**Methods**

**Media and Isolate Preparation**

The 97 isolates of *B. cinerea* used were obtained previously from single spore isolations from a natural collection. Preparation of the potato dextrose agar (PDA) consisted of a 0.75% concentration of commercial agar (Difco) in a 39g/L solution using milliQ H2O. The agar was poured into 10cm diameter sterile Petri plates. A 1cm x 1cm block was cut with a scalpel of fresh hyphae of each isolate and placed on each new PDA plate. Following spore maturation, spores from each isolate were harvested with a glass rod and 3mL of water. The isolates were diluted with filter-sterilized 50% grape juice to a concentration of 0.2 spores/uL. Fresh plates were inoculated with 1mL of spore solution and grown for 3 days.

Each plate Each plate was divided into a 3 x 3 grid, and hyphal waviness was quantified in XX blocks per plate. We randomized the 97 isolates into inoculation groups, as not all observations could be recorded on a single day. We marked individual spore locations and measured hyphae on a 0-10 scale of increasing waviness. Hyphae with a measurement of 0 would follow a linear path while 10 would have tightly waving hyphae. We noted any contamination on plates, and photographed a subset of plates.

**Data Analysis**

The hyphal waviness phenotype was analyzed using a linear mixed-effect model including the effects of isolate (B. cinerea), isolate interaction with plate block, and the date of observation (lme4; Douglas Bates 2015). Not all of the 97 isolates’ hyphae were measured in the same period so we could not include the interaction between isolate and date. Randomized effects of the plate block term were omitted as the impact showed similar results to the interaction between isolate and plate block in a mixed-effect model. Also, PDA concentration, ordering and plate block were all omitted for the insignificant change they had on the model. This model allowed for the significance of each term to be calculated through least-squared means of the hyphal waviness phenotype for each *B. cinerea* isolate. We calculated heritability as the ratio of of sum of squares per term over total sum of squares. We used the R statistical environment to generate figures and complete statistical analysis (ggplot2; Hadley Wickham 2016)

For GWA mapping with the 91 isolates genotyped in this study, we utilized a total of 272,672 SNPs with minor allele frequency (MAF) 0.20 or greater, and less than 10% missing calls across the isolates (SNP calls in at least 82/ 91 isolates).

The model means for Hyphal Waviness were used as the phenotypic input for GWA using bigRR, a heteroskedastic ridge regression method that incorporates SNP-specific shrinkage (Shen, Alam et al. 2013). This approach has previously had a high validation rate (Ober, Huang et al. 2015, Corwin, Copeland et al. 2016, Francisco, Joseph et al. 2016, Kooke, Kruijer et al. 2016). The B. cinerea GWA used 272,672 SNPs at MAF 0.20 or greater and <10% missing SNP calls as described above. Because bigRR provides an estimated effect size, but not a p-value, significance was estimated using 1000 permutations to determine effect significance at 95%, 99%, and 99.9% thresholds (Doerge and Churchill 1996, Shen, Alam et al. 2013, Corwin, Copeland et al. 2016). SNPs were annotated using SNPdat (Doran and Creevey 2013) with gene transfer format file construction from the T4 gene models for genomic DNA by linking the SNP to genes within a 2kbp window (http://www.broadinstitute.org, (Staats and van Kan 2012)). Functional annotations are based on the T4 gene models for genomic DNA (http://www.broadinstitute.org, B. cinerea; (Staats and van Kan 2012)). Additional genes of interest, based on a broad literature search of known virulence loci, were taken from NCBI (https://www.ncbi.nlm.nih.gov/) and included by mapping sequence to the T4 reference using MUMmer v3.0 (Kurtz, Phillippy et al. 2004). We used the program InterProScan within BLAST2GO for functional gene ontology (GO) annotation of the gene models (http://www.blast2go.com).