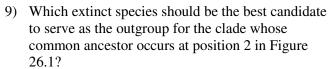
Unit 2 Prac	ctice l'est	Name:
1)	Which of the following is (are) problematic wheevolutionary history? A) polyphyletic taxa B) paraphyletic taxa	cen the goal is to construct phylogenies that accurately reflect C) monophyletic taxa D) Two of the responses are correct.
2)	The term <i>homoplasy</i> is most applicable to which A) the legless condition found in various linear B) the five–digit condition of human hands and C) the β hemoglobin genes of mice and of human b) the fur that covers Australian moles and Note b) the bones of bat forelimbs and the bones of	ges of extant lizards d bat wings nans orth American moles
3)		the bear family (Ursidae) but place the lesser panda in the the morphological similarities of these two species are
4)	possessed three-chambered hearts (two atria, or	vere very early (stem) reptiles, which almost certainly ne ventricle). Birds and mammals, however, are alike in entricles). The four–chambered hearts of birds and D) the result of shared ancestry. E) molecular homologies.
5)	•	which of the following is considered most important for D) the number of homoplasies E) overall phenotypic similarity
6)	 domains, rather than assigning all prokaryotes t A) molecular B) behavioral C) nutritional 	D) anatomical E) ecological
7)	Which eukaryotic kingdom is polyphyletic, andA) PlantaeB) FungiC) Animalia	D) Protista E) Monera
8)	with high acidity, salinity, and/or temperature. Sommon on the primitive Earth. Thus, modern abecame adapted to long ago. Which of the followextremophiles, assuming that their habitats have A) Among themselves, they should share related ancestral forms to adapt to extreme conditions.	ively few ancestral traits, especially those that enabled

D) They should currently be undergoing a high level of horizontal gene transfer with non–extremophilic archaeans.

branches of the extremophiles should be shorter than the non–extremophilic archaeans.

C) They should contain genes that originated in eukaryotes that are the hosts for numerous species of

bacteria.



- A) A
- B) B
- C) C
- D) D
- E) E
- 10) If Figure 26.1 is an accurate depiction of relatedness, then which of the following should be correct?
 - 1. The entire tree is based on maximum parsimony.
 - 2. If all species depicted here make up a taxon, this taxon is monophyletic.
 - 3. The last common ancestor of species B and C occurred more recently than the last common ancestor of species D and E.
 - 4. Species A is the direct ancestor of both species B and species C.
 - 5. The species present at position 3 is ancestral to C, D, and E.



Present

- A) 1 and 3
- B) 3 and 4
- C) 2, 3, and 4
- D) 1, 2, and 3

Genetic Relatedness

Use Figure 26.1 to answer the following questions.

Traditionally, whales and hippopotamuses have been classified in different orders, the Cetacea and the Artiodactyla, respectively. Recent molecular evidence, however, indicates that the whales' closest living relatives are the hippos. This has caused some zoologists to lump the two orders together into a single clade, the Cetartiodactyla. There is no consensus on whether the Cetartiodactyla should be accorded order status or superorder status. This is because it remains unclear whether the whale lineage diverged from the lineage leading to the hippos before or after the other members of the order Artiodactyla (pigs, camels, etc.) diverged (see Figure 26.2).

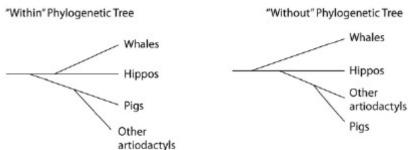


Figure 26.2

Figure 26.2 contrasts the "Within the artiodactyls" origin of the whale lineage with the "Without the artiodactyls" origin of the whale lineage.

- 11) If it turns out that the whale lineage diverged from the lineage leading to hippos *after* the divergence of the lineage leading to the pigs and other artiodactyls, and *if* the whales continue to be classified in the order Cetacea, then what becomes true of the taxon Cetartiodactyla?
 - A) It should be considered as one monophyletic order.
 - B) It should be considered a superorder that consists of two monophyletic orders.
 - C) It should be established as a paraphyletic order.
 - D) It should be thrown out or modified by taxonomists if classification is to reflect evolutionary history.
- 12) If cetaceans are determined to have diverged from the lineage leading to the artiodactyls *before* the divergence of lineages leading to the modern artiodactyls (including hippos), then the cetaceans can be considered
 - 1. a sister order to the order Artiodactyla.
 - 2. an ingroup of the order Artiodactyla.
 - 3. the common ancestor of the order Artiodactyla.
 - A) 1 only
- B) 3 only
- C) 1 and 2
- D) 1 and 3
- E) 2 and 3

- 13) It was once thought that cetaceans had evolved from an extinct group of mammals called the mesonychids. If, in the future, it is determined that some organisms currently classified as cetaceans *did* actually evolve from mesonychids, whereas other cetaceans evolved from artiodactyl stock, then what will be true of the order Cetacea?
 - A) It will be paraphyletic.
 - B) It will be polyphyletic.
 - C) It will need to be thrown out or modified if classification is to reflect evolutionary history.
 - D) Two of the responses are correct.

