**RESULTS**

We examined all genes expressed in the *B. cinerea* - *A. thaliana* pathosystem, including transcripts from the host and from the pathogen. Previous analysis showed that the vast majority of transcripts are affected by variation in the *B. cinerea* genome. Of the 9,284 differentially expressed *B. cinerea* genes, 74% (5,244) 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 23,898 differentially expressed *A. thaliana* genes, 85% (20,328) 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). In this study, we performed genome-wide association (GWA) for each transcript expressed in the pathosystem to look for evidence of eQTL.

**eQTL indicate polygenic transcriptome modulation**

To look for 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 performed Genome-wide Efficient Mixed Model Association (GEMMA). 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 phenotype as a p-value. In total, genetic variation in *B. cinerea* appeared to significantly affect the expression of X *A. thaliana* genes and X *B. cinerea* genes. Overall, we find a polygenic basis of loci modulating transcriptome variation.

**Randomization to define hotspots**

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 phenotypes, one from each measured *B. cinerea* 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 X3). We defined hotspot thresholds from the maximum hotspot size across these permutations, and applied these thresholds to all data to define significant hotspots.

**Hotspots indicate mostly trans-eQTL transcriptome-wide**

To search for hotspots of eQTL, for the SNP with the strongest evidence (lowest p-value) of association by GEMMA per transcript, we plotted the p-value and location of each top SNP. Hotspots are defined as peaks of significant SNPs above the permutation threshold. The regulatory hotspots we identified are spread throughout the genome, present on chromosomes 2-6, 8-10, 12-15 (Figure X3a). These hotspots of controlling variation may be due to a mix of *cis*- and *trans*-eQTL. Genome-wide, we identified XX hotspots, from X to X per chromosome. Hotspots were defined by X to X SNPs, with an average length of X kb.

To look for *B. cinerea* loci that are *trans*-acting to control expression variation in the affected host, we also examined patterns of association between *A. thaliana* expression variation and *B. cinerea* genomic variation. We identified hotspots putatively controlling *A. thaliana* expression variation for all *B. cinerea* chromosomes except 17 and 18 (Figure X4b). These *B. cinerea* loci may contribute to regulation of gene expression in the host. We looked for evidence of eQTL hotspots that are common across both *B. cinerea* and *A. thaliana* (Figure XX). We find that X% of hotspots are shared among both transcriptomes, X% are unique to *B. cinerea*, and X% are unique to *A. thaliana.*

**Gene functions of expression modulating hotspots**

We mapped genes to selected hotspots to identify possible functions associated with our eQTL. At hotspot XX shared between *B. cinerea* and *A. thaliana*…

Lack of evidence for cis-effect patterns transcriptome-wide

Previous eQTL mapping studies show evidence for large-effect *cis-*eQTL [CITATIONS]. To search for a pattern of transcriptome-wide *cis* effects in this study, 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 X6a). These distances are similar to those from the association of random transcript profiles to top SNPs (Figure Xb). 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.

In these transcript-to-SNP associations, we find that *cis*- control of gene expression is largely drowned out by patterns of *trans*-acting variation. 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 to *cis*-acting 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 X5). We again 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 X5), the top 10 SNPs per transcript (Figure SX1), or the top 100 (Figure SX2).

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

We did not see enrichment for local SNPs as the top loci controlling expression variation; rather, the top SNPs are distributed across the genome. Thus, we are mostly detecting *trans*-eQTL. As we did not detect a transcriptome-wide pattern of *cis*-effect variation controlling expression patterns of *B. cinerea* on *A. thaliana*, we narrowed our focus to a subset of localized biosynthetic gene networks with known presence-absence polymorphism to identify the role of *cis*-eQTL. These focal networks were among those most highly conserved across *B. cinerea* isolates (Zhang, Corwin et al. 2018). These include the botcynic acid biosynthetic pathway (13 genes, 55.8 kb), botrydial biosynthesis (7 genes, 26 kb), and Network 5 (Zhang, Corwin et al. 2018), which contains XX (10 genes, 46.5 kb).

We focused analysis on the botcynic acid biosynthesis network, which has a known presence-absence polymorphism. Upon visualizing SNP-level variation surrounding genes in this pathway, we found evidence of a deletion common to 12 of the 96 isolates (Figure X7c). 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 X7c). 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. We find evidence of many haplotypes within the pathway. Hierarchical clustering based on these loci assigned the 96 isolates into three major clusters, and one small two-isolate cluster (B05.10, Fd1) (Figure X7a). The largest cluster (cluster 4) includes a sub-cluster containing all of the isolates in the deletion group (cluster 3). We removed isolates with the whole-region deletion, then performed ANOVA across the 3 major clusters (1, 4, 5) to see whether SNP variation within the botcynic acid biosynthetic network predicts expression level of genes within the region. We found no significant effect of cluster membership on expression profile (F(1,74)=0.36, p=0.55). This suggests that the major *cis*-effect loci controlling expression variation in this network are not captured by SNP-level variation. Rather, our GWA analysis misses the major cis-eQTL signal of the network deletion.

To look for patterns of expression variation that may be controlled by undetected *cis*-acting loci, we examined mean botcynic acid pathway expression across all isolates, grouped by cluster membership. Expression levels across the network are reduced in the deletion group (cluster 3) but we also see independent outliers of low-expression isolates with additional loss-of-function polymorphisms (Noble Rot, 01.04.03, Apple 517, 02.04.09) (Figure X7b). These isolates also contain deletions within the botcynic acid biosynthetic network (Figure X7c), likely of independent origin. As such, the major *cis­*-effect variation controlling expression in the botcynic acid region appears to be explained by deletion events, which are not captured by our SNP analysis. 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.

The botrydial biosynthetic network, and network 5, exhibit similar cis-effect patterns to the botcynic 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… 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 9).

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

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 9). These range from 114 to 634 linked *A. thaliana* transcripts, with very low overlap with *B. cinerea* transcripts (a maximum of 3 genes).

**Annotation of eQTL hotspots**

We annotated the genes at these eQTL hotspots with functional information, including links to coexpression networks from previous RNAseq analysis of these transcripts {Zhang 2016; Zhang 2018} (Table X1). 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.* Among the 11 *B. cinerea* hotspot *trans-*eQTL, three of these 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* coexpression on Col-0 *A. thaliana* {Zhang 2018}. 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.

**eQTL correlation to co-expression networks**

Previous analysis of these RNAseq data clustered transcripts in *B. cinerea* and *A. thaliana* into coexpression networks {Zhang 2016; Zhang 2018}. eQTL hotspots linked to these coexpression networks could indicate regulatory points for these modules of expression variation. We looked for gene overlap between transcripts linked to eQTL hotspots and coexpression networks. Nine of the *B. cinerea* eQTL hotspots were also linked to genes in one or more of four major *B. cinerea* coexpression networks on *A. thaliana* (Figure 9). Nine of the *A. thaliana* eQTL hotspots were also linked to genes in one or more of six major genotype-dependent *A. thaliana* coexpression networks when infected with *B. cinerea* (Figure 9).

**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). 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 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 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.

**Permutation and defining 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 20 transcripts in *A. thaliana*, we removed these SNPs from further analysis as likely false positives. We then conservatively defined actual hotspots as SNP peaks exceeding 20 transcripts in *B. cinerea* and 150 transcripts in *A. thaliana*. We then collapsed hotspots into genes, such that all SNPs were annotated to the nearest gene within 2kb.

**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%.

FIGURE LEGENDS

(For now, see figures PPT)

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