

# Integrating Host–Pathogen Dynamics and Quantitative Resistance for Sustainable Blight Management in Solanaceous Crops

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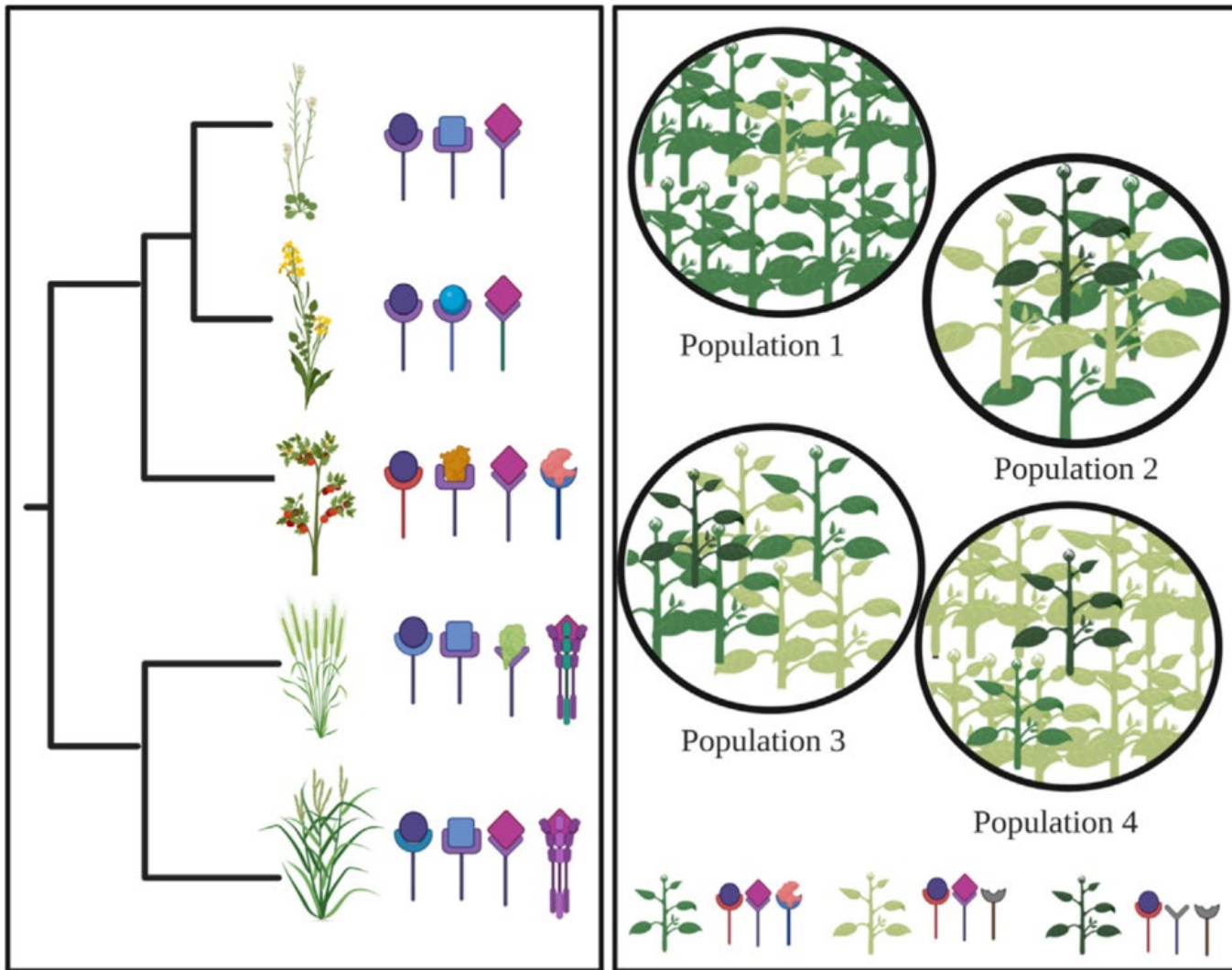
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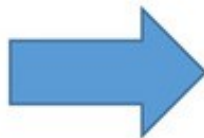
## Qualitative Resistance



Healthy

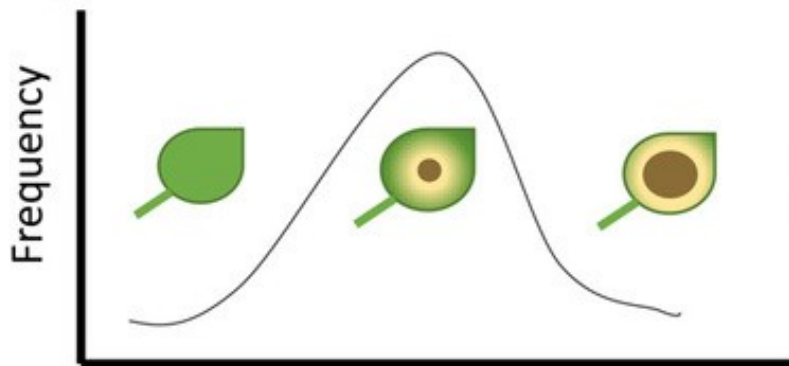
Infected

3 (R-) : 1 (rr)

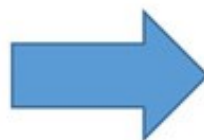


Genomic Position

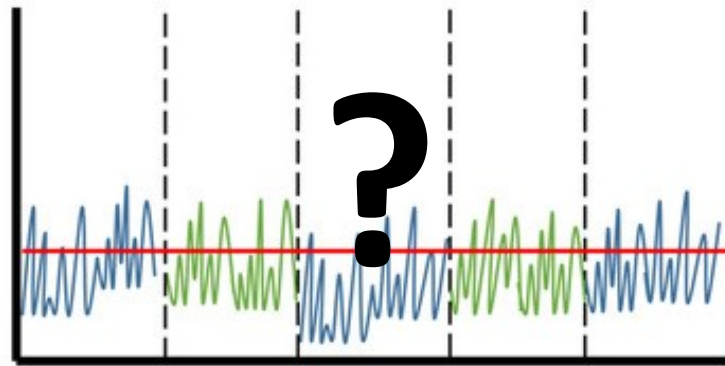
## Quantitative Resistance



Disease Severity



Effect



Genomic Position

How do plants and their pathogens evolve & interact in natural pathosystems?

How can we measure the interactions between host, pathogen and environment?

Which mechanisms are involved?

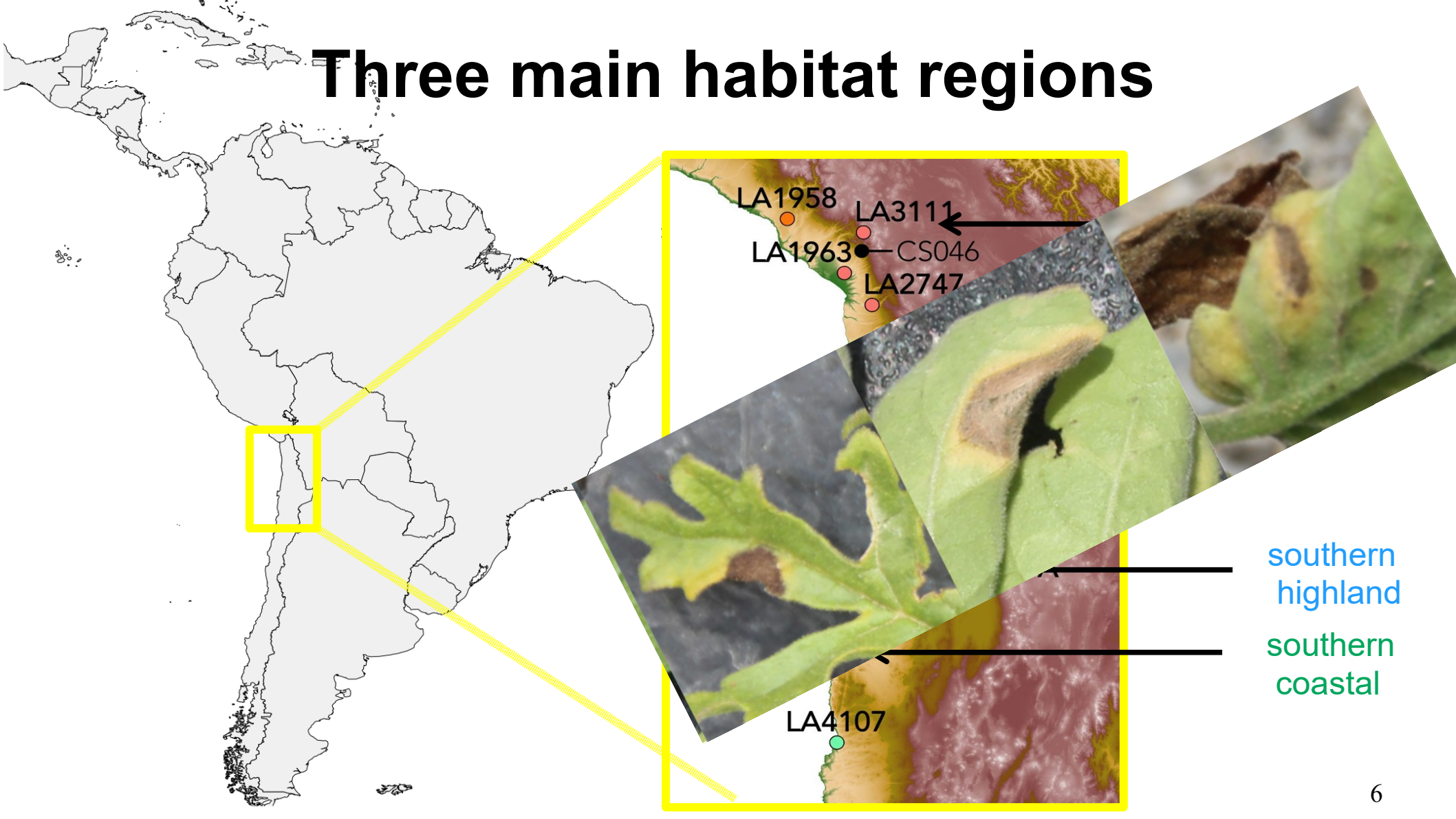
What can we learn from host and pathogen dynamics for agriculture?

