**FIGURES**

Figure R1. *Botrytis cinerea* x tomato detached leaf assay and digital image analysis. Individual tomato leaflets of 6 *S. lycopersicum* genotypes and 6 *S. pimpinellifolium* genotypes are in randomized rows, spore droplets of individual *B. cinerea* isolates are in randomized columns. Digital images are collected 72 hours post inoculation (A). Digital masking of leaf and lesion (B) is followed by automated measurement of area for each lesion.

Figure R2. Relative susceptibility of tomato genotypes to *B. cinerea* infection. Violin plots are of lesion size due to *Botrytis cinerea* growth on each tomato host genotype. Individual points are mean lesion size for each isolate-host pair.

Figure R3. *B. cinerea* virulence responds to host domestication. The violin plots include each *B. cinerea* lesion on the host species. The interaction plot traces the average lesion size of a single *B. cinerea* isolate across the host species.

Figure R4. *Botrytis cinerea* virulence varies due to isolate-host interactions. Interaction plot of lesion size due to individual *B. cinerea* isolates on tomato host genotypes. The x-axis includes each plant host genotype. Each line traces the average lesion size of a single *B. cinerea* isolate across hosts. A is a plot of all isolates, B-G highlight a subset of isolates. B is B05.10, C is the 10 most highly-virulent isolates, D is the 10 most saprophytic (low-virulence) isolates, E is host-sensitive isolates, F is 5 isolates collected from tomato tissue, G is 3 domestication-sensitive isolates.

Figure R5. *B. cinerea* lesion size is a polygenic trait on tomato.

Figure R6. Overlap in lesion size SNPs > 99.9% threshold across multiple host plant phenotypes. Chromosomes are differentiated by shading. Frequency is number of phenotypes in which the SNP exceeds the threshold.

Figure R7. Top 50 SNPs for lesion size phenotype on each host plant. Points are color coded by plant host.

Figure R8. Overlap in lesion size SNPs > 99.9% across individual-host phenotypes and domestication phenotypes.

Figure R9. Top 50 SNPs for lesion size for each domestication phenotype. Domestication sensitivity is (domesticated – wild / domesticated).

Figure R10. Venn diagram of SNPs identified >99.9% for each domestication phenotype.

Figure R11. Venn diagram of genes with a significant SNP identified >99.9% for each domestication phenotype.