1. (*1 mark; 0.5 each*) Select from the list of words and phrases to complete this sentence.

Note that some words/phrases will be used more than once, some might not be used at all.

non-random mating	random	unpredictable
mutation	smaller	phenotype
fitness	genetic drift	
probability	larger	

__Non-random mating__ occurs when the _probability____ that two individuals in a population will mate is not the same for all possible pairs of individuals.

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*	*= 0.00203² = .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*	*= .99797² = .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. (3 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? Explain how each of these pre-requisites *might* be met based on the data given. **(8 marks)**
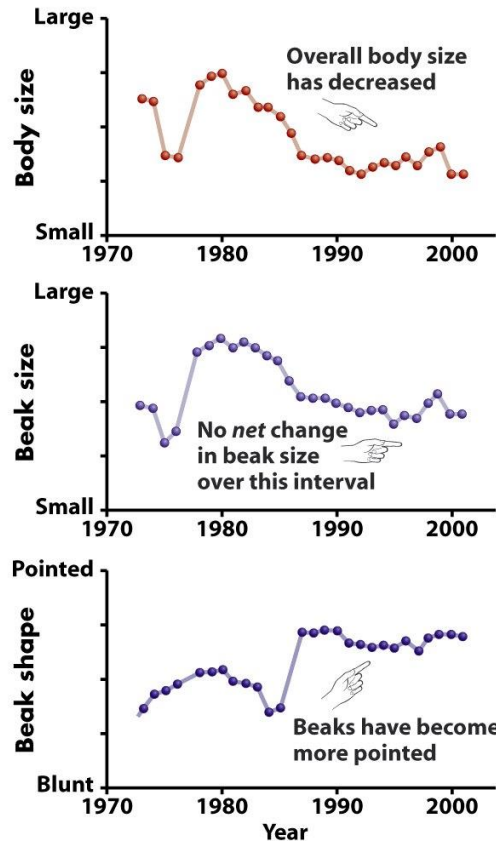
*(**1 mark** for each component and **1 mark** for each application or explanation)*

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 (e.g. more pointed or larger beaks) have a greater chance of survival and having more offspring

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

Phylogenetic relationship among extant land plants
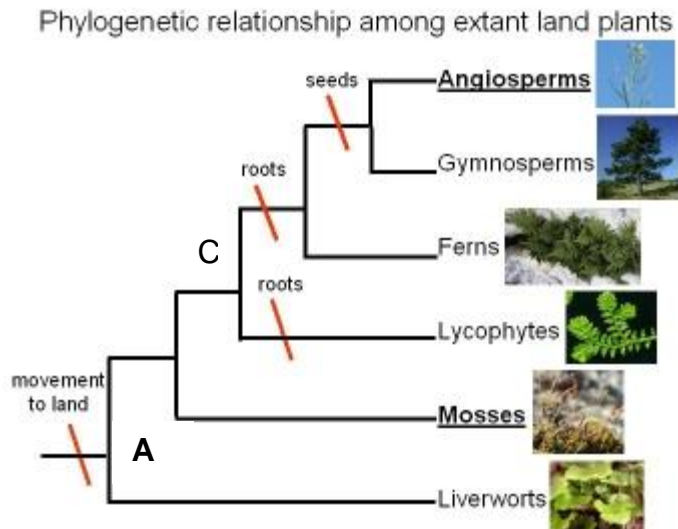
a) Which of the following groups form monophyletic clades (all members of a monophyletic clade must share a common ancestor)? Circle the correct answer(s). For those that are not a monophyletic clade, explain why not. (4 marks).
i)   Angiosperms, Gymnosperms (plus common ancestor)
ii) Angiosperms, Gymnosperms, Ferns (plus common ancestor)
iii) Ferns, Lycophytes (plus common ancestor)
iv). Lycophytes, Mosses (plus common ancestor)
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. In the Lake Erie region of Ontario there are two kinds of non-poisonous water snakes (*Nerodia* spp.). On the shores of the lake most of the snakes have a banded colouration, while on the islands in the lake most snakes are not banded. You have been hired by the Ontario government to work on a project designed to protect these threatened snakes from becoming endangered. (13 marks total)

a) The first thing you have to do is to determine whether banded and unbanded snakes represent different morphological forms (morphs) of one species or are two separate species. In the table below, indicate what would you expect to observe if these were separate species and what would you expect if they were the same species but with different morphs (6 marks).

b)

Species Concept	Expectations if only one species (1 mark each)	Expectations if two species (1 mark each)
Morphological	*Only small morphological differences (e.g. only banding pattern)*	*Additional morphological differences (e.g. jaw structure, reproductive structures)*
Phylogenetic	*Individuals from the two populations are part of the same monophyletic group defined by synapomorphies, the banding is just variation with the one species*	*Individuals from two populations are from two different monophyletic groups defined by synapomorphies such as banding pattern or DNA sequences*
Biological	*Individuals from two populations are able to mate and produce viable, fertile offspring*	*Individuals from two populations unable to mate or produce viable, fertile offspring*

b) Suppose you determine that these two morphs are in fact one species. What could be causing the difference in distribution of the two morphs? (2 marks)
many answers are possible; they just have to be logical and biologically possible.
e.g., perhaps the environment on the shore or on the island is such that the less common morph is more visible to predators (2)
Banded morphology confers more protection from predators because it acts as camouflage. There are few predators on the islands, so the selection pressure for bands is much lower.

c) Talking to the locals, you discover that the population on the island was founded by a snake breeder who accidentally released five snakes 25 years ago. Given this new information, what evolutionary factor(s) could be responsible for the difference between the island and the mainland population? Briefly explain your answer (3 marks)
Drift – the original population was small and allele frequencies in the released snakes not likely representative of the mainland population and gene flow restricted between island and mainland.

d) Suppose you determine that they are in fact two species. What are two reproductive isolating mechanisms that could be causing them to remain separate species? (2 marks)
any two of: non-random mating, habitat isolation, behavioural isolation e.g. courtship behavior, temporal Isolation, d) mechanical isolation, e) gametic isolation, Postzygotic barriers such as reduced hybrid fertility

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.