

AP[®] BIOLOGY
2011 SCORING GUIDELINES (Form B)

Question 4

Phylogeny reflects the evolutionary history of organisms.

- (a) **Discuss** TWO mechanisms of speciation that lead to the development of separate species from a common ancestor.
(2 points maximum)

Mechanisms that lead to the development of separate species from a common ancestor (1 point each)

- Geographic isolation (or allopatric speciation) takes place when a population of one species becomes physically separated by some geographic barrier such as a river, mountain range, etc. Long-term isolation of two populations eventually leads to reproductive isolation.
- Sympatric speciation happens when new species arise as a result of reproductive isolation within the population range — for example, because of polyploidy or switching mating behaviors (fruit flies going from hawthorn to apple to lay eggs). Eventually the two populations are unable to interbreed.
- Reproductive isolation by prezygotic barriers, such as habitat, temporal, behavioral, mechanical, or gametic incompatibility.
- Reproductive isolation by postzygotic barriers (e.g., reduced hybrid viability or fertility) leads to speciation.

- (b) **Explain** THREE methods that have been used to investigate the phylogeny of organisms. **Describe** a strength or weakness of each method.
(6 points maximum)

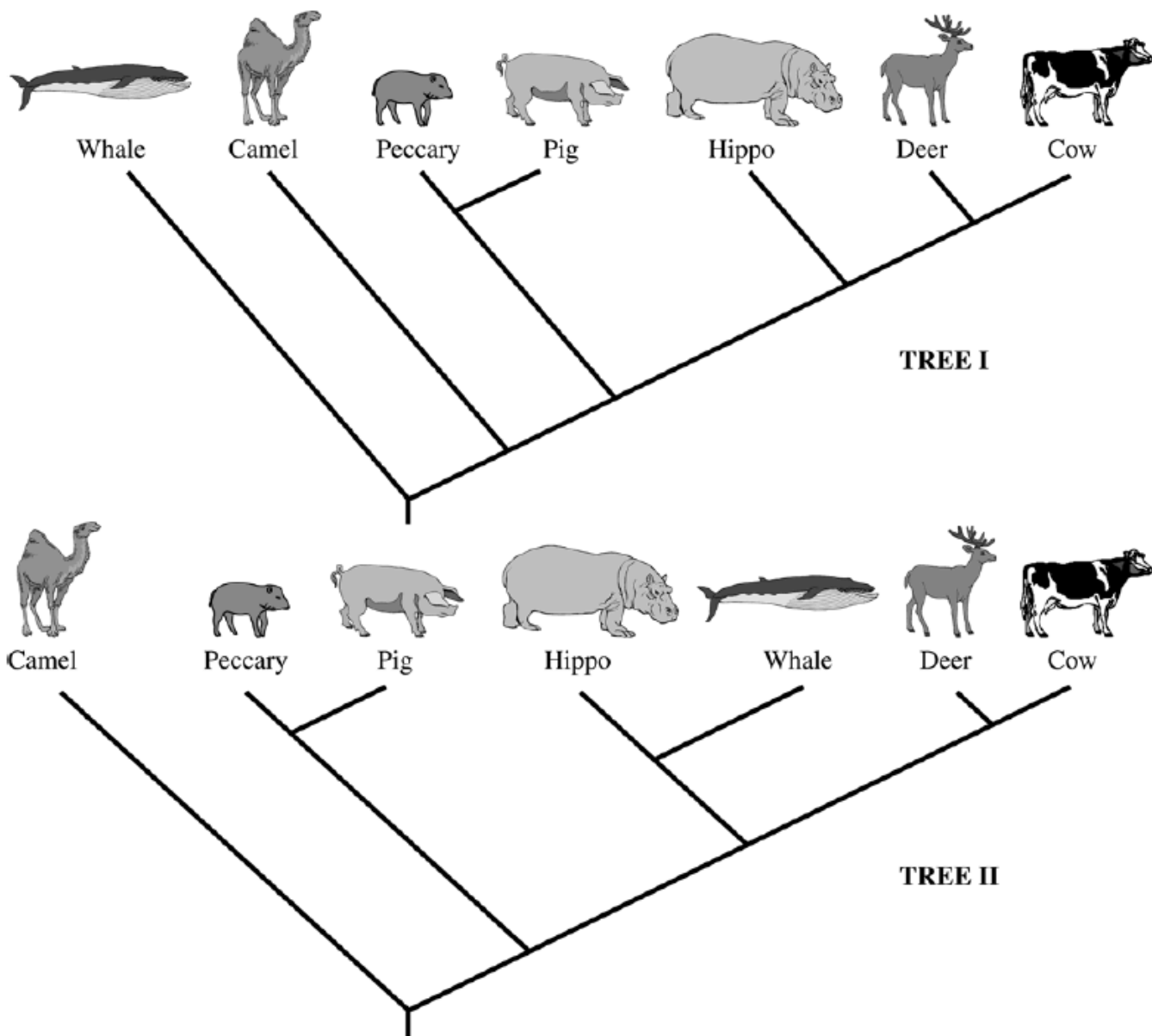
Response earns 1 point for each method explained and 1 point for either a strength *OR* a weakness.

