Running title: Botrytis eQTL of co-transcriptome

**Pathogen genetic control of transcriptome variation in the *Arabidopsis thaliana* – *Botrytis cinerea* pathosystem**

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**ABSTRACT**

**INTRODUCTION**

Plant-pathogen interactions can be classified in two groups; qualitative interactions, in which few genetic variants interact to determine binary disease outcomes, or quantitative interactions, in which a spectrum of outcomes may occur due to genetic variation between the host and pathogen. The genetic basis of quantitative plant-pathogen interactions is less clear and is being elucidated through the study of phenotypic variation across genetically diverse hosts and pathogens, finding links to genetic variation. Interactions between plants and generalist pathogens, which do not specialize on particular hosts, are more often quantitative due to a lack of reciprocal co-evolution, and generalist pathogens often harbor higher genetic diversity (Williamson, Tudzynski et al. 2007).

There is a lack of evidence for qualitative virulence/ resistance genes underlying quantitative disease outcomes in plant-pathogen interactions. Rather, the genetic basis of plant resistance in these interactions is highly polygenic (Glazebrook 2005, Nomura, Melotto et al. 2005, Goss and Bergelson 2006, Rowe and Kliebenstein 2008, Barrett, Kniskern et al. 2009, Corwin, Copeland et al. 2016, Fordyce, Soltis et al. 2018). On the pathogen side, recent studies have accumulated evidence for a polygenic basis of virulence as well (Corwin, Copeland et al. 2016, Bartoli and Roux 2017, Wu, Sakthikumar et al. 2017, Zhang, Corwin et al. 2017, Atwell, Corwin et al. 2018, Soltis, Atwell et al. 2019). These studies provide many candidate loci for pathogen resistance, with diverse functional annotations. Some of these loci appear to modulate virulence across multiple virulence phenotypes, including lesion size across multiple hosts and independent phenotypes of lesion growth (Corwin, Copeland et al. 2016, Fordyce, Soltis et al. 2018, Soltis, Atwell et al. 2019). However, thus far we know little about the molecular mechanism of action by which these genes affect virulence outcomes, or how the host and pathogen genetics interact.

One study has taken a genome-wide association (GWA) approach to the plant and pathogen genomes simultaneously, as well as their genetic interactions (Zhang, Corwin et al. 2018). In this system, most of the variation in disease resistance was determined by a polygenic structure in the pathogen, with small genetic effects from the host genome or the interaction between them. Similarly, viral load in the human x HIV pathosystem is better explained by pathogen than host diversity (Bartha, McLaren et al. 2017).

Many quantifiable phenotypes result from the interaction of plant and pathogen and can be used in GWA studies, including gene expression responses. Each expression profile may be considered a unique indicator of the progression of the interaction between host and pathogen. As such, analysis summarizing information across transcriptomes can elucidate the common and specific genetics underlying virulence phenotypes and hypothesize causal relationships between genetic variation and expression responses. Individual gene expression profiles can be treated as phenotypes for analysis using recombinant inbred lines (RIL) or GWA. Expression quantitative trait loci (eQTL) are the markers correlated with variation in transcripts’ expression profiles and are hypothesized as points of direct or indirect genetic control over expression variation. Locally acting (*cis*) eQTL may indicate regulatory variation within the expressed gene itself, or nearby. Additional markers distant from the responding gene are classified as *trans*-eQTL. *trans*-eQTL may be due to genes present in a common regulatory network, or transcription factors acting upon the expressed gene. *trans*-eQTL hotspots (loci linked to expression variation across many transcripts) may point to master regulators, with extensive pleiotropy across many genes.

eQTL analysis focusing on one side of the plant-pathogen interaction can identify pathogen loci controlling pathogen gene expression in planta, or plant loci controlling plant gene expression over the course of infection. This provides a view of how variation in one of the interacting organisms leads to the shared disease phenotype and can identify virulence loci in the pathogen and resistance loci in the plant (Chen, Hackett et al. 2010, Christie, Myburg et al. 2017). However, few studies have conducted genome-wide association for any disease traits on the pathogen side, let alone expression traits for eQTL studies (Bartoli and Roux 2017). Further, these analyses cannot account for the signaling and decision-making that occur between the two organisms’ genomes over the course of infection.

