Past-paper walk-through

Common Ancestry ▪ 7.7

eXercise

Questions in this set

- 2023 Q5
- 2015 Q2
- 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

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

Question 5

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

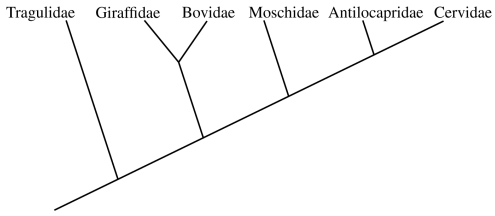
Characteristic Number	Morphological Characteristic	Tragulidae	Giraffidae	Bovidae	Moschidae	Antilocapridae	Cervidae
1	Extra tooth material			X		X	
2	Third stomach	X	X	X	X	X	
3	Double opening for tear ducts					X	X

Question 5

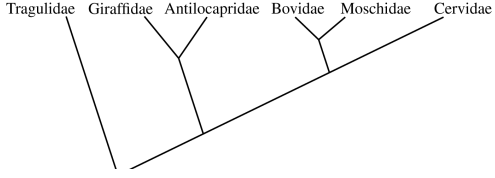
(a) Describe how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
(b) Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
(c) Using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

Question 5

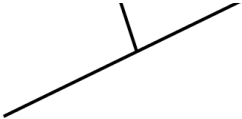
A



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.

Question 2

2015 ▪ Q2

[Figure 1. Glycolysis and pyruvate oxidation: Glucose (chain of 6 circles) reacts with 2 ADP + 2 Pi and 2 NAD^+ to yield 2 ATP, 2 NADH, and 2 Pyruvate (chain of 3 circles). The 2 Pyruvate are converted to 2 CO_2, 2 NADH, and 2 Acetyl-CoA (chain of 2 circles).]

[Figure 2. Krebs cycle: 2 Acetyl-CoA (2 circles) enters a cycle; 2 OAA (4 circles) combines with it going into the cycle, producing 2 TCA (6 circles) coming out. Around the cycle: inputs 2 NADH and 2 $FADH_2$ feed in; outputs are 2 CO_2, 2 NADH (first turn), 2 GTP (bottom), and 2 CO_2, 2 NADH (second turn).]

[Figure 3. Electron transport chain: A membrane diagram showing Complex I, Complex II, Complex III, and Complex IV embedded in a phospholipid bilayer. NADH and NAD^+ enter at Complex I; 2 electrons ($2e^-$) pass from Complex I and Complex II to Complex III, then to Complex IV. H^+ ions are pumped across the membrane at

Question 2

Complex I, Complex III, and Complex IV (shown by upward H^+ arrows). At Complex IV, $\frac{1}{2}O_2$ combines (with H^+) to form H_2O.]
Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.
(a) Using the information above, **describe** ONE contribution of each of the following in ATP synthesis.
- Catabolism of glucose in glycolysis and pyruvate oxidation - Oxidation of intermediates in the Krebs cycle - Formation of a proton gradient by the electron transport chain

Question 2

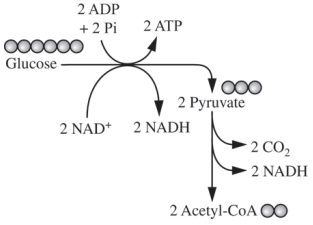


Figure 1. Glycolysis and pyruvate oxidation

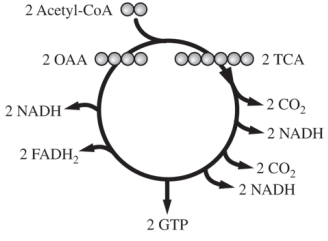
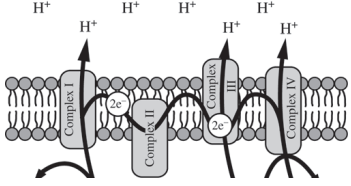


Figure 2. Krebs cycle



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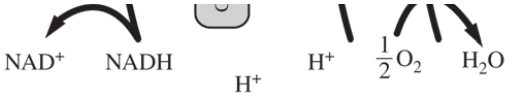

Question 2

2015 ▪ Q2

[Figure 1. Glycolysis and pyruvate oxidation: Glucose (chain of 6 circles) reacts with 2 ADP + 2 Pi and 2 NAD^+ to yield 2 ATP, 2 NADH, and 2 Pyruvate (chain of 3 circles). The 2 Pyruvate are converted to 2 CO_2, 2 NADH, and 2 Acetyl-CoA (chain of 2 circles).]
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Question 2

Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.

