

**© Biology 121, UNIVERSITY OF BRITISH COLUMBIA.**  
**Practice Midterm**  
**Midterm 2, March 2020**

**Name :** \_\_\_\_\_  
 \_\_\_\_\_  
 FAMILY NAME FIRST NAME

**Student Number :** \_\_\_\_\_

### Instructions:

1. Answer all questions in the space provided. The back of the exam will not be marked unless it is an exact replacement for material that is crossed out.
2. Writing can be in pencil or ink, but pencil or erasable ink answers **cannot** be remarked.
3. Answers may be in sentences or point form. Illustrations are acceptable but must be annotated.
4. Students suspected of any of dishonest practices will be immediately dismissed from the examination and will be subject to disciplinary action.
5. Other than a **one page** study sheet based on the provided template and a **non-programmable calculator**, no other memory devices are permitted.
6. Students may not speak or in any other way communicate with other students while in the examination room.
7. Students may not expose their written paper to other students. The excuse of accidental exposure, forgetfulness, or ignorance will not be accepted.
8. Make sure you have **6** written pages (3 pieces of paper) including this cover page.

**I have read and fully understand these instructions.**

**Student signature** \_\_\_\_\_

**Mark allocation:**

| Question    | Marks possible | Your mark |
|-------------|----------------|-----------|
| 1.          | 10             |           |
| 2.          | 11             |           |
| 3.          | 11             |           |
| 4.          | 13             |           |
| Concept Map | 1              |           |
| Total       | 46             |           |

1) You are a scientist studying populations of field mice and effects of predation on the mice by hawks. These mice have a single gene that controls fur colour. Mice with the F allele have light brown fur, but mice with the f allele have black fur. F is dominant to f. In your study, there are two populations of mice, one that lives in a field with short, sparse grass; and another population that lives in a separate field with abundant tall grass. The population in the field with abundant tall grass is in Hardy-Weinberg equilibrium (**10 marks total**).

Data from mice in the field with short, sparse grass. Data from mice in field with abundant tall grass not shown.

| Genotype | Observed | Observed frequencies | Predicted frequencies |
|----------|----------|----------------------|-----------------------|
| FF       | 55       | 0.385                |                       |
| Ff       | 85       | 0.594                |                       |
| ff       | 3        | 0.021                |                       |

a) What are the respective frequencies of the 'F' and 'f' alleles in the population of mice found in the field with short sparse grass? Show your calculations for full credit, and show your answers to at least two decimal places. (**2 marks**)

$$\text{frequency of F} = p = (55+85/2)/(55+85+3) = 0.682$$

$$\text{frequency of f} = q = (3+85/2)/(55+85+3) = 0.318$$

b) Based on the data you collected, is the population of mice found in the open field with short sparse grass in Hardy-Weinberg equilibrium? Show your work and briefly justify your answer. (**4 marks**)

$$\text{Expected frequency of FF} = 0.682^2 = 0.465 \quad (\text{observed} = 0.385)$$

$$\text{Expected frequency of Ff} = 2 \times 0.682 \times 0.318 = 0.434 \quad (\text{observed} = 0.594)$$

$$\text{Expected frequency of ff} = 0.318^2 = 0.101 \quad (\text{observed} = 0.021)$$

The population is not in HW equilibrium.

The observed GENOTYPE frequencies don't match the expected.

The frequency of the ff genotype is much less than expected; frequency of Ff higher than expected; frequency of FF lower than expected.

c) Based on specific information given in the question, provide brief reasoning that supports your answer to 'part b'. With specific reference to the scenario and possible evolutionary mechanisms, provide an explanation for why the population of mice found in the field with short, sparse grass is, or is not in Hardy-Weinberg equilibrium. (**4 marks**)

This is likely due to Natural Selection.

In the open field, the darker mice (ff) stand out against the soil versus the light brown mice.

