PLSC 731: Paper Review

Cummings and Clegg - Nucleotide sequence diversity at the alcohol dehydrogenase 1 locus in wild barley (*Hordeum vulgare* ssp. *spontaneum*): an evaluation of the background selection hypothesis

1. What is the goal of population genetics? What forces drive changes in genetic diversity?

2. What is the value of gene trees?

3. What does a significant deviation from Tajima's D imply with regards to the neutrality of the evolution of a gene?

4. Describe the relationship between diversity and recombination?

5. What is the relationship between selection intensity and recombination on the breadth of selection sweep? What is the relationship between background selection and reduced diversity?

6. What is alcohol dehydrogenase a good gene for population genetics studies?

7. What features make barley an ideal species to study background selection?

8. Describe the sequence strategy.

9. Describe the sequence diversity patterns observed in this barely population.

10. What test statistics were used to detect deviation from the neutral model of gene evolution? Which sequences exhibited significant deviation from neutral model?

11. What is the effective population size?

12. What degree of recombination was observed?

13. What is the effect of a population bottleneck and selective sweep on the degree of localized genetic variation?

14. What factors and data in this paper favor background selection at Adh in barley?