

Past-paper walk-through

Phylogeny ■ 7.9

eXercise

Questions in this set

- 2024 Q5
- 2023 Q5
- 2019 Q5
- 2018 Q1
- 2015 Q3
- 2014 Q2

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 5

2024 ■ Q5

Researchers study mechanisms that enable or prevent speciation.

New genes can evolve from noncoding regions of DNA. It is not until certain regulatory elements are present in the DNA that a noncoding region becomes a new, functional gene that encodes a protein. These regulatory elements include a promoter, a 5' untranslated region (UTR) followed by a start codon, and a 3' UTR following a stop codon (Figure 1).

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[Figure 1. Basic structure of a functional *ag* gene. A linear diagram of a gene, drawn left to right as a rectangle divided into segments: a white “Promoter” segment, then a “5’ UTR” segment, then a region labeled “*ag* Repeat Sequences” bracketed over several dark “Exons” segments alternating with white intron/gap segments, and finally a white “3’ UTR” segment at the right end.]

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Researchers studied the evolution of the family of antifreeze-glycoprotein (AG) encoding genes in Gadidae, a family of marine fish known as cods. When present in the fish, these glycoproteins reduce the freezing temperature of the fish. The researchers compared genomic sequences in nine cod species and one non-cod fish species, *B. brosme*. They recorded the presence or absence of the elements of functional *ag* genes as well as *ag*-like sequences that are similar to a functional gene but have undergone mutation and do not contain all the elements required to enable protein production (Figure 2).

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[Figure 2. Phylogenetic tree showing the evolution of *ag* genes. Left side: a phylogenetic tree with x-axis “Time Before Present (millions of years ago)” running from 40 down to 0 in increments of 5. The tree root is labeled “Gadidae” and branches split over time; a vertical gray shaded band marks the “Period of Freezing Temperatures” roughly between 15 and 10 million years ago. Branch labels along the tree indicate “5’ UTR” arising at one internal node and “*ag*-like” sequences arising at another (later) internal node, with the tree then splitting into the ten terminal branches (species) listed at right. Right side: a table with columns “Promoter”, “*ag* Repeat Sequences”, “3’ UTR” (each showing “+” for present or “–” for absent, aligned to each species’ branch tip), followed by the species name and, where relevant, a code letter “(L)” or “(P)”; then a column “Average Water Temperature of Habitat”. The rows, top to bottom, are:

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Promoter	ag	Repeat Sequences	3' UTR	Species	Average Water Temp of Habitat
---	---	---	---	---	---
-	-	-	-	*B. brosme* (non-cod fish)	5-10°C
-	-	-	-	*G. argenteus*	5-10°C
-	-	-	-	*T. minutus*	5-10°C
-	-	-	-	*P. virens*	5-10°C
+	+	+	+	*M. aeglefinus* (L)	5-10°C
+	+	+	-	*M. merlangus* (L)	5-10°C
+	+	+	+	*A. glacialis* (P)	1.2-6°C
+	+	+	+	*B. saida* (P)	1.2-6°C
+	+	+	+	*G. chalcogrammus* (P)	1.2-6°C
+	+	+	+	*G. morhua* (P)	1.2-6°C

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A legend below the table reads: “—” Element is absent. “+” Element is present. “L” Functional *ag* genes are lost. “P” Functional *ag*-encoded proteins are present.]

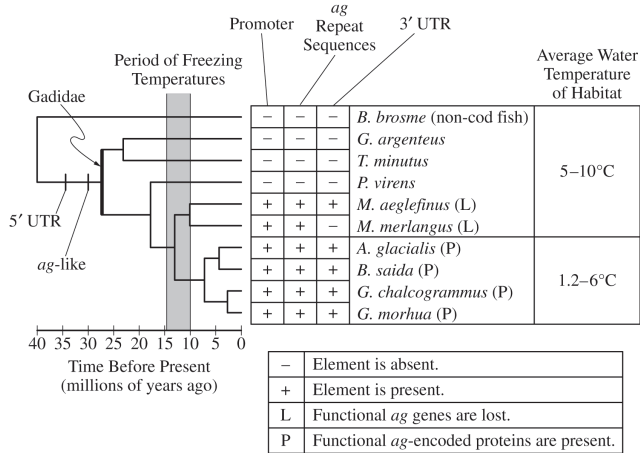
(a) Describe a post-zygotic mechanism that prevents gene flow and thus enables speciation.