Studies encompassing transcriptomic variation in both the host and pathogen, and genomic variation within one of the interacting organisms, can look for signs of interspecific *trans*-eQTL; loci in the pathogen that modulate expression in the infected host, or loci in the host that modulate expression in the infecting pathogen. A few studies have examined variation in host-pathogen interactions in this way, validating the ability of this approach to identify pathogen loci modulating host expression levels, and thus candidate loci for interspecific signals (Wu, Cai et al. 2015, Guo, Fudali et al. 2017). These cross-species *trans*-eQTL can be used to hypothesize causal relationships between individual genes in the interspecific interaction (Wu, Cai et al. 2015, Guo, Fudali et al. 2017).

Previous studies have identified hundreds of plant host genes with one or more eQTL in the pathogen modulating their expression (Wu, Cai et al. 2015, Guo, Fudali et al. 2017), and one small study identified 3 bacterial parasite genes modulated by human host eQTL (Guo, Fudali et al. 2017). Hundreds of pathogen eQTL linked to host expression changes (Wu, Cai et al. 2015), and a single eQTL may modulate expression of over 60 host genes (Guo, Fudali et al. 2017). Genes from the same host network often shared the same eQTL (Wu, Cai et al. 2015). However, these studies work with limited natural variation; one with 98 F2 nematode progeny from a recombinant inbred line (RIL) between two geographically distant parents (Guo, Fudali et al. 2017), and one with 24 progeny from a RIL between two parental lines from distinct subspecies within *Plasmodium* (Wu, Cai et al. 2015).

In this study, we focus on an extreme generalist pathogen with high genetic diversity, *B. cinerea*, and the model plant host, *A. thaliana*. *B. cinerea* exhibits highly quantitative virulence, facilitated through natural genetic variation (Rowe, Walley et al. 2010, Corwin, Copeland et al. 2016, Zhang, Corwin et al. 2018). These interactions are well-characterized phenotypically, and we have previous information on some of the potentially relevant genetic factors on both the pathogen and host sides of the interaction (Denby, Kumar et al. 2004, Rowe and Kliebenstein 2008, Zhang, Corwin et al. 2017, Atwell, Corwin et al. 2018, Soltis, Atwell et al. 2019). This also gives us the opportunity to connect our findings, particularly in plant genetic targets and affected pathways, to many previous datasets.

Previous studies in the *A. thaliana* - *B. cinerea* pathosystem point to transcriptome variation on both sides of the interaction. Detached leaves of wildtype *A. thaliana* and major immune pathway mutants were inoculated with 96 genetically variable isolates of *B. cinerea,* and at 18 hours post inoculation, mRNA was collected. Variation in expression of *A. thaliana* genes was very sensitive to pathogen genetic variation; expression of host genes was under approximately equal regulation from genetic variation across the *B. cinerea* isolates, and host immune-pathway responsive variation across the *B. cinerea* isolates (Zhang, Corwin et al. 2017). This far exceeded the contribution of the major host immune pathway variants to variation in gene expression (Zhang, Corwin et al. 2017). The host-pathogen genetic interactions target four major host response networks; jasmonic acid and salicylic acid signaling and camalexin biosynthesis, defense and cell cycle, and two photosynthesis networks (Zhang, Corwin et al. 2017). The authors analyzed co-expression of genes across the *B. cinerea* isolates and *A. thaliana* immune pathway mutants. Genes were condensed into co-expression networks, which hypothesize causal links between many genes in an interacting web. Within this host-pathogen system, all transcriptome variation is a result of the interaction of the two species, and not independently determined by one of the organisms. However, these analyses do not untangle the directionality of effect from one gene, one pathway, or one genome to another.

In this study, we ask how genetics within the pathogen may modulate expression variation over the course of infection. We work with the gene expression data from Zhang *et al*., performing genome-wide association (GWA) of variation in individual transcript expression profiles with SNP level variation within the *B. cinerea* genome when infecting the wildtype host Col-0 *A. thaliana*. This gives us a hypothesis of directionality; any locus in *B. cinerea* linked to expression variation in the host or pathogen is directly or indirectly modulating expression. With numerous traits in this analysis, we focused on general patterns of eQTL distribution across the genome, and identification of major hotspots of eQTL.

Any genes linked to expression variation of many members of the previously described *A. thaliana* and *B. cinerea* virulence co-expression networks both affirms the biological relevance of the pathway and suggests a genetic control factor in pathway-level expression variation. Determining the pathogen genetic control of both host and pathogen gene expression over the course of infection can give us inference into points of genetic control over virulence pathways in the pathogen. Further, it can elucidate the sensitive host pathways, to inspire a search for potential resistance alleles among host variants. If we consider the full transcriptome of host and pathogen, this provides us thousands of phenotypes to test in genome-wide association, and we can deepen our search for loci which control multiple phenotypic measures of the progression of the plant-pathogen interaction. We can build inference on which genes in the pathogen are core factors in the virulence interaction, and which are uniquely controlling specific attributes of the interaction.

