**Linkage: Study guide and readings**

***Required readings:*** Cistue et al. 2011. Theor. Appl. Genet. 122: 1399-1410

1. Abstract, Introduction, Conclusions. Pay particular attention to Figure 2.
2. What is linkage and what does it represent in terms of genetic loci and their chromosomal locations?
3. Explain how, in the case of a species with complete linkage maps, the number of linkage groups will equal the n number of chromosomes.
4. What is intragenic recombination and what are the implications if the cross-over event is reciprocal vs. if the cross-over event is non-reciprocal?
5. Distinguish between coupling and repulsion linkages.
6. What is a bivalent and how might cross-overs be distributed across sister chromatids?
7. Can there be more than one cross-over per bivalent?
8. Summarize, in your own words, key points in non-sister chromatid exchange.
9. Why the emphasis on non-sister chromatid exchange vs. sister chromatid exchange?
10. Even when DNA compaction is not an issue, are crossovers occurring at equal frequency at all points in the chromosome?
11. Explain how independent assortment of loci on different chromosomes, and at loci on opposite ends of a chromosome, can lead to non-parental combinations of alleles.
12. Explain how recombination between linked loci can lead to lead to non-parental combinations of alleles.
13. Demonstrate to your satisfaction that the maximum frequency of non-parental (non-recombinant) combinations of games at two loci is 50%.
14. Can linkage analysis be conducted with types of populations other than doubled haploids?
15. If you observed a high frequency of repulsion linkages (using the term to describe linkage of favorable and unfavorable alleles) alleles, how could repeated cycles of selfing, or intermating, potentially be more useful than doubled haploids?
16. In the slides shown in class, why were chi square tests accepted for three of the tests and rejected for one of them?
17. To be sure you understand there where, when and how of meiosis, diagram two meiosis events per the VvNnLl examples shown in class.
18. “The recombination frequency between two linked loci is the sum of the recombinant phenotypic classes divided by the total population size.”
    1. True
    2. False
19. Why are double cross-overs less frequent at recombination frequencies of <10% and more frequent at recombination frequencies >10%?
20. Explain why the centiMorgan is useful, even though there is not a direct conversion to Mbp..
21. Three loci (A, B, and C) are linked in that order. Does the recombination frequency between A and C (*r*AC) equal the sum of the recombination frequencies between A and B (*r*AB) and B and C (*r*BC)?
22. What are reasons for making linkage maps within a species?
23. What are reasons for making linkage maps in different species, and then aligning the maps?
24. In the graphical genotype slides shown in class, does a continuous series of alleles from one parent mean that there were no crossovers in that region?
25. In the linkage maps shown in class slides, there are often gaps without markers. Give two possible explanations for these gaps.
26. Does chromosome 1A of bread wheat show homoeology with or synteny with chromosome 1H of barley?
27. *Do Fragaria* and Prunus show homoeology or syntney?
28. Explain why molecular markers, rather than morphological markers, are used to create high density linkage maps.
29. If you were constructing a linkage map using an F2 population, would you prefer using dominant or codominant markers?
30. Why are the high density maps shown in class based on SNPs rather than SSRs?
31. In 2019, why might SNPs - assayed using KASP or Illumina platforms - be more useful for some applications than whole genome sequence?
32. Based on your answer to question #47, do think that in the future, for plant breeding purposes, hole genome sequence will replace targeted genotyping? Defend your answer.

Based on assigned reading

* + What is meant by sampling female gametes with the *Hordeum bulbosum* system vs. male gametes with anther culture?
  + Were there major differences in recombination between megasporogenesis and microsporogenesis?
  + Why was it “reassuring” that there were no difference in locus ordering between the two mapping populations?
  + What is segregation distortion?
  + Why was pleiotropy discussed in a paper on linkage?

**Supplementary resources: Not required.**

JoinMap demo

<https://www.kyazma.nl/index.php/JoinMap/>

Barley World website on Oregon Wolfe Barley

<https://barleyworld.org/owb>

Chutimanitsakun et al. (2011) on Oregon Wolfe Barley mapping

<https://www.ncbi.nlm.nih.gov/pubmed/21205322>