**Introduction**

* For generalist necrotrophs, virulence & susceptibility are quantitative traits
  + Most plant immunity studies on large-effect genes (qual-R)
* genetics of Botrytis virulence
  + virulence loci on tomato
  + Quantitative genetics of resistance in Arabidopsis – Jason’s GWAS
* Domestication in pathogen resistance
  + Theory: loss of resistance alleles in domestication & cultivation
    - Email JRI for assumptions in maize genomics
  + Assumptions
    - domestication model holds for disease resistance
    - Resistance is low across all domesticated varieties
    - applies to plants domesticated for fruit
* Approach: detached-leaf GWAS using genetics of Botrytis
  + Work with variation in pathogen
  + Can expand to additional host species - generalist
* Questions
  + Does domestication give us a strong hypothesis about susceptibility?
    - Is this dependent on: pathogen genotype, host genotype
  + Genetic basis of virulence in Botrytis
    - Do the same loci confer virulence across host genotypes?
* Summary of major findings
  + Contributions of host, domestication, isolate and interactions
  + Highly quantitative: Number of SNPs/genes associated with phenotype
  + GO terms associated with multi-host candidate genes

Section 1.

Pathogen virulence and host susceptibility are highly complex traits. Virulence and susceptibility can be viewed as the cumulative outcome of interactions between host pathways and pathogen pathways. Specialist pathogens are only pathogenic (and therefore exhibit virulence) on a narrow range of hosts. Suitable hosts may be limited to a single species or genus, leading to coevolution between host and pathogen which allows crosstalk between genes contributing to pathogen virulence and genes contributing to host susceptibility. Generalist pathogens, in contrast, can affect diverse hosts across taxa. They may be less sensitive to variation in host phenotypes, including some resistance strategies.

Most known genes for plant resistance to pathogens confer qualitative resistance through plant innate immunity. A common genetic basis of plant resistance involves R-gene mediated resistance, in which alleles at a single plant resistance locus (R-gene) and a single pathogen avirulence locus determine susceptibility, based on recognition by the R gene. For example, pattern recognition receptors in plants induce defense pathways following sensing of a conserved pathogen signal, such as cell-wall polymers or flagellin. The R gene strategy often induces programmed cell death, a strategy which is effective against biotrophic pathogens feeding on living tissue {Glazebrook 2005}. This gene-for-gene resistance depends upon specific recognition, and requires close coevolution between host and pathogen if the host is not responding to highly conserved pathogen signals. The reciprocal selective pressures present in interactions between hosts and specialist pathogens make evolution of these specific genetic interactions relatively likely. In contrast, generalists respond to evolutionary pressures from many host species, making the evolution of gene-for-gene resistance unlikely. It is unclear what effect domestication of host plants would have on R-gene mediated resistance. Domestication may lead to loss of some R-genes, or reduce diversity at those loci.

Domestication is also expected to affect the path of coevolution between host and pathogen. Domestication poses a strong genetic bottleneck for many species. This may also reduce genetic variation contributing to pathogen resistance, particularly if pathogen pressures are reduced in cultivation. In contrast, persistent pathogen pressures throughout cultivation could select for resistance loci. Host domestication may affect the path of pathogen coevolution as well, likely more strongly in host-restricted specialists than in generalists. Cultivation practices such as greenhouse growth can affect the evolution of necrotrophic pathogens {Decognet 2009}.

Section 2.

In plants, most naturally variable genes for generalist pathogen resistance likely contribute to quantitative, rather than qualitative, resistance. There are no known naturally variable large-effect resistance loci for plant defense against generalist pathogens. Further, there are no known naturally variable large-effect virulence loci in generalist pathogens.

Additionally, virulence phenotypes and the underlying genetics are highly variable between *B. cinerea* isolates. Production of the toxin botrydial affects virulence in only some isolates {Siewers 2005}. The effect of jasmonates in inhibiting *B. cinerea* virulence on *A. thaliana* depends upon the isolate {Rowe 2010}. Quantitative resistance to *B. cinerea* in *A. thaliana* appears to be largely isolate-specific; GWAS identified mostly non-overlapping sets of candidate loci for resistance to each of four *B. cinerea* genotypes {Corwin 2016}. Such inter-isolate variation for virulence related traits suggests possible host specialization for individual isolates.

Single isolates of B. cinerea exhibit extreme host ranges in contrast to other pathogens. Fusarium oxysporum is a fungal species which is pathogenic on diverse plant hosts. Many of the individual strains, however, are highly host specific {Katan 1999}. In contrast, *B. cinerea* isolate B05.10 pathogenesis has been studied on *A. thaliana*, *Phaseolus vulgaris*, *Capsicum annuum*, *Solanum lycopersicum*, multiple wild *Solanum* *spp*., among other host species {Deighton 2001; Finkers 2007; Corwin 2016; ten Have 2007}. A few genes are known to contribute to quantitative plant resistance to pathogens. Genes involved in secondary metabolite biosynthesis regulate quantitative resistance {Ferrari 2007}. Additional transporters and kinases contribute to resistance. To identify the genomic basis of resistance to generalist and necrotrophic pathogens, we must work with genetic variation within pathogens and their plant hosts.

To look at the interactions between genetic variation in plants and pathogens and the role of evolutionary processes including differentiation by lineage and domestication, we chose to focus on *Botrytis cinerea*. *B. cinerea* causes major pre- and post-harvest crop losses in many species, in the field and greenhouse {Nicot 1996; Elad 2007}.

