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## ANSC 446 / IB 416 Population Genetics Exam 3, November 14, 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.

- (12) 1. The Seeing Eye maintains a kennel of approximately 36 female German Shepherds and 10 male German Shepherds in their breeding population.
  - (3) a. What is the effective population size for an autosomal gene?

Answer: 
$$N_e = \frac{4 N_f N_m}{N_f + N_m} = \frac{4(36)(10)}{36 + 10} = \frac{1440}{46} = 31.3$$

(3) b. What is the effective population size for an mtDNA gene?

Answer: 
$$N_e = N_{ef} = 36 = 18$$

(3) c. What is the effective population size for a Y-chromosome gene?

Answer: 
$$N_e = N_{em} = 10 = 5$$

(3) d. What is the effective population size for an X-chromosome gene?

Answer: 
$$N_e = 9 \times N_f N_m = 9 \times (36) \times (10) = 3240 = 28.9$$
  
 $2N_f + 4N_m = 2(36) + 4(10) = 112$ 

- (6) 2. Effective population size
  - (3) a. Over 3 recent generations, the number of guppies in a stream has been 100, 100 and 100. What is the effective population size?

Answer: 
$$N_e = 3 / ((1/100) + (1/100 + 1/100)) = 3/(3/100) = 100$$

(3) b. In a second stream, the number of guppies has been 100, 10, and 100. What is the effective population size?

Answer: 
$$N_e = 3 / ((1/100) + 1/10 + 1/100)) = 3/(12/100) = 25$$

- (15) 3. For the South China tiger, a population size of 50 is maintained in zoos. Assume that this population size is constant across generations.
  - (3) a. For a population of this size, how much of the current generation's heterozygosity will be lost in the next generation due to drift?

 $H_{t+1} = (1 - (1/(2N)) \times H_t = (1 - 1/(2X50)) H_t = (1 - 0.01) H_t = 0.99 H_t$ Since .99 of heterozygosity is retained each generation, **.01 or 1%** of any remaining heterozygosity is lost due to drift each generation.

(3) b. If drift is the only force operating to alter genotypic frequencies, how many generations will it take for a reduction in heterozygosity to approximately 50% of the initial value in populations of size 50?

ANS: 
$$t = -2$$
 (N)  $ln(x) = -2(50) ln(.5) = 69.3 generations$ 

(3) c. If drift is the only force operating to alter allele frequencies, how many generations will it take to reach fixation for an allele with an initial frequency of .5 when the population size is 50?

ANS: 
$$T(q) = [-4 (N) (1-q) ln(1-q)] / q = [-4(50)(1-.5) ln(1-.5)] / .5$$
  
=  $[-100 ln(.5)] / .5 = 138.6$  generations

(Note that this twice the value of the answer in part b)

(3) d. Assuming that the effective population size equals the census size of 50, and assuming no selection or migration. How long is it expected to take on average for a new neutral mutant allele to become fixed in this population?

Answer: 
$$T1(p) = 4 N_e = 4(50) = 200$$
 generations

(3) e. For a new neutral mutation in this population, what is the probability that it will become fixed in the population?

Answer: 
$$1/(2N) = 1/100 = 0.01$$

(3) 4. Give an example of a population that has undergone a bottleneck or a founder effect.

Florida Panther, humans on Tristan da Cunha, etc.

- (5) 5. Assuming Neutrality, circle the letters for those of the following statements that are true. Assume that Kimura's Neutral Theory and Ohta's Nearly Neutral Theory are accurate. a b d
  - a. selection plays a greater role relative to drift as populations get larger
  - b. theta calculated based on nucleotide diversity should be the same as or similar to theta calculated based on segregating sites
  - c. in large populations, frameshift mutants will more frequently reach fixation.
  - d. most mutations have little or no impact on fitness.
  - e. absorbing states will not be present in large natural populations
- (13) 6. The ostrich farm on Route 57, owned by Mr. Jones, still only has single combed birds. Single comb is recessive to double comb. However, the Jones farm has now decided to double their flock size by adding an equal number of individuals from the ostrich farm on Route 47, owned by the Smiths. Mrs. Smith has estimated the allele frequency of single comb in their flock as 0.2
  - (3) a. Estimate the allele frequency of single comb in the new Jones flock.

$$q_1 = (1-m)q_0 + mq_m = (.5)(1) + (.5)(.2) = 0.6$$

(3) b. What would be the migration rate for the first generation?

