

**EEB 2245: Evolutionary Biology**  
**Spring 2008**  
**Answer Key to Selected Problems from Problem Sets 1 and 2**

**Problem Set 1:**

2.) a. genotype frequency of  $MM = 30/1315 = 0.0228$ ; genotype frequency of  $MN = 335/1315 = 0.255$ ; genotype frequency of  $NN = 950/1315 = 0.722$

b. allele frequency of  $M = [2(30) + 335] / [2(1315)] = 0.150$ ; allele frequency of  $N = [2(950) + 335] / [2(1315)] = 0.850$  or, another way to find the frequency of  $N$ ,  $1 - 0.150 = 0.850$

c. expected genotype frequency of  $MM = 0.150^2 = 0.0225$ ; expected genotype frequency of  $MN = 2(0.15)(0.85) = 0.255$ ; expected genotype frequency of  $NN = 0.850^2 = 0.7225$

d. If you see observed and expected frequencies that are this similar, for our purposes you can assume they are in HW equilibrium.

3.) a. genotype frequency of  $AA = 25/ 130 = 0.192$ ;  $AB = 90/ 130 = 0.692$ ;  $BB = 15/ 130 = 0.115$

b. allele frequency of  $A = [2(25) + 90] / [2(130)] = 0.538$ ; allele frequency of  $B = [2(15) + 90] / [2(130)] = 0.462$  or, another way to find the frequency of  $B$ ,  $1 - 0.538 = 0.462$

c. expected genotype frequency of  $AA = 0.538^2 = 0.289$ ; expected genotype frequency of  $AB = 2(0.538)(0.462) = 0.497$ ; expected genotype frequency of  $BB = 0.462^2 = 0.213$

d. No, the expected genotype frequencies don't match the observed very closely.

e. We expect the frequencies to return to HW equilibrium, which will give us the expected frequencies from c.,  $AA = 0.289$ ,  $AB = 0.497$ ,  $BB = 0.213$

4.) The frequency of black horses only depends on the frequency of the  $a$  allele. If there is a high frequency of the  $a$  allele there will be relatively many black horses, but if there is a low frequency of the  $a$  allele, there will be relatively few black horses. The frequency of  $aa$  genotype is independent of whether it is composed of dominant or recessive alleles.

5.) observed frequency of  $SS = 1,194 / 1,778 = 0.672$ ; observed frequency of  $Ss = 526 / 1,778 = 0.296$ ; observed frequency of  $ss = 58 / 1,778 = 0.033$

The observed allele frequency of  $S = [2(1,194) + 526] / [2(1,778)] = 0.819$ ; the observed frequency of  $s = [2(58) + 526] / [2(1,778)] = 0.181$

The expected genotype frequencies assuming HW equilibrium are:

$$SS = 0.819^2 = 0.671; Ss = 2(0.819)(0.181) = 0.296; ss = 0.181^2 = 0.033$$

Because our expected genotype frequencies and our observed genotype frequencies match, we can assume that this population is in HW equilibrium with respect to the *COL1A1* locus. You could also take your observed genotype frequencies and determine your expected allele frequencies from these, and then compare your observed and expected allele frequencies. These should match if the population is in HW equilibrium.

In order to know whether this population will be in HW equilibrium in the next generation, we would need to know whether or not any of the HW assumptions are being

violated. If no HW assumptions are being violated, then we can assume the population will stay in HW equilibrium.

**Problem Set 2:**

1.) Remember, populations lose diversity in  $4N_e$  generations. So, populations with smaller values of  $N_e$  are expected to lose diversity faster, or in less generations. So for question 1, whichever population has the lower value for  $N_e$  is expected to lose diversity faster. In part c, both populations have the same effective population size, so we expect neither to lose diversity faster than the other. (in part d, it should read  $N_e = 90$ )

2.) a. If a population has an allele frequency for  $A$  of 0.4, then we know the probability of that allele reaching fixation is 0.4. Likewise if we know the probability of the  $A$  allele reaching fixation in any particular population is 0.4, then we also can expect it to reach fixation in 0.4 of the number of populations. The same logic dictates that 0.6 of the populations will become fixed for  $a$ .

b. In a population of 50 individuals, there are a total of 100 alleles at a given locus. If a mutation occurs in one of these alleles, **then this new allele only has a frequency of 1/100 or 0.01**. So, we only give this allele a probability of 0.01 of becoming fixed in a particular population. If we have 100 populations of size 50, each with a frequency of 0.01 for this new allele, then **we expect 0.01(100), or just 1 population to become fixed for the new mutant allele.**

