**Title: The role of tomato domestication in the quantitative genetic basis of Botrytis cinerea virulence**

**Introduction:**

* For generalist necrotrophs, disease is a quantitative trait
  + Or, describe as quantitative resistance *studied from the pathogen side*
  + Most plant immunity studies on large-effect genes (qualitative resistance)
* Applied goal: to control common, economically costly pathogen
* Previous knowledge of quantitative genetics of virulence in Botrytis
  + Jason’s GWAS
    - Botrytis x At as model of quant R
  + Known virulence genes
* Multigenic basis of plant resistance to Botrytis
  + Genetics in Arabidopsis – Jason’s GWAS
  + Mutant analysis in Arabidopsis
* Approach: detached-leaf GWAS using genetics of Botrytis
  + Can extend to additional host species
* Domestication in pathogen resistance
  + Theory: selection against defense alleles in domestication & cultivation
  + Assumes: low resistance in all domesticated varieties
    - But, does this depend on pathogen/ host genotype?
* Summary of findings
  + Number of genes associated with phenotype
  + Gene functions associated with phenotype
  + Number of genes/ loci that are conditional on domestication or host genotype

**Materials & Methods:**

* Plant growth & choice of accessions
* Pathogen propagation & population of isolates
  + Number of genes in Bc genome
  + Number of SNPs at MAF > 0.20 (plus MAF > 0.10 / > 0.05?)
    - Number of genes with at least 1 SNP
    - Number of genes with >= 2 SNPs
  + address population structure
    - reference Atwell in prep.
* Detached leaf assay
  + Whole-plant translatable
  + Lesion size as approximation of virulence
* Linear models
* bigRR
  + reference JAC 2016
* gene identification

**Results:**

* variation in lesion size
  + domesticated lines more susceptible on average BUT overlap with wild
  + **Figure R0.** Violin plot of lesion size on domesticated vs. wild tomato hosts.
  + analysis of GLM
  + **Table R1.** Mixed model analysis of lesion area. Interaction ( : ) and nesting ( / ) of terms are included. Lesion size is significantly affected by pathogen and host genotypes, and domestication status. Further, host and isolate effects differ between the two replicate detached leaf experiments.
* genetic control of lesion size
  + due to plant, pathogen, and INTERACTION
    - **Figure R1.** Bar plots of average lesion area on each tomato plant genotype, across all *B. cinerea* isolates. Tomato accession names are listed.
    - **Figure R2.** Interaction plot of lesion area for each isolate across tomato plant genotypes. Tomato accession names are listed, and each isolate is traced by a single color.
      * How best to draw these?
    - variation between Bc genotypes affects virulence on tomato
      * Where does B05.10 fall?
  + spearman’s rank correlation among phenotypes
    - Is isolate ranking (based on lesion size) more consistent between domesticated or wild varieties?
* Candidate genes for lesion size
  + **Figure R3a-l.** Manhattan plots of lesion size on all 12 tomato genotypes. Plots with high thresholds include sub-plot showing peaks.
  + number of significant loci > threshold
    - phenotype-conditional loci (single host genotype)
    - total loci (across phenotypes)
    - quantitative resistance to Botrytis depends on both plant and pathogen genetics
  + Role of domestication
    - **Figure R4a-c.** Manhattan plots of lesion size on domesticated, wild, and “domestication effect” phenotypes.
    - loci which are conditional on domestication
  + Gene functions
    - GO annotation
      * within each phenotype
      * across all phenotypes
      * for domesticated / wild comparison
    - SNPs for previously-IDed virulence genes not found in our GWAS list?
  + quantitative – importance of study beyond single-pathogen level.

Discussion:

* Next steps:
  + condense loci into co-expression networks
  + Additional host species
    - Are high-virulence isolates on tomato also virulent across hosts?
    - Genetics of virulence conserved/ variable?
    - Is the effect of domestication consistent across taxa?

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