**Study Questions on Quantitative Inheritance**

1. How would you calculate allele and genotype frequencies from sample data? For practice, consider a sample of your favorite outcrossing wildflower that has 78 A1A1, 65 A1A2, and 27 A2A2 genotypes at an SSR locus.
2. Be able to use the Hardy-Weinberg principle to make predictions about the distribution of genotypes in a random-mating population. If 16% of a population is homozygous for a recessive allele, what proportion of the population would you expect to be heterozygotes? With a total of 200 plants, how many would you expect to be homozygous for the dominant allele?
3. Describe what is meant by linkage disequilibrium. Is it possible to have disequilibrium between loci that are on different chromosomes? How can you tell if two loci are in equilibrium?
4. Discuss some of the possible origins of linkage disequilibrium.
5. For two unlinked loci, at what rate will linkage disequilibrium decay in a population that is random mating? In addition to linkage, what other factor(s) might delay the rate of LD decay?
6. What is the definition of inbreeding? How can you tell from a pedigree if there is the potential for an individual to be inbred?
7. Six seeds of a weed species hitchhiked to an island on the shoe of a tourist, and were left in a patch where they were able to intermate and reproduce. Assuming that there was no prior inbreeding in the population, what would the level of inbreeding be after one generation on the island?
8. Be able to estimate the additive and dominance effects for the single locus model. For example, if the A1A1 genotype has a genotypic value of 20, and the A2A2 genotype has a value of 12, what is the additive effect (*+a*) for this locus? If the heterozygote has a genotypic value of 18, what is the dominance effect? Is there complete dominance?
9. What is the value of the additive genetic covariance between a parent and its offspring? Could you explain the same concept using simpler language?
10. If a kinship matrix for a given group of individuals is calculated from pedigrees, will that be identical to a kinship matrix estimated from molecular markers? Why or why not?
11. The variance in height among identical clones is 100 cm2. The variance among noninbred individuals is 500 cm2. How would you estimate genetic variance? What is the estimate of broad sense heritabiltiy?
12. Describe how narrow sense heritability can be used to predict the response to natural or artificial selection.
13. Discuss the advantages and disadvantages of using linkage analysis in a biparental mapping population for mapping quantitative trait loci.
14. Recombinant inbred lines and doubled haploids are two common types of mapping populations. In what respects are they similar? How are they different? Why might you choose to use one over the other for mapping QTL?
15. Name two commonly used mapping functions. Why are they needed?
16. What are the limitations of using single-marker analysis (SMA) for QTL detection?
17. Describe how the use of composite interval mapping (CIM) might provide better estimates of QTL effects than simple interval mapping (SIM).
18. What information is obtained from a QTL analysis that can help us to understand the inheritance of quantitative traits?
19. How can the results of a QTL analysis be used to further other basic and applied research objectives in plant genetics?
20. Discuss at least three potential advantages of GWAS compared to linkage analysis for QTL mapping.
21. Why is there a higher risk of detecting false QTL when using GWAS?
22. Discuss how the rate of LD decay affects the density of markers required to detect QTL (power) and the resolution of the position of QTL on chromosomes.
23. Describe how the mating system of a plant species and breeding history might affect the rate of LD decay.
24. What is meant by “population structure”? What general approaches are available to account for it in association mapping?
25. Describe in a general way how the Q + K statistical model improves the accuracy of GWAS.
26. The Nested Association Mapping (NAM) and Multi-parent Advanced Generation Intercrosses (MAGIC) designs are intended to combine the benefits of linkage analysis and GWAS for QTL analysis. Do you think they have achieved that goal? Explain your answer.