Previous analysis showed that the vast majority of transcripts are affected by variation in the *B. cinerea* genome. Of the differentially expressed *B. cinerea* genes, 74% showed significant variation in their expression due to *B. cinerea* genetic variation, with an average broad-sense heritability of 0.152 attributed to *B. cinerea* isolate (Zhang, Corwin et al. 2018). Of the differentially expressed *A. thaliana* genes, 85% showed significant variation in their expression due to *B. cinerea* genetics, with an average broad-sense heritability of 0.108 due to *B. cinerea* isolate (Zhang, Corwin et al. 2017). As such, we conducted genome-wide association (GWA) to look for evidence of loci in *B. cinerea* that may be modulating this heritable expression variation.

**RESULTS**

**eQTL indicate polygenic transcriptome modulation**

We performed genome-wide association (GWA) for eQTL detection across all genes expressed in the *B. cinerea* - *A. thaliana* pathosystem, including transcripts from the host and from the pathogen. To perform genome-wide association (GWA) and identify expression quantitative trait loci (eQTL) for both host and pathogen, we associated the expression profiles of these 9,267 *B. cinerea* genes and 23,947 *A. thaliana* genes to genome-wide SNP variation in the *B. cinerea* genome. We used a previous genome-wide SNP dataset that has 237,878 SNPs with a minimum minor allele frequency of 0.20 (Atwell, Corwin et al. 2018). We performed Genome-wide Efficient Mixed Model Association (GEMMA) (Zhou and Stephens 2012) to rapidly estimate the significance of all markers for each expression profile. We first controlled for the effects of population structure within our *B. cinerea* isolates by calculating and including a relatedness matrix in the downstream analysis. GEMMA estimates the significance of effects of each SNP on the focal trait as a p-value. To determine significance of SNP effects across tens of thousands of traits (individual expression profiles in *B. cinerea* and *A. thaliana*), we permuted each trait across the 96 B. cinerea isolates five times, and repeated GEMMA analysis for each. We calculated the minimum p-value per SNP per transcript across these five permutations and used this to threshold our data. However, we found this approach overly conservative due to the magnitude of variation from one trait to another. Instead, we considered p-values below the 5% permutation threshold as significant. For individual gene expression traits, we find 0 to 16,818 loci with significant p-values for *B. cinerea*, and 0 to 24,623 loci for *A. thaliana* transcripts (Figure N1). In total, genetic variation in *B. cinerea* appeared to significantly affect the expression of 5,213 *A. thaliana* genes and 1,616 *B. cinerea* genes.

In looking at only the top 1 SNP per trait, we find that in *B. cinerea* 69% of the genes show a lower p-value of SNP-trait association from the observed data than the maximum across all 5 permutations. In *A. thaliana*, 58% of genes … thus, we focus on the top 1 SNP per trait.

Overall, we find a highly polygenic basis of loci modulating transcriptome variation.

**Absence of transcriptome cis-effect dominance**

Previous eQTL mapping studies using both GWA or structured mapping populations in a wide range of species show a predominance of loci that map to the gene itself, i.e. *cis-*eQTL (Brem, Yvert et al. 2002, Schadt, Monks et al. 2003, Monks, Leonardson et al. 2004, Keurentjes, Fu et al. 2007, West, Kim et al. 2007). To test if the *B. cinerea* transcriptome shows a similar cis-eQTL dominance, we looked for a *cis*-diagonal signature of associations between transcript center and GWA SNP hits. We first focused on the single top SNP hit per transcript, with the highest probability (lowest p-value) of significant effect on expression in the gene of interest. If control of gene expression is localized to the gene itself or toproximate loci, we would expect a strong linear (*cis*-diagonal) association between the center of each gene and the genomic location of its top SNP hit. However, we find that few genes have a top SNP hit within the same chromosome, and even fewer within 1Mb (Figure N2). We conclude that most of this genetic variation is *trans*-acting, as we do not see a strong *cis*-diagonal signal when comparing transcript center to top SNP hit. This pattern holds whether we examine the top 1 SNP per transcript (Figure N2a) or the top 10 SNPs per transcript (FigureN2b). Further, we do visualize vertical stripes of SNPs, indicative of *trans*-eQTL hotspots; loci which modulate expression variation across many of the pathogen genes (Figure N2).

