1. Abstract
2. Introduction
3. Methods
   1. Botrytis collection
      1. Sequencing
      2. Reference, alignment, SNP info
   2. Arabidopsis accessions
   3. Transcriptome experiment
      1. Experimental design
      2. RNA isolation & sequencing
      3. Vivian’s transcript analysis pipeline
   4. GWA for trans eQTL
      1. My linear models & lsmeans
      2. bigRR to B05.10 (if applicable)
      3. GEMMA to B05.10
   5. Cis eQTL
      1. Haploview methods
4. Results
   1. Heritability of transcript variation
      1. Done – refer to Vivian’s paper
         1. For At genes
         2. For Bc genes
   2. Broad summary – ideas from West 2006 paper
      1. Approx.. # eQTL per gene?
         1. Figure X1. Plot an example GWAS of a randomly selected gene?
      2. Total # eQTL?
      3. Organelle vs. nuclear encoded genes?
      4. Likelihood ratio test statistics from composite interval mapping analysis of eQTL?
         1. Heatmap: color LRT stats vs. global permutation threshold
            1. Could color by positive fx B05.10 allele vs. neg
         2. Or, heatmap: x axis is top
   3. Cis eQTL – WITHIN gene
      1. Comparison: avg effect within gene vs. outside?
      2. For Bc genes only
         1. Haploview: ID LD blocks
            1. Specific networks

For botrydial network, ~2 blocks in cis fx. But effect size distribution suggests more loci/ more continuous trait variation. Suggests that trans eQTL have LARGER effect size than expected.

* + - 1. HCA on SNPs in network
         1. Concordance with haploview – YES
      2. Cluster isolates according to SNP HCA?
         1. Done.
      3. Association analysis with few HCA SNPs
         1. Include as covariates in GWA?

Can do in bigRR – try?

* + - 1. Grab large fx (+-8?) SNPs from across all genes from GEMMA outputs – cis signal?
  1. Trans eQTL
     1. GWA B05.10 GEMMA
        1. Summarize across top SNPs
           1. Top 1/gene
           2. Top 10/gene
           3. Top 100/gene
        2. Z-scaled effect sizes
           1. Check effect size distributions for genes with random variation
           2. Compare to real genes
     2. GWA B05.10 bigRR (if applicable)
     3. Repeat each For Bc genes
        1. Col0
        2. Npr1
        3. x
     4. Repeat each For At genes
        1. Col0
        2. Npr1
        3. x

1. Discussion