UNIVERSITY OF BRITISH COLUMBIA
Biology 121 Midterm 2, 2022

You may once again bring a study sheet that is a **SINGLE** 8.5 x 11inch piece of paper with **HAND-WRITTEN/DRAWN** notes (printed tablet notes fine) on **BOTH** sides of the paper. Your study sheet must be **UNIQUE** to you. Please **DO NOT** include copy/pasted textbook figures, class slides, homework questions, etc. on your study sheet.

Why no copy/pasted notes? Because the act of creating the study sheet, of decided what to include and compiling it all onto your document is a form of studying. You are processing the information you've been given as you create your study sheet: deciding what is most important, condensing your notes, drawing pictures. When you copy and paste, you're not getting that same benefit of studying as you create.

2. Variegated porphyria (VP) is a disease caused by a dominant allele; it affects the nervous system and other organs. This disease is more common in South Africa than elsewhere in the world and its origins there can be traced back to a Dutch man who emigrated from The Netherlands and married a woman in South Africa in 1688. (15 marks total)

a) A blood test has been developed to determine if individuals are homozygous dominant (AA), heterozygous Aa) or homozygous recessive (aa). In a population of 100,000 there are 1 AA, 404 Aa and 99,595 aa individuals. Is this population in HW equilibrium? Justify your answer. Show all your calculations to six decimal places and show all your work. (**6 marks**)

Frequency of the A allele = p = (1 + 404/2)/100,000 (number of individuals)
  = 203/100,000 = .00203
OR   *p = [(1 x 2) + 404]/200,000 (number of alleles)*
       = 406/200,000 = 0.00203

Frequency of the a allele = q = (404/2 + 99595)/100,000 (number of individuals)
  = 99797/100,000 = .99797
OR q = (404 + 99595 x 2)/200,000 (number of alleles) = 0.99797
OR   q = 1-p = 1-0.00203 = 0.99797

		Observed Frequency	*Expected Frequency*	*Expected Number*
AA	*1*	*= 1/100000 = .00001*	*= 0.00203^2 = .00000412*	*= 0.00000412 x 100000 = 1*
Aa	*404*	*= 404/100000 = 0.00404*	*= 2 x 0.00203 x 0.99797 = 0.004052*	*= 0.004059 x 100000 = 406*
aa	*99595*	*= 99595/100000 = .99595*	*= .99797^2 = .991916 0.995944*	*= 0.995944x 100000 = 99594*

Not in HWE (1): The expected and observed values for AA are both very small numbers; however, 0.00001/0.00000412 = 2.4. There are 2.4X as many AA observed as expected.

b) List two assumptions of the HW equilibrium that may have been violated in this example and indicate how each violation could account for the results obtained. (4 marks)

1 mark for each assumption and 1 mark for each explanation. e.g.

Gene flow. AA is very rare in the general population. since the man leaves the Netherlands, and enters South Africa, where he has children, we expect South Africa to have more AA than expected.

Selection: we do not know from the question when the disease, Variegated porphyria strikes, but individuals with the disease will likely have lower fitness. The A allele is dominant, and we see that the AA and Aa genotypes are at a very low frequency in the population. There are more AA in the population than expected because of the man's immigration to South Africa.

Non-random mating: If the disease has a visible phenotype there may be less mating between A individuals than expected by chance. Again, AA are higher than expected because of immigration to South Africa, but a is by far the dominant allele.

c) What evolutionary mechanism is illustrated in this example (not considering the original origin of the variegated porphyria allele in humans)? Explain (2 marks)

Gene flow (1) because a man left the Netherlands gene pool and entered the South African gene pool where he successfully reproduced. (1)

d) Individuals with VP are sensitive to sunlight and develop skin ulcers as a consequence of ultraviolet light exposure. Explain how this illustrates that Phenotype is a combination of genotype plus the interaction of genotype with the environment (Phenotype= Genotype + Environment). (3 marks)

*VP is due to the dominant allele in the **genotype** (1)*
*The development of skin ulcers is an **environmental** effect caused by UV (1).*
Together genotype and environmental influence result in the phenotype of skin ulcers (1).