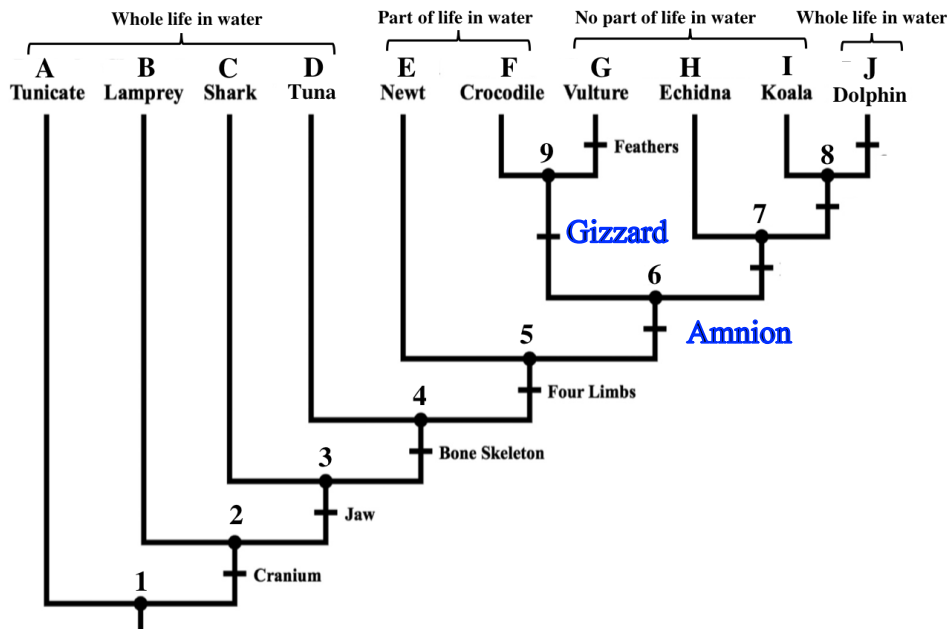
Darker mice face higher predation pressure as they are more likely to be seen by predators, such as hawks, and are not surviving to reproduction. This could change the GENOTYPE frequencies in the population.

OR

Darker mice face higher predation pressure as they are more likely to be seen by predators and are not surviving to reproduction in the open field, there are fewer ff (black) than expected.

Could get full or partial marks for Gene Flow or Genetic Drift if explained correctly and related to scenario (e.g. gene flow from the other field).

- 2) The figure below is a simplified phylogeny of the Chordates, a group of animals belonging to phylum Chordata that includes mammals, reptiles, fishes, tunicates (sea squirts) and more. Numbers refer to nodes, letters refer to taxa and lines indicate when a trait first evolved. (11 marks total)



- a) The table below lists a selection of traits found in some Chordates. An “X” tells you whether a species has a trait. On the phylogeny, label where the gizzard and amnion evolved, applying the principle of parsimony. (2 marks)

The labels must be on the vertical branches between the nodes. We already supplied the short horizontal hash-marks where they should be labelled.

- b) Fill in the blanks below.

Node 6 represents the most recent common ancestor of the **echidna** and **crocodile**. (0.5 marks)

Node 2 represents the most recent common ancestor of the **lamprey** and the **tuna**. (0.5 marks)

- c) Draw a circle around one monophyletic group (clade) on the phylogenetic tree.

Explain how you can tell it is monophyletic. (2 marks)

Need a circle around a clade. Explanation: A node/ancestor and all of its descendants. Other answers are possible.

Any example that includes an ancestor, and all possible descendants, could be one branch, a number, or the entire tree.

- d) According to the phylogenetic tree, did **koalas** and **dolphins** evolve from **echidnas**? Explain your answer. (2 marks)

No.

Acceptable examples (there are others):

The echidna is an extant species and is not the same species as the ancestor to echidnas, river dolphins, koalas.

OR Echidnas are currently living and have therefore experienced the same passage of time as the koala and river dolphin lineages.

OR Just because the echidna lineage doesn't have any nodes doesn't mean this species hasn't experienced evolution [changed] since the time of the common ancestor to echidnas, koalas and river dolphins

(not enough to say they have a common ancestor)

e) According to the phylogenetic tree, which of these two taxa is more closely-related to the **shark**?

Lamprey / **Koala** / Equally Related (circle one).

Explain your answer below, making reference to **specific nodes** on the phylogenetic tree. (2 marks)

Sharks and koalas share a more recent common ancestor (node 3) than shark does with lamprey (node 2).  
(must include reference to specific nodes)

f) Is a life spent entirely in water likely to be a homologous trait for **tuna** and **dolphins**? (yes or no).  
Explain your reasoning, and make reference to **specific nodes** on the phylogenetic tree (2 marks)

No (must include a node, likely node 4). Explanation needs to say something to the effect that the common ancestor to tuna and dolphins was aquatic, but after node 4, the lineage that eventually lead to dolphins evolved to live on land and dolphins evolved an aquatic lifestyle from a terrestrial ancestor.

**Q3) 11 marks total.** The table below lists different traits found in a selection of plants. An “X” tells you that a genus has a trait (X=present, blank=absent). Each table row is a plant genus and each table column is a trait. Each genus and trait has an associated number or letter, which you may use instead of writing out the full genus/trait name.