Methods (1 point)	AND Strengths (1 point)	OR Weaknesses (1 point)
Fossils (paleontology)	Determine time; reveal extinct species.	Not all species leave fossils. Fossil record is incomplete.
Anatomy/morphology	Homologous structures indicate evolutionary relationships.	Analogous structures. Some taxa have little diversity (e.g., bacteria). Some morphology reflects environment or diet.
Embryology/development	Reveals similarities in structures and patterns of development that are not evident in adults.	Similarities between species may be lost in later development.
Molecular traits (amino acid sequence in proteins or base sequence in DNA)	Large numbers of traits. Allow study of evolution between closely related species. Most accurate.	No (or little) data for extinct species. Variation within species blurs differences between species.
Behavioral traits	Some behaviors are genetic (e.g., frog calls).	Behavior maybe culturally transmitted or learned (e.g., bird calls).

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Question 4 (continued)

- (c) The two phylogenetic trees represent the relationship of whales to six other mammals. All of the organisms shown have a pulley-shaped astragalus bone in the ankle except for the whale.



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Question 4 (continued)

Locus	DATA ON PRESENCE OF SPECIFIC DNA SEQUENCES												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Cow	-	-	-	-	-	+	+	+	+	+	+	+	-
Deer	-	-	-	-	-	+	?	+	+	+	+	+	-
Whale	+	+	+	+	+	-	?	+	+	-	?	+	-
Hippo	?	-	+	+	+	-	+	+	+	-	?	+	-
Pig	-	-	?	-	-	-	?	-	?	-	-	+	+
Peccary	?	?	?	?	?	?	?	?	?	?	?	?	+
Camel	-	-	-	-	-	-	-	-	-	-	-	-	-

+ sequence present
- sequence absent
? undetermined

- For each tree, **describe** a monophyletic group, the closest relative to the whale, and the point at which the pulley astragalus was lost or gained.
(3 points maximum)
 - Correctly identifying a monophyletic group in *BOTH* Tree I and II (a number of correct possibilities) or correctly defining a monophyletic group as a species and all of its descendants. **(1 point)**
 - Correctly identifying the camel as the closest relative to the whale in Tree I *AND* the hippo in Tree II. **(1 point)**
 - Stating that the gain of the pulley astragalus bone in Tree I occurs between the whale and the camel, *OR* that the loss of the bone occurs on the line to whales, *AND* that the loss of the pulley astragalus bone in Tree II occurs between the common ancestor of the hippo and the whale. **(1 point)**

- Based on the principle of parsimony (the simplest explanation is the best) and the genomic information in the table shown, **identify** which tree is the best representation of the evolutionary relationship of these animals, and **justify** your answer.
(1 point maximum)

Identification of correct tree	Justifications include but are not limited to
Tree II	<ul style="list-style-type: none"> • The camel is the out-group, with none of the 13 sequences. • The peccary and pig have the fewest sequences, but they are similar. • The deer and cow share the same half of the 13 sequences. • The whale and hippo have a similar pattern of DNA sequences.

Note: No point is earned for using the pulley astragalus bone to justify Tree II, nor for discussing common environments, body shapes, or feeding habits.