How do we translate our findings to breeding and management solutions?

*Solanum chilense*



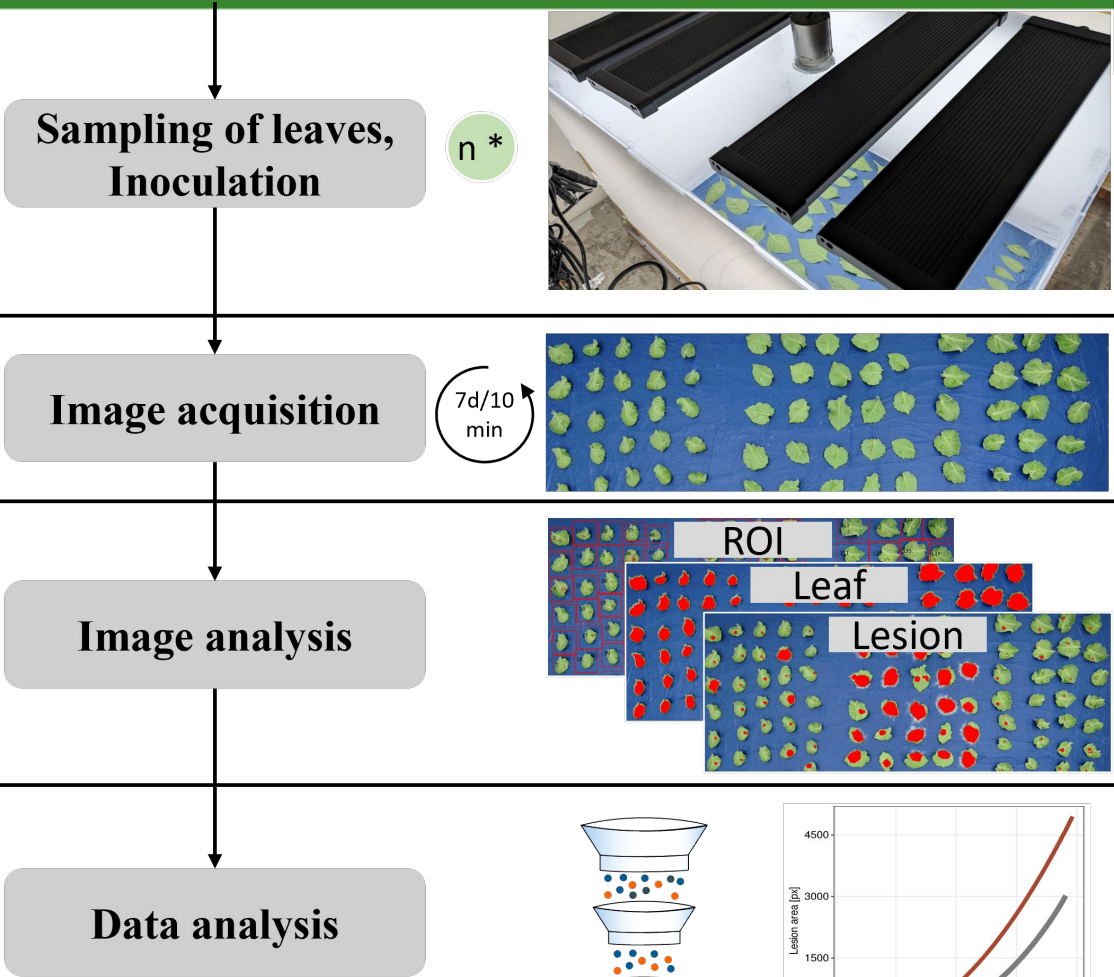
# Three main habitat regions



southern  
highland

southern  
coastal

# Low-cost automated phenotyping



$n^*$

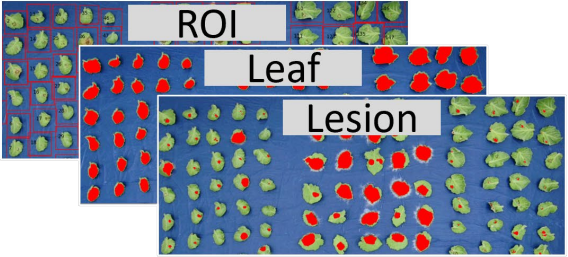
Sampling of leaves, Inoculation

7d/10 min

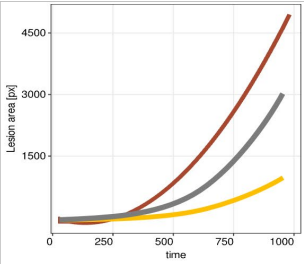
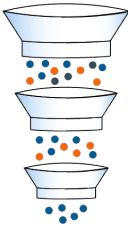
Image acquisition



Image analysis



Data analysis



(Einspanier *et al.*, 2024 Plant phenomics)

