Other projects: Y1H, brassica RILs (Vivian), transcriptomics (Jason – Vivian)

GWAS for Botrytis

Justification: crop loss

Genetics of necrotrophic disease resistance across domesticated plants

6 wild and 6 domest individuals per 7 spp

100 genotypes Botrytis

One phenotype = one lesion trait ON ONE plant genotype?

ANOVA for lesion phenotypes

ID candidate genes responding to defense evo across eudicots

(Differential phenotype of one Botrytis genotype across eudicot genotypes)

filter candidates: fungal networks

(and expect resistance network-for-network interactions that vary by genotype)

use cufflinks for RNA seq

Used ATTED-II for network clustering of Arabidopsis candidates from coexpression data

Validation: transgenic complementation in Botrytis

essentially: map plant eQTLs to pathogen genome

Questions

One phenotype = one lesion trait ON ONE plant genotype?

How well characterized botrytis networks? – existing transcriptomics data?

Rotation projects

Image analysis on cucumbers

HPLC output analysis

Phenotyping Botrytis

Classes to take?

Mol, Biochem, Genomics group

MATH

Taken: Math 135A (probability)

Sp 14: Math 135B (probability: MCMC, HMM)

DEFICIENCY

Plant morphology and evolution (Jernstedt, Wi 15)

XX Plant biochem? Winter 15

AREA OF EMPHASIS

Plant pathology (PLP 210 with Gitta Coaker, Wi 15)

BioInformatics (ECS 124) Sp 15

Molecular genetics and genomics (MCB 210) Fa 14

Molecular genetics of fungi?

Network biology?

Funding

full over 4 year including GSR

partial 5th year (grant)

TAing?