# PRACTICE MIDTERM #3 - BIOL 121 Midterm 2 – Evolution – ANSWER GUIDE

Please note, the purpose of the answer guide is to help you understand the logic of the answers as well as providing some of the points we were looking for when grading. For the specific grade breakdown, please see the rubric in Gradescope.

## QUESTION 1. (9 Marks Total)

Grey squirrels were introduced to Stanley Park in 1909 when a small number of squirrels from Eastern Canada were released into the park. Grey squirrels have since become common throughout Vancouver. Squirrels eat seeds, fruits, insects and scavenge from human trash. Squirrels are preyed upon by coyotes, birds, domestic animals and humans. In cities, cars are the major cause of mortality.

Coat coloration is determined by a single gene with two alleles that are incompletely dominant: grey = $C^G C^G$, black = $C^B C^B$ and brown-black = $C^G C^B$.

| Allele | Initial Frequency in Vancouver | Current Frequency in Vancouver |
|---|---|---|
| $C^G$ | 0.7 | 0.370 |
| $C^B$ | 0.3 | 0.630 |

a. You used historical records to estimate allele frequencies in the initial population in Stanley Park. Would you expect the allele frequencies in the initial population in Stanley Park to be the same as the original population from Eastern Canada? Briefly explain your reasoning with specific reference to evolutionary mechanisms. (**3 marks**)

For this question you should have taken note of the idea that a small number of squirrels from Eastern Canada were introduced to Stanley Park in 1909. Squirrels have since become common throughout Vancouver

Given that the population in Stanley Park/Vancouver was founded by a small number of individuals from Eastern Canada, you should consider the role of genetic drift due to the founder effect as the initial evolutionary force affecting the allele frequency in the population in Stanley Park. It is reasonable to expect the allele frequencies in Stanley Park to be different from the frequencies in the Eastern Canada population due to the effect of genetic drift.

The answer should correctly identify the role of genetic drift due to the founder effect and discuss the role of sampling in altering allele frequencies in the Stanley Park population relative to the Eastern Canada Population.

b. Squirrels with black coats are most abundant in cities; squirrels with grey coats are more abundant in forests (Gibbs et al.). Black squirrels are more easily recognized by humans and stand out against the grey asphalt of roads in comparison to the grey squirrels. In cities, the frequency of black squirrels killed by cars is about 10 times lower than grey squirrels. Could natural selection be the cause for the increase in frequency of the black allele in the Vancouver population? List the criteria and provide an explanation for each. (**6 marks**)

For this question you should be listing the requirements for selection as outlined in class and clearly describe how they are met or not.

| Requirement for Selection | Explanation |
| --- | --- |
| **Variation in the population** | **There is variation in coat color in the population, squirrels have black, grey or brown-black coats** |
| **Variation is heritable** | **Coat color is determined by a single gene with two alleles ($C^B$ and $C^G$) – can indicate that the alleles are co- or incompletely dominant** |
| **Variants differ in fitness** | **For this part there needs to be clear logical connections between coat color and fitness.** <br><br> **Black individuals are more visible to drivers (humans) and have reduced mortality due to car accidents _relative_ to the grey morphs. More black individuals would be expected to survive to reproduce therefore have higher fitness.** |

## QUESTION 2. (8 Marks Total)

a) What are two characteristics in living organisms that appear to be homologies that support the conclusion that all living organisms shared a common ancestor? (**2 marks**)

The key to this question is thinking about characteristics that were inherited by ALL living organisms from a common ancestor. Basically, you need to list characteristics that are present in all living organisms (e.g. made of one or more cells, DNA as genetic material, universal genetic code, same 20 amino acids)

The question asks for two characteristics. Therefore, it is not acceptable to list general classes of evidence that organisms are related (e.g. genetic homology).