Studies of plant resistance have identified several mechanisms contributing to quantitative plant resistance and *B. cinerea* virulence. The *B. cinerea* toxins botrydial and botcinic acid increase virulence on several host plants including tomato {Siewers 2005; Dalmais 2011}. VELVET is necessary for oxalic acid production and *B. cinerea* mutants exhibit reduced virulence on multiple hosts {Schumacher 2012}. B. cinerea also has virulence genes for cell wall degradation in the plant {ten Have 1998}.

Tomato is one of the numerous hosts to *B. cinerea*, in which it causes major crop loss due to both pre- and post-harvest infection. Resistance to *B. cinerea* is a quantitative trait in tomato. QTL have been identified for *Solanum* susceptibility to *B. cinerea*, explaining up to 15% of phenotypic variation in a stem bioassay {Finkers 2007}. There is evidence for quantitative resistance to *B. cinerea* in the closest wild relative to tomato as well as other Solanum species, though this has not been directly tested in comparison to domesticated *S. lycopersicum* {Egashira 2000; Nicot 2002}. Further, tomato domestication has altered genetic variation for the circadian clock phase {Muller 2016}, which likely contributes to modulation of pathogen resistance. In *A. thaliana*, multiple genes incorporate signaling from the circadian clock and pathogen attack {Sauerbrunn 2003; Bhardwaj 2011; Weyman 2006}, suggesting connections between these response pathways.

The effect of domestication on plant-pathogen interactions is largely untested. Domestication poses a strong genetic bottleneck, reducing diversity genome-wide. We assume that this extends to pathogen resistance loci; resistance alleles are likely lost during the domestication bottleneck. Further, selective pressures from pathogens may be reduced under cultivation. In contrast, domesticated plants may experience increased selective pressures from some pathogens. *B. cinerea* causes extensive preharvest damage in *S. lycopersicum* cultivation, so it is unclear what the effect of domestication will be on plant susceptibility and pathogen virulence.

In this study, we examined the contributions of tomato variation, domestication, and *B. cinerea* genetic variation to lesion size in a detached leaf assay. We inoculated individual tomato leaflets from 6 domesticated varieties of *S. lycopersicum*, and 6 wild accessions of *S. pimpinellifolium* with spore suspensions of 91 *B. cinerea* isolates. In our analysis of lesion images at 72 hours post inoculation, both host and pathogen genotype contribute to virulence. However, we found no significant interaction between host and *B. cinerea* genotype species-wide. We also find no species-wide evidence of a significant domestication effect upon *B. cinerea* virulence, though domesticated varieties are slightly more susceptible on average. This suggests that individual isolates are generalists across tomato genotypes and across domestication in *Solanum.* A subset of single isolates, however, are sensitive to tomato domestication. All three of these show increased virulence on domesticated tomato varieties. No isolates are significantly affected by individual tomato genotypes. Further, lesion size is more variable on domesticated than wild genotypes, in contrast to the expected reduction in variation at resistance loci following the domestication bottleneck. We do not find evidence for host specialization; *B. cinerea* isolates collected from tomato tissues are not within the most-virulent isolates on tomato.

Scraps and bits:

*Botrytis cinerea* is one such generalist necrotroph, with a sequenced genome and over 200 host plants {Elad 2007}, including nearly all eudicots. Previous experiments found evidence of quantitative resistance in the response of *Arabidopsis thaliana* to *B. cinerea*, due to an interaction between plant host genotype and isolate genotype {Corwin 2016}. Additional evidence for isolate-dependent resistance comes from the fact that candidate genes for *A. thaliana* quantitative resistance were largely unique to each of the 4 *B. cinerea* isolates tested. The plant response likely varies depending on molecular patterns perceived from individual pathogen genotypes. [add more about specific genes in Botrytis/ Arabidopsis interactions?]

Much of what we know about pathogen resistance comes from the Arabidopsis model. Something about Arabidopsis genetic diversity- weedy but selfing?

For domesticated plants, in theory the population bottleneck of plant breeding has led to a reduction in genetic diversity genome-wide, including regions contributing to pathogen resistance. [evidence from maize]

Breeding durable resistance necessitates a quantitative genetic approach.

These assumptions are also applied to species domesticated for fruit and leaf traits.

If the domestication bottleneck did indeed reduce genetic diversity genome-wide, it is expected to reduce genetic diversity for pathogen resistance loci as well. This would likely lead to reduced pathogen defense, and reduced variation for defense, in domesticated hosts compared to wild relatives. However, these assumptions are untested, particularly in relation to different pathogen life histories.

For genes in Botrytis/host, simply put together a list of citations on genes in Botrytis and genes in Tomato/Arabidopsis.

Say that they affect a diversity of processes.

Then say that most of these studies do not look at which genes function in diverse roles across the pathogen genotypes or how they interact with diverse hosts.

Then talk briefly about Jason’s paper and how there is isolate x host interactions.

Then the Botrytis velvet paper and Botrytdial papers talk about genetic variation in Botrytis genes.

Then finish off saying that there is a need for genome wide analysis in the pathogen to understand how the host broadly handles host variation.

Thought: We know relatively little about how genetic variation in a generalist pathogen impacts its ability to infect diverse hosts.

How does Botrytis evade/ survive non-host resistance in such diverse species?