**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 at 25°C with 12 hours of light for 3 days.

For each isolate, five plates were inoculated and divided into a 3 x 3 grid, and hyphal waviness was quantified in 5 observations 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 PlateBlock, our randomization technique of distributing isolates among plates, 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 PlateBlock term were also omitted as the effect of the term on the sum least squared means when making the linear model were very minimimal. Also, the 0.75% PDA concentration, isolate ordering and PlateBlock terms were all omitted for the insignificant change on the linear 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 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). A total of 345,485 SNPs were used to produce GWA map using all 95 genotyped isolates. With less than used 10% missing calls across all isolates (SNP calls in at least 86/ 95 isolates), these SNPs contained a minor allele frequency (MAF) of 0.20 or greater.

To use a heteroskedastic ridge regression method that incorporates SNP-specific shrinkage, bigRR (Shen, Alam et al. 2013), the phenotypic input for GWA was given by the model means of hyphal waviness. This ridge regression method, or bigRR, has had previously high validation rate(Ober, Huang et al. 2015, Corwin, Copeland et al. 2016, Francisco, Joseph et al. 2016, Kooke, Kruijer et al. 2016). To generate a GWA, as listed above, a MAF of 0.20 or greater and <10% missing SNP calls combined with 345,485 SNPs of B. cinerea. Estimated using 1000 permutations, an estimated effect size, not a p-value in bigRR, was determined with an effect significance of 95%, 99% and 99.9% thresholds (Doerge and Churchill 1996, Shen, Alam et al. 2013, Corwin, Copeland et al. 2016). as well as SNP annotations were done using SNPdat (Doran and Creevey 2013). Gene transfer format file construction from the T4 gene models for genomic DNA was done by linking the SNP to genes within a 2kbp window (http://www.broadinstitute.org, (Staats and van Kan 2012)). Taken from NCBI (https://www.ncbi.nlm.nih.gov/), broad literature search of known virulence loci were used as additional genes of interest and provided mapping sequences to the T4 reference using MUMmer v3.0 (Kurtz, Phillippy et al. 2004). For the functional gene ontology (GO) annotation of the gene models (http://www.blast2go.com), the program BLAST2GO was used with an internal feature, InterProScan.