**Results**

**Experimental Design**

We wanted to directly measure the impact of tomato domestication and genetic variation on quantitative resistance. To measure quantitative resistance, we infected tomato leaflets with a collection of 91 diverse *B. cinerea* isolates. *B. cinerea* is an endemic necrotroph, and host resistance to this generalist pathogen is largely quantitative (CITE). We selected tomato genotypes including 6 domesticated *Solanum lycopersicum* cultivars and 6 wild *S. pimpinellifolium* genotypes. Previous studies have examined the contrast in *B. cinerea* resistance between wild and domesticated tomato using distantly related species such as *S. chilense* {ten Have 2007}, *S. habrochaites* {Finkers 2007, ten Have 2007}, *S. hirsutum* {Egashira 2000}, *S. lycopersicoides* {Guimaraes 2004}, *S. neorickii* {Finkers 2008, ten Have 2007}, *S. peruvianum* {Egashira 2000}, and *S. pimpinellifolium* { Egashira 2000}. We selected *S. pimpinellifolium*, the closest wild relative of *S. lycopersicum*, to directly study the selection associated with the impact of domestication. We infected all 91 *B. cinerea* isolates onto each plant genotype in 3-fold replication across 2 independent experiments in a randomized complete block design, giving 6 measurements per plant-pathogen combination, for a total of 3,276 lesions. We digitally measured the area of the developing lesion at 72 hours post infection (HPI) (Figure R1). At 72 hours, significant lesion growth is visible, but no lesions have grown to completely consume infected leaflets. Lesion area is a composite phenotype from the interaction of host and pathogen genetics.

We performed statistical analysis of lesion size with a generalized linear model (GLM). Within the model, we tested the fixed effects of isolate genotype, plant species (domesticated or wild), plant genotype (which is nested within species), and position of sampled leaflet (apical or basal). We also considered the random effects of experiment, block (nested within experiment), individual plant, and individual leaf (nested within sample plant). The terms for individual plant, leaf, and leaflet position did not significantly improve the model, so we omitted them from further analysis. Our final model also included the interaction terms of isolate by plant species, and isolate by plant genotype (nested within species). The final model shows that genetic variation within both the host plant and the pathogen affect lesion growth, as does domestication (Table R1). Further, there are significant effects of tomato genetic variation between domesticated and wild species. We did not find evidence for significant interaction effects between isolate and plant genotypes, but the F-test did suggest that the isolate-plant interactions contribute a large proportion of the variance in lesion size (Table R1).

**Domestication and lesion area**

Existing literature, largely drawing from evidence of qualitative resistance to biotrophic pathogens, has proposed that domestication increases pathogen susceptibility and decreases genetic variation for disease resistance due to genetic bottlenecks in domestication (CITE).

As expected due to domestication, lesion size is significantly greater on average (18% increase) on domesticated tomato compared to wild tomato (p = XXX, Table R1) (Figure R2).

On domesticated tomato, the range of lesion sizes is broader by 15% compared to wild hosts (5% to 95% interval: 2.03 on domesticated, 1.76 on wild). This increased range of lesion size contradicts the hypothesis of decreased range of resistance due to the domestication bottleneck. Additionally, the coefficient of variation (CV) of lesion size is broadly consistent across domestication (Wilcoxon signed-rank test, V=2275, p=0.7163), indicating no significant effect of domestication on lesion size variance (Figure R3).

We also asked whether domestication interacts with pathogen genetics to determine lesion size. Lesion size varies across host for many of the isolates, suggesting an interaction between the genomes of *B. cinerea* and tomato (Figure R4). However, domestication did not have a significant interaction effect with isolate genotype (Table R1). This is likely due to the many degrees of freedom in calculating this interaction effect.

Second, isolate ranking by mean lesion size differs between domesticated and wild hosts (Wilcoxon signed-rank test, V=4322, p=2.586e-12) (Figure R3).

**Host variation and lesion area**

Domestication does impact lesion size, but most variance is due to genetic variation in the isolate and in host plant genetics (Table R1). However, tomato genotype within each species did not have a significant interaction effect with isolate genotype (Table R1). These interaction effects are likely not significant via F-test due to the many degrees of freedom in the combinations of isolates and tomato genotypes. As such, we took an additional approach to statistically test for an interaction between *B. cinerea* and host genotype. Through single-isolate GLM analysis, a subset of isolates show a significant (p < 0.05) interaction with host genotype when including the fixed effects of domestication and plant genotype nested within domestication, and the random effect of experiment (Figure R4E) \*\*still need to use FDR correction\*\*.

Isolates collected from tomato stem or fruit tissue are not among the most virulent group (Figure R4F). In fact, one isolate collected from tomato tissue (KGB1) is within the 10 least-virulent isolates (Figure R4F). This may suggest a generalist strategy for individual isolates, due to this apparent lack of host-specificity.

**FIGURES**

Figure R1. Will be an image of the detached leaf assay and leaf/ lesion calls.

Figure R2. Violin plots of lesion size due to Botrytis cinerea growth on tomato host genotypes. Plots include all replicates of lesion size measurements across isolates.

Figure R3. Interaction plot for domestication. Each line traces the average lesion size for a single Botrytis isolate.

Figure R4. Interaction plot of lesion size due to individual Botrytis cinerea isolates on tomato host genotypes. Each line traces the average lesion size across plant genotypes for a single Botrytis isolate.