In these genome-wide transcript-to-SNP associations, we find that *cis*- control of gene expression is largely drowned out by patterns of *trans*-acting variation. To further search for a signature of dominant cis-effects, we calculated the distance between the center of each transcript and the top associated SNP. If *cis*- acting loci contribute the bulk of genetic control of expression variation, we would expect to see a high frequency of short-distance associations, and a rapid decline to a plateau moving away from the gene of interest. However, we observe that distances between transcript center and top SNP as far as 2 Mb are common (Figure N3). These distances are similar to those from the association of random transcript profiles to top SNPs (Figure SX1). As such, we do not see evidence for *cis*-effect loci overrepresented in the top candidates for control of expression variation. Rather, most control of gene expression variation in *B. cinerea* on *A. thaliana* appears to be *trans*-acting.

**Search for *cis*-effects through focus on gene networks with presence-absence polymorphism**

The absence of a dominant signal for *cis*-eQTL could arise from *B. cinerea* having a different pattern of causal eQTL variation from our expectation. Alternatively, this could arise from *B. cinerea* having a sufficiently high genetic diversity that leads to false-negatives due to complex haplotype structures at causal loci (Atwell, Corwin et al. 2015, Atwell, Corwin et al. 2018). To test between these possibilities and to identify the role of *cis*-eQTL, we narrowed our focus to a set of three biosynthetic pathways that exist as gene clusters and have known presence-absence polymorphisms (Zhang, Corwin et al. 2018). These biosynthetic pathways contribute to *B. cinerea* virulence and the botcinic acid biosynthetic pathway (13 genes, 55.8 kb), botrydial biosynthetic pathway (7 genes, 26 kb), and a putative cyclic peptide pathway (10 genes, 46.5 kb) (Deighton, Muckenschnabel et al. 2001, Colmenares, Aleu et al. 2002, Porquier, Morgant et al. 2016, Zhang, Corwin et al. 2018). Critically, the transcripts within each of these pathways are highly correlated across the isolates suggesting that their genetic variation is controlled by pathway-specific variation (Zhang, Corwin et al. 2018). None of the genes showed a *cis*-eQTL within the GWA suggesting that the identified causal variation is solely in *trans* to the pathways.

To test if this result may be complicated by the architecture of loci within the pathway, we initially focused on the botcinic acid biosynthesis network, which is known to have presence-absence polymorphisms in the species {Siewers 2005; Pinedo 2008; Zhang 2018}. We obtained all of the SNPs for this biosynthetic cluster and conducted an alignment of the *B. cinerea* isolates. This showed evidence of a number of distinct haplotypes with some relatively isolated isolates (e.g. B05.10, Fd1) (Figure N4a). Looking at the expression of the transcripts for the biosynthetic pathway showed a single clade that had a distinctly lower level of expression than the other clusters. Using SNP-level variation surrounding genes in this pathway showed that these 12 isolates share a 53.5 kb deletion that removes the entire biosynthetic cluster (Figure N4c). We then tested if the remaining clusters had any link to transcript expression by performing ANOVA across the 3 major clusters (2, 5, 6). After removing the major deletion, we found no remaining significant effect of cluster membership on expression profile (F(1,74)=0.36, p=0.55). Although within each of these clusters there are independent isolates with low pathway expression polymorphisms (Noble Rot, 01.04.03, Apple 517, 02.04.09) (Figure N4b), these isolates each contain smaller independent deletions that likely abolish expression of the botcinic acid biosynthetic pathway (Figure N4c). This suggests that for this locus, there is a major *cis*-effect deletion and a number of rarer additional deletions that control expression variation. However, this *cis*-effect is not captured by the SNP-level data utilized for the GWA. Rather, our GWA analysis misses the major *cis*-eQTL signal of the network deletion. If insertion and deletion events account for the majority of localized control of expression variation, our GWA analysis will not detect these *cis*-effect loci. Thus, we investigated the other two biosynthetic pathways for additional evidence of *cis*-acting genetic variation.

The botrydial biosynthetic network, and the cyclic peptide pathway, exhibit a similar lack of dominant *cis*-effect SNP patterns to the botcinic acid biosynthetic network. Hierarchical clustering within each of these networks by genic SNP variation divides the isolate population into two groups, and mean pathway expression across all isolates is not differentiated by this clustering for either network (Figure S1, Figure S2). We find that SNP state does not detect the major *cis*-effects polymorphisms. Within the botrydial biosynthetic pathway, we detect small deletions in the intergenic regions, but these also do not predict expression level within the pathway and likely do not abolish pathway function (Figure S3). Within the cyclic peptide pathway, minor deletions within the intergenic regions correlate with low expression of the pathway genes, and two isolates with partial deletions within the genes early in the pathway exhibit very low pathway expression (1.05.16, 1.05.22) (Figure S4).

