

Past-paper walk-through

Evidence of Evolution ■ 7.6

eXercise

Questions in this set

- 2025 Q4
- 2023 Q5
- 2019 Q5
- 2018 Q1
- 2015 Q3

Reading the mark scheme

- **B1** a mark that stands on its own – the point is either made or not.
- **M1** a *method* mark: the right approach, even if the number is wrong.
- **A1** an *answer* mark, and it usually needs its M mark first.
- **C1** a working mark on the way to the answer.
- **//** separates answers the examiner accepts equally.
- **ecf** = error carried forward: a later part is marked on your own earlier answer.
- **owtte** = “or words to that effect” – the wording need not match.

Question 4

2025 ■ Q4

Twenty million years ago the Caribbean Sea and Pacific Ocean were connected, and water flowed freely between the two bodies of water. Many of the same marine species were found in both areas. Over millions of years, the land referred to as the Isthmus of Panama formed, eventually closing off the connection between the Caribbean Sea and Pacific Ocean and creating two separate bodies of water. The ecology of these two marine habitats was dramatically altered by this land formation. The warmer Caribbean water could no longer flow west, so the Pacific water cooled and became more nutrient-rich, while the Caribbean water became warmer.

- (a)** Describe the genetic evidence that evolution is occurring in a population.
- (b)** Explain how the isolation of marine species by the formation of a land barrier can lead to divergent evolution of those species.

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(c) The formation of the Isthmus of Panama connected two continents, North America and South America. Many North American land animal species migrated to South America after the formation of the isthmus and occupied similar niches as South American species.

Predict the effect the formation of the isthmus had on resource availability for South American species.

(d) Justify your prediction in part C.

Solution 4

(a)

Mark scheme

- Genetic evidence of evolution occurring in a population includes changes in allele/gene frequencies over time, and/or heritable changes in phenotypes across generations.

Solution 4

(b)

Mark scheme

- A land barrier isolating marine species results in reproductive isolation / lack of gene flow between the separated populations (allopatric speciation); different environmental conditions/pressures on each side then select for different alleles/genotypes/phenotypes, so selective pressures produce different allele frequencies, driving divergent evolution.

Solution 4

(c)

Mark scheme

- Resource availability for South American species would have decreased, since migrating North American land animals now occupy niches similar to those of South American species and compete for the same resources.

Solution 4

(d)

Mark scheme

- More species (native South American plus the migrated North American species) would now be competing for the same set of resources, resulting in fewer resources available to each individual — justifying the prediction that resource availability decreased.

Question 5

2023 ■ Q5

Ruminants are hoofed animals, including cattle and sheep, that have a unique four-chambered stomach specialized to digest tough, fiber-filled grasses. Researchers studying ruminants are investigating the morphological and molecular characteristics of different ruminant families in order to determine the evolutionary relationships among the families. Cladograms of several ruminant families were constructed based on morphological data (Figure 1A) and molecular data (Figure 1B). Table 1 shows a sample of the morphological characteristics present in each family used to construct the cladogram in Figure 1A.

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[Figure 1, two cladograms labeled A and B, each showing six ruminant family names (Tragulidae, Giraffidae, Bovidae, Moschidae, Antilocapridae, Cervidae) at branch tips connected by a tree of internal nodes/branch points, with a shared basal branch line running to the lower left. Panel A (“Cladogram of six ruminant families based on morphological data”): from left to right along the tips, the branch order is Tragulidae, Giraffidae, Bovidae, Moschidae, Antilocapridae, Cervidae. Giraffidae branches off first (closest to the base) from a node shared with (Bovidae, Moschidae, Antilocapridae, Cervidae); Bovidae and Moschidae share a nearer common node together, forming a pair; that pair’s node then joins with a node leading to Antilocapridae and Cervidae, which themselves diverge from a shared node closer to the tips. Panel B (“Cladogram of six ruminant families based on molecular data”): from left to right along the tips, the branch order is Tragulidae, Giraffidae, Antilocapridae, Bovidae, Moschidae, Cervidae. Giraffidae and Antilocapridae share a nearer common node together, forming a pair; Bovidae and Moschidae share a separate nearer common node together, forming

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another pair; these two pairs then join at a shared internal node closer to the base; Cervidae diverges separately, joining nearer the base of the tree.]

