

## PLSC 731 – Study Questions

Zhao et al – Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*.

1. What research materials were used in this paper?
2. Describe the population structure and LD decay in the rice populations? Why is this information important?
3. Why is estimating phenotypic correlations important?
4. How was it determined that there was a strong population structure confounding effect.
5. What are the tradeoffs between using a naïve statistical model to detect significant SNPs and a model that accounts for population structure?
6. Was it important to determine if subpopulations had different loci controlling the same traits? How was this assessed?
7. How was it determined that different genetic networks controlled the same trait in different subpopulations? How does this relate to genotype-by-environment interactions?
8. Distinguish between linkage and pleiotropy. How does Fig. 6a display the concept that the multiple linked genes controlled a trait or that the same gene controls several traits.
9. How does this paper demonstrate the value of using a world-wide genotype panel?
10. What relevant results are observed in this paper regarding the use of a naïve statistical model and comparing it with a model that controls for population structure?
11. What is it difficult to uncover domestication traits in a panel of cultivated genotypes?
12. What information useful to plant breeders can be drawn from an association mapping study?