Name:
Student Number:

EVOLUTIONARY MECHANISMS: Sea Otter Answer Key

1. As part of your graduate studies, you are studying a large, isolated population of sea otters (*Enhydra lutris*). Imagine that geneticists have identified two polymorphic, heritable traits in this population:
   - Fur colour is influenced by gene *C*: C^L is dominant over C^D, and produces light brown fur; C^D/C^D individuals have dark brownish-black fur.
   - Foraging behaviour appears to be associated with variation at a single locus (gene *B*): F^B/F^B individuals tend to spend more time foraging in the benthic zone (on the sea floor); F^S/F^S individuals tend to spend more time foraging in the intertidal zone (close to shore). Heterozygous individuals (F^B/F^S) appear to do a little of both.

   There are only two known alleles for each of these genes. The table on the left gives the number of individuals of reproductive age with for each genotype.

   a. Fill in the table on the right with the frequency of each genotype in the population:

Genotype	# Sea otters
C^L/C^L; F^B/F^B	56
C^L/C^L; F^B/F^S	12
C^L/C^L; F^S/F^S	57
C^L/C^D; F^B/F^B	113
C^L/C^D; F^B/F^S	25
C^L/C^D; F^S/F^S	112
C^D/C^D; F^B/F^B	56
C^D/C^D; F^B/F^S	13
C^D/C^D; F^S/F^S	56

Genotype	# Sea otters	Observed frequency
C^L/C^L	125	**0.25**
C^L/C^D	250	**0.5**
C^D/C^D	**125**	**0.25**
F^B/F^B	225	**0.45**
F^B/F^S	50	**0.1**
F^S/F^S	**225**	**0.45**

b. Fill in the table below with the frequency of each allele in the population.

Allele	#	Freq	Allele	#	Freq
C^L	500	0.5	F^B	**500**	**0.5**
C^D	**500**	**0.5**	F^S	**500**	**0.5**

c. Fill in the table below with the predicted frequency of each allele in the population, assuming the genes are in Hardy-Weinberg equilibrium.

Genotype	Predicted frequency	Genotype	Predicted frequency
C^L/C^L	**0.25**	F^B/F^B	**0.25**
C^L/C^D	**0.5**	F^B/F^S	**0.5**
C^D/C^D	**0.25**	F^S/F^S	**0.25**

2. **CLICK IN!** Is this population of otters in Hardy-Weinberg equilibrium with respect to:
   - **Gene *C*?** Please briefly explain your answer. **Yes – observed genotype frequencies match predicted genotype frequencies**
   - **Gene *F*?** Please briefly explain your answer. **No – observed genotype frequencies don't match predicted genotype frequencies (there are fewer heterozygotes than expected)**

Possible explanations for why allele frequencies for each gene are (or aren't) in equilibrium:

Gene *C*:
Possible explanation for why gene *C* is in equilibrium: The phenotypes influenced by gene *C* (colour) are neutral with respect to fitness in this particular environment. The population is isolated (no gene flow); mutation rates are likely low (long generation time); mating is random with respect to this locus/gene. The population is large enough (500 individuals) that sampling bias in terms of who survives and reproduces is relatively low (genetic drift is weak).

Gene *F*:
Possible explanation for why gene *F* is not in equilibrium: There are many more homozygotes than expected. Maybe phenotypes influenced by gene *F* result in assortative mating in this particular environment   (individuals tend to mate with other individuals who forage in the same area they do), but do not appear to affect fitness. Or maybe there is a fitness disadvantage to trying to forage in both the intertidal and benthic   zones (i.e., generalists have lower fitness than specialists). For the reasons listed above, gene flow, genetic   drift, and mutation arguably will not have much of an effect on the frequency of alleles for this gene.

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3. A population of bald eagles establishes itself in the area. Young sea otter pups are easy prey for adult eagles – <u>particularly if they have light brown fur</u>, which shows up more easily on the surface of the water. In one year, the sea otter population shrinks from 500 individuals to 90 due to predation by eagles.

   The table on the left gives the number of individuals in the population with each genotype, before the arrival of the bald eagles versus one year after the arrival of the bald eagles. The table on the right gives the frequency of each genotype after the eagle's arrival.