Question 5

Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

TABLE 1. MORPHOLOGICAL CHARACTERISTICS FOUND IN EACH RUMINANT FAMILY

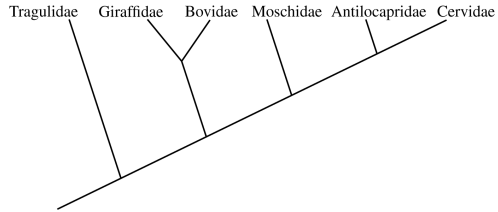
Characteristic Number	Morphological Characteristic	Tragulidae	Giraffidae	Bovidae	Moschidae	Antilocapridae	Cervidae
1	Extra tooth material			X		X	
2	Third stomach		X	X	X	X	X
3	Double opening for tear ducts					X	X

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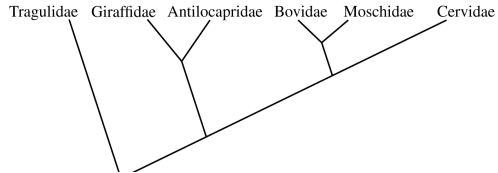
- (a) **Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
- (b) Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
- (c) Using the template in the space provided for your response, **represent** the point(s) at which characteristic 1, listed in Table 1, evolved by marking “X” on the line(s) of the cladogram in the correct location(s).
- (d) Based on Figure 1A, **explain** why a characteristic found only in the Cervidae and Bovidae families is more likely evidence of convergent evolution than it is of common ancestry.

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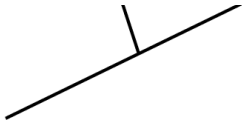
A



B



Question 5



Solution 5

(a)

Mark scheme

- A scientist compares DNA sequences across organisms and infers that organisms whose sequences are more similar to one another are more closely related evolutionarily (share a more recent common ancestor) than organisms whose sequences are more different/less similar.

Solution 5

(b)

Mark scheme

- Based on Figure 1B (the molecular-data cladogram), Bovidae and Moschidae are placed as more closely related to each other (sharing a more recent common node) than either is to Giraffidae. Molecular (DNA sequence) data are generally considered more reliable than morphological data for inferring evolutionary relatedness, because morphological similarities can evolve independently (convergently) and may not accurately reflect true relatedness — so the molecular tree's grouping of Bovidae with Moschidae is taken as the better estimate of their relationship.

Solution 5

(c)

Mark scheme

- Mark an "X" on the two branches of the Figure 1A (morphological) cladogram where characteristic 1 (extra tooth material) independently evolved: one X on the line/branch leading to Bovidae, and one X on the line/branch leading to Antilocapridae. This is because, per Table 1, only Bovidae and Antilocapridae possess characteristic 1, and on the Figure 1A tree they are not sister taxa (Moschidae branches between them without the trait), so the characteristic must have arisen independently on each of their two lineages rather than once in a shared ancestor.

Solution 5

(d) Mark scheme

- A characteristic found only in Cervidae and Bovidae (with Giraffidae, Moschidae, and Antilocapridae — which branch between them on the Figure 1A cladogram — all lacking it) is more likely due to convergent (independent) evolution than common ancestry, because if the trait had arisen in the common ancestor of Cervidae and Bovidae, the families that share that same common ancestor (Giraffidae, Moschidae, Antilocapridae) would also be expected to display it. Since those intermediate families do not have the characteristic, it is more parsimonious/likely that the trait evolved independently in the Cervidae and Bovidae lineages than that it arose once and was subsequently lost in three separate lineages.

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2019 ■ Q5

TABLE 1. DIVERGENCE (IN PERCENT) OF MITOCHONDRIAL DNA SEQUENCES AMONG FIVE PRIMATE SPECIES

	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

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A researcher studying the evolutionary relationship among five primate species obtained data from a sequence of mitochondrial DNA (mtDNA) from a representative individual of each species. The researcher then calculated the percent divergence in the sequences between each pair of primate species (Table 1).

(a) Based on fossil data, the researcher estimates that humans and their most closely related species in the data set diverged approximately seven million years ago. Using these data, **calculate** the rate of mtDNA percent divergence per million years between humans and their most closely related species in the data set. Round your answer to two decimal places.

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	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

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