UNIVERSITY OF BRITISH COLUMBIA

Midterm 2, November 3rd, 2022

BIOL 121-121 ANSWER GUIDE

QUESTION1 (8 marks) – EVIDENCE FOR EVOLUTION

1A (2 marks) List two characteristics of living organisms that are interpreted as evidence that all living organisms share a common ancestor? (2 mark)

Examples of acceptable answers:
a) DNA as genetic material
b) All organisms made of cells
c) Common information flow DNA-RNA-protein
d) Near universality of Genetic code

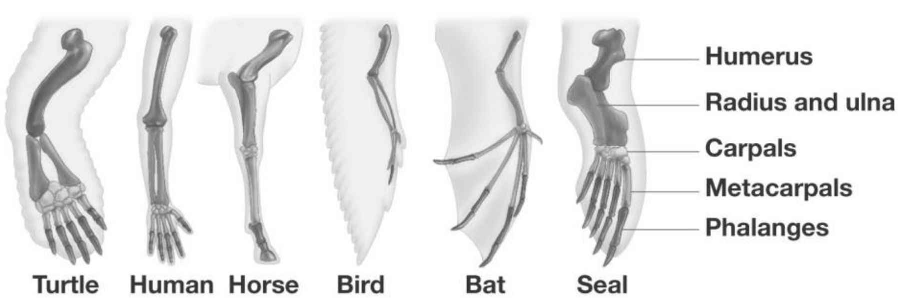
1B (2 marks) Kiwi wings

The wings and eyes are an example of a ______Vestigial______trait. (1 mark)

Their wings and eyes support the conclusion that (circle your choice): (1 mark)

a) All living organisms share a common ancestor
b) Organisms are related
c) Organisms have changed through time
d) All of the above
e) None of the above.

The figures below show the bones that make up the limbs of various vertebrates (Fig. 1) and the evolutionary relationships between these taxa (Fig. 2).



1C (1 mark) Based on Figure 1 (above) and Figure 2 (next page), the presence of a humerus in the forelimbs of turtles, seals and humans is an example of a:

a. Structural homology
b. Developmental homology
c. Transitional form
d. Analogous trait
e. A, B, C & D (all of these are correct)
f. None of these are correct

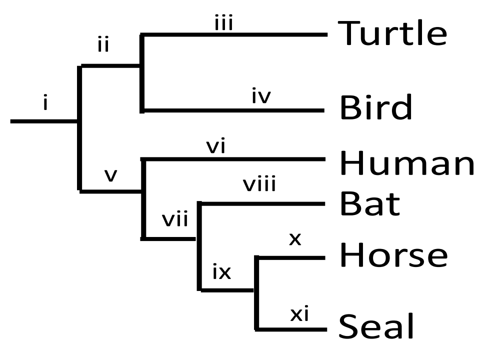


Figure 2. Phylogenetic relationships among six tetrapods (animals with four limbs). Branches are labelled with Roman numerals.

Answer the next 3 questions (1C-1E) using Figure 2 (above) and the principle of parsimony:

1D (1 mark) In the space below write the branch number(s) where the humerus most likely evolved.

branch I (note – all 6 taxa have a humerus)

1E (1 mark) Bats and birds both have wings that are used for flight. The common ancestor of bats and birds most likely (circle your choice)

a) Had wings
b) Lacked wings
c) Had vestigial wings
d) Not possible to determine

1F (1 mark) In the space below, write the branch number(s) where wing(s) likely evolved (were gained).

branch iv and viii

QUESTION 2 (4 marks total)
Obtaining elephant tusks for ivory requires killing the elephant. The illegal hunting of African elephants for ivory has reduced their populations. In areas where illegal hunting is common, the frequency of tusklessness (= lacking tusks) in female African elephants has increased, from 19% to 51% over a period of 15 years. The genetic basis for tusklessness is found on the X chromosome. Note – tuskless males do not occur because this mutation in lethal in males.

2A (1 mark) The mutation resulting in tusklessness occurred because of:

a. Illegal hunting, so female elephants could avoid being killed for their ivory
b. A chance change in the DNA on the X-chromosome
c. Female elephants required an adaptive mutation to improve their fitness
d. Impossible to choose between the provided answers.

