**Results**

**Experimental Design**

To test how genetic variation between *Botrytis cinerea* isolates interacts with tomato domestication, we infected a collection of 91 diverse Botrytis cinerea isolates onto tomato leaflets. This included 6 domesticated *S. lycopersicum* cultivars and 6 wild *S. pimpinellifolium* genotypes. We infected all 91 *B. cinerea* isolates onto each plant genotype in 3-fold replication across two independent experiments in a randomized complete block design. We measured lesion size at 72 hours post infection (HPI) on each leaflet using digital image analysis (Figure R1).

Lesion area is a composite phenotype including contributions from both host and pathogen genetics. We analyzed lesion size with a generalized linear model (GLM), and found statistically significant effects of [isolate genotype, plant genotype, plant species]. \*\* need to rerun model and write this section \*\* The random effects of [experiment, replicate] were also significant. Terms for individual plant, individual leaf, and leaflet position (apical or basal) did not significantly improve the model, so we omitted them from further analysis.

**Contributions to lesion area phenotype**

Lesions were significantly larger on average (18% increase) on domesticated tomato compared to wild tomato (t-test; t=7.0248, df=6214.3, p= 2.373e-12) (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).

Isolate ranking by mean lesion size differs between domesticated and wild hosts (Wilcoxon signed-rank test, V=4322, p=2.586e-12) (Figure R3), but CV of lesion size is broadly consistent across domestication (Wilcoxon signed-rank test, V=2275, p=0.7163) (Figure R3).

Lesion size varies across host for many of the isolates, indicating an interaction between the genomes of *B. cinerea* and tomato (Figure R4). A subset of isolates show a significant (p<0.05) interaction with host genotype in a single-isolate GLM analysis including the fixed effects of domestication and plant genotype nested within domestication, and the random effect of experiment (Figure R4E) \*\*need to use multiple-testing correction\*\*. Isolates collected from tomato stem or fruit tissue are not among the most virulent group (Figure R4F).

**Genome wide association mapping of lesion area**

The B. cinerea population includes X SNPs with minor allele frequency > 0.2.

We used XXX to estimate broad-sense heritability of isolate-specific, host genotype-specific lesion size and their interactions. Heritability is the fraction of lesion area variations that can be attributed to genetic variation in host or pathogen.

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.

* Botrytis lesions are slightly larger on domesticated than wild tomato
* No large domestication effect
* average lesion size varies depending on tomato genotype, slightly
* lesion size is more variable between domesticated tomato lines than between wild varieties

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.