(b) Based on the data in Figure 2, **explain** how changes to the genome enabled cods to survive and reproduce after a period of freezing temperatures between 10 and 15 million years ago.

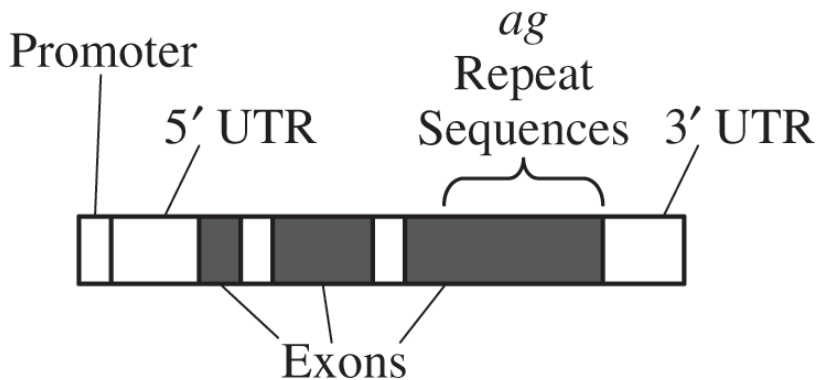
(c) Using the template in the space provided for your response, place an “X” on the phylogenetic tree to **represent** the origin of the functional *ag* gene.

(d) Based on Figure 2, **explain** how genetic differences among the species in the Gadidae family determine the habitats in which they can survive.

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Solution 5

(a)

Mark scheme

- A post-zygotic mechanism that prevents gene flow: the offspring do not survive long enough to reproduce, or cannot successfully reproduce (e.g., hybrid inviability or hybrid sterility), so genes cannot flow between the diverging populations even though fertilization/zygote formation occurred.

Solution 5

(b)

Mark scheme

- Over time, the addition/gain of the promoter, ag repeat sequences, and 3' UTR (the regulatory/functional elements) led to the emergence of new, functional ag genes/gene products (antifreeze glycoproteins) from the previously nonfunctional ag-like sequence; these antifreeze proteins lower the freezing point of body fluids, allowing cods to survive and reproduce through the period of freezing temperatures 10–15 million years ago.

Solution 5

(c)

Mark scheme

- An X placed anywhere along the highlighted L-shaped branch segment in the figure — i.e., on the branch of the phylogenetic tree between the ag-like ancestral lineage and the node/lineage where all three elements (promoter, ag repeat sequences, 3' UTR) first become jointly present (the lineage leading to the (L)- and (P)-labeled species). On this typed practice system, credit the leaf if the student's stated location correctly identifies this branch/interval as the origin point of the functional ag gene.

Solution 5

(d)

Mark scheme

- Species with the functional ag gene/antifreeze glycoprotein (all three elements "+") are able to live in colder water/lower temperatures (species labeled (P), habitat 1.2–6°C), while species lacking the functional gene are restricted to warmer water (habitat 5–10°C); species that lost the functional gene (labeled (L)) also live in the warmer range.

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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.]

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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

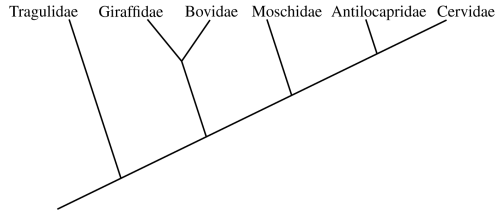
Characteristic Number	Morphological Characteristic	Tragulidae	Giraffidae	Bovidae	Moschidae	Antilocapridae	Cervidae
1	Extra tooth material			X		X	
2	Third stomach		X	X	X	X	X
3	Double opening for tear ducts					X	X

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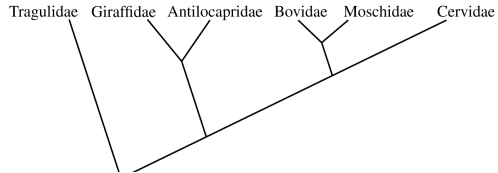
- (a) Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
- (b)** Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
- (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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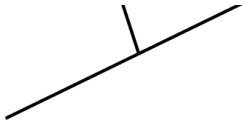
A



B



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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.

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(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.

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(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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