ERFs
- § ABA responsive
- § WRKY
- § TCP Family TFs (Fragments 2&3)

6. Conclusion
Extended local networks of three hub genes
- - Can use this information in further modellings
Further work:
- § Mutagenise portions of the promoter
  - Which TFs no longer bind?
  - Identify sections that are the most important
- § Test other members of the same TF family
  - Specificity of the interaction