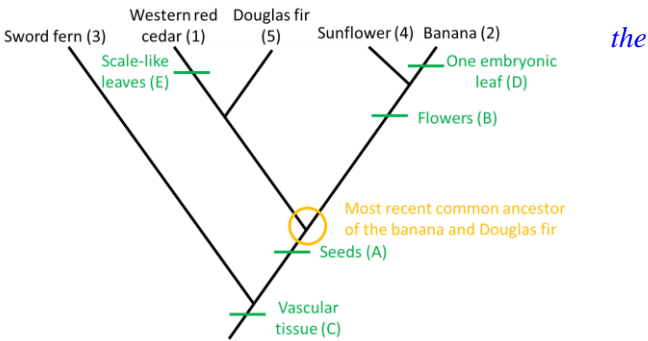
**2a) 6 marks.** Using the information in the table, create a phylogeny of these plants in the space provided below. Then, using the principle of parsimony, indicate where each trait arose using clear hash marks along the phylogenetic tree.

| Plant genus            | Produces seeds (A) | Produces flowers (B) | Vascular tissue (C) | One embryonic leaf (D) | Scale-like leaves (E) |
|------------------------|--------------------|----------------------|---------------------|------------------------|-----------------------|
| <i>Thuja</i> (1)       | X                  |                      | X                   |                        | X                     |
| <i>Musa</i> (2)        | X                  | X                    | X                   | X                      |                       |
| <i>Polystichum</i> (3) |                    |                      | X                   |                        |                       |
| <i>Helianthus</i> (4)  | X                  | X                    | X                   |                        |                       |
| <i>Pseudotsuga</i> (5) | X                  |                      | X                   |                        |                       |

Draw your phylogeny here.

**3.5 marks for the correct topology.** (0.5 marks for the root of tree; 0.5 marks for the sword fern as an outgroup; 1 mark for having the Western red cedar and Douglas fir in a clade; 1 mark for having the sunflower and banana in a clade. -0.5 marks for taxa not being along a vertical or horizontal axis).

**2.5 marks for the correct placement of traits** (0.5 marks per trait). Students can earn marks for placing traits even if there are some mistakes with the topology



**2b) 1 mark.** Circle the node indicating the most recent common ancestor of *Pseudotsuga* (5) and *Musa* (2).

**2c) 1 mark.** On your tree, put a star (\*) next to the synapomorphy for the clade containing all five taxa. *Vascular tissue*

**2d) 1 mark.** Draw a circle around one monophyletic group. Explain why it is monophyletic.

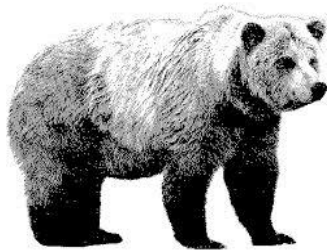
*A monophyletic group includes a common ancestor and all of its descendants (0.5 marks). They can circle any such group: e.g. the banana (*Musa*), sunflower (*Helianthus*), and their shared node (0.5 marks).*

*Students can receive full marks for this question, even if they made a mistake with the branching order in their phylogeny.*

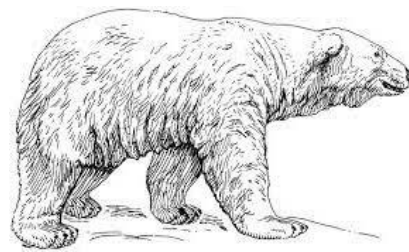
**2e) 2 marks.** Based on your phylogenetic tree, would you expect the *Thuja* genome to be more similar to the *Helianthus* genome, or to the *Polystichum* genome? Briefly explain your answer.

*The *Thuja* genome should be more similar to the *Helianthus* genome (1 mark). This is because they share a more recent common ancestor (1 mark).*

**4)** The figures below show two species of bear. Brown bears (*Ursus arctos*) are generally smaller and lighter of the two (1.5-2.8 m long, 220 kg) and most have brown coats, short faces and larger ears. They are found in diverse habitats such as forests and meadows and eat both plants and many kinds of animals. Polar bears (*Ursus maritimus*) are larger (2-3 m long, 450 kg), have coats that appear white, longer faces and smaller ears. They thrive in arctic environments, and are completely carnivorous, eating prey such as seals and walruses. In occasions when their ranges overlap, brown bears and polar bears can mate and produce viable hybrid offspring. **(13 marks total)**



Brown bear (*Ursus arctos*)



Polar bear (*Ursus maritimus*)

a. Which species concept (choose only one) would justify the classification of brown bears and polar bears as one species? Explain your answer using only the information provided. **(2 marks)**

*Biological species concept – they do interbreed / no reproductive isolation.*

b. Under which species concept (choose only one) would polar bears and brown bears be considered two species? Explain your answer using only the information provided. **(2 marks)**

*Morphological species concept - observe specific morphological differences in body size, mass, or coat colour, face/ear size.*

*OR*

*Ecological species concept – (Not as strong an answer as their ranges overlap)*

*For full marks, must specifically address that they mainly live in different habitats (forests and meadows vs. arctic environment) AND eat different prey items (plants and animals for brown and only animals such as seals and walruses for polar).*

c. What specific evidence would a biologist need to determine that brown bears and polar bears were different species using the phylogenetic species concept? Explain how this evidence would allow them to make their decision. (3 marks)

- 1) Needs specific evidence (such as DNA, fossils, morphological measurements), that can be used as unique defining characteristics (or synapomorphies).
- 2) This allows for different monophyletic groups (or clades) for the brown bear lineage and the polar bear lineage.
- 3) Needs to be in the context of phylogenetic information, e.g. unique evolutionary histories after split from common ancestor.

