

Past-paper walk-through

Mutations ■ 6.7

eXercise

Questions in this set

- 2019 Q1
- 2018 Q1
- 2017 Q6
- 2015 Q1
- 2014 Q8

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 1

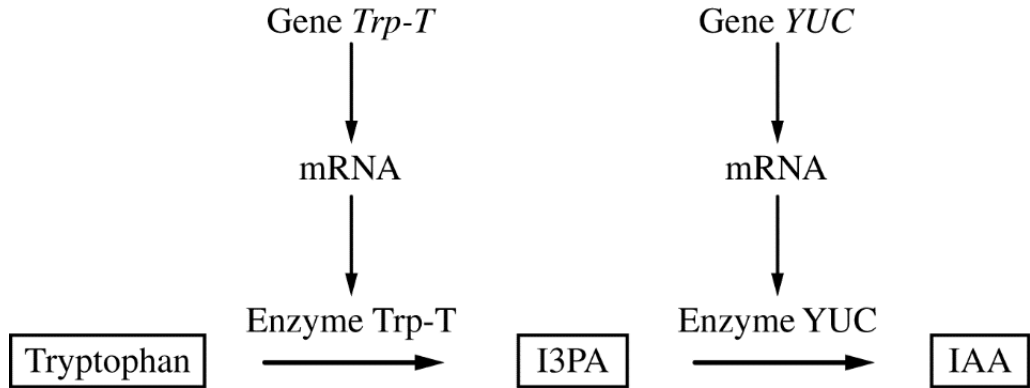
2019 ■ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene *Trp-T* $\rightarrow$ (arrow down) mRNA $\rightarrow$ (arrow down) Enzyme *Trp-T*; Tryptophan $\xrightarrow{\text{Enzyme Trp-T}}$ I3PA. Gene *YUC* $\rightarrow$ (arrow down) mRNA $\rightarrow$ (arrow down) Enzyme *YUC*; I3PA $\xrightarrow{\text{Enzyme YUC}}$ IAA.]

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*.

(a) Circle ONE arrow that represents transcription on the template pathway. **Identify** the molecule that would be absent if enzyme *YUC* is nonfunctional.

Question 1



Question 1

2019 ■ Q1

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(b) Predict how the deletion of one base pair in the fourth codon of the coding region of gene *Trp-T* would most likely affect the production of IAA. **Justify** your prediction.

Question 1

2019 ■ Q1

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(c) Explain one feedback mechanism by which a cell could prevent production of too much IAA without limiting I3PA production.

Question 1

2019 ■ Q1

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(d) Rhizobacteria are a group of bacteria that live in nodules on plant roots. Rhizobacteria can produce IAA and convert atmospheric nitrogen into forms that can be used by plants. Plants release carbon-containing molecules into the nodules. Based

Question 1

on this information, **identify** the most likely ecological relationship between plants and rhizobacteria. **Describe** ONE advantage to the bacteria of producing IAA.

Question 1

2019 ■ Q1

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(e) A researcher removed a plant nodule and identified several “cheater” rhizobacteria that do not produce IAA or fix nitrogen. **Describe** the evolutionary advantage of being a bacterial cheater in a population composed predominantly of noncheater bacteria.

Question 1

Plants can adjust the amount of carbon-containing molecules released into nodules in response to the amount of nitrogen fixed in the nodule. **Predict** the change in the bacterial population that would cause the plant to reduce the amount of carbon-containing molecules provided to the nodule.

Solution 1

(a)

Mark scheme

- Circle: Circle either arrow that points from a gene (Trp-T or YUC) to its mRNA — this represents transcription. [1 point] Identify: If enzyme YUC is nonfunctional, the molecule IAA would be absent, because YUC catalyzes the conversion of I3PA to IAA (the final step of the pathway); with no functional YUC, I3PA cannot be converted to IAA. [1 point]

Solution 1

(b)

Mark scheme

- Prediction: Deletion of one base pair in the fourth codon of the Trp-T coding region would most likely reduce IAA production, or result in no IAA production. [1 point] Justification (any one): the frameshift mutation results in translation of an inactive/nonfunctional Trp-T enzyme; OR the mutation results in no translation of the Trp-T enzyme (e.g., a premature stop codon); OR the mutation results in no/reduced production of I3PA (since Trp-T is needed to convert tryptophan to I3PA, and I3PA is the precursor for IAA). [1 point]

Solution 1

(c)

Mark scheme

- This is a negative feedback (feedback inhibition) mechanism: as IAA accumulates, increasing amounts of IAA inhibit the pathway that produces it. [1 point] Specifically, the rising IAA level inhibits production of the YUC enzyme, or inhibits YUC enzyme activity — this blocks only the second step ($\text{I3PA} \rightarrow \text{IAA}$), so I3PA production (via Trp-T, the first step) is not limited. [1 point]

Solution 1

(d)

Mark scheme

- Identification: The relationship between plants and rhizobacteria is mutualism — both organisms benefit. [1 point] Description: One advantage to the bacteria of producing IAA is that IAA promotes root growth, which increases the plant's habitat/number of nodules available to house the rhizobacteria; in exchange, the bacteria receive carbon-containing molecules released by the plant (as a result of the increased plant growth). [1 point]

Solution 1

(e)

Mark scheme

- Description: 'Cheater' bacteria that benefit from nodule resources without expending energy to produce IAA or fix nitrogen have more energy available for their own reproduction, giving them a reproductive/evolutionary advantage over noncheater bacteria as long as cheaters remain a minority. [1 point]
Prediction: A decrease in the nitrogen-fixing/noncheater bacteria (or a decrease in the total amount of nitrogen fixed in the nodule) would cause the plant to reduce the amount of carbon-containing molecules it releases into that nodule. [1 