Results

Interaction of genetic diversity in B. cinerea and tomato

Purpose-

To assess the contributions of genetic diversity within the genomes of Botrytis and its host, and the interactions between them.

Approach-

Outcome-

Impact of domestication on pathogen-host interaction

Factors in lesion size phenotype

F-test from a GLM of lesion size revealed a significant effect of XXX on lesion size, which we were able to account for in the model. There was a statistically significant interaction between XX and YY for lesion size (interpretation). The effects of XXX terms were non-significant for lesion size (interpretation).

Given the effect of host genotype on lesion size, we conducted GWA analysis for lesion size individually within each host.

Interspecific comparisons

Consistent genetic basis of lesion size between tomato and Arabidopsis?

Any shared SNPs/ gene models?

Shared networks? … network based on SNP co-occurrence between plant/ isolate genotypes

How many isolates remained in same “rank category” across species?

How many isolates were saprophytic on Arabidopsis but virulent on tomato?

Genetics of isolates with “strong” rank-order shift?

Questions

How does variation between genotypes of Botrytis affect virulence on tomato?

Does virulence of one genotype on tomato correspond to virulence on Arabidopsis?

Does tomato species affect the contribution of Botrytis genotype to virulence?

How does variation between genotypes of tomato affect defense against Botrytis?

Does tomato species consistently affect Bc defenses?