Results

1. Genome-wide scans for SNP associations with gene expression variation
   1. Botrytis gene expression to Botrytis genome
      1. Lack of evidence for cis control
         1. Plot: gene center from SNPs vs. gene center from transcript
         2. Manhattan style plot: x = SNP location, y = distance SNP to read center
      2. Association hotspots (mostly trans// cis x trans)
         1. Top 1/ 10/ 100 SNP fx
   2. Arabidopsis gene expression to Botrytis genome
      1. Association hotspots
         1. Top 1/ 10/ 100 SNP fx
2. Localized search for evidence of cis control of gene expression variation
   1. Focus on gene networks: Botrydial, Botcynic Acid, Network 5
      1. Haplotype diversity and LD
         1. High LD within network edges
         2. Breaks down rapidly outside cluster
         3. Figure N1: Haploview plots
      2. Does SNP variation within network explain gene expression variation within network?
         1. Figure N2: Phylogeny of isolates from SNP variation within networks
            1. Isolate clustering by SNP variation

Indels—difficulty defining neighbors?

* + - * 1. Poor sampling of some clusters
      1. Figure N3: Expression variation within SNP-based clusters // Excel plots
         1. Botrydial

Mix of cis x trans expression loci

Zeros within gene cluster ~ 3 unique deletion events?

Transposon between genes?

Deletion not correlated with low expression?

Huge deletion between genes: likely TE?

* + - * 1. Botcynic Acid

02.04 low expression, but scattered throughout tree

Deletions within gene?

02.04s mostly one deletion across whole cluster!

* + - * 1. Network 5

01.01.06, 01.05.22: shared origin?

Major cis effects as independent, rare events

Two large intergenic deletions

* + - * 1. Trends overall from excel plotting:

B05.10 SNP haplotype, 2nd haplotype, random admixture?

* 1. Focus on Botcynic Acid
     1. Figure X1. Pvclust tree BoA
        1. Isolates cluster into 4 groups based on SNP diversity
     2. Figure X2. Excel gene deletions
        1. One sub-cluster defined by ~whole-cluster deletion. Deletion is polymorphic.
        2. Additional isolates outside cluster with deletions – independent events
     3. Figure X3. Violin plot of whole-network expression based on clustering
  2. Figure X4. Frequency of distance between gene and top SNP
     + 1. From top 10 SNPs/ gene, lsm
       2. For Col0?
       3. From top 1/ 100 SNP/ gene
  3. Figure X5. Cis-diagonal plot for gene to top SNP
     + 1. From top 10 SNPs/gene, lsm
       2. Col0
       3. Top 1/ 100 SNP/gene