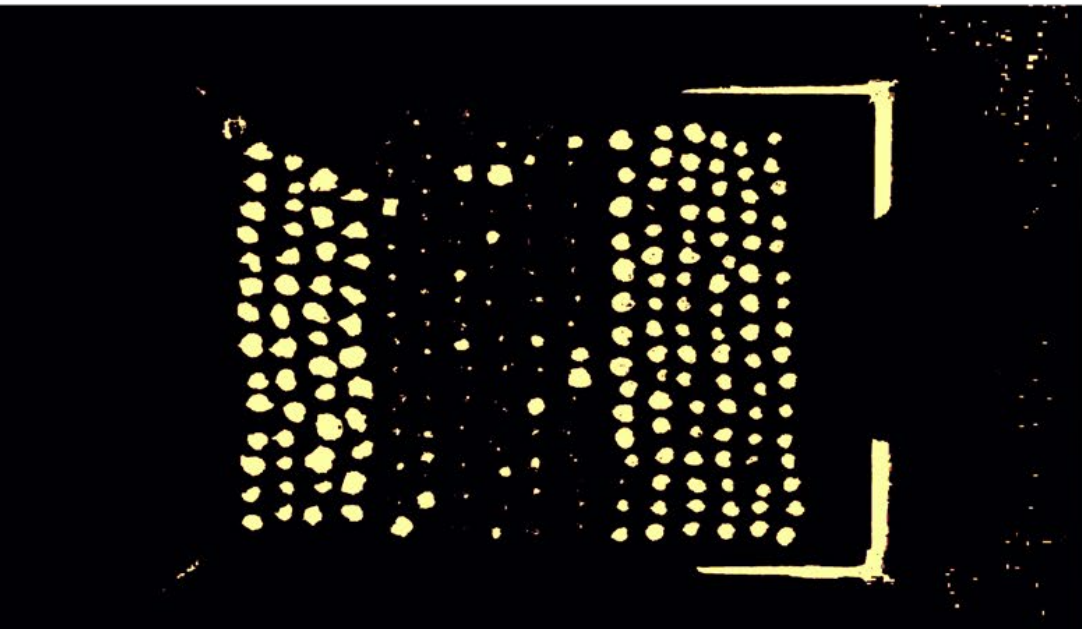


Experiment 2

# Different infection dynamics

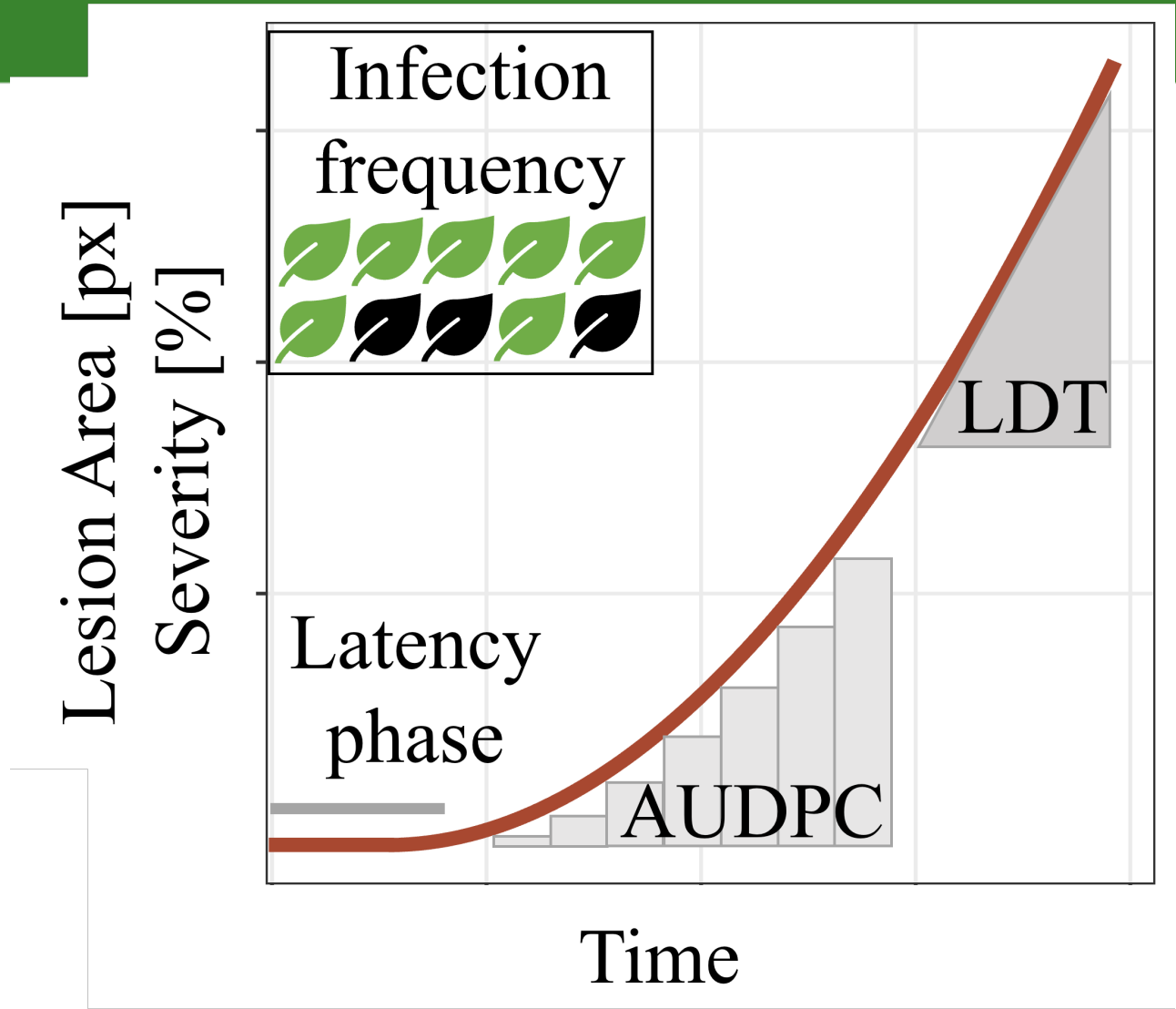


# Different infection dynamics

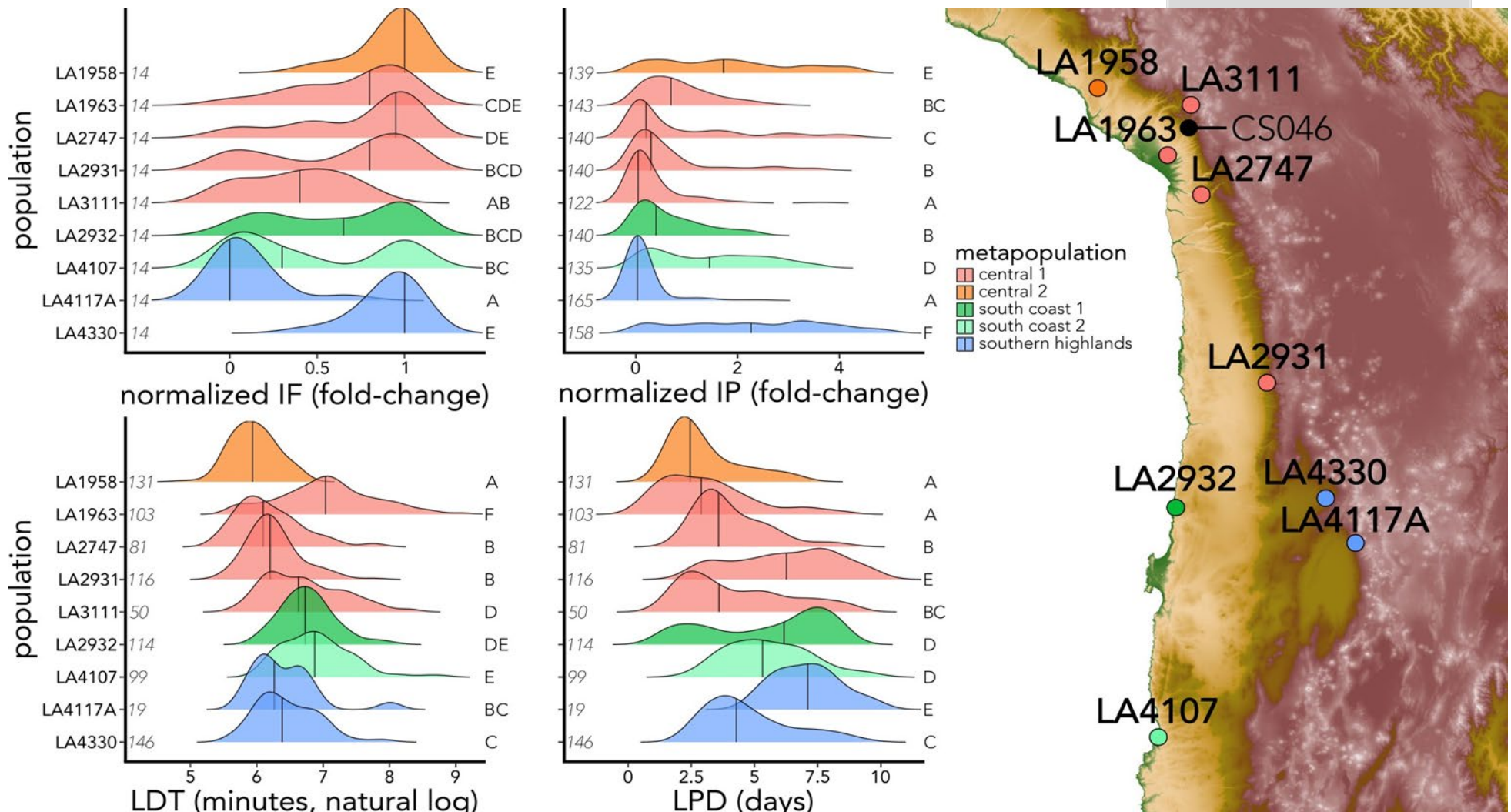


Infected





# Different QDR strategies?

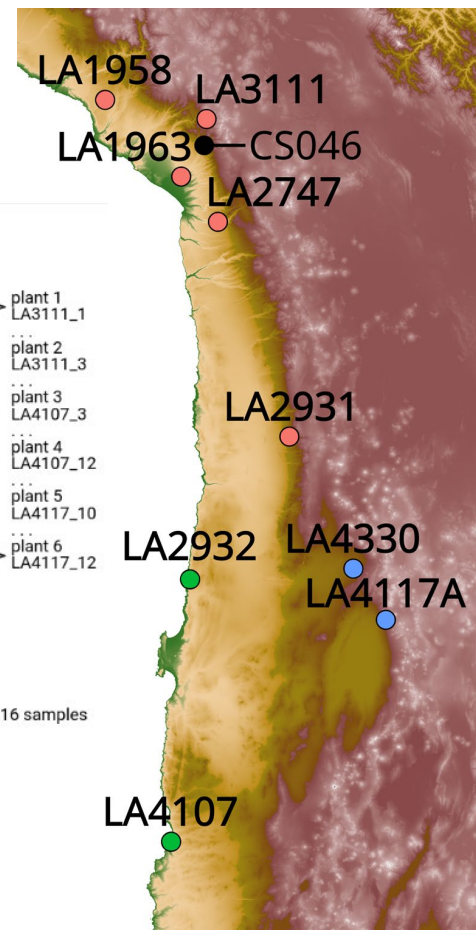
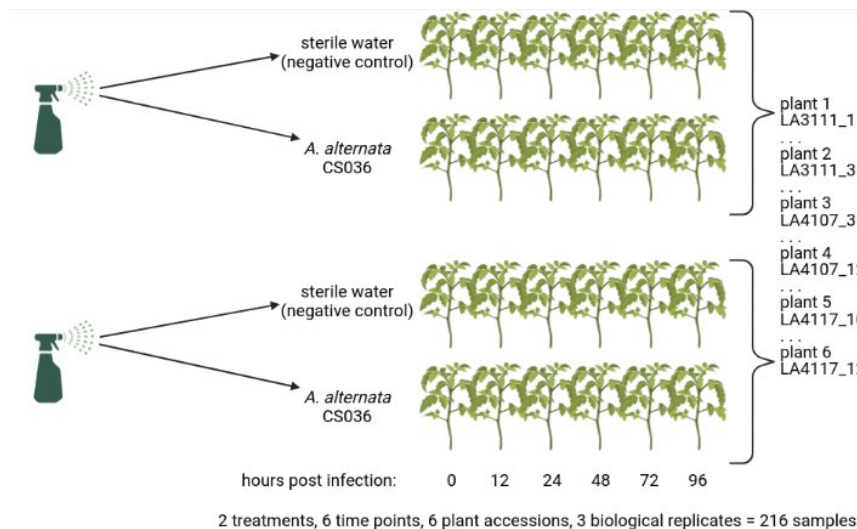


# RNASeq to unravel complex response

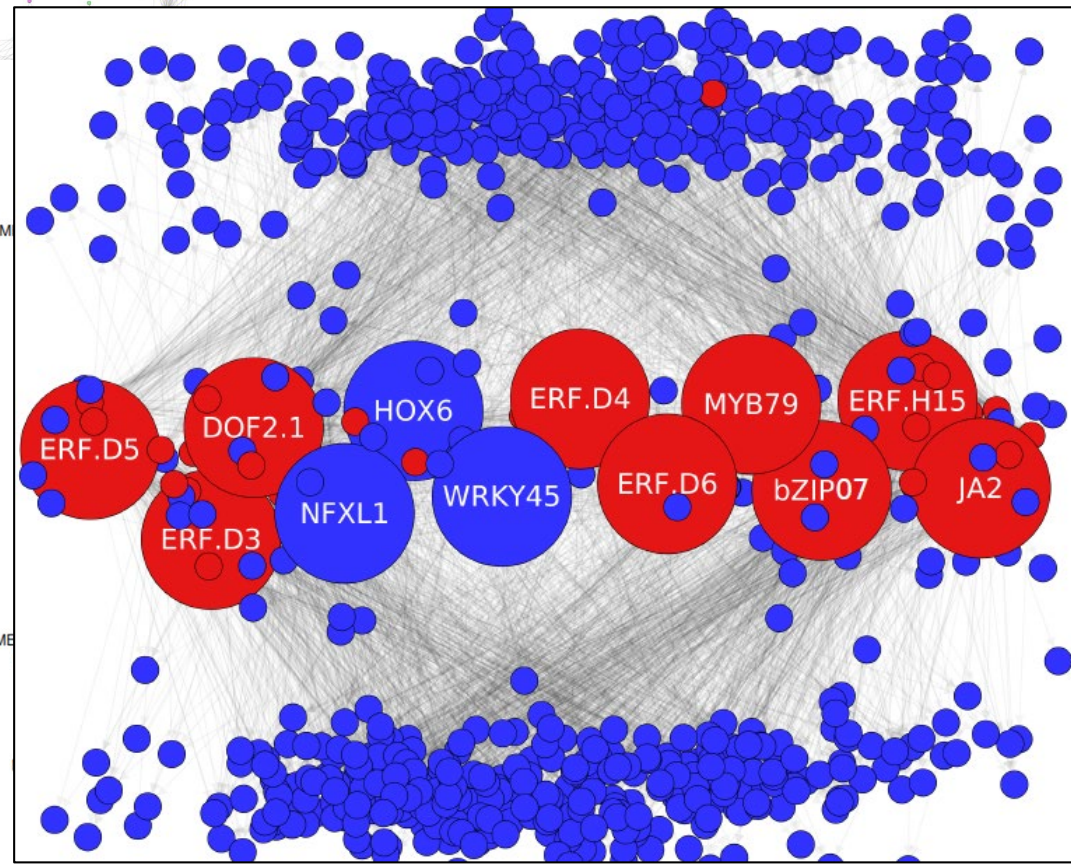
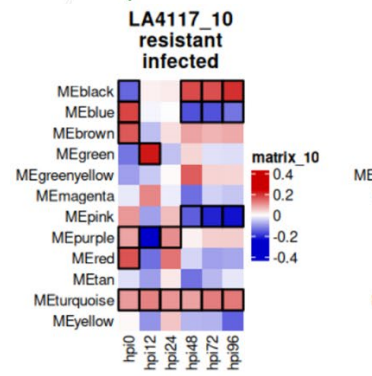
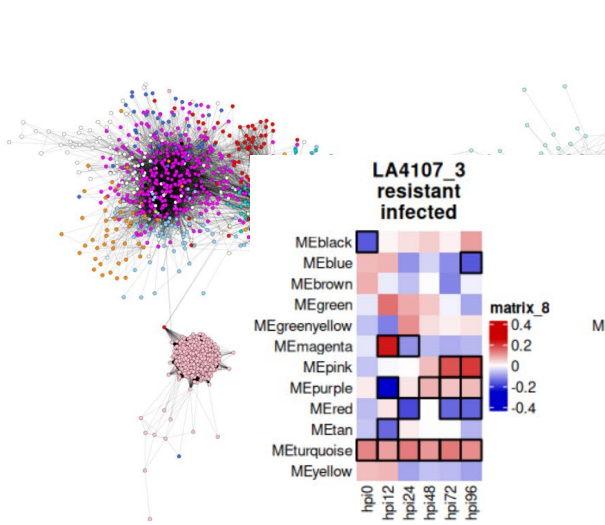
RNAseq

Whole plants spray-infected

3 populations of plants; 2  
genotypes per population



# We construct regulatory networks



**The role of ET is evident**

**ABA only in coastal populations!**

Advanced phenotyping can help score QDR in solanaceae

Phenotypes are complex; RNASeq dissects them

Defence response is wired differently in different populations

> incompatibility/trade-offs when crossing?

What are implications on management strategies?

# How can we translate this?

Most work can be translated to wild or cultivated potato (or other crops)

>> *Alternaria* (QDR) in Rape Seed



>> *Sclerotinia* in some wild solanaceous



>> *Alternaria* and *Sclerotinia* QDR in Quinoa

# What is the role of pathogen diversity?



Christian-Albrechts-Universität zu Kiel

Pathogen monitoring

Assess aggressiveness of populations on cultivars

Predict evolutionary trajectories

Goal: pathogen informed solutions

>> Talk Gonne Clasen in *Alternaria* session



Incorporating the CBS and the NCCB Culture Collections



**UF** UNIVERSITY of FLORIDA

**UFV** Universidade Federal de Viçosa



Stiftung  
Schleswig-Holsteinische  
Landschaft  
**Ackermann**  
Der Gerstenzüchter  
seit 1903



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# What else do we do?