As such, we are able to detect cis-acting variation in the form of deletions for two of the biosynthetic pathways, but still have not identified the controlling variation for the botrydial pathway. However, we conclude that large *cis-*effect loci exist for transcriptional regulation in this pathosystem, but that GWA across SNPs misses these patterns. This missing *cis*-effect likely amplifies the apparent magnitude of *trans*-acting loci.

**Detection and annotation of *trans*-eQTL hotspots**

Our 11 significant *trans­-*eQTL hotspots for *B. cinerea* range from 22 to 129 linked genes, with minimal overlap to expression modulation in *A. thaliana* (a maximum of 56 genes). These hotspots are dispersed across the genome, at least 0.1 Mb apart and across 9 chromosomes (Figure N7). The 11 significant cross-species *trans*-eQTL hotspots for *A. thaliana* are also dispersed across the genome of *B. cinerea*, covering 8 chromosomes with at least 0.1 Mb between hotspots (Figure N7). These range from 114 to 634 linked *A. thaliana* transcripts, with very low overlap with *B. cinerea* transcripts (a maximum of 3 genes).

The other typical predominant pattern in eQTL studies is the presence of hotspots, whereby variation in numerous transcripts links to specific loci. These are considered positions where there is a causal polymorphism that influences the regulation of numerous genes in *trans*, i.e. a *trans*-eQTL hotspot. In this dataset, we can extend this analysis to look for *trans*-eQTL hotspots that extend beyond *B. cinerea* and influence the expression of genes in the host, *A. thaliana*. To conduct a conservative search and to simplify the analysis, we focused on solely the single most-significant SNP (i.e. strongest evidence) that is linked to a given transcript. Taking these top SNPs for all *the B. cinerea* and *A. thaliana* transcripts, we queried for hotspots per transcriptome (Figure N6). By permuting the SNP positions, we identified maximum permuted hotspot sizes for *B. cinerea* as 11 genes, and 80 genes for *A. thaliana*. For further analysis of hotspots, we utilized a conservative threshold of 20 linked transcripts for *B. cinerea* and 150 transcripts for *A. thaliana*. This analysis identified 13 SNPs as potential *trans*-eQTL hotspots for the *B. cinerea* transcriptome and 12 SNPs as potential cross-species *trans*-eQTL hotSNPs influencing *the A. thaliana* transcriptome (Figure N6, Figure N7). The *trans*-eQTL hotSNPs are spread throughout the genome, present on all chromosomes except 7, 11, 14, 15 (Figure N6, Table N1).

One possibility is that a *trans*-eQTL hotSNP for *B. cinerea* transcripts may control virulence pathways and thus cause an associated *trans*-eQTL hotSNP in the *A. thaliana* response. However, we found no significant overlap in eQTL hotspots across the two genomes; hotSNPs targeting *B. cinerea* gene expression linked to 0 to 56 transcripts in *A. thaliana*, and hotSNPs targeting *A. thaliana* gene expression linked to 0 to 3 *B. cinerea* transcripts. To test the dependency of these results on using solely the top SNP, we repeated the full analysis by selecting the top 10 SNPs per transcript. This again identified a limited number of *trans*-eQTL hotSNPs with little overlap between the two species’ transcriptomes (Table SX1; Figure SX3). This suggests that the pathogen’s influence on the host’s transcriptome is not solely limited to major interactions between *tran*s-eQTL hotSNPs but can involve more limited changes in the pathogen that are magnified in the host’s response.

**Annotation of hotSNPs and eQTL hotspot targets**

We annotated these hotSNPs with gene and functional information, to understand possible mechanisms of expression modulation in the host and pathogen transcriptomes. While we find annotation information suggestive of metabolic interactions between host and pathogen, and known virulence mechanisms, X of our hotSNP genes and X of the downstream targets do not yet have gene ontology (GO) information. Thus, this study identifies a large number of loci potentially involved in novel virulence mechanisms of B. cinerea.

From *A. thaliana* expression profiles, the 11 hotSNP gene annotations included 4 enzymes and 2 genes associated with isolate compatibility (Table N1). From *B. cinerea* expression profiles, the 11 hotSNP gene annotations included 4 enzymes (Table N1).

