

Name:

Student number:

**MID-TERM BIOL 434: October 2009**

Points

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Q1

Q2

Q3

Q4

Q5

Q6

Total      100

**Check that your copy of the test has all 7 pages.**

The following are UBC's rules governing formal examinations:

- 1) Each candidate must be prepared to produce, upon request, a Library/AMS card for identification.
- 2) Candidates are not permitted to ask questions of the invigilators, except in cases of supposed errors or ambiguities in examination questions.
- 3) No candidate shall be permitted to enter the examination room after the expiration of one-half hour from the scheduled starting time, or to leave during the first half hour of the examination.
- 4) Candidates suspected of any of the following, or similar, dishonest practices shall be immediately dismissed from the examination and shall be liable to disciplinary action.
  - a) Having at the place of writing any books, papers or memoranda, calculators, computers, audio or video cassette players or other memory aid devices, other than those authorized by the examiners.
  - b) Speaking or communicating with other candidates.
  - c) Purposely exposing written papers to the view of other candidates. The plea of accident or forgetfulness shall not be received.
- 5) Candidates must not destroy or mutilate any examination material; must hand in all examination papers; and must not take any examination material from the examination room without permission of the invigilator.

1. (8 points each) You are studying the evolution at a locus in a wild population. There are two alleles at this locus, which we will call  $B$  and  $b$ .  $BB$  individuals have a 20% chance of surviving to adulthood, for  $Bb$  individuals the probability of survival is 45%, and for  $bb$  the probability is 30%.

a. A large population starts with an allele frequency of 0.2  $B$  alleles. What is the allele frequency expected to be after one generation?

$$\begin{aligned}
 p' &= \frac{p^2 w_{11} + pq w_{12}}{\bar{w}} \\
 &= \frac{0.2^2(0.2) + 2(0.2)(0.8)(0.45)}{0.2^2(0.2) + 2(0.2)(0.8)(0.45) + 0.8^2(0.3)} \\
 &= 0.2326
 \end{aligned}$$

b. What would we expect the allele frequency to be after a very long time had passed, assuming that the strengths of selection stayed constant?

This is a case of overdominance. We can calculate the relative fitnesses of the three genotypes as 1-s:1:1-t by dividing each by the fitness of heterozygotes:

$1-s = \frac{0.2}{0.45}$ ;  $1-t = \frac{0.3}{0.45}$ , so  $s = 0.5555$  and  $t = 0.3333$ . Therefore at equilibrium, the

allele frequency should be  $\hat{p} = \frac{t}{s+t} = \frac{0.3333}{0.5555 + 0.3333} = 0.375$ .

2. (5 points each) *Drosophila melanogaster* and *D. simulans* share their most recent common ancestor 6 million years ago. Assume that these flies have about 5 generations per year, and that *D. melanogaster* has an effective population size of  $10^6$  and *D. simulans* has  $N_e = 10^5$ . We examine a stretch of DNA with 1000 base pairs, and each base pair has a mutation rate of  $10^{-9}$ .

a. On average, how many base pairs will differ between the two species out of these 1000 base pairs?

The two species have been separated for about 6,000,000 years at 5 generations/.year, or 30,000,000 generations. Substitutions in one species occur at a rate equal to the mutation rate for neutral mutations, or  $10^{-9}$  per base pair per generation. So each species will have  $10^{-9}$  substitutions per generation per base pair, times 30,000,000 generations times 1000 base pairs, or about 30 substitutions. Given that this process is occurring in both species, the two species will differ by about 60 base pairs.

b. What is the expected heterozygosity at equilibrium at any base pair in this sample, for *Drosophila melanogaster*?

$$H = \frac{4N\mu}{4N\mu + 1} (= 1 - \hat{F})$$

For neutral genes at equilibrium we expect

$$= \frac{4(10^6)10^{-9}}{4(10^6)10^{-9} + 1}$$

$$= 0.00398$$

c. If some of these mutations turn out to be deleterious, rather than neutral, would this cause the expected heterozygosity to increase, decrease or stay the same? Why?

If some mutation are deleterious, this would reduce the heterozygosity, because these deleterious mutations would be removed more rapidly by selection.

d. If some of the mutations turn out to be beneficial in one species but not the other, would this increase, decrease, or not change the expected number of differences between the two species? Why?

It would increase the number of expected differences between the species, because the substitution rates would be higher than expected for neutral alleles.