Develop further Phenotyping

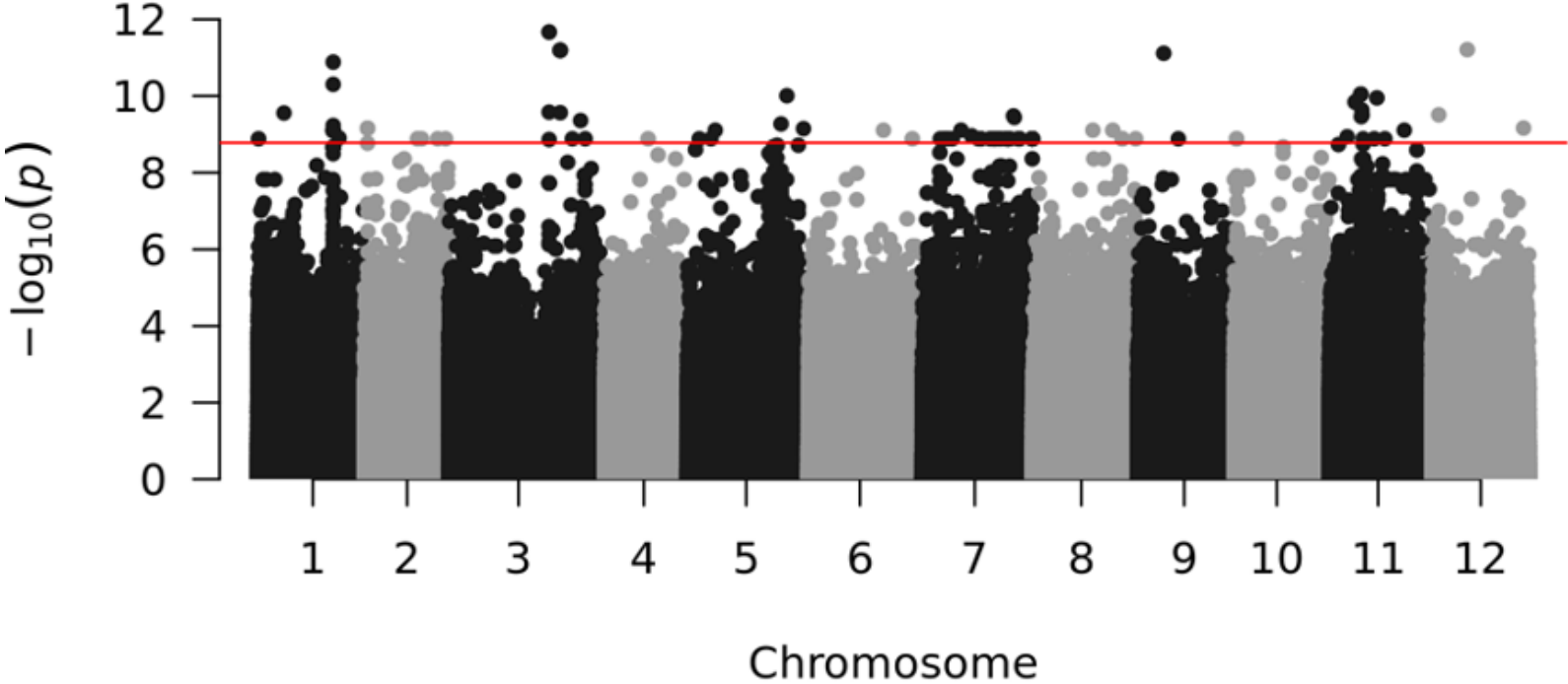
>> Light source? (tolerance)

>> Whole plants? (but keeping it simple)

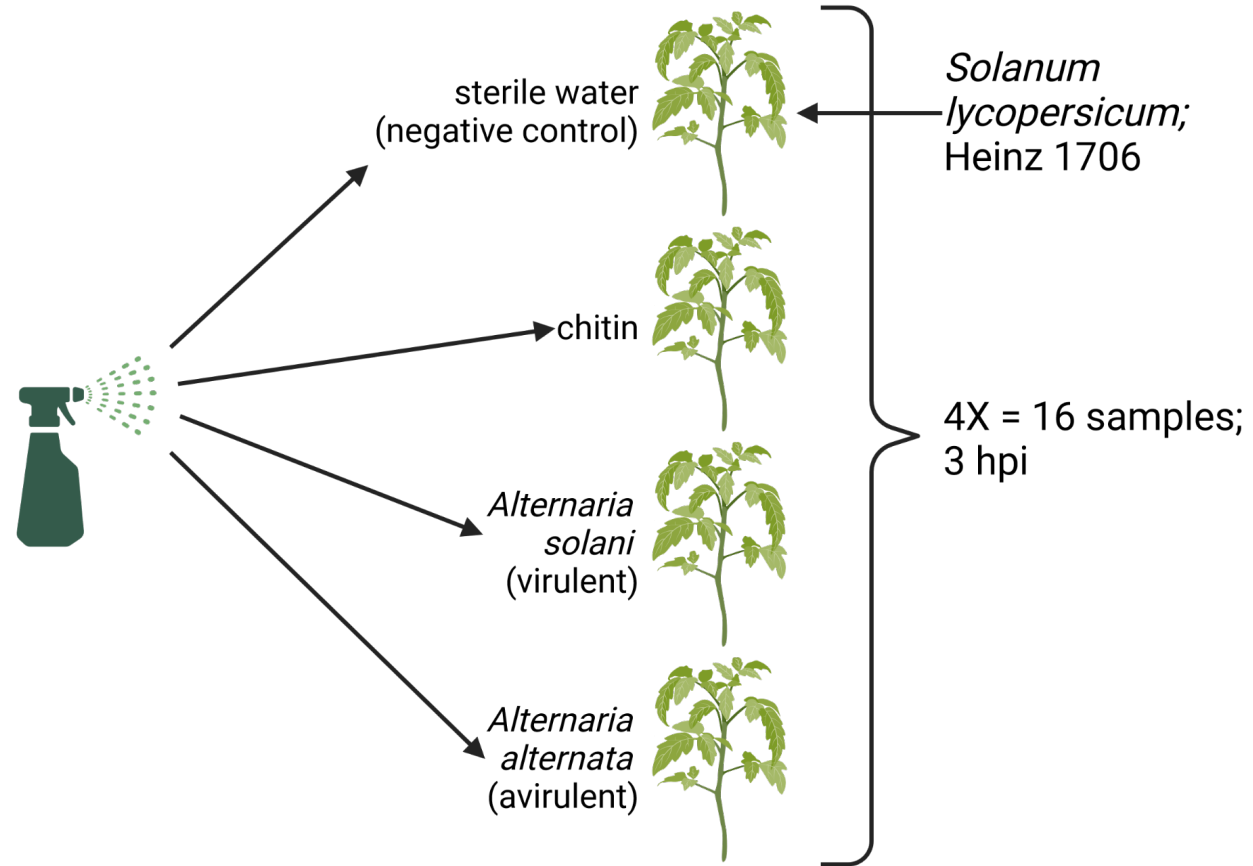
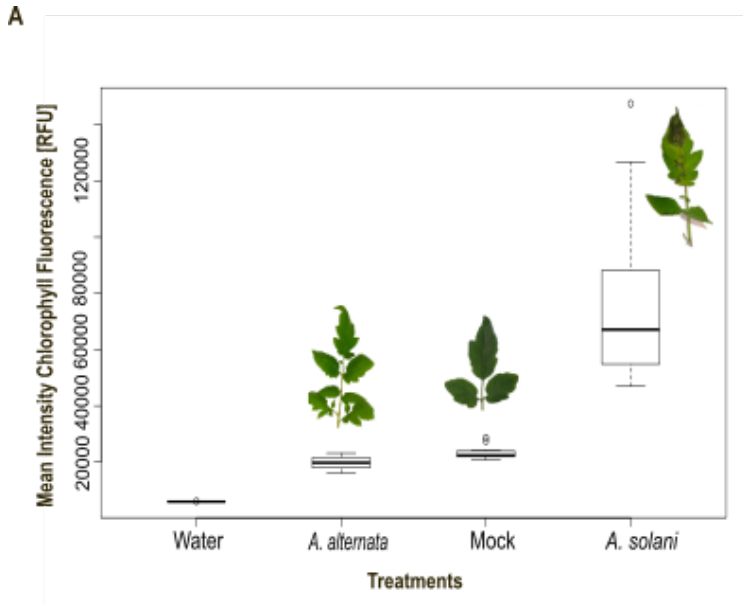
>> Completely different pathogenic organisms (Phytoplasma!)



