ANSC 446 / IB 416
Population Genetics
Exam 2, October 17, 2008

Name _____

(5 pages) Please underline or indicate your answer. If rounding, use 3 significant digits. Show your work or describe your logic to earn partial credit for incomplete answers.

(8) 1. At a diploid biallelic locus, calculate the expected heterozygosity for the first four generations, given $H_0 = 0.4$, for the following:

(4) a. lineages where there is complete selfing

(4) b. lineages where there is continuous full-sib mating

(8) 2. A population of 400 cattle is surveyed at a locus with two codominant alleles. The genotype A_1A_1 is found to be present in 80 cattle, A_1A_2 is present in 40 cattle, and A_2A_2 is present in 280 cattle.

(4) a. What are the allele frequencies?

(4) b. Estimate the level of inbreeding (inbreeding coefficient) in the population.

(4) 3. Assume that the initial and final allele frequencies before and after selection are 0.2 and 0.1. How many generations does it take for this amount of change when there is a recessive lethal?

(18) 4. The relative fitnesses found for alleles at a locus in the major histocompatibility complex are 0.5, 1, and 0.75 for alleles A_1A_1, A_1A_2, and A_2A_2, respectively.

(2) a. What are the values of the selection coefficients s_1 and s_2?

(2) b. What is the name given to this type of fitness array?

(4) c. What is the equilibrium frequency for A_2?

(2) d. Would the equilibrium frequency be stable? Why or why not?

(4) e. What is the genetic load at the equilibrium frequency?

(4) f. Four isolated populations have initial allele frequencies for A_2 of 0.0, 0.45, 0.55 and 1.0. At what frequency will allele A_2 stabilize in each of these four populations?

(14) 5. Give the best definition for the following terms:

(2) a. Philopatry:

(2) b. Coefficient of inbreeding

(2) c. Fisher's fundamental theorem of natural selection:

(2) d. Inclusive fitness:

(2) e. Antagonistic pleiotropy:

(2) f. Meiotic drive:

(2) g. Indel:

(10) 6. Determine the frequencies at generation t+1 for the following:

(5) a. At a biallelic autosomal locus, a deleterious allele with a dominance level of 0.4 and selection coefficient of 0.4 is found at a frequency of 0.2. Assuming random mating, what will be the frequency of the allele in the next generation?

(5) b. For the situation described in (a), and assuming the Basic Selection Model, what was the frequency of the three genotypes among only those progeny that were inviable?

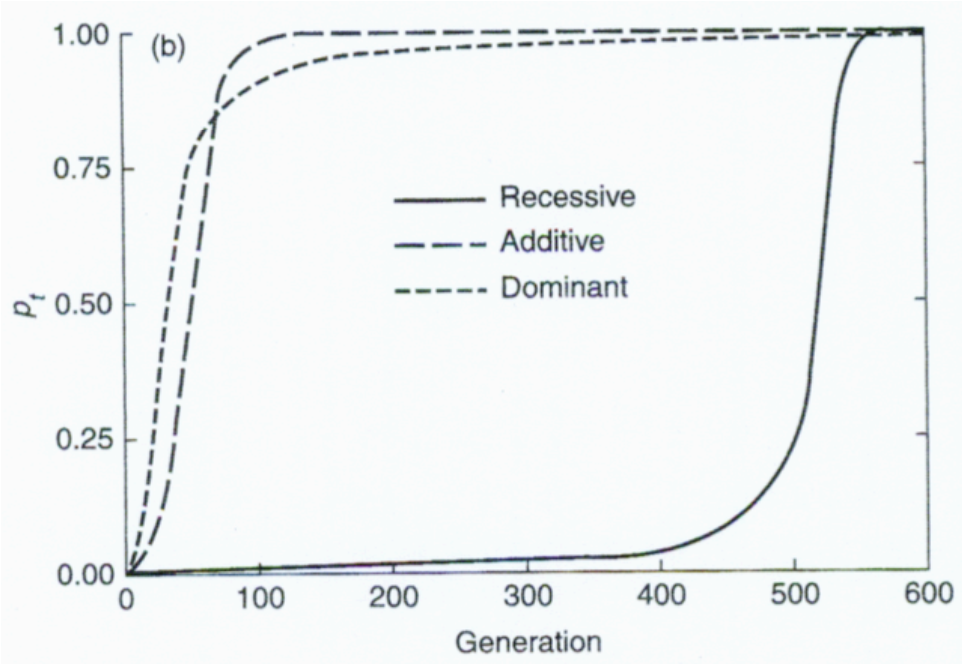
(3) 7. Give an example of positive assortative mating.

(6) 8. For a diploid lineage with no history of inbreeding,

(3) a. What is the coefficient of relationship between parent and offspring?

(3) b. What is the kinship coefficient between parent and an offspring?

(4) 9. The following Figure from Hedrick's text shows the rise in frequency for an allele at an initially low frequency ($p_0 = 0.01$) undergoing positive Darwinian selection ($s = 0.1$), in cases where the allele is recessive, dominant, or additive:



Given that the fitness value for an additive allele is exactly half way between the fitness of a dominant allele and the fitness of a recessive allele, why doesn't the curve showing increase in an additive allele fall exactly intermediate between the curve for a dominant and the curve for a recessive allele?

(4) 10. Four alleles (A_1, A_2, A_3, A_4) at a single locus (A) have been identified on a plant that prevents self-fertilization by self-incompatibility. If the A locus is at equilibrium, what is the expected allele frequency of allele A_3?

(8) 11. Assume that the fitnesses are 0.9, 1.0 and 0.6 for alleles A_1A_1, A_1A_2, and A_2A_2, respectively.

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(4) a. Calculate the mean fitness when q = 0.4.

(4) b. Is the mean fitness higher for any other allele frequency? Why or why not?

(4) 12. What is the difference between purifying and Darwinian selection?

(9) 13. In the pedigree on the right, CA1 and CA2 are outbred.

(3) a. What is the inbreeding coefficient for individual U?

(3) b. What is the inbreeding coefficient for individual Z?

(3) c. Genotypes are shown for the A locus for individuals included in the pedigree. What are the possible genotypes for individual Z to have at the A locus? Which of these would be identical by descent, and which have identity in state?