We also annotated the genes targeted by these hotSNPs with functional information, including links to co-expression networks from previous RNAseq analysis of these transcripts (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018) (Table X1). eQTL hotspots linked to these co-expression networks could indicate regulatory points for these modules of expression variation.

Among the 11 *B. cinerea* hotspot *trans-*eQTL, three of these hotspot genes are linked to lesion size variation across all tested *A. thaliana* genotypes. A fourth gene is linked to lesion size variation on Col-0 *A. thaliana*. This gene is also linked to the major vesicle/ virulence network of *B. cinerea* co-expression on Col-0 *A. thaliana* (Zhang, Corwin et al. 2018).

Nine of the 11 *B. cinerea* eQTL hotspots were also linked to genes in one or more of four major *B. cinerea* co-expression networks on *A. thaliana* (Figure N8). In particular, two of these were host-specific networks functionally associated with virulence, with 7 of the 11 *B. cinerea* eQTL hotspots associated with one of these virulence co-expression networks. As such, we hypothesize that these major points of *B. cinerea* gene expression modulation may also exhibit regulation of virulence strategies on *A. thaliana*.

Among the 11 *A. thaliana* hotspot trans-eQTL, two of these genes are correlated to *B. cinerea* lesion size across all tested *A. thaliana* genotypes, including immune pathway mutants. An additional gene is correlated with lesion size variation on Col-0 *A. thaliana*, and one on *coi1-1* *A. thaliana.*

Nine of the *A. thaliana* eQTL hotspots were also linked to genes from two major genotype-dependent *A. thaliana* co-expression networks when infected with *B. cinerea* (Figure N8). These networks contain genes pointing to network function in jasmonate and salicylic acid signaling processes and camalexin biosynthesis (Network I), or photosynthesis in the host (Network IV). We observe particularly strong links between 4 of the 11 eQTL hotspots of *B. cinerea* modulation of *A. thaliana* gene expression and immune networks in *A. thaliana* (Figure N8). These frequent links suggest that our eQTL hotspots may exhibit regulatory control over co-expressed modules of genes active in virulence interactions between *B. cinerea* and its host.

If these eQTL are modulating expression of many genes, and affecting lesion size, they may be major *B. cinerea* control points in the plant-pathogen interaction.

We further examined functional annotation of the genes linked to our eQTL hotspots, to hypothesize mechanisms of regulation by these hotSNPs.

Many of the *B. cinerea* genes targeted by the hotSNPs are enzymatic (34% of our list of annotated hotSNP target genes, 140/412) (Table N2). These genes also include 11 transcription factors and two genes associated with virulence.

**DISCUSSION**

**METHODS**

**Experimental design**

We used a previously described collection of *B. cinerea* genotypes that were isolated as single spores from natural infections of fruit and vegetable tissues collected in California and internationally (Atwell, Corwin et al. 2015, Zhang, Corwin et al. 2017, Fordyce, Soltis et al. 2018, Zhang, Corwin et al. 2018). We focused analysis on the *A. thaliana* accession Columbia-0 (Col-0), and all plants were grown as described in a previous study, with 4-fold replication of the full randomized complete block experimental design across two independent experiments (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018). The original study included wildtype Col-0 A. thaliana hosts, as well as knockouts to the salicylic acid pathway (*npr1-1*) and to jasmonic acid sensitivity (*coi1-1*). Leaves were harvested 5 weeks after sowing, and inoculated in a detached leaf assay with spores of each of 96 *B. cinerea* isolates (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018).

**Expression analysis**

RNASeq libraries were prepared as previously described (Kumar, Ichihashi et al. 2012, Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018). Briefly, we prepared mRNA from leaves frozen at 16 hours post inoculation, and pooled amplified, size-selected libraries into four replicate groups of 96 barcoded libraries. Sequencing was completed on a single Illumina HiSeq 2500 (San Diego, CA) lane as single 50bp reads at the U.C. Davis Genome Center- DNA Technologies Core (Davis, CA). Individual libraries were then separated by adapter index from fastq files, evaluated for read quality and overrepresentation (FastQC Version 0.11.3, www.bioinformatics.babraham.ac.uk/projects/), and trimmed (fastx, http://hannonlab.cshl.edu/fastx\_toolkit/commandline.html). Reads were aligned to the *A. thaliana* TAIR10.25 cDNA reference genome, followed by the *B. cinerea* B05.10 cDNA reference genome, and we pulled gene counts (Langmead, Trapnell et al. 2009, Li, Handsaker et al. 2009, Van Kan, Stassen et al. 2017, Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018). We summed counts across gene models, and normalized gene counts as previously described (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018).

