Results

Interaction of genetic diversity in B. cinerea and tomato

\*\* violin plot domesticated vs. wild

Overall, domesticated varieties show higher susceptibility to diverse B. cinerea isolates (Table R1) (Figure R0), and the three highest-susceptibility varieties are within S. lycopersicum. However, one domesticated variety, LA4345 (Heinz 1706) is relatively resistant to B. cinerea isolates even compared to wild varieties.

Figure R2. Lesion area for each isolate by tomato plant interaction. Tomato accession names are listed, and each isolate is traced by a single color. Virulence of isolates changes across tomato genotypes within both the domesticated and wild groups.

Susceptibility is higher overall in tomato hosts compared to *A. thaliana* (Figure R3). virulence of several isolates changes across host species (Figure R4).

Factors in lesion size phenotype

Table R1. Mixed model analysis of lesion area. Interaction ( : ) and nesting ( / ) of terms are included. Lesion size is significantly affected by pathogen and host genotypes, and domestication status. However, genotype effects differ across the two replicate detached leaf experiments.

F-test from a GLM of lesion size revealed a significant effect of B. cinerea genotype, tomato genotype, and tomato domestication on lesion size. The interactions between B. cinerea and tomato genotypes were non-signficant under our model (\*\* interpretation). The F-test also revealed significant effects of experimental replicates and flat blocking, which we were able to account for in the model. The effect of individual plant was non-significant for lesion size (\*\* interpretation).

There was a statistically significant interaction between XX and YY 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?

Genetics

For top 50 SNPs/ geno:

* Table of effect-size estimates per association
* Table of MAF per association

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Figure R0. Violin plot of lesion size on domesticated vs. wild tomato hosts.

Figure R1. Average lesion area on each tomato plant genotype, across all *B. cinerea* isolates. Tomato accession names are listed.

Figure R2. Lesion area for each isolate by tomato plant interaction. Tomato accession names are listed, and each isolate is traced by a single color. Virulence of isolates changes across tomato genotypes within both the domesticated and wild groups.

Figure R3. Variation in lesion area for each *B. cinerea* isolate, averaged across plant host genotypes. Lesion size data from *S. lycopersicum* and *S. pimpinellifolium* is compared to the same set of isolates on *A. thaliana*.

Figure R4. Variation in lesion area for each *B. cinerea* isolate, averaged across plant host genotypes. Lesion size data from *S. lycopersicum* and *S. pimpinellifolium* is compared to the same set of isolates on *A. thaliana*. Each isolate is traced by a single line color. Relative virulence of several isolates changes across host species.