Wei Zhang 2018 on Heritability:

Of 9,284 detectable *B. cinerea* genes, 8,603 genes and 5,244 genes were significantly influenced by genetic variation in pathogen and host, respectively (74% and 45% of predicted *B. cinerea* genes, respectively) (Figure 2A and Supplemental Data Set 3 and 5). In addition, the host effect was also less than that of the pathogens own natural genetic variation, average H2Host = 0.010 while average H2Isolate = 0.152.

Broad-sense heritability of individual transcripts was estimated as the proportion of variance attributed to *B. cinerea* genotype, Arabidopsi*s* genotype, or their interaction effects.