

PLSC 731 – Paper Review

Wang et al – Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars

1. Why are genome-wide association studies (GWAS) experiments feasible now? (p233)
2. What are the advantages of GWAS to plant breeding? (p233)
3. Why are plants especially well-suited for GWAS experiments? (p234)
4. What has led to the highly-structured nature of barley cultivars and why is this important for GWAS experiments? (p234)
5. Why is barley useful for testing various statistical methods for controlling population structure? (p234)
6. Describe the cultivars used in these experiments. Are they appropriate for the experiments described here? (p234)
7. Describe the genotyping platform. Is it appropriate for the experiments described here? (p234)

Dr. McClean will cover the statistical methods.

8. Describe the LD results found in this paper. (p237)
9. Why was the number of subpopulations not adequately determined? (p237)
10. How was the barley population structured based on the first principal component? third principal component? (p237)
11. Were the phenotypic values distributed the same in the winter and spring subsets? (p238)
12. What results suggested skewed results could result from population structure? (p 238)
13. Why was the “chromosomal bin” approach used? (p 239)
14. What statistical models performed best? Why was one chosen rather than use either one? (p239-240)
15. What feature of the STRUCTURE approach is violated when using inbred breeding lines like barley? (p244)