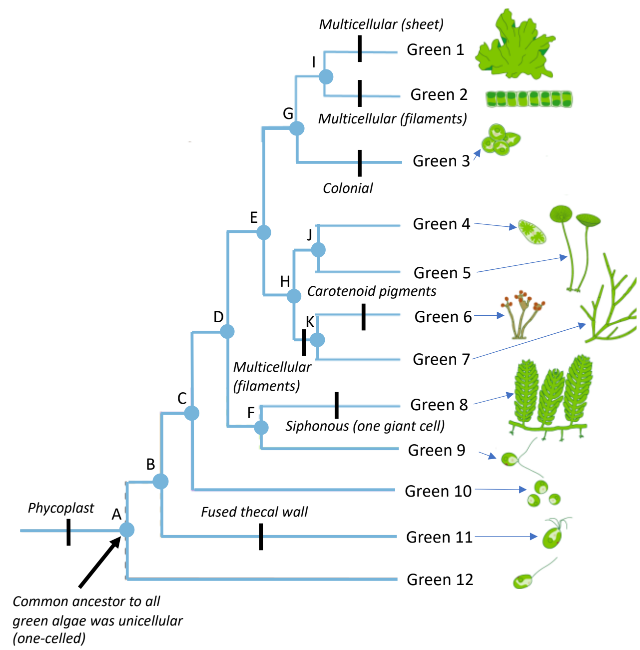
2B (1 mark) Elephants normally use their tusks for a variety of tasks such as defense, stripping bark from trees to eat, and digging for water during dry periods. The loss of tusks in female elephants in areas with illegal hunting is most likely due to:

a. Tusks being lost because they are no longer useful in the current environment.
b. Tuskless females outcompeting tusked males for food and water, therefore passing on the tuskless allele to more offspring.
c. Consistent increase in the frequency of the tuskless mutation due to genetic drift.
d. Females without tusks having an increased chance of survival and therefore passing on the tuskless mutation to more offspring
e. A high mutation rate generating new individuals with the tusklessness allele in the population.

2C (2 marks) If a nearby African elephant population initially lacks the tuskless allele, what evolutionary mechanism would be most likely to result in the tuskless trait occurring in this population? Briefly (in one sentence) describe how this could occur?

Gene flow
Female elephants carrying the tuskless allele moved to this population
Mated with members of the local population

QUESTION 3 (9 marks total) To the right is a figure of the phylogeny of the Chlorophyta, a group of green algae. Capital letters (A, B, C, etc.) refer to nodes and vertical lines indicate when a trait first evolved.



A) (3 marks) Fill in the blanks below.

Section 121-121

___Node B_____ represents the most recent common ancestor of **Green 1** and **Green 11**.

____Node E____ represents the most recent common ancestor of **Green 3** and **Green 4**.

____Green 1 & 2____ represents the closest living relative(s) of **Green 3**. (All or none)

B) (3 marks) Based on the phylogeny above, which of the following groups are monophyletic? Fill in the chart below with an X indicating whether the suggested groups are monophyletic or not.

Groups	Monophyletic	Not monophyletic	Can't Tell
Greens 7 and 8, plus node D		X	
Greens 4, 5, 6, 7, plus nodes J, K, H	X		
Greens 1, 2, 3, plus nodes I, G, E		X	

C) (1 mark) You discover a new type of green algae ("Green 13") that DNA sequencing suggests is most closely related to **Green 3**. According to the principle of parsimony, **list the traits** you expect "Green 13" to have in the space below.

Phycoplast, either Unicellular or Colonial

D) (2 marks) Which type of algae, **Green 11** or **Green 12**, is more evolved? Briefly explain your answer and make specific reference to the tree above.

- they are equally evolved
- both species have been continuing to experience evolution / continue to evolve
- since they diverged from the common ancestor at node A.

QUESTION 4. (14 marks total)

The northern leopard frog (*Rana pipiens*) exhibit three genetically-based skin phenotypes (color, spots, and mottling).

In the 1970s, biologists determined the allele frequencies for spots in a small, isolated population (= 120 individuals). In 2000, biologists returned to this population and re-calculated allele frequencies for spots. The population size of the frogs did not change.

(Spots = T gene, T1 allele = spots, T2 allele = no spots)

Skin phenotype (gene)	Allele frequencies (1970)	Allele frequencies (2000)
Spots (*T* gene)	0.4 : 0.6 (*T1* : *T2*)	0.6 : 0.4 (*T1* : *T2*)

4A) (2.5 marks) Explain how genetic drift could explain the change in allele frequencies for skin spots/skin colour for this specific northern leopard frog population. Provide evidence and reasoning.

For full marks student must demonstrate an understanding that genetic drift can occur with no change in population size due to chance/random events

Marks for details specific to scenario

- Acceptable mechanism (e.g. differences in mating opportunities, cannot invoke bottleneck event as there was no change in population size)

- Linked to specific alleles (T1/T2 alleles)

  - e.g. Individuals carrying the T1 allele had more mating opportunities than individuals carrying the T2 allele.

