**Methods**

**Media and Isolate Preparation**

The 97 isolates of *B. cinerea* used were obtained previously from harvested single spore natural collection. Preparation of the potato dextrose agars (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 plastic disposable Petri plates. Utilizing previous collections of mature isolates, a 1cm x 1cm block was cut with a scalpel of matured forms of each isolate and placed on each plate. After given time to form a lawn, new inoculations were done using grown isolates harvested with a glass rod and 3mL of water. The spores were then centrifuged for isolation and counted. After counting, the isolates were diluted with filter-sterilized 50% grape juice to a concentration of .2 spores/uL. Fresh plates were inoculated with 1mL of this concentration of spores and grown for 3 days.

Each plate contained a 3 x 3 block system that organized spore location using a plate block system for overall categorization. The recording process consisted of marking individual spore locations and measuring hyphae on a 0-10 scale of increasing waviness. Hyphae with a measurement of 0 would be completely straight while 10 would have \_\_\_\_\_ hyphae. Plates with contamination were noted, pictures were taken of the recording process and not all isolates were measured on the same days.

**Data Analysis**

The hyphal waviness phenotype was analyzed using a linear mixed-effect model of isolate (B. cinerea), isolate interaction with plate block, and the date of recording (lme4; Douglas Bates 2015). Not all 97 isolate’s hyphae were measured in the same period and we therefore dropped 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. Heritability was able to be calculated using proportion of sum of squares per term over total sum of squares. For the graphical generation (ggplot2; Hadley Wickham 2016) and statistical analysis, were done using an R statistical environment

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 and 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).