(**Incorrect answer** if only says they are on different branches on a tree or have different common ancestors or have no common ancestor. They will be in the same monophyletic group/clade no matter what, if they are one species (a single species clade) or two species (genus *Ursus* clade).

d. Suppose there is a population of brown bears in the mountains of central British Columbia [mountain bears] which form a sister clade to the brown bears of northern coastal British Columbia [coastal bears]. The coastal bears specialize on a marine diet such as whale carcasses, clams and salmon.

Describe the process of a large, single species of BC brown bears becoming two species: mountain brown bears and coastal brown bears. Explain what could happen during each step, each one leading to the next, to cause this result. Use the biological species concept and include references to appropriate evolutionary mechanisms in your answer, and be as specific as possible. (6 marks)

Correct answer would be a description of events leading to allopatric speciation. Could be in a different order if logical.

Step 1

1) Identify the fact that there would need to be a lack of gene flow between coastal brown bears and mountain brown bear populations.

E.g., The populations have become physically isolated from one another by dispersal or vicariance, like a river forming, which prevents gene flow between coastal and mountain populations and/or allows the populations to diverge from one another.

[\*Note that they start off as a “large, single species of BC brown bears”, so there has to be something that divides them, can’t start as two isolated populations.]

Step 2

2) Propose an evolutionary mechanism that would cause the populations’ allele frequencies to diverge from one another.

E.g., If coastal brown bears are a small population, then allele frequencies might change due to genetic drift. Genetic drift is random, so allele frequencies for many different genes could change in different ways for each population, and populations that are isolated from one another could diverge from one another evolutionarily.

**or**  
frequencies of alleles related to ecological / morphological / behavioural / physiological differences will change in the coastal brown bear and mountain brown bear populations due to (disruptive) natural selection, e.g. skull differences related to feeding on different diets; morphological differences related to swimming vs terrestrial locomotion, etc. The isolated populations will diverge in morphology/behaviour/physiology over time because of different selection pressures in the coastal vs mountain environments.

Step 3

3) Describe a specific reproductive isolating mechanism that could evolve between coastal brown bears and mountain brown bears.

E.g., Difference in allele frequencies might lead to gamete incompatibilities / or behavioural differences / between coastal brown bears and mountain brown bears / poor survival and/or fitness of hybrids.

If coastal brown bears and mountain brown bears can no longer mate or produce any viable offspring with members of the other group, then they would be considered separate species according to the biological species concept.

4) Red-billed queelas are common birds in parts of Africa. These birds make nests and breed in large, very dense colonies. A male and a female mate and occupy a shared nest to raise offspring. During the year, both male and female birds have identical light brown coloration. **(13 marks total)**

During the breeding season, males produce more colorful feathers ranging from red to yellow. Red and yellow pigments come from the bird's food. It was assumed birds with red feathers had a more nutritious diet than birds with yellow feathers.

Biologists have hypothesized that female queelas may prefer to mate with males that have red feathers.

a) Based on all of the information above, briefly explain the reasoning underlying this hypothesis. Your answer should make specific reference to the fitness effect of female choice on female fitness (females who choose males with red feathers compared with females that choose males with yellow feathers). **(6 marks)**

- 1) Color correlates with higher quality **males** and/or better genes
- 2) **Female** fitness increases if she picks the male with red feathers (must have specific reference to female fitness)
- 3) because she has healthier/better **offspring** with a higher chance of survival

Decades later, James Dale studied coloration in queelas. He found that the male plumage color is highly correlated with the plumage color of their father. The birds' diet did not affect coloration after all. All birds have the same average number of offspring regardless of their feather color.

b) Your friend suggests that the feather coloration (red vs. yellow) in red-billed queelas indicates that sexual selection is occurring and feather coloration is a signal used by females to evaluate male quality. Do you agree with his claim? **(1 mark)**

**Yes / No** (circle one)

c) Explain why or why not with specific reference to each of the three main criteria required for selection. **(6 marks)**

| Criteria for Selection   | Explanation  |
|--|--|
| Genetic basis  | Since the offspring look like their fathers and the colour is not effected by diet, the trait does seem to be heritable.   |
| Variation in phenotype   | Males have different colour feathers, so there is variation.   |
| Differential success in survival and reproduction or just reproduction | Since all birds approximately the same number of offspring regardless of the parents' feather colour, we <u>cannot</u> conclude that this trait is under sexual selection. |