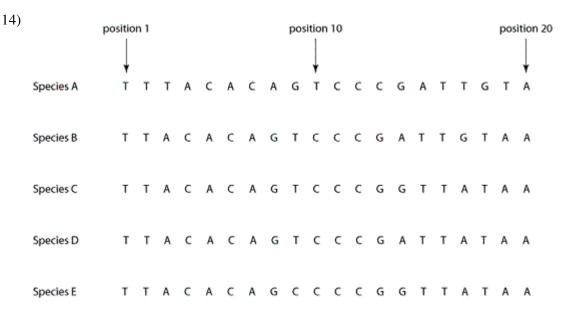


Figure 26.3. Morphologically, species A is very similar to four other species, B–E. Yet the nucleotide sequence deep within an intron in a gene shared by all five of these eukaryotic species is quite different in species A compared to that of the other four species when we study the nucleotides present at each position.

If the sequence of species A in Figure 26.3 differs from that of the other four species due to simple misalignment, then what should the computer software find when it compares the sequence of species A to those of the other four species?

- A) The nucleotide at position 1 should be different in species A, but the same in species B–E.
- B) The nucleotide sequence of species A should have long sequences that are nearly identical to those of the other species, but offset in terms of position number.
- C) The sequences of species B–E, though different from that of species A, should be identical to each other, without exception.
- D) If the software compares the amino acid sequence of the actual protein product rather than the nucleotide sequence, then the amino acid sequences of species B–E should be similar to each other, but very different from that of species A.
- E) Computer software is useless in determining sequences of introns; it can only be used with exons.
- 15) Which structure–function pair is *mismatched*?
 - A) nucleolus; production of ribosomal subunits
 - B) lysosome; intracellular digestion
 - C) ribosome; protein synthesis

- D) Golgi; protein trafficking
- E) microtubule; muscle contraction
- 16) What is the most likely pathway taken by a newly synthesized protein that will be secreted by a cell?
 - A) $ER \rightarrow Golgi \rightarrow nucleus$
 - B) Golgi \rightarrow ER \rightarrow lysosome
 - C) nucleus \rightarrow ER \rightarrow Golgi
 - D) $ER \rightarrow Golgi \rightarrow vesicles$ that fuse with plasma membrane
 - E) ER \rightarrow lysosomes \rightarrow vesicles that fuse with plasma membrane

17) Which cell would be best for studying lyosomes?

A) muscle cell

B) nerve cell

C) phagocytic white blood cell

D) leaf cell of a plant

E) bacterial cell

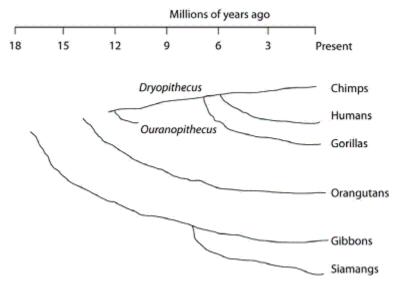


Figure 26.5. Humans, chimpanzees, gorillas, and orangutans are members of a clade called the great apes, which shared a common ancestor about 18 million years ago (Figure 26.4). Gibbons and siamangs comprise a clade called the lesser apes. Tree-branch lengths indicate elapsed time.

- 18) Assuming chimps and gorillas are humans' closest relatives, removing humans from the great ape clade and placing them in a different clade has the effect of making the phylogenetic tree of the great apes
 - A) polyphyletic.
 - B) paraphyletic.
 - C) monophyletic.
 - D) conform with Linnaeus' view of great ape phylogeny.
- 19) What is true of the phylogeny in Figure 26.5?
 - 1. It is rooted.
 - 2. The gibbons and siamangs represent an outgroup of the great apes.
 - 3. Chimps and humans are the closest extant sister taxa depicted here.
 - 4. It is absolute, meaning *free of error*.
 - 5. The last common ancestor of the great apes lived about 14 million years ago.
 - A) 1, 2, 3
- B) 1, 2, 5
- C) 1, 2, 3, 4
- D) 1, 2, 3, 5
- E) 2, 3, 4, 5
- 20) From Figure 26.5, which other event occurred closest in time to the divergence of gorillas from the lineage that led to humans and chimps?
 - A) the divergence of chimps and humans
 - B) the divergence of *Dryopithecus* and *Ouranopithecus*
 - C) the divergence of gibbons and siamangs
 - D) could be either the divergence of chimps and humans OR of Dryopithecus and Ouranopithecus
 - E) could be either the divergence of chimps and humans OR of gibbons and siamangs

Answer Key

1) D	26.1
2) A	26.2
3) D	26.2
4) C	26.2
5) C	26.3
6) A	26.6
7) D	26.6
8) B	26.3/26.6
9) A	26.3
10) D	26.3

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