Genotype	# Sea otters	
	Before eagles	**After** eagles
$C^L/C^L; F^B/F^B$	56	6
$C^L/C^L; F^B/F^S$	12	4
$C^L/C^L; F^S/F^S$	57	5
$C^L/C^D; F^B/F^B$	113	5
$C^L/C^D; F^B/F^S$	25	4
$C^L/C^D; F^S/F^S$	112	7
$C^D/C^D; F^B/F^B$	56	20
$C^D/C^D; F^B/F^S$	13	14
$C^D/C^D; F^S/F^S$	56	25

	Genotype frequency	
	After eagles	
Genotype	# Sea otters	Observed	Predicted
C^L/C^L	15	0.17	**0.07**
C^L/C^D	16	0.18	**0.38**
C^D/C^D	59	0.65	**0.55**
F^B/F^B	31	0.34	**0.22**
F^B/F^S	22	0.25	**0.50**
F^S/F^S	37	0.41	**0.28**

Allele	#	Freq	Allele	#	Freq
C^L	46	**0.26**	F^B	84	**0.47**
C^D	134	**0.74**	F^S	96	**0.53**

   a. Please fill in the table above (lower right) with the frequency of each allele in the population.

4. **CLICK IN!** Following the arrival of the eagles, is the population of otters in Hardy-Weinberg equilibrium with respect to each gene? You can use the upper right hand table to record predicted genotype frequencies under Hardy-Weinberg equilibrium.
   ' **Gene *C*?** Please propose an explanation for why or why not.

Possible explanation for why gene *C* is not in equilibrium: The light fur phenotype was selected against (death of lighter fur pups changed the phenotype frequencies à genotype frequencies à allele frequencies). Remember that before the eagles, the frequency of C^L/C^L = 0.25, and the frequency of C^L/C^D = 0.50. Now *freq*. (C^L/C^L) = 0.17, and *freq*. (C^L/C^D) = 0.18. So, the frequency of individuals with lighter fur has decreased. We are told that C^L/C^L and C^L/C^D individuals have identical phenotypes (lighter brown fur), and that the eagles are more likely to prey upon this phenotype, so the fact that the frequency of C^L/C^D individuals has decreased more than the frequency of C^L/C^L individuals may just be due to chance (i.e., some unknown factor with an unpredictable effect). Either way, it appears that there was a slightly unpredictable/random component to the way in which allele frequencies have changed in this population.
Imagine that we didn't have the information about what the allele frequencies were like before the eagles; all we have are the current genotype frequencies. Calculating the predicted genotype frequencies (under H-W equilibrium assumptions) show us that the population is *not* in H-W equilibrium. We would see that there are fewer heterozygotes, and more homozygotes than predicted. What could we conclude? …Maybe non-random mating is occurring? Or maybe allele frequencies have changed because of an evolutionary mechanism (…maybe because of natural selection)?

One last point: notice that, even though the eagles find it easier to prey upon lighter brown fur pups, it looks like some of the dark brown-black fur pups were also lost. Even though the lighter fur pups are more visible, occasionally the eagles also preyed upon darker fur pups (and pups of either colour may have died due to other, non-eagle-related reasons). Lighter fur is selected against in this environment, but selection isn't a perfect filter. The stronger selection is (i.e., the more specific it is/the more discriminatory it is), the greater its effect on the population.

- **Gene *F*?** Please propose an explanation for why or why not.

Possible explanation for why gene *F* isn't in equilibrium: When the population decreased in size (down to about a fifth of the size it used to be) due to eagle predation, the number of F^B and F^S alleles also decreased in an unpredictable (random) way. Based on the predatory behaviour of the eagles (i.e., the fact that eagle are more likely to prey on C^L/C^L and C^L/C^D individuals), we had no way of predicting that the frequency of F^B alleles in the population would decrease slightly – gene *C* and gene *F* do not appear to be linked, and the eagles did not prey on particular otters based on genotype at the *F* locus. Therefore, this is considered to be a random change in allele frequencies. In other words, the population has evolved at the gene *F* locus due to genetic drift.

Note that, if the otter population stays at this relatively low size, or if it decreases in size even further, there's a good chance allele frequencies may continue to change in unpredictable ways (that included alleles that belong to other genes, as well as gene *F*). Or, if the otter population manages to recover, it could grow back up to ~500 individuals but would likely have lower frequencies of the F^B allele than it did before – this would be an example of a bottleneck effect.