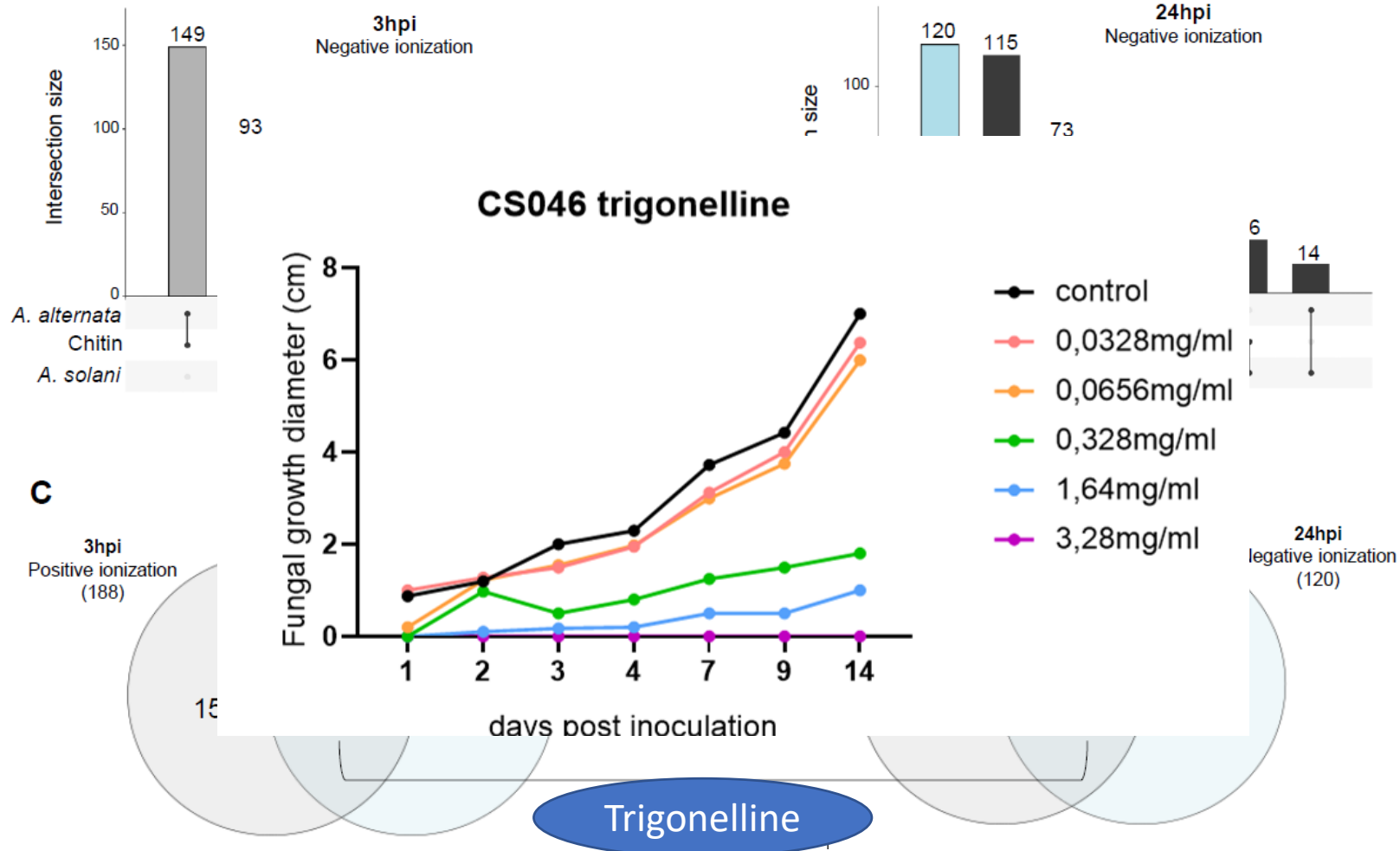
# GWAS identifies SNPS for IF



# Defence response to Alternaria

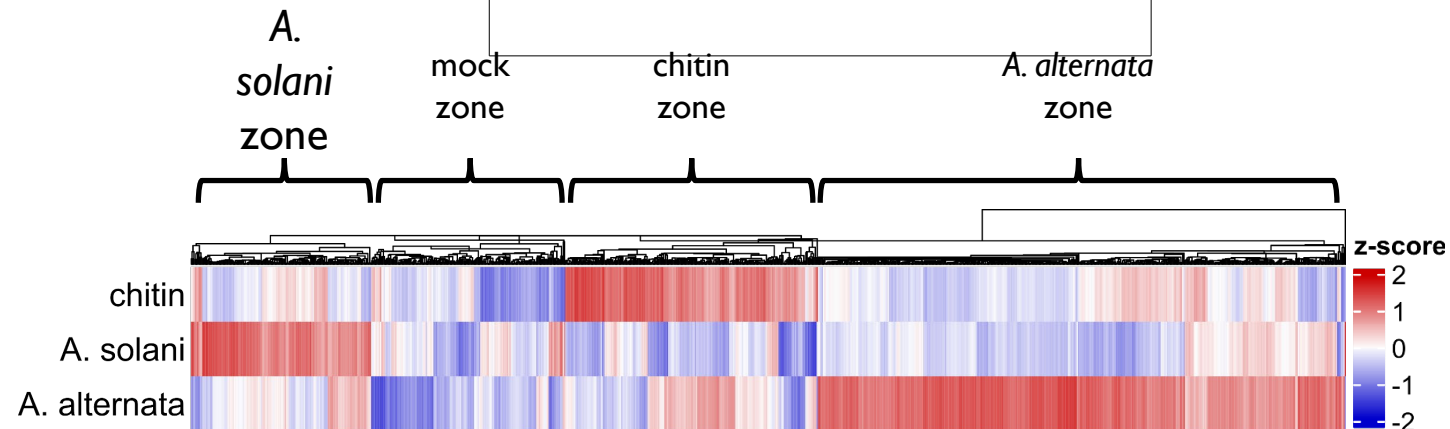


# Metabolic response to *Alternaria*



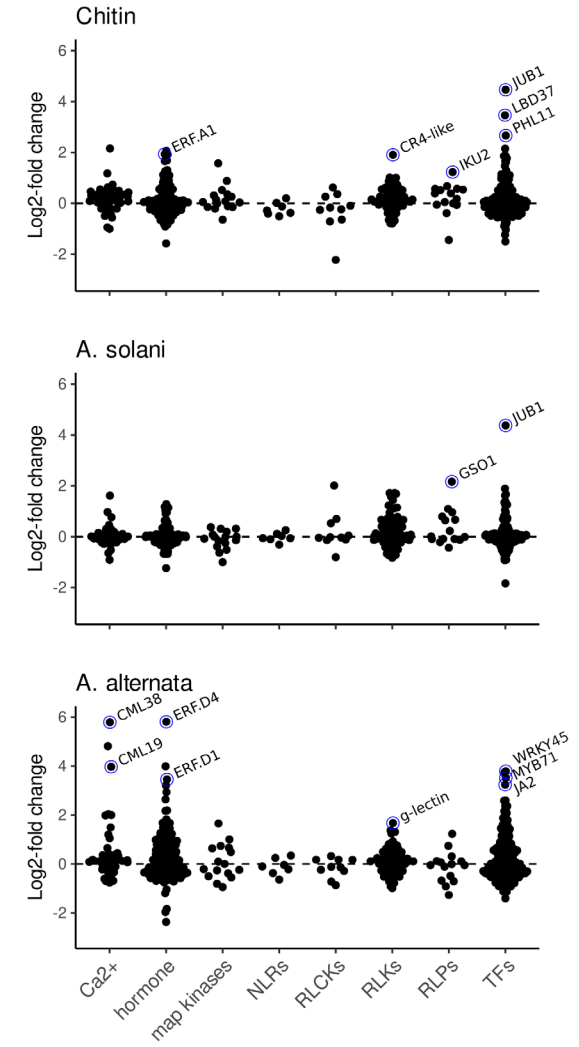
# Distinct DEG patterns

- Genes up-/downregulated vs. mock treatment are **D**ifferentially **E**xpressed **G**enes
- 910 high quality DEGs; strict filtering