As well, it is important to make sure that the traits listed are not specific only to certain groups of organisms (e.g. meiosis, mitosis are specific to eukaryotes); developmental homologies are specific to animals and are not relevant for unicellular life (so not evidence that all living organisms share a common ancestor)

b) List two vestigial traits discussed in class. (**1 mark**)

Review the class sides or text for examples of vestigial characters. In some cases, a lack of specificity was a problem (e.g. not indicating the organism that the vestigial trait was found in) or incomplete / incorrect description of the vestigial trait (e.g. feathers in kiwis – the

characteristic of feathers is not vestigial, the reduced wings in flightless birds are vestigial traits).

c) Explain how vestigial traits are evidence supporting the conclusion that organisms have changed through time. (**2 marks**)

To start this question, you should begin by thinking about the definition of a vestigial trait. "*"a reduced or incompletely developed structure that has no function or reduced function but is clearly similar to functioning organs or structures in closely related species"* the definition itself does not answer the question asked however it is a starting point for formulating an answer.
  1) If the vestigial trait is clearly similar to functioning organs or structures in closely related (extant) species then it suggests that the functional trait was present in the common ancestor of species that possess the trait as well as organisms with the vestigial trait.
  2) If the ancestor of species with the functional trait and the vestigial trait possessed the functional trait then the trait must have been reduced or become non-functional through time.
  3) If a trait has changed from a functional form to a non-functional or reduced form, species have changed through time.

d) For each of the statements in the table below, indicate the type of evidence that it is an example of and the conclusion that it supports. Fill in the circle beside the answer you choose.(**3 marks**)

| | Is an example of : | Supports the Conclusion that: |
|---|---|---|
| The flagella in eukaryotes (that have flagella) have a common 9+2 arrangement of microtubule bundles. | o Developmental Homology<br>o Extinction<br>o Genetic Homology<br>o Geographical Relationships<br>o Structural Homology<br>o Transitional Forms<br>o Vestigial Traits<br>o An analogous character | o Organisms are related<br>o Organisms have changed through time<br>o Neither |

| | Is an example of : | Supports the Conclusion that: |
|---|---|---|
| Silverswords are a group of plants containing ~30 species in three genera (*Agryroxiphium*, *Dubautia* and *Wilkesia*) that are only found on islands in the archipelago of Hawai'i. | o   Developmental Homology<br>o   Extinction<br>o   Genetic Homology<br>o   <mark>Geographical Relationships</mark><br>o   Structural Homology<br>o   Transitional Forms<br>o   Vestigial Traits<br>o   An analogous character | o   <mark>Organisms are related</mark><br>o   Organisms have changed through time<br>o   Neither |
| Both bacteria and eukaryotic cells have flagella that are used for swimming. The eukaryotic flagella are all composed filaments of proteins called tubulin and are surrounded by the cell's plasma membrane. Bacterial flagella are formed from different proteins and not surrounded by the cell's plasma membrane. | o   Developmental Homology<br>o   Extinction<br>o   Genetic Homology<br>o   Geographical Relationships<br>o   Structural Homology<br>o   Transitional Forms<br>o   Vestigial Traits<br>o   <mark>An analogous character</mark> | o   Organisms are related<br>o   Organisms have changed through time<br>o   <mark>Neither</mark><br>o |

## QUESTION 3. (11.5 Marks Total)

Millipedes are small, slow-moving animals that eat dead leaves Figure 1. Millipedes are eaten by rodents that feed at night (nocturnal predators). Millipedes produce cyanide to deter predators. To signal their toxicity to nocturnal predators, some millipedes are bioluminescent (they glow at night). Brightness of bioluminescence can vary within a population from faint to bright. The millipedes are blind and cannot see this light, but the light is visible to nocturnal predators.

Bioluminescence has a genetic basis. Imagine a simple system where the brightest of the glow is determined by one gene with two alleles G1 and G2.   Millipedes that are homozygous for the G1 allele glow faintly. Millipedes that are homozygous for the G2 allele glow brightly. Millipedes that are heterozygous have a mid-level of brightness.

In an **isolated** millipede population of 200 individuals, 18 millipedes glow faintly, 140 millipedes glow brightly, and 42 millipedes glow at a mid-level of brightness.
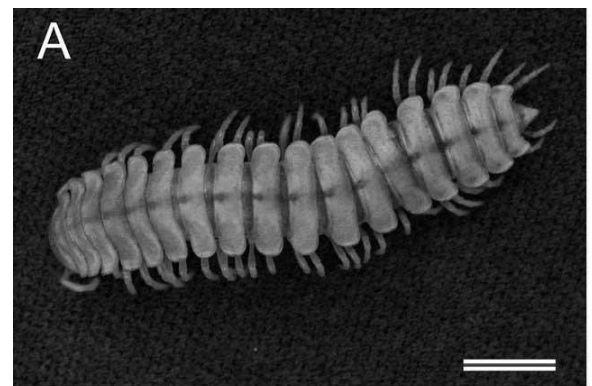