We used as input the model-adjusted means per transcript from negative binomial linked generalized linear models in previously published studies in the *A. thaliana* transcriptome and *B. cinerea* transcriptome (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018). *A. thaliana* and *B. cinerea* transcript phenotypes were from least square means of normalized gene counts in a negative binomial generalized linear model (nbGLM) (Zhang, Corwin et al. 2017, Zhang, Corwin et al. 2018). We calculated linear models from the transcript data including the effects of isolate and host genotype. We z-scaled all transcript profiles prior to GWA.

**Genome wide association**

For GEMMA mapping, we used 95 isolates with a total of 237,878 SNPs against the *B. cinerea* B05.10 genome (Atwell, Corwin et al. 2018). We used haploid binary SNP calls with MAF > 0.20 and <20% missingness. We ran GEMMA once per phenotype, across 9,267 *B cinerea* gene expression profiles and 23,947 *A. thaliana* gene expression profiles.

**Genome wide association of permuted phenotypes**

To validate SNPs as significantly associated with transcript variation, we performed a comparative analysis of randomized phenotypes. Taking each transcriptional profile, we randomized the assignment of phenotypes across the 96-isolate collection. This analysis includes 9,267 randomized *B. cinerea* phenotypes and 23,947 randomized *A. thaliana* phenotypes, one from each measured expression profile. We repeated this randomization in a 5x permutation. We ran GEMMA on each of these permutations, and plotted SNP p-value vs. position (Figure N5). To threshold our individual expression profile GEMMA outputs, we considered p-values below the average 5% permutation threshold as significant; p < 1.96e-05 for *B. cinerea* and p < 2.90e-05 for *A. thaliana*. Permutation approaches are often more effective than p-value thresholding for determining significance across GWA studies with many phenotypes {CITE}.

**Defining significant hotspots**

We plotted the number of transcripts linked to each SNP, summed across all 5 permutations, to calculate permuted hotspot size. For any SNPs that linked to permuted hotspots of over 5 transcripts in *B. cinerea* or 10 transcripts in *A. thaliana*, we removed these SNPs from downstream analysis as likely false positives. The maximum hotspot size across any of the 5 permutations was 11 genes in *B. cinerea* and 80 genes in *A. thaliana*. We then conservatively defined significant hotspots as SNP peaks exceeding 20 transcripts in *B. cinerea* and 150 transcripts in *A. thaliana*. We further annotated hotspot SNPs to the nearest gene within a 2kb window. The average LD decay in the B. cinerea genome is < 1kb, so we can be relatively confident of SNPs tagging particular genes at the hotspot peaks (Atwell, Corwin et al. 2018). Three genes are annotated to pairs of neighboring hotSNPs, the rest are unique genes. Two genes on chromosome 12 denoting hotSNPs from *A. thaliana* gene expression appear closely linked; in fact, they are separated by ~80kb on the *B. cinerea* genome.

**Annotation of gene ontology and network membership**

*A. thaliana* co-expression analysis identified 131 genes across four major networks (Zhang, Corwin et al. 2017). Network architecture varied by plant host, but a constitutive core was conserved across *A. thaliana* genotypes. We compared our eQTL hotspots (both the gene at eQTL hotspot SNP and all associated transcript profiles) to the largest *A. thaliana* network lists (*npr1-1* background) to estimate all possible regulatory ties. We identified gene overlap with two of the major networks; Network I, camalexin biosynthesis; Network IV, chloroplast function.

*B. cinerea* co-expression analysis identified ten major co-expression networks containing 5 to 242 genes (Zhang, Corwin et al. 2018). We identified gene overlap with four of these networks, including one likely involved in fungal vesicle virulence processes including growth and toxin secretion (vesicle/ virulence), one involved in translation and protein synthesis (translation/ growth). These networks maintained a consistent core across the 3 *A. thaliana* host genotypes, but linkages varied; as such we compared our gene lists with the networks across all 12 hosts, and included both host-dependent and host-independent annotations of our hotspots.

**Pathway focus**

We focused further *cis*-effects analysis on three networks which were highly conserved across *B. cinerea* isolates (Zhang, Corwin et al. 2018). We clustered isolates by SNP data within focal networks. Hierarchical clustering was computed using the R package pvclust based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications (Suzuki and Shimodaira 2015). AU p-values are reported in red, BP values in green. Edges with high AU values are considered strongly supported by the data, and clustering is drawn according to these edges with AU > 95%.

