**Results**

**Experimental Design**

In this study, we directly measure the impact of tomato domestication on quantitative resistance to *Botrytis cinerea*. To do this, we infected tomato leaflets with a collection of 91 diverse *B. cinerea* isolates. The selected tomato genotypes included 6 domesticated *Solanum lycopersicum* cultivars and 6 wild *S. pimpinellifolium* genotypes. Previous studies have examined the contrast in resistance between wild and domesticated tomato across evolutionary time (CITE). We selected *S. pimpinellifolium*, the closest wild ancestor of *S. lycopersicum*, to more directly study the impact of domestication itself. 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 a total of 6 measurements per plant-pathogen combination, for a total of 3,276 lesions. We measured the area of the developing lesion, which is a composite phenotype from the interaction of host and pathogen genetics. Specifically, we examined lesion size 72 hours post infection (HPI) on each leaflet using digital image analysis (Figure R1).

We performed statistical analysis of lesion size with a generalized linear model (GLM). We considered 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 did not significantly improve the model, so we omitted them from further analysis. Our final model also included the interaction terms of isolate with plant species, and isolate with plant genotype (nested within species). Analysis of this model indicates the genetics of both the host plant and the pathogen affect lesion growth, as does domestication (Table R1).

**Domestication and lesion area**

Based on the literature, we expect domestication to increase pathogen susceptibility and decrease genetic variation for disease resistance due to genetic bottlenecks in domestication (CITE).

Lesions were significantly larger on average (18% increase) on domesticated tomato compared to wild tomato (p = XXX, Table R1) (Figure R2). Further, the range of lesion sizes was broader by 15% on domesticated tomato (5% to 95% interval: 2.03 on domesticated, 1.76 on wild). This increased range of lesion size is surprising, given the hypothesized decrease in range of resistance due to the domestication bottleneck.

Lesion size varies across host for many of the isolates, indicating an interaction between B. cinerea and tomato domestication (Figure R3), as well as between the genomes of *B. cinerea* and tomato (Figure R4). However, neither domestication nor tomato genotype within each species had 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. First, 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\*\*. 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).

d

**Random bits**

CV of lesion size, however, is broadly consistent across domestication (Wilcoxon signed-rank test, V=2275, p=0.7163) (Figure R3).

Isolates collected from tomato stem or fruit tissue are not among the most virulent group (Figure R4F).

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.