Figure 1. Millipede image from Marek and Moore 2015

| Genotype | Phenotype | # individuals | observed genotype frequencies | expected genotype frequencies |
|----------|-----------|---------------|-------------------------------|-------------------------------|
| G1G1 | Low glow | 18 | 0.09 | 0.04 |
| G1G2 | Mid-level glow | 42 | 0.21 | 0.32 |
| G2G2 | Bright glow | 140 | 0.70 | 0.64 |

a. What are the observed genotype frequencies for the genotypes in this millipede population? Answer to 2 decimal places. Please show your work and enter your answer in the table provided. (**2 marks**)


to calculate the observed frequencies of the genotypes divide the number of individuals with a specific genotype by the total number of individuals

for example the frequency of G1G1 = 18/(18+42+140)


b. What are the allele frequencies for the G1 and G2 alleles in this millipede population? Answer to 2 decimal places. (**2 marks**)


Recall there are two ways to think about this calculation, counting individuals or counting alleles.

If we count individuals we count the heterozygotes as ½. If we count alleles we need to double the number of individuals to determine the total number of alleles

Counting individuals – the frequency of the G1 allele is p

p = (18+42/2)/(18+42+140) = 0.195    p=0.20 after rounding

counting alleles – the frequency of the G1 allele is p

p = (18*2+42)/((18+42+140)*2) = 0.195 p=0.20 after rounding


c. What are the expected genotype frequencies for the genotypes in this millipede population? Answer to 2 decimal places. Please show your work and enter your answer in the table provided. (**2 marks**)

expected genotype frequencies

G1G1 = p^2 = 0.195^2 = 0.038 rounded to 0.04 (note that the un-rounded values of p and q should be used here) when grading, I accepted answers that used the rounded values of p and q in calculations, however, credit was not given if calculations using rounded or un-rounded values were not performed consistently

G1G2 = 2pq

G2G2 = q^2

d.  Is this isolated millipede population in Hardy-Weinberg Equilibrium for the G gene? Yes or no. Please circle your choice below. (**0.5 marks**)

<div align="center">

**Yes**          **No**

</div>

e.  Briefly explain your answer to 4d above, referring to specific genotypes. Do not refer to assumptions for this question. (**1.5 marks**)

In this question, you need to compare the observed genotype frequencies to the expected frequencies. As I outlined in the answer guide for the group exam, if values differ by more than 0.01 then they should be considered different enough that the population is not in equilibrium.

As in the answer guide for the group midterm, your answer should refer to specific observed and expected values for the genotypes. The purpose of having you do this is to practice supporting an argument (the population is not in equilibrium) with use of specific data from observations and calculations.

f. Given your answers to parts d and e, choose one evolutionary mechanism that could be responsible for the observed versus the expected genotype frequencies. Clearly state the hypothesis, then evidence, and reasoning to explain why the population is or is not in Hardy-Weinberg (**3.5 marks**)

Given that the population is not in equilibrium, you need to choose an evolutionary mechanism that could affect this population. Given the scenario, gene flow is not a reasonable mechanism since the population is isolated. Mutation, as discussed in class can generate new alleles but has a negligible effect of altering allele frequencies.

For your answer you should consider one of: natural selection, genetic drift or non-random mating and provide a reasonable explanation as to how this evolutionary force could alter allele frequencies in the population.

