1. Guo 2017 symbiosis paper
   1. eQTL hotspots may be pleiotropic—one gene modulating expression of many genes
      1. interspecific pleiotropy!
      2. From paper “Host Expression Modulator” for parasite loci
   2. Could add a co-expression analysis across host and pathogen?
      1. Gene co-expression with isolate genotype as the independent variable
      2. Gene co-expression with isolate genotype \*at specific loci\* as the independent variable
   3. Evaluate effect size of eQTL on each gene?
      1. How can I calculate the predicted effect of the single top SNP hit locus on gene of interest? Include SNP state within a block as the factor?
   4. Overrepresentation analysis of eQTL hotspots
   5. Look at transcripts modulated by a hotspot
      1. Overrepresentation analysis in functions of transcripts affected by a hotspot!
      2. // function of genes in hotspot
   6. Overrepresentation of which genes have significant cis effects?
   7. Network analysis of polymorphic genes and affected transcripts?
   8. Can I calculate LOD scores? Goal: find nearby loci with LOD scores in opposite directions
   9. Recombination map?
      1. Can tell multiple vs. single causal locus per eQTL based on clustering of recombinant vs. nonrecombinant individuals within region of eQTL
   10. Interpretation of local eQTL: “genes for which expression/ mRNA abundance is strongly associated with genotype near their genomic position”
   11. Prominent vertical bands: “genomic loci that influence the expression of genes located throughout the genome” = trans-eQTL hotspots
2. Meta-analysis:
   1. GWAS (Bc virulence on Col0) vs. eQTL hotspots
   2. transcriptome (Bc expression on Col0 // Col0 expression) vs. eQTL hotspots
   3. GWAS vs. transcriptome
3. Pei 2018 Kiwifruit Botrytis
   1. Geographical origin did not predict pathogenicity
   2. “relatively uniform species diversity”
   3. Phenotype & genotype variation/ differentiated within population
4. Hernandez 2012
   1. Method for cis eQTL detection:
      1. Per SNP, take all transcripts within 500kb, incorporate them into linear model. Estimate “association between the allelic does of each SNP as a predictor of proximal gene expression levels”
5. Ideas for policy paper
   1. Action: research genetic basis of virulence across wild and domesticated prior to focusing efforts on introducing genes from wild
   2. Action: maintain (incentivize?) biodiversity within crops
      1. To prevent selection of highly virulent specialist pathogens
      2. To maintain gene pool for virulence loci