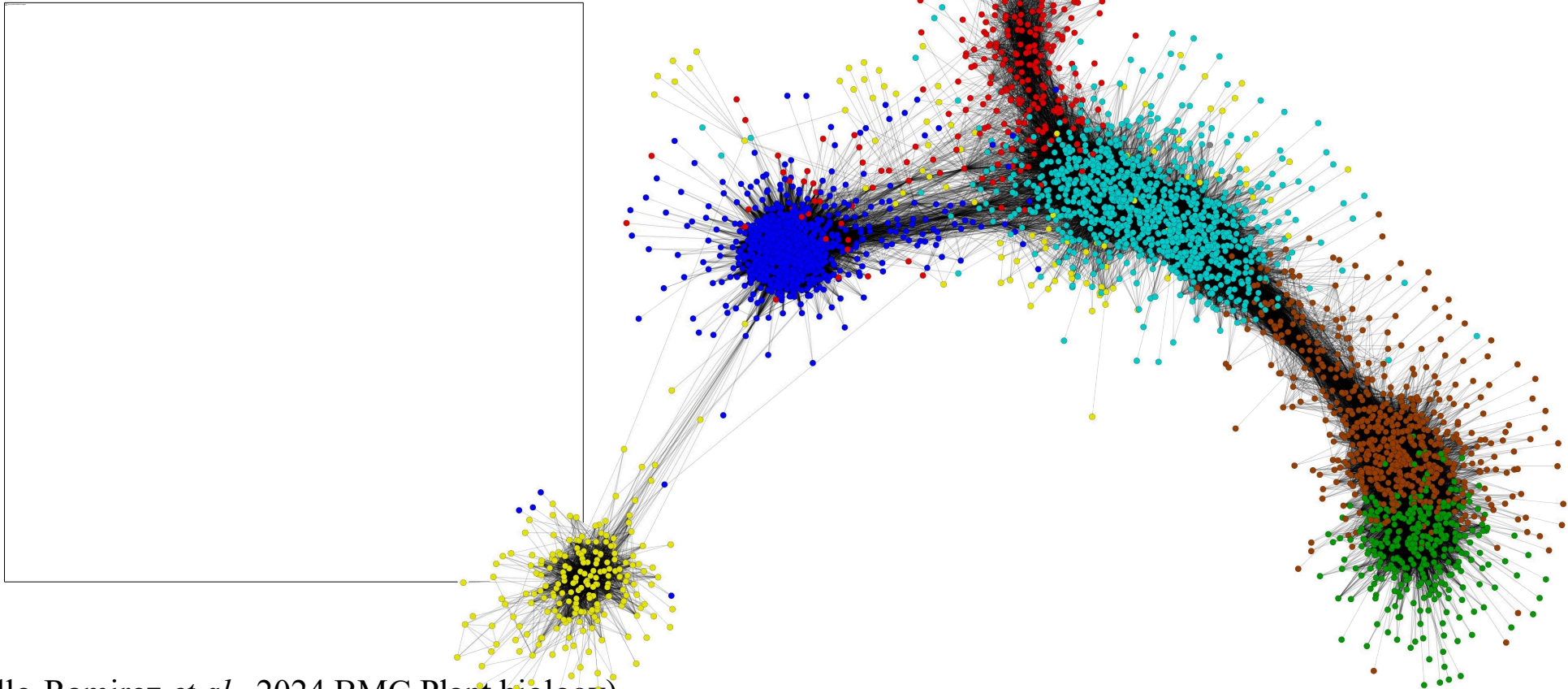


# Little role: canonical mechanisms

- NLRs and PRRs show little induction 3 hpi
- $\text{Ca}^{2+}$  signaling, hormone signaling, and transcription factors show largest changes
- *A. solani* has the least induction of immune system components *in general*



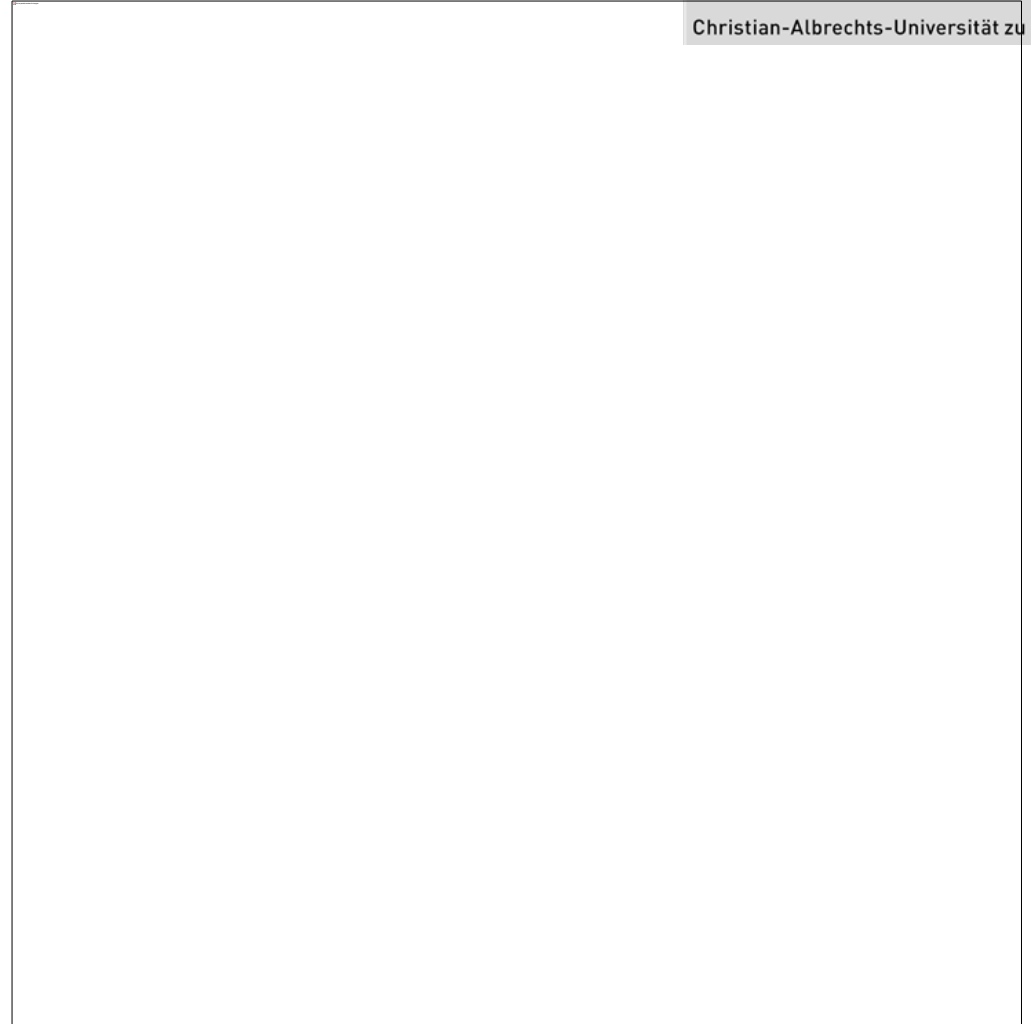
# WGCNA reveals 7 modules



(Tominello-Ramirez *et al.*, 2024 BMC Plant biology)

# Hub genes have various roles

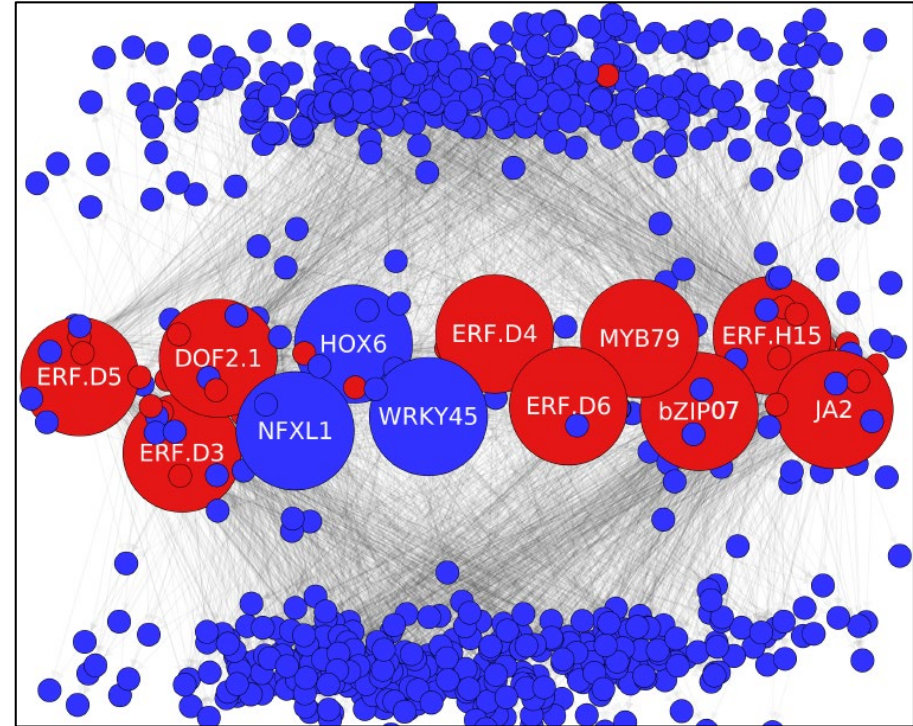
**Blue Module contains hub genes with various roles, incl hormone signalling**



# Hub genes have ET role

**GRE defines 12 major regulators amongst the hub genes.**

**9 of whose associated with ET responses!**





# Wild Plant Pathosystems: Focus Issue

And I will be recruiting postdocs!