3. The medium ground finches on an island in the Galapagos have been studied in detail by Peter and Rosemary Grant over the last 30 years. A summary of changes in their body size, beak size and beak shape are shown below. (There was a drought in 1977, and a return to full plant growth by 1983). In chickens, a related species of bird, beak size and shape are determined by known genes. What are the pre-requisites for evolution by natural selection? Explain how each of these pre-requisites *might* be met based on the data given. **(8 marks)**
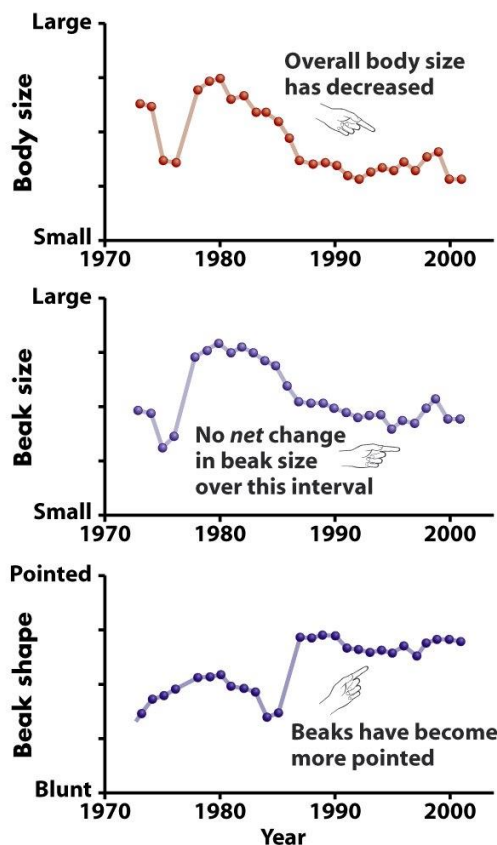
*(**1 mark** for each component and **1 mark** for each application or explanation)*

1. Variation – the birds must have varied morphologically in these three traits.

2. Heritiblity – the birds must have varied genetically and been able to pass on the genes that influences these three traits.

3. Differential survival and reproduction – individuals with the better traits (eg. more pointed or larger beaks) survive and have offspring

4. Increase in better performing variants – the next generation will have a smaller body, larger beak or more pointed beak

4. The following phylogenetic tree shows the relationship among terrestrial plants alive today. (7 marks total)

Phylogenetic relationship among extant land plants
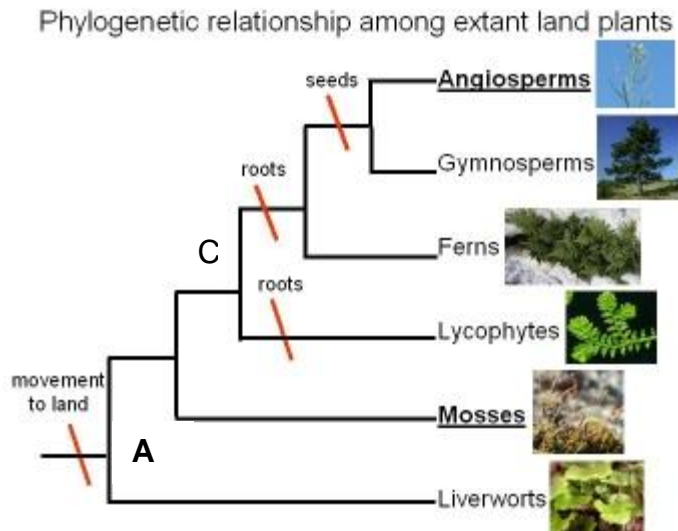
a) Which of the following groups form monophyletic clades (all members of a monophyletic clade must share a common ancestor)? Circle the correct answer(s). For those that are not a monophyletic clade, explain why not. (4 marks).
i) Angiosperms, Gymnosperms
ii) Angiosperms, Gymnosperms, Ferns
iii) Ferns, Lycophytes
iv). Lycophytes, Mosses
i and ii 1 mark each Penalty for wrong answers. Right – ½ wrong – so if you check all of them you get 1 mark.
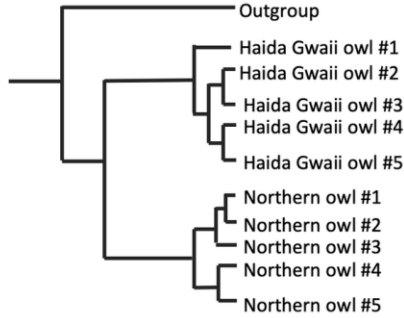
b) The first node by the root is labeled A, label the remaining nodes in order, from B to E. For one of the monophyletic groups you have identified, explain why it is a monophyletic group. (2 marks)
Angiosperms and Gymnosperms are the descendants of E; there are no other descendants of E.
(or Angiosperms, gymnosperms and ferns are the descendants of D; there are no other descendants of D)

c) What is a synapomorphy (shared derived character) for angiosperms and gymnosperms? (1 mark)

   seeds

5. British Columbia is home to two subspecies of Saw-whet owls: the Common Northern Saw-whet owl (*Aegolius acadicus acadicus*) and the Haida Gwaii Saw-whet owl (*Aegolius acadicus brooksi*). Some researchers believe that the two subspecies should be classified as two different species. The table below shows key characteristics of the two subspecies:

	Common Northern Saw-When Owl	Haida Gwaii Saw-Whet Owl
Population size	1900	200,000
Feather colour	Light brown	Dark brown
Body length	18-21 cm	17.5-22 cm
Body weight	65-151 g	75-145 g
Diet	~80% mice, rest other small mammals or birds	Marine invertebrates (e.g., crabs, snails)
Behaviour	Migratory	Not migratory
DNA, and phylogeny built using DNA		

Outgroup
Haida Gwaii owl #1
Haida Gwaii owl #2
Haida Gwaii owl #3
Haida Gwaii owl #4
Haida Gwaii owl #5
Northern owl #1
Northern owl #2
Northern owl #3
Northern owl #4
Northern owl #5

Scale bar for phylogeny:
— = a single nucleotide difference

Q5.1 Does the phylogenetic species concept support the argument that these two owls are separate species? Briefly explain your answer, using information from the table above (2 sentences maximum). (2 marks)

Yes, the PSC holds here. In the given phylogeny, all owls identified as Haida Gwaii owls form a monophyletic group, while all Northern owls form a separate monophyletic group.

Q5.2 Using information from table above, identify one other species concept that would support the argument that these two owls are separate species. Briefly explain your answer, using information from the table above (2 sentences maximum). (2 marks)

Your answer should directly connect a) your chosen species concept, biological, morphological or ecological, b) evidence from the table, and c) reasoning that makes the connection between your concept and evidence. For example, if you choose the morphological, you would need to let us know what the MSC requires (clear and consistent differences in physical or behavioural features to be different species) and what evidence supports this. In this case, you could argue that HG owls are different in several ways: always dark brown while N owls light brown, HG owls are slightly larger and heavier than N owls and (if you include behaviour in morphology — I'd accept it here or with ecological), HG owls don't migrate while N do.

6. You are studying an isolated population of a flowering plant species, the Common Silverweed. Two alleles for gene *A* exist in this population (*A1* and *A2*). The function of gene *A* is currently unknown. (**8 marks total**)

    a.   Explain how a single, <u>large</u> change in population size could possibly result in a random change in the frequencies of *A1* and *A2* in this population. (**2 marks**)

A sudden <u>decrease</u> in population size/<u>population bottleneck</u> (partial mark if all you say is genetic bottleneck or bottleneck, without connecting it to this population), could result in a random change in allele frequencies if:
- *the individuals who survived and/or reproduced were a small **random subset/sample** of individuals from the original population*
  AND
- *the individuals who survived and/or reproduced after the bottleneck were a **non-representative** sample/subset of the original population*

[Note: In order to get full marks, you need to clearly communicate how a change in allele frequencies could occur. I.e., it's not enough to just say that a random subset of individuals survived, because it's possible that, by chance, a random subset would have the same allele frequencies as the original population – in which case evolution has not occurred.]

    b.   Explain how the frequencies of *A1* and *A2* could change randomly between generations, even if there is <u>no change</u> in population size. Assume there are no mutations affecting gene *A*. (**2 marks**)

If the population is <u>small</u> OR because it is <u>finite/not infinite</u> ...
...then random survival and reproduction of some individuals will have a measurable/noticeable/significant affect on allele frequencies in the population.
OR
...then sampling error will affect allele frequencies OR The next generation is more likely to be non-representative of the previous generation

    c.   Several years later, you discover a third allele for gene *A* in the population (i.e., *A3*), which was not there previously. Briefly describe <u>two</u> different evolutionary mechanisms that could have possibly resulted in the appearance of the new allele in this population. (**4 marks**)

1 mark per mechanism and 1 mark for each description.

Mutation *an error during DNA synthesis/replication/meiosis resulted in a new version of the gene/a new DNA sequence/new allele in a gamete*

*AND **Gene flow/Migration** individual(s) with the A3 allele migrated to this population from another population and interbred with residents/joined the gene pool*

Other logical phrasings/descriptions may also be acceptable.

Q3 Phylogenetic Tree

Below is a phylogenetic tree showing the evolutionary relationships among hornets. (repeated in the sub-questions, where needed)

Q3.2 If *P. barthelemyi*, *P. anomala* and their common ancestor had a mutation that changed their appearance, would this be an example of a homologous trait or convergent evolution? Explain your answer (2 sentences maximum). (2 marks).

Homologous trait. To be a homologous trait is to be [your wording here]. Present in *P. barthelemyi*, *P. anomala* because it was inherited from a shared common ancestor.

Q3.3 Hornets are venomous. Your friend gets stung by a *V. mandarinia* and needs antivenom. Antivenom for *V. baslis* and *V. affinis* is available. Which antivenom do you think your friend should receive? Explain your answer, make specific reference to the phylogeny. 2 sentences maximum. (2 marks)

Antivenom from *V. affinis. It is more closely-related to V. mandarinia than V. baslis [you know this because of what evidence from the tree? You should include that evidence in your explanation by referring to specific nodes from the tree]*