3. (4 points each) In each part below, there are two cases listed, and all other evolutionary parameters are assumed to be equal. Choose which of each pair would have the *higher* total genetic variance at equilibrium, and indicate your choice by circling the case with higher genetic variance.

a.	Positive frequency dependent selection	Negative frequency dependent selection
b.	Variance in reproductive success is 4.	Variance in reproductive success is 8.
c.	High migration rate	Low migration rate
d.	Equal sex ratio	Unequal sex ratio
e.	Fitnesses equal to $w_{BB} = 1$ ; $w_{Bb} = 1.5$ ; $w_{bb} = 1.2$	Fitnesses equal to $w_{BB} = 1$ ; $w_{Bb} = 0.75$ ; $w_{bb} = 1.2$

4. (6 points each) A population of cats has variance in reproductive success of 5, and the population size stays constant at 20 individuals. We examine one locus which initially has three alleles, present in 14, 18, and 8 copies. There are no selective differences between the alleles.

a. After four generations have passed, what is the expected heterozygosity of this population?

$$N_e = \frac{4N - 2}{V + 2} = \frac{4(20) - 2}{5 + 2} = 11.14$$

$$H_0 = 1 - \left( \left( \frac{14}{40} \right)^2 + \left( \frac{18}{40} \right)^2 + \left( \frac{8}{40} \right)^2 \right) = 0.635$$

$$H_t = \left( 1 - \frac{1}{2N} \right)^t H_0 = \left( 1 - \frac{1}{2(11.14)} \right)^4 (0.635) = 0.5284$$

b. What is the probability of fixation for each of the three alleles?

The probability of fixation of each allele is its starting frequency, because these alleles are neutral. Therefore the probability of fixation of the three alleles are 0.35, 0.45, and 0.2, respectively.

c. Assume that the variance in reproductive success were doubled. How would this affect the probability of fixation of each allele, and how would it affect the expected time to fixation?

The probability of fixation would not be changed, and the time to fixation would be lower, because the effective population size would be less.

d. Assume that the variance in reproductive success were doubled. How would this affect the expected time until one allele reaches fixation? (A qualitative answer is sufficient.)

The effective size would be lower, so the time to fixation would be faster.

5. (15 points) Two populations of fish are being followed at two genetic loci, which we will call  $A$  and  $C$ . The first population is fixed for the genotype  $AAcc$ . The second population is fixed for the  $a$  allele and has 80%  $C$  alleles. The recombination rate between  $A$  and  $C$  loci is 0.2.

Large and equal samples of both populations are artificially mixed to create a new lab population of this fish species. After two generations of random mating in the lab, what is the genotype frequency of  $AACC$  expected to be, assuming no selection?

The initial allele frequency for the two loci is  $p_A = 0.5$  and  $p_C = 0.4$ . The initial frequency of the  $AC$  haplotype is 0. Therefore we can find the initial linkage disequilibrium  $D$  from

$$P_{AC} = p_A p_C + D$$

$$0 = 0.5(0.4) + D$$

$$D = -0.2$$

After two generations of random mating,  $D'' = (1 - r)^t D = (1 - 0.2)^2 (-0.2) = -0.128$ .

Because the alleles are neutral, the allele frequencies will not be changing, and the gamete frequencies will be

$$P_{AC} = p_A p_C + D = (0.5)(0.4) - 0.128 = 0.072$$

$AACC$  individuals are made by pairing two  $AC$  gametes, which will occur with random mating at frequency  $(0.072)^2 = 0.0052$ .

6. (5 points) A deleterious allele is completely recessive. Homozygotes for this allele reduce fitness by 20%. Give the marginal fitness for this allele and the wild type allele when the deleterious allele is at frequency 1% and when the allele is at frequency 50%. Use these calculations to predict which case would show more effective selection against the allele.

For the allele at frequency 0.01,  $w_{\text{deleterious}} = 0.01 (0.8) + 0.99 (1) = 0.998$ , and  $w_{\text{wildtype}} = 1$ .

For the allele at frequency 0.5,  $w_{\text{deleterious}} = 0.5 (0.8) + 0.5 (1) = 0.9$ , and  $w_{\text{wildtype}} = 1$ .

The difference in the fitness of the two alleles is only 0.002 when the allele is rarer, but 0.1 when they are at equal frequency. Therefore the recessive allele will have more effective selection against it when it is more common.