## QUESTION 4. (10 Marks Total)

Many species of toads deter predators by producing toxins that can cause heart failure in predators if the toads are eaten. Some snakes and lizards have evolved a resistance to the toad's toxin. The phylogeny shown in the figure above shows the evolution of toxin resistance in some reptiles. Nodes are labelled with numbers (1-15). The ancestor to the snakes and lizards on this tree was not resistant to toad toxins. **In this system there have been both gains of resistance and losses of resistance to the toxin**.
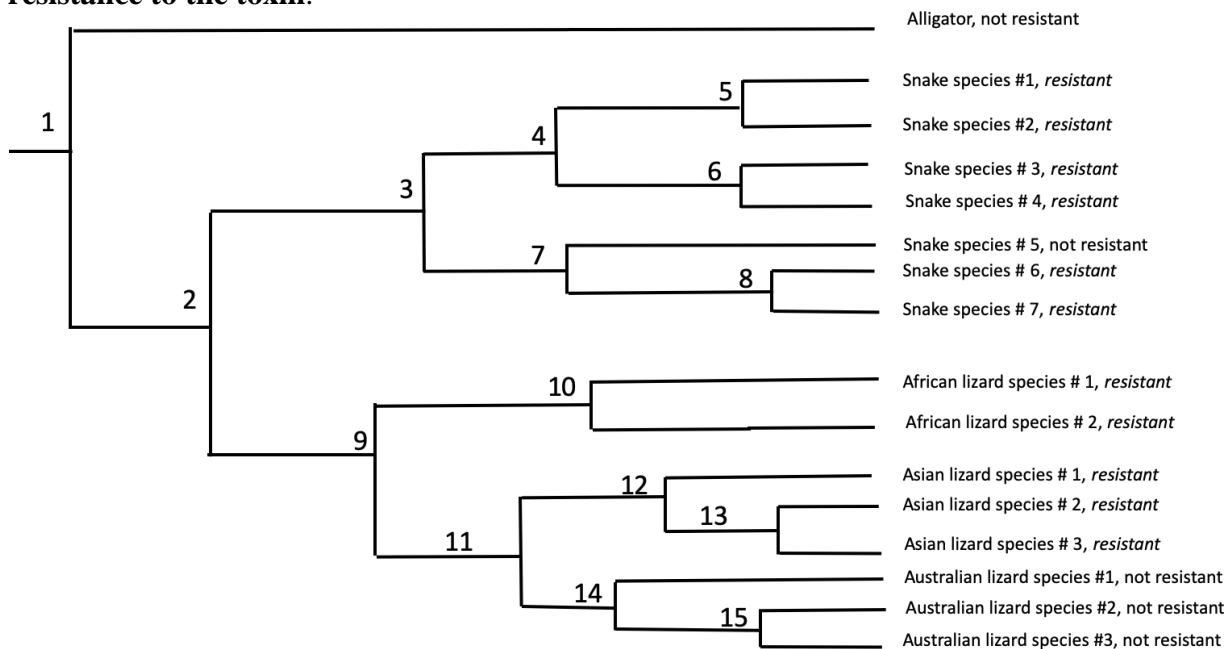


For parts a and b there are multiple combinations of gains and losses that are possible. Note that in the stem of the question, it is indicated that the ancestor of snakes a lizards (#2) was "not resistant" . Since Alligators are not resistant, and #2 (the descendant of #1) is "not resistant" then #1 is likely not resistant.

The combination of gains and losses needs to be internally consistent. For example if a gain was inferred between 2 and 3, then it is reasonable to indicate a loss between 7 and snake species #5. However, if a gain was inferred between 3 and 4 and 7 and 8, it is not reasonable to infer a loss between 7 and snake species 5 since there was no trait to lose.

The gains and losses occur along the branches not at the nodes.

a)  Using the principle of parsimony (the smallest number of changes possible), how many times has toad toxin resistance been gained in this phylogeny? Indicate on the phylogeny with a "G" for gain. (**2 marks**)

b)  Using the principle of parsimony (the smallest number of changes possible), how many times has toad toxin resistance been lost based on this phylogeny? Use the letter "X" on the branch to indicate where resistance to toad toxin was lost. (**2 marks**)

c)  Is the presence of resistance to toad toxin in both snake species #1 and African lizard species #1 an example of a homology or an analogy (homoplasy)? Explain your reasoning with specific reference to the tree. You answer should show your understanding of both homologies and analogies (homoplasies). (**3 marks**)

The answer to this question depends on the specific combination of gains and losses that you have inferred in the tree. For full marks, you will need to make specific reference to where characters evolved and which ancestors possessed the trait.

**d)**  Which extant taxon/taxa is/are most closely related to snake species #5? (**1 mark**)

*Snake species #6 and #7  (original answer of species #3, Snake species #2 is incorrect)#*

**e)** Are snakes a monophyletic group based on this phylogeny? Explain why or why not with specific reference to the tree. (**2 marks)**

To answer this question, you should refer to your definition of a monophyletic group. A monophyletic group contains an ancestor and all of its descendants.

Depending on the reasoning you provided, either monophyletic or non-monophyletic could be acceptable. See the rubric in gradescope for details.