(b) Use each of the following observations to **justify** the claim that glycolysis first occurred in a common ancestor of all living organisms.

- Nearly all existing organisms perform glycolysis.
- Glycolysis occurs under anaerobic conditions.
- Glycolysis occurs only in the cytosol.

Question 2

2015 ▪ Q2

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Question 2

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(c) A researcher estimates that, in a certain organism, the complete metabolism of glucose produces 30 molecules of ATP for each molecule of glucose. The energy released from the total oxidation of glucose under standard conditions is 686 kcal/mol. The energy released from the hydrolysis of ATP to ADP and inorganic phosphate under standard conditions is 7.3 kcal/mol. **Calculate** the amount of energy available from the hydrolysis of 30 moles of ATP. **Calculate** the efficiency of total ATP production from 1 mole of glucose in the organism. **Describe** what happens to the excess energy that is released from the metabolism of glucose.

Question 2

2015 ▪ Q2

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Question 2

Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.

(d) The enzymes of the Krebs cycle function in the cytosol of bacteria, but among eukaryotes the enzymes function mostly in the mitochondria. **Pose** a scientific question that connects the subcellular location of the enzymes in the Krebs cycle to the evolution of eukaryotes.

Solution 2

(a) Mark scheme

- 1 point per box, max 3 points. Catabolism of glucose in glycolysis and pyruvate oxidation: produces NADH for use in the electron transport chain (ETC), produces acetyl-CoA for entry into the Krebs cycle, and provides energy for substrate-level phosphorylation of ADP. Oxidation of intermediates in the Krebs cycle: produces NADH or FADH2 for use in the ETC, releases high-energy electrons for the ETC, provides energy to pump protons against their concentration gradient, and produces GTP via substrate-level phosphorylation of ADP. Formation of a proton gradient by the electron transport chain: the flow of protons through membrane-bound ATP synthase generates ATP, providing energy for oxidative phosphorylation of ADP.

Solution 2

(b) Mark scheme

- 1 point per box, max 3 points. Nearly all existing organisms perform glycolysis: the trait/gene/process originated early and was inherited/passed down/highly conserved because glycolysis provided a selective advantage passed on to descendants. Glycolysis occurs under anaerobic conditions: the origin of glycolysis pre-dates free atmospheric oxygen/photosynthesis. Glycolysis occurs only in the cytosol: the origin of glycolysis pre-dates cell types with membrane-bound organelles/eukaryotes/endosymbiosis. Each observation is used to justify that glycolysis is ancient enough to trace to a common ancestor of all life.

Solution 2

(c)

Mark scheme

- 1 point per box, max 3 points. Calculate available energy in ATP: 30 mol ATP $\times$ 7.3 kcal/mol $=$ 219 kcal. Calculate efficiency: 219 kcal / 686 kcal $\approx$ 0.31–0.32, i.e., 31–32%. Describe fate of excess energy: the remaining energy ($686 - 219 \approx 467$ kcal) not captured in ATP is released as heat, which increases entropy.

Solution 2

(d)

Mark scheme

- 1 point for any valid, testable scientific question connecting the subcellular location of Krebs-cycle enzymes to the evolution of eukaryotes, e.g.: 'Since the Krebs cycle occurs in the "cytoplasm" of the mitochondria (the matrix), does this suggest that mitochondria were once free-living prokaryotes (i.e., arose via endosymbiosis)?' Any comparable question linking enzyme location to eukaryotic organelle origin earns the point.

Question 2

2014 ▪ Q2

Mammalian milk contains antibodies that are produced by the mother's immune system and passed to offspring during feeding. Mammalian milk also contains a sugar (lactose) and may contain proteins (protein A, protein B, and casein), as indicated in the table.