- Change in allele frequencies
  - e.g. resulted in an increase in the T1 allele and a decrease in the T2 allele from 0.4 to 0.6 and from 0.6 to 0.4
  - must be quantified

- Connection to small population size
  - small population
  - quantified – 120 frogs

- Acceptable if students refer to gametes instead of individuals. For example, it could be random which gametes (or individuals) make the next individuals, in this case individuals with T1 allele randomly occurring more

In 2000, the researchers also collected observational data on skin colour in the leopard frogs. Skin colour in frogs is controlled by a single gene (R gene) and two alleles (R1 and R2 allele).

Frogs with two copies of the R1 allele have green skin. Frogs with two copies of the R2 allele have brown skin. Frogs that are heterozygotes have patches of brown and green skin.

The table below shows the data collected by the researchers.

Table 1: Data from study population of frog skin colour				
Phenotype	Genotype	# of observed frogs	Observed genotype frequencies	Expected genotype frequencies
Green Skin	*R1/R1*	18	0.150	0.303
Patches of Green and Brown Skin	*R1/R2*	96	0.800	0.495
Brown Skin	*R2/R2*	6	0.050	0.203

4B (2 marks) What are the frequencies of the R1 and R2 alleles in this population? Please show your work and retain 3 decimal places.

R1 frequency = 0.550
Work: (18+18+96)/(120*2) = 0.55 <u>OR</u> *T1*=(18+0.5*96)/(120) = 0.55. Other approaches acceptable

R2 frequency = 0.450
Work: 1-0.55 = 0.450 (okay if students do not use p + q = 1 equation)

must report to 3 decimal places; okay if last digit is different by +/0.001

4C (2 marks) Using the Hardy-Weinberg Equation, calculate the **expected frequency for the two missing genotypes.** Show your calculations and write the expected frequencies in the blank spaces in the table above. Retain 3 decimal places.

R1/R1 genotype:	Heterozygotes
p2 = 0.55*0.55 = 0.303	2pq = 2*0.55*0.45=0.495

must report to 3 decimal places.

4D (2.5 marks) Is this population in Hardy-Weinberg Equilibrium (HWE) with respect to genotype frequencies?

Circle one answer: Yes **No** We need more information

Explain your answer, referring to specific genotypes. There is no need to refer to assumptions of HWE.

- compared expected and observed genotypes frequencies of each genotype (or at least one homozygous genotype and one heterozygous genotype) – values not simply listed.

- genotype frequencies had to be quantified for full marks.

- had to be clear that more heterozygotes were observed than expected and fewer homozygotes were observed than expected.

- explain that there is a greater than 0.10 difference between the exp. & obs. genotype frequencies.

4E) (5 marks) Research suggests that visual predators may have more difficulty detecting frogs with more than one skin colour (e.g. green and brown) = 121-121 or spot pattern (121-124)....because the patches (or spots) break up the outline of the frog making it more difficult to see the frogs, which could potentially give heterozygotes a selective advantage.

Given this information, can you conclude with certainty that the difference between observed and expected values for this leopard frog population could be due to natural selection? Circle one answer:

Yes / **No**

Explain why or why not with specific reference to each of the three criteria required for selection.

Criterion for selection	Explanation
Skin colour is heritable	- must refer to specific gene (R gene) for full marks
Skin colour is a variable trait	- must describe the variation that exists in skin colour (green, brown, and green/brown)
There are differences in fitness associated with differences in skin colour	For students who answered "no" - marks for their claim (no) - marks for stating that although it has been suggested that frogs with green/brown skin are less visible to predators compared to frogs with brown skin or green skin there is no evidence that frogs with patchy skin colour have a higher fitness (i.e. higher reproductive success/more offspring) than frogs that are green or brown - optional - there are other explanations for differences for why patchy frogs were observed more frequently than expected (e.g. genetic drift, non-random mating)

	- for full marks, must demonstrate understanding of fitness (i.e. relative reproductive success) and refer to all three skin phenotypes. For students that answered yes, they can receive up to 1 mark for: - pointing out that there is some suggestion that frogs with patchy green/brown skin are less visible to predators compared to frogs with just one skin colour (green or brown). - refer to differences in frequencies (quantified) of the different phenotypes. - explanation must demonstrate an understanding of differences in fitness (i.e. differences in relative reproductive success of the frogs).

Bonus: 1 mark