Migration rate =
$$(1-0.6)/(1-0.2) = .4/.8 = .5$$

(3) c. If instead Mr. Jones would replace a random sample of 10% of his flock with a random sample of birds from Mrs. Smith each generation for 5 generations, what is the expected frequency of the single comb allele?

$$q_{t+5} = ((1-.1)^5 \times 1.0) + (1 - (1 - .1)^5) \times 0.2 = 0.5905 + 0.0819 = 0.6724$$

(4) d. Would (c.) represent an example of the continent-island model of migration, or of the general model of migration. Why?

Continent-island model of migration. Gene flow is unidirectional.

(3) 7. What is the approximate probability of loss of a new mutation in the first generation if the number of offspring per family follows a Poisson distribution and averages 2 offspring per family.

ANS: 
$$P(loss) = .368$$
 (See Hedrick page 367)

(4) 8. What is the equilibrium frequency of  $A_2$  if the forward mutation rate from  $A_1$  to  $A_2$  is  $10^{-4}$  and the reverse mutation rate is 6 x  $10^{-5}$ ?

ANS: 
$$q_e = u / (u + v) = .00010 / .00016 = 5/8 = 0.625$$

- (10) 9. Give the best definition for the following terms:
- (2) a. Infinite allele model: assumes that every new mutation does not match any previous mutation (and is thus a novel allele). Model is used to examine the balance between the creation of new alleles by mutation and the elimination of alleles by drift
- (2) b. Metapopulation: subpopulations in discrete habitat patches, that turnover with extinction and recolonization from other patches. The newly colonized patches may display the results of founder effects
- (2) c. Cline: a directional change in allele frequencies across (geographic) space or between subpopulations (or between species), potentially due to selection or substructure. May be stable or transient.
- (2) d. Coalescence: the point at which common ancestry for two alleles occurs
  - (2) e. Admixture: the proportion of gene flow from an outside population.
- (7) 10. Under neutrality:
  - (4) a. Why is the rate of substitution independent of population size?

This independence occurs because in a smaller population, there are fewer mutants, but their initial frequency is higher; in a large population there are more mutants, but the probability of fixation for a mutant is lower. Thus the higher or lower number of new mutants is matched, respectively, by a lower or higher probability of fixation.

(3) b. What is the time between substitutions if the rate of mutation is 10<sup>-6</sup>?

1/u = 1 million generations

- (22) 11. Assume that for two isolated subpopulations of the same size, frequencies of alleles  $A_1$  and  $A_2$  are 0.6 and 0.4, respectively, in the first subpopulation; and frequencies of alleles  $A_1$  and  $A_2$  are 0.4 and 0.6, respectively, in the second subpopulation.
  - (3) a. Assuming Hardy-Weinberg proportions, what is the frequency of heterozygotes in the first subpopulation?

$$2pq = 2 \times 0.6 \times 0.4 = 0.48$$

(3) b. Assuming Hardy-Weinberg proportions, what is the frequency of heterozygotes in the second subpopulation?

$$2pq = 2 \times 0.4 \times 0.6 = 0.48$$

(4) c. If the two subpopulations were merged into a single panmictic (freely interbreeding) population, what would be the frequency of heterozygotes after Hardy Weinberg equilibrium was reached in the combined population?

$$2 \times p$$
-bar  $\times q$ -bar =  $2 \times 0.5 \times 0.5 = 0.5$ 

(4) d. What is the term used in cases where subpopulation structure results in a reduction in overall heterozygosity, even though the subpopulations themselves are in Hardy-Weinberg equilibrium?

Wahlund effect.

(4) e. Calculate  $G_{\text{ST}}$  between the two subpopulations (before they were merged)

$$G_{ST} = (H_T - H_S) / H_T = (0.50 - 0.48) / 0.5 = 0.02/0.5 = 0.04$$

(4) f. Would you expect  $F_{ST}$  to be positive, negative or zero between the original two subpopulations (before they were merged)? Why?

 $F_{ST}$  would be positive because there are allele frequency differences between the two subpopulations; equally importantly, Nei's  $G_{ST}$  is an estimator of  $F_{ST}$ . (Also,  $F_{ST}$  ranges in value from zero to one and thus can never be a negative value.)