MILK COMPONENTS IN DIFFERENT MAMMALS

Character	**Cat**	**Cow**	**Horse**	**Human**	**Pig**
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	−	+	+	−	+
Casein	−	+	+	−	+

Question 2

- indicates the presence of the character, and – indicates the absence of the character

[Below the parts is a blank cladogram template: a horizontal trunk line branching rightward into an upper branch (which itself splits into two terminal branches) and a lower branch (which splits into two terminal branches, one of which further splits into two more terminal branches), for the student to label and annotate.]
(a) Using the data in the table, **construct** a cladogram on the template provided to indicate the most likely evolutionary relationships among the different mammals. **Indicate** on the cladogram where each of the characters most likely arose in the evolutionary process, and **justify** the placement of the characters on the cladogram.

Question 2

(b) Describe FOUR steps in the activation of the mother's specific immune response following exposure to a bacterial pathogen. **Predict** how the mother's immune response would differ upon a second exposure to the same bacterial pathogen a year later.

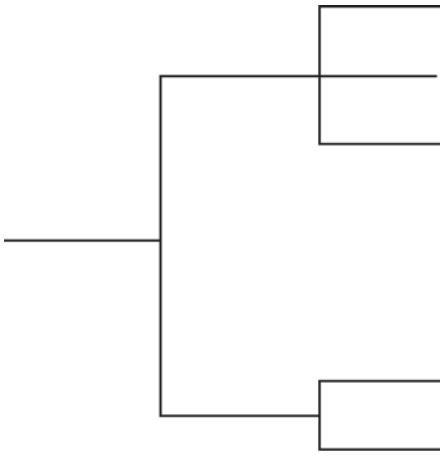
(c) Predict the most likely consequence for a nursing infant who is exposed to an intestinal bacterial pathogen (e.g., *Salmonella*) to which the mother was exposed three months earlier. **Justify** your prediction.

Question 2

MILK COMPONENTS IN DIFFERENT MAMMALS

Character	Cat	Cow	Horse	Human	Pig
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	–	+	+	–	+
Casein	–	+	+	–	+
+ indicates the presence of the character, and – indicates the absence of the character					

Question 2



Solution 2

(a) Mark scheme

- Construct a cladogram from the character table (points earned in ONE column/option only, 3 points max). Option 1: Lactose and Protein A arose in a common ancestor to all 5 animals; Casein and Protein B arose in the common ancestor to the pig/cow/horse clade — topology ((Cat, Human), (Horse, (Pig, Cow))) with Lactose+Protein A marked at the base and Casein+Protein B marked at the pig/cow/horse branch. Option 2: Lactose, Casein, Protein A, and Protein B all arose in a common ancestor to all 5 animals, and Casein and Protein B were subsequently lost in the common ancestor of the cat/human clade — topology ((Pig,(Cow,Horse)),(Cat,Human)) with all four characters marked at the base and a 'loss of both Casein & Protein B' mark at the cat/human branch. 1

Solution 2

point for correct tree topology/branching, 1 point for correctly placed character-origin marks, 1 point for the matching written justification.

Solution 2

(b) Mark scheme

- Description (1 point each, 4 points maximum) — any four of: endocytosis of antigen by a dendritic cell/macrophage/B-cell; degradation of antigen; antigen complexed with an MHC molecule; presentation of antigen on the cell surface; recognition of antigen on the antigen-presenting cell's surface by a (helper) T-cell; activation of a signal transduction mechanism in the T-cell; activation of the (helper) T-cell; (helper) T-cells release chemicals that recruit/activate B-cells; antigen recognition by the B-cell; activation of a signal transduction mechanism in the B-cell; the activated B-cell or T-cell clones itself; plasma cells/B-cells produce antibodies; antibodies recognize the antigen; antibody binding to antigen is specific; memory B cells/memory helper T cells are produced. Prediction (1

Solution 2

point): upon a second exposure a year later, the response is more rapid — any of: results in a more rapid immune response; presence of memory cells; greater production of antibodies; antibodies circulate longer; antibodies have greater affinity for the antigen.

Solution 2

(c)

Mark scheme

- Points earned in a single row only (2 points max). Option 1: Prediction — the infant will be protected/not get sick (1 pt); Justification — antibodies are passed to the infant in utero/via breast milk, or the infant receives B-cells in breast milk (1 pt). Option 2: Prediction — the infant will become sick/die (1 pt); Justification — insufficient antibodies were transferred to the offspring, or the infant was exposed to a high infecting dose of the pathogen (1 pt).