For botcinic acid biosynthesis, the major deletion extends 53.5 kb and includes SNP 4kb from the 5’ end of the chromosome, indicating a teleomeric loss on chromosome 1. We selected a focal region encompassing the deletion endpoints (1.4029, 1.82614) and an additional 2 genes beyond the deletion boundaries (Bcin01g00170, Bcin01g00190) (Figure N4c). We removed 10 SNPs that were likely miscalled (SNP state ~ inverse compared to surrounding region) and called all SNPs within the deletion region as missing.

**TABLE LEGENDS**

**Table N1. Annotation of the hotSNPs identified from *B. cinerea* and *A. thaliana* eQTL.**

**Table N2. Annotation of the *B. cinerea* genetic targets of *B. cinerea* hotSNPs.**

**Table N3. Annotation of the *A. thaliana* genetic targets of *B. cinerea* hotSNPs.**

**FIGURE LEGENDS**

**Figure N1. Manhattan plot examples for 1 transcript per species.** Panel a is an example plot of p-values for all *B. cinerea* SNP associations to a single *B. cinerea* transcript, from Bcin01g00170. Panel b is an example plot of p-values for all *B. cinerea* SNP associations to a single *A. thaliana* transcript.

**Figure N2. *cis*-diagonal plot comparing *B. cinerea* gene center to position of top associated SNP, for all 9,284 transcripts.** We retained only the SNPs with highest probability (lowest p-value) of significant effect on expression for each transcript. Panel a depicts the single top SNP per transcript. Panel b depicts the top 10 SNPs per transcript. Chromosomes are delimited by red bars along the x-axis. Vertical striping of SNP positions indicate genomic locations of putative *trans*-eQTL hotspots.

**Figure N3. Distance between transcript center and top SNP location for all *B. cinerea* expression profiles on Col-0 *A. thaliana*.** Data include the top 1 SNP identified by GEMMA association with each transcript expression profile (lowest p-value for association). Distances are in Mb, including only top SNPs on the same chromosome as the focal gene.

**Figure N4. *cis*-effect analysis of the botcinic acid biosynthetic gene network.** Panel a is hierarchical clustering of *B. cinerea* isolates from SNPs within the botcinic acid biosynthetic gene network. Clustering was based on mean linkage (UPGMA), with correlation distance and 1000 bootstrap replications. AU p-values are reported in red, BP values in green. Edges with high AU values are considered strongly supported by the data, and clustering is drawn according to these edges with AU > 95%. Panel b is Violin plots of botcinic acid network-level expression within *B. cinerea* clusters. Isolates are clustered based membership in groups defined by hierarchical clustering of the SNPs within the botcinic acid biosynthesis network (Figure X5). Panel c is the gene models of the biosynthetic gene network, with the cluster 3 deletion indicated as a triangle.

**Figure N5. Manhattan-type plot of GEMMA results of transcriptome-wide *B. cinerea* expression phenotypes.** Panel a is a Manhattan-type plot of the top 1 SNP hit per *B. cinerea* transcript on Col-0 *A. thaliana*. Panel b is a Manhattan-type plot of the top 1 SNP hit per *A. thaliana* transcript when infected by *B. cinerea*.

**Figure N6. All eQTL hotspots across the *B. cinerea* and *A. thaliana* transcriptomes.** We counted the number of genes (transcripts) associated with each SNP. Panel a is for all *B. cinerea* transcripts, panel b is all *A. thaliana* transcripts.

**Figure N7. Interspecific hotspot comparison on the *B. cinerea* genome.** For each SNP that is a top hit for one or more transcripts, the number of associated transcripts is counted, across both the *B. cinerea* transcriptome and the *A. thaliana* transcriptome.

**Figure N8. Genes linked to eQTL hotspots are in virulence and defense co-expression networks.** Circles along the *B. cinerea* genome map are eQTL hotspots, centered at the gene containing the eQTL and with radius proportional to the number of transcripts linked to this hotspot. The gene center is marked with a white dot. Hotspots for *B. cinerea* transcripts are drawn in blue, hotspots for *A. thaliana* transcripts are drawn in green. The *A. thaliana* networks depicted are the most inclusive of the host-dependent networks, from *npr1-1*. Links between hotspots and co-expression networks are drawn according to the number of genes shared between them. Variable line weight represents the percent of hotspot target genes shared with the co-expression network; 1-25% is dashed, 25-50% is dotted, 50-75% is solid, 75-100% is heavy solid.

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