Introduction

Plant-pathogen interactions are classified as qualitative, in which few genes or few individual genotypes interact to determine binary disease outcomes, or quantitative, in which a spectrum of interactions may occur due to genetic variation between the host and pathogen. The genetic basis of quantitative plant-pathogen interactions is just beginning to be explored, through studying phenotypic variation across genetically diverse hosts and pathogens and finding links to genetic variation. Interactions between plants and generalist pathogens are more often quantitative, due to a lack of reciprocal co-evolution.

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 2005; Goss 2006; Rowe 2008; Barrett 2009; Corwin 2016; Fordyce 2018}.

On the pathogen side, recent studies have accumulated evidence for a polygenic basis of virulence {Atwell 2018; Soltis 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; lesion size across multiple hosts, independent attributes of lesion size {Corwin 2016; Soltis 2019; Fordyce 2018}. However, we know little about the molecular mechanism of action by which these genes affect virulence outcomes.

Many measurable phenotypes occur during the interaction of plant and pathogen, including gene expression. Determining the pathogen genetic control of both host and pathogen’s gene expression over the course of infection can give us inference into points of genetic control over virulence pathways. Further, it can elucidate the sensitive host pathways, to inspire a search for potential resistance alleles in among host variants. If we consider the full transcriptome of host and pathogen, this offers 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.

Expression quantitative trait loci (eQTL) are the markers associated with variation in these transcripts’ expression profiles. Locally linked (cis) eQTL may indicate regulatory variation within the responding gene, or nearby. Additional markers distant from the responding gene are classified as trans-eQTL. Trans-eQTL may be due to

Previous studies in the A. thaliana x B. cinerea pathosystem point to control of expression variation on the host side of the interaction …

The authors assessed co-expression of genes across different B. cinerea isolates and A. thaliana immune mutants. Genes were condensed into co-expression networks, which hypothesize causal links between many genes in an interacting web. Any genes linked to expression variation of many members of this pathway both affirms the pattern of the pathway and suggests a control factor in pathway-level expression variation.

Introduction outline

1. Plant-pathogen interactions
   1. ~~Qualitative: binary disease states~~
   2. ~~Quantitative: continuous disease states~~
   3. ~~Little information on quantitative disease genetics~~
      1. ~~So far: evidence for lack of qualitative R genes in plants/ virulence genes in quantitative disease pathogens~~
      2. ~~Patterns of quantitative disease genetics~~
         1. ~~Quantitative genetic basis on plant side of virulence as lesion size: Corwin (and earlier), Fordyce 2018, Zhang 2017~~
            1. ~~Highly quantitative/ polygenic~~
            2. ~~Patterns of which loci are involved~~
            3. ~~Other species/ labs… LIT REVIEW~~
         2. ~~Quantitative genetic basis on pathogen side of virulence as lesion size: Soltis 2019, Atwell 2019~~
            1. ~~Also highly quantitative/ polygenic~~
            2. ~~Patterns of which loci are involved~~
            3. ~~Other species/ labs… LIT REVIEW~~
         3. Shared loci across multiple phenotypes? Larger emerging patterns of genetic players in quantitative virulence outcomes
            1. Soltis 2018, commonalities across plant hosts
            2. Fordyce 2018 (multiple measures of lesion), Corwin/ Zhang for lesion size or expression on multiple host genotypes…
            3. Other species/ labs…
2. Transcriptome variation (gene expression profiles) as many quantitative phenotypes describing the interaction between host and pathogen.
   1. Insight into shared and unique bases of virulence phenotypes?
   2. Quantitative genetic basis on plant side of expression variation: Zhang
      1. Patterns of how many loci
      2. Patterns of which loci
      3. Something about networks, idk
   3. Other species/ labs… LIT REVIEW
3. eQTL to learn genetic control of expression phenotypes
   1. cis eQTL: regulatory variation within target gene, or closely linked
      1. (promoter, local structure, ~ operon analogue?)
   2. trans eQTL: regulatory variation distant from target gene.
      1. Mechanism? Shared network/ transcription factor/ other reasons for correlation…
   3. Trans eQTL hotspot: “master regulator” idea
      1. could be transcription factor/ core of interacting pathway/ ???
4. need a logical link here
5. eQTL in plant-pathogen interactions
   1. eQTL in plant host
      1. LIT REVIEW, major findings – number of loci, function?
         1. Any hotspot analyses/ validation?
   2. eQTL in pathogen
      1. examples from Malaria…
         1. Gonzalez 2008
         2. Zhu 2018
      2. do a deeper LIT REVIEW… is there anything here? Haven’t really found it
6. interspecific trans eQTL in plant-pathogen interactions
   1. very few studies
      1. Major patterns?
      2. Guo 2017
         1. Medicago + parasitic nematode (parasite eQTL, host expression)
         2. Human + Salmonella (host eQTL, parasite expression)
      3. Wu 2015
         1. Mouse + Plasmodium (parasite eQTL, host expression)
   2. What would these hits mean?
      1. Vaguely, signs of network-network crosstalk between plant and pathogen
         1. Network x network coevolution rather than gene x gene
            1. Do I talk about generalists here? Or earlier? Or never?
7. Our study system for cis eQTL, trans eQTL hotspots, and interspecific trans eQTL
   1. Botrytis
      1. quantitative virulence… cite
      2. quantitative genetics of virulence… cite
   2. Arabidopsis
      1. Model host, efficient system – cite plant path studies
      2. Well defined genetics for validation, pathway information
   3. Botrytis-Arabidopsis pathosystem
      1. Botrytis genetic component describing Arabidopsis infection phenotypes
         1. Zhang
8. Our study methods
   1. Detached leaf assay
   2. mRNA isolation from infected leaf, 18hpi
   3. transcript expression levels
   4. GWA to X Botrytis SNPs
   5. Selection for top SNP per transcript

Corwin, J. A., D. Copeland, J. Feusier, A. Subedy, R. Eshbaugh, C. Palmer, J. Maloof and D. J. Kliebenstein (2016). "The quantitative basis of the Arabidopsis innate immune system to endemic pathogens depends on pathogen genetics." PLoS Genet **12**(2): e1005789.

Fordyce, R. F., N. E. Soltis, C. Caseys, R. Gwinner, J. A. Corwin, S. Atwell, D. Copeland, J. Feusier, A. Subedy and R. Eshbaugh (2018). "Digital Imaging Combined with Genome-Wide Association Mapping Links Loci to Plant-Pathogen Interaction Traits." Plant physiology **178**(3): 1406-1422.