**DISCUSSION**

1. **Dispersed interactions across host and pathogen genomes**

Theories of filamentous pathogen genomics suggest a two-speed genome model, in which diverse fungal virulence effectors are enriched in regions of the genome containing repetitive sequences and transposable elements {Dong 2015}. This predicts patterns of virulence loci in small regions of the genome with high mutation rates, and slower evolution in the rest of the genome, with little virulence effect. Previous studies in cross-species eQTL conformed with this expectation, as in the system of *Medicago truncatula* x *Meloidogyne hapla*, in which few cross-species eQTL hotspots (termed Host Expression Modulators) clustered on only a few of the parasite chromosomes (termed i-chromosomes) {Guo 2017}. The targeted plant genes, on the other hand, were dispersed across the host genome {Guo 2017}. Our findings contrast these expectations; half the chromosomes in the *B. cinerea* genome appear to harbor one or more loci with expression modulation of *A. thaliana* genes which are dispersed across the host genome. Expanding analysis to additional hosts could reveal specific chromosomes with more common, or more concentrated, expression modulation effects, but thus far we have not found evidence of the two-speed genome for *B. cinerea* expression modulation on *A. thaliana*.

1. **Haplotype diversity and polygenic genetic modulation of expression**

Our results are suggestive of the highest-diversity model of a generalist pathogen, in which specialization occurs at the gene or allele level, which would select for very high diversity and low population structure as the different genetic strategies are intermixed within individuals. This is consistent with the high SNP diversity and low population structure observed in previous studies of *B. cinerea*, due to a combination of random mating and frequent recombination {Williamson 2007; Rowe 2010; Atwell 2015; Corwin 2016; Zhang 2016}.

1. **Detection of pathogenicity genes and novel loci**

Approximately 1/3 of our hotSNP loci and 1/5 of the hotSNP target genes currently lack gene ontology information (Table N1, Table N2). This study is additionally identifying a large number of novel virulence-associated loci within *B. cinerea*.

1. **Connecting from genome to transcriptome to phenotype (future directions)**

**Conclusion**

The 25 hotSNPs identified in this study provide potential targets for breeding low-virulence *B. cinerea*. These loci may control modular virulence strategies, serving as decision points in the course of *B. cinerea* infection on *A. thaliana*. The target genes in plants, and their associated networks, may provide targets for disease resistance in plants.