Resistance plants show transcriptome shift

Network analyses narrow down gene lists

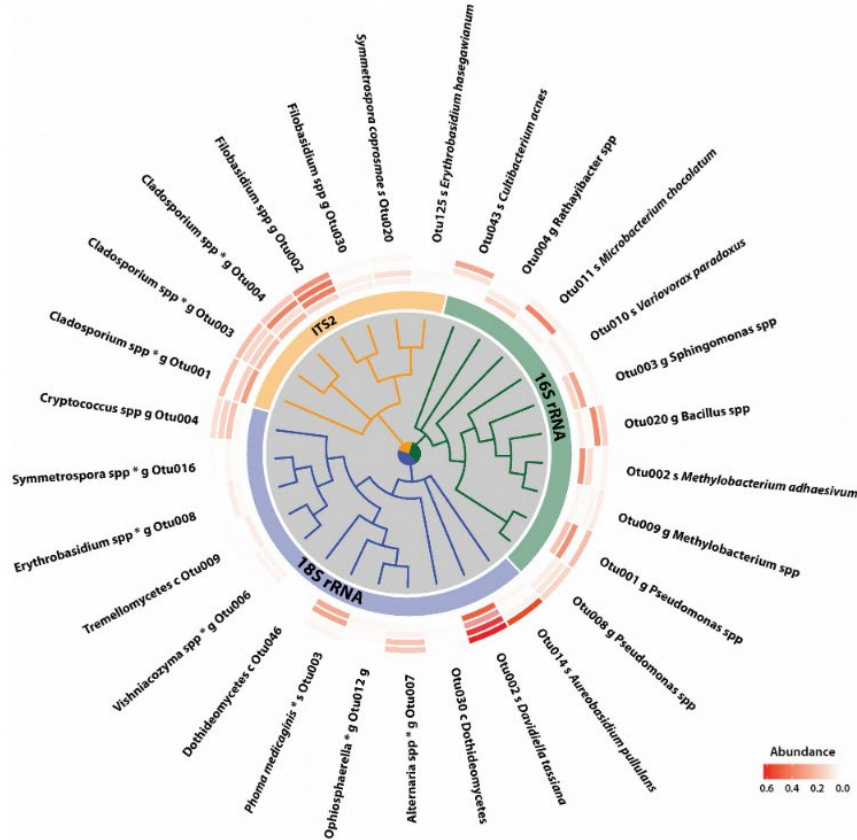
and we identify major regulators

A new clade of ERFs drive EB resistance

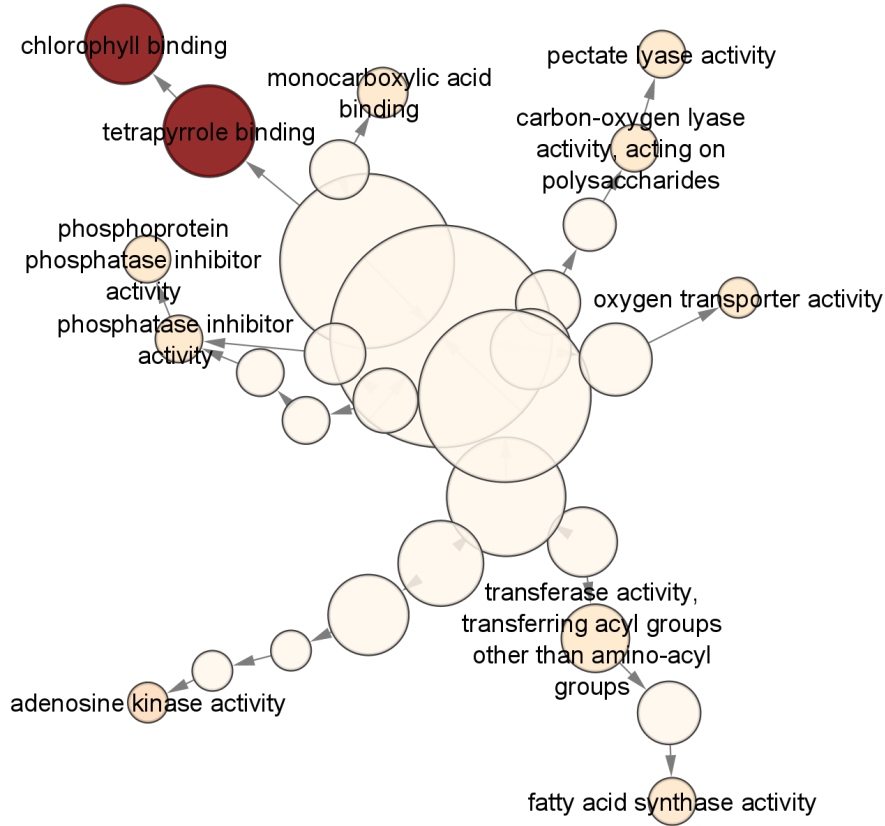
> Next up validate!



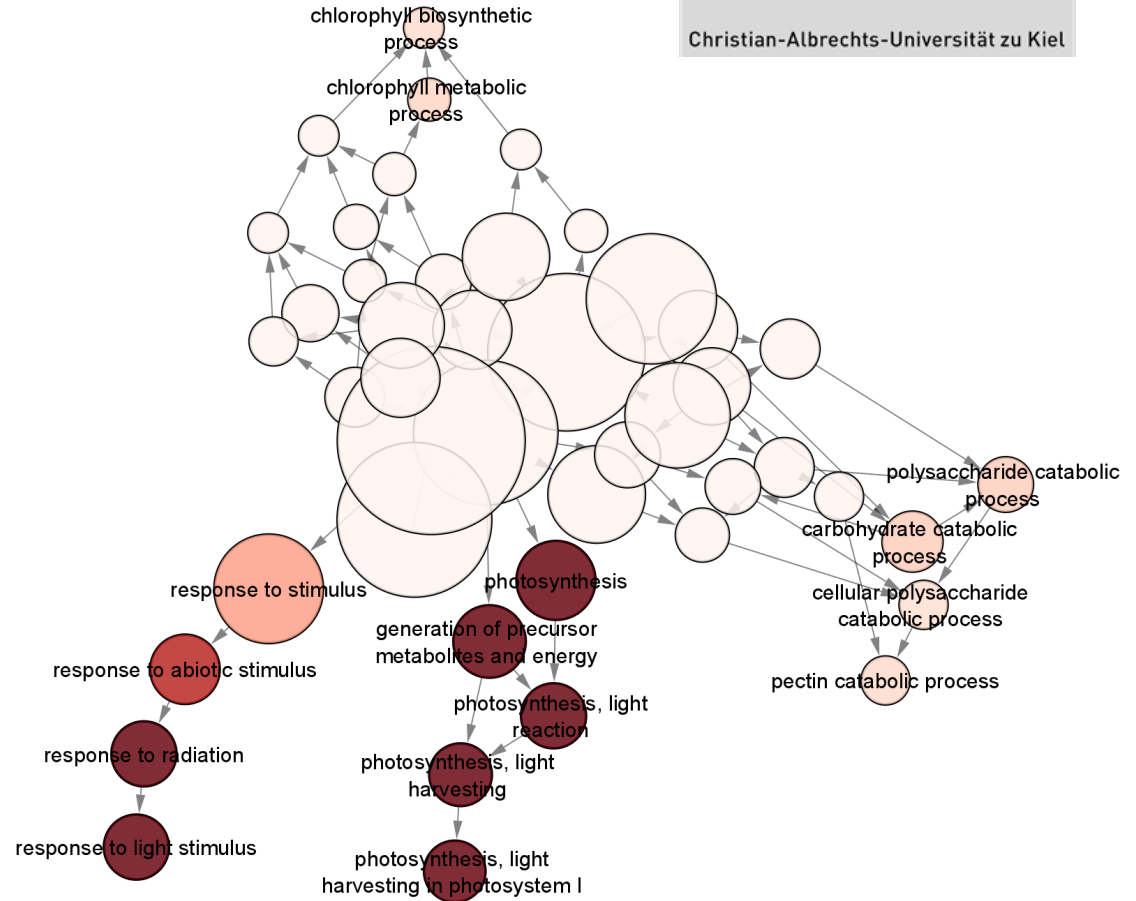
# Always part of the leaf microbiome



# Red module: photosynthesis



molecular



biological process

