BcSolGWAS\_redraft\_todo.docx

1. Add GEMMA analysis
   1. Run linear model association test
      1. Manhattan plots of output
   2. Calculate relatedness matrix
   3. Run linear mixed model association test using relatedness matrix
   4. Compare bigRR T4 to GEMMA B05.10
      1. QQ plot
         1. Remove excess bigRR SNPs. Pair SNPs based on location order. Plot effect size from each method
            1. This is negatively correlated, which seems weird. But it does give us a set of SNPs that are “more significant” across both methods
         2. Remove excess bigRR SNPs. Pair SNPs based on relative effect size. Plot location from each method.
            1. This is just a big mess
   5. Add plots
      1. make a figure similar to the final figure using Gemma. And possibly make mimics of Figure 4 and 5 as well.
2. Address reviewer comments
   1. Broad comments: reviewer 1
      1. Phenology of domesticated vs. wild tomato
         1. Phenology is a mechanism of disease resistance -- incorporated into design (rather than flaw in experiment)
         2. should check how we wrote about making sure the plants were mid-way between flowering and germination to minimize phenological differences and see if we need to strengthen the comment about how the leaflet and leaf position did not matter in the model. We should also write in the phenology is an ecological form of resistance known as evasion and that we consider this as valid to study as classical resistance mechanisms.
      2. Selection of leaflets
         1. 2nd true leaf and younger
      3. Inoculation droplet position
         1. Quantify lesion area AND lesion shape. 2 separate measures, interested in both (incl. how much does the lesion track the vasculature). Simply focusing on lesion area here.
      4. Inoculation solution
         1. Spore concentration
         2. Spore germination -- timing
      5. Replication
         1. THREE replicates at TWO timepoints per interaction
         2. How to justify this as sufficient?
         3. Test removing 1 replicate -- change conclusions?
      6. GWA mapping on gapless B05.10 genome
         1. bigRR?
         2. Done in GEMMA
      7. Annotation windows
         1. Smaller windows
         2. Test for assigning >1 gene to SNP?
   2. Broad comments: reviewer 2
      1. Only include GENETIC factors in % variance explained by model (omit experiment, block)
      2. Kinship across tomato lines - sampling bias?
         1. Maloof paper
         2. cite the Maloof/Zamir paper to say that these tomato genotypes are well distributed in the distribution from wild to domestication and do not cluster meaning they are as randomized a sample as possible.
      3. Figure 3 redundant. No phenotypic bottleneck. Less discussion of variance in lesion size
      4. Figure 1c-h an interaction of 2 genomes? Random non-genetic variation?
      5. Interaction effect of 2 genomes: use random effect
      6. Table 2. Wilcoxon with FDR
         1. Include table 2
         2. Clarify FDR correction of p-value
         3. Is population structure of Botrytis considered?
         4. Independence of individuals
         5. Null distribution of Wilcoxon statistic?
      7. Account for population structure
         1. Standard mixed-model GWAS?
      8. Figure 5a
         1. Statistical analysis: overlap > expectation?
      9. Domestication GWAS
         1. Account for population structure
         2. Why genetic effect domest =/= wild
      10. Remove table 1 redundancy (SS vs. F-value)
      11. Report p = XX NOT p < XX.
      12. Figure 2: too small a wild vs. domesticated effect
   3. Reviewer 3 comments
      1. Phylogenetic distance in host?
      2. Line 283: “we identified a significant increase in the resistance of wild tomato in comparison to domesticated tomato”
         1. Reword: observe expected decreased resistance in domesticated tomato --- not direct change/ causative
      3. Pathogen Specialization to Host Variation section
         1. Retitle. There is specialization to genotypes within the host variation (host x pathogen genotypic interactions)
      4. Include caveats in focusing on 2/97 isolates with significant domestication effect
      5. Figure 5
         1. Better explain in figure legend + text
         2. Explain inset graphs
         3. Line 406: how to interpret inset graphs for “levels of overlap exceed the expected overlap due to random chance”
      6. Ancestry of domesticated genotypes
         1. What is known about origins? Multiple domestication events?
   4. Additional edits from Celine
      1. Redraw black/ grey figures as color figures (esp. GWAS)
      2. Figure 1
         1. put into the text that we inoculated close to the central vasculature and measured both lesion size and lesion shape. While both traits showed genetic variation due to the plant and the pathogen that we are going to focus on lesion size in this manuscript. This approach tells the reader that both are informative but we don’t have time to talk about both.
         2. We should however comment tighter in the figure legend of Figure 1 about the statistical test used to make these calls.
      3. Cartoon to explain experimental design
      4. Figure 3 highlight different patterns with colors -- according to statistical threshold
         1. Figure 3 could be colored using a rank plot like Vivian did where she colored the isolates based on their lesion in Wild and kept that color across to domestication. It helps visualize the interaction a bit better.
   5. Cover letter