In a population of 100 individuals, there are a total of 200 alleles at a given locus. If a mutation occurs in one of these alleles, **then this new mutant allele only has a frequency of 1/200, or 0.005**. So we only give this allele a probability of 0.005 of becoming fixed in a particular population. If we have 100 populations of size 100, each with a frequency of 0.005 for this new allele, **then we expect 0.005(100), or just ½ of a population to become fixed for this allele.**

In total, we would expect 1½ populations to become fixed for this allele.

c. With what we know, we can't determine exactly how many generations it will take for this allele to become fixed in a population, but we know if it happens it should happen by  $4N_e$  generations. So, **for a population with an effective population size of 50, if the allele becomes fixed, it should happen by 4(50) or 200 generations. For a population with an effective population size of 100, if the allele becomes fixed, it should happen by 4(100) or 400 generations.**

3.) a. The probability that an allele will become fixed due to drift alone is always the same as the allele's frequency.  **$A = 0.63$ ,  $B = 0.37$ .**

b. Because the ratio of male to females does not equal one, we know this is not an ideal population, and that  $N$  will not equal  $N_e$ . In this case we must use the formula

$N_e = [4N_m N_f] / [N_m + N_f]$ . So, in this case the effective population size equals

$[4(25)(75)] / [25 + 75]$ , or **75**.

c. We expect to lose diversity in  $4N_e$  generations, or  $4(75) = 300$  generations.

4.) a. Probability  $B$  allele becomes fixed is 0.54; probability  $b$  allele becomes fixed is 0.46.

b. By  $4N_e$  generations, or  $4(350) = 1,400$  generations.

5.) a. the migration rate is equal to the fraction of the total population that were born in a different population, or in this case  $10/360 = 0.02778$ .

b. In the original population of water snakes we had 0.54 (700), or 378  $B$  alleles and 0.46(700), or 322  $b$  alleles. Remember, we use 700 because each of the 350 water snakes has 2 alleles. Now we are adding  $2(3) + 6$ , or 12  $B$  alleles from the migrants and  $2(1) + 6$ , or 8  $b$  alleles. So that gives us a total of 390  $B$  alleles and 330  $b$  alleles. Our new population size is 360,  $350 + 10$ , which gives us a total of 720 alleles. So,  $390/720$ , or 0.542 is our new allele frequency of the  $B$  allele, and  $330/720$ , or 0.458 is our new frequency of the  $b$  allele.

c. If we know the allele frequency in this generation and the migration rate we can estimate the allele frequencies in the next generation using the formula

$p' = p(1-m) + p_m m$ , where  $p'$  equals the frequency of  $p$  in the next generation,  $p$  equals the frequency in the current generation,  $m$  equals the migration rate, and  $p_m$  equals the frequency of  $p$  in the home population of the migrants. Since it was given that the allele frequencies of the migrants are representative of the allele frequencies of their home population, we know that their home population has an allele frequency of  $[2(3) + 6]/20$ , or 0.6 for the  $B$  allele and  $[2(1) + 6]/20$ , or 0.4 for the  $b$  allele. So, plugging all these numbers into our formula and solving for the frequency of  $B$  in the next generation, we

have  $p' = 0.542(1 - 0.02778) + 0.6(0.02778) = 0.544$ .  $1 - 0.544$  will give us the frequency of the  $b$  allele, which equals **0.456**.

d. In order to determine whether or not to expect populations to diverge or become more similar we use  $2N_e m$ , where  $m$  is the migration rate. If this quantity is less than 1, this means effective population size is very small and/or migration rate is very low, and that drift will be a more powerful evolutionary factor than migration. In these cases we expect populations to diverge. If this quantity is greater than 1, this means effective population size is very large and/or migration rate is high, and that migration will be a more powerful evolutionary factor than drift. In these cases we expect the populations to become more similar. In our case  $2(360)(0.02778) = 20$ , so we expect these populations to become more similar. Eventually, we expect the island population to have identical allele frequencies as the mainland population:  $B = 0.6$  and  $b = 0.4$ .

e. For this question use the same formula you used above, but substitute 0.4 and 0.6 for 0.02778. The only thing that has changed in this question is the migration rate.

If  $m = 0.4$ ,  $B$  will = 0.565 and  $b$  will = 0.435 in the next generation.

If  $m = 0.6$ ,  $B$  will = 0.578 and  $b$  will = 0.422 in the next generation.

f. we calculate these the same as we calculated migration rate above in 5a.

if 20 water snakes migrate the migration rate will = 0.054

if 50 migrate, the migration rate will = 0.125

6. We use the same formula that we used in 3b to solve these problems.

a.  $N_e = 99$

b.  $N_e = 36$

**c.  $N_e = 100$**