

1. After learning about the human *MN* locus in class, you decide to replicate a previous study in order to confirm the published results, which suggested that the *M* and *N* alleles are in Hardy-Weinberg equilibrium. 1315 fellow UCONN students volunteer to have their blood type characterized for your study. You discover 30 students with the *MM* genotype, 335 students with the *MN* genotype, and 950 students with the *NN* genotype.

- What are the genotype frequencies for your sample population of UCONN students?
- What are the allele frequencies?
- Given the allele frequencies, what are the expected Hardy-Weinberg genotype frequencies.
- What will be the genotype frequencies of the next generation, assuming none of the assumptions of Hardy-Weinberg are broken?
- Is this population in Hardy-Weinberg equilibrium with respect to the *MN* locus?

2. The major histo-compatibility complex (MHC) consists of a suite of genes that play an important role in the immune system. While studying a particular MHC locus in a population of field mice found in Connecticut, you discover ample genetic variation. There appears to be two common alleles residing at this particular MHC locus. You characterize the genotype of 130 individuals from this population. You discover 25 individuals with genotype *AA*, 90 individuals with genotype *AB*, and 15 individuals with genotype *BB*.

- What are the genotype frequencies of your sample population of field mice?
- What are the allele frequencies?
- Given the allele frequencies, what are the expected Hardy-Weinberg genotype frequencies.
- Is the population in Hardy-Weinberg equilibrium with respect to the *AB* MHC locus?

3. Black color in horses is governed primarily by a recessive allele at the *A* locus. *AA* and *Aa* horses are nonblack colors, while *aa* horses are black all over. In the internet group "rec.equestrian", one person asked why there are relatively few black horses of the Arabian breed. One response was, "Black is a rare color because it is recessive. More Arabians are bay or gray because those colors are dominant." What is wrong with this explanation? (Assume that the *A* and *a* alleles are in Hardy-Weinberg equilibrium, which was probably true at the time of this discussion.) Generally, what does the Hardy-Weinberg model show us about the impact that an allele's dominance or recessiveness has on its frequency?

4.) In humans, the *COL1A1* locus codes for a certain collagen protein found in bone. The normal allele at this locus is denoted with *S*. A recessive allele *s* is associated with reduced bone mineral density and increased risk of fractures in both *Ss* and *ss* women. A recent study of 1,778 women showed that 1,194 were *SS*, 526 were *Ss*, and 58 were *ss* (Uitterlinden et al. 1998).

- a) Are these two alleles in Hardy-Weinberg equilibrium?
- b) How do you know?
- c) What information would you need to determine whether the alleles will be in Hardy-Weinberg equilibrium in the next generation?

5.) In each example below, identify which of the two populations will lose diversity faster due to genetic drift?

- a) A population with  $N = 2000$ ,  $N_e = 300$ ; a population with  $N = 10,000$ ,  $N_e = 200$ .
- b) A population with  $N = 500$ ,  $N_e = 459$ ; a population with  $N = 678$ ,  $N_e = 650$ .
- c) A population with  $N = 3000$ ,  $N_e = 1430$ ; a population with  $N = 1550$ ,  $N_e = 1430$ .
- d) A population with  $N = 100$ ,  $N_e = 95$ ; a population with  $N = 100$ ,  $N_e = 90$ .

How many generations do you expect it to take to lose genetic diversity in each of the above populations?

6.) For a diploid species, assume one set of 100 populations, each with a constant size of 50 individuals, and another set of 100 populations, each with 100 individuals. Assume these are all ideal populations.

- a) If in each population the frequencies of alleles  $A$  and  $a$  are 0.4 and 0.6 respectively, what fraction of populations in each set are likely to become fixed for allele  $A$  versus  $a$ ?

7.) A small population of wolves consists of 25 males and 75 females. At a particular major histocompatibility locus (MHC), the  $A$  allele has a frequency of 63% and the  $B$  allele has a frequency of 37%.

- a) What is the probability that the  $A$  locus will become fixed in the population, assuming genetic drift is the only evolutionary factor acting on the population. What is the probability that the  $B$  locus will become fixed?
- b) What is the effective population size?
- c) How many generations do you predict will pass before there is a loss of genetic diversity?

8.) A particular population of 350 water snakes lives on an island off the coast of Lake Erie. At a particular locus involved in determining color patterning, this population has a frequency of 0.54 for the  $B$  allele and 0.46 for the  $b$  allele. Assume that this is an ideal population (none of the genetic drift assumptions are violated,  $N = N_e$ ).

- a) What is the probability that the  $B$  allele will become fixed in the population?  
What about the  $b$  allele?
- b) How many generations do you predict will pass before there is a loss of genetic diversity?
- 9.) Imagine that 10 water snakes migrate from the mainland and join the island population. 3 of these snakes have a  $BB$  genotype, 6 have a  $Bb$  genotype, and 1 has a  $bb$  genotype. Imagine that the allele frequencies of the migrants are representative of those of the mainland population.
- a) What is the migration rate?  
b) What are the new allele frequencies?  
c) What do you expect the allele frequencies to be in the next generation?  
d) Do you expect these two populations to diverge, why or why not? If not, what do you expect the equilibrium frequencies of the island population to be?  
e) What do you expect the allele frequencies to be in the next generation if the migration rate is 0.4? What about 0.6?  
f) What would the migration rate be if 20 water snakes migrated from the mainland? What about 50 migrants?
- 10.) What is the population size and the effective population size for a population of water snakes with the following sex-ratios, assuming constant population size and non-overlapping generations.
- a) 45 males and 55 females  
b) 10 males and 90 females  
c) 50 males and 50 females

How many generations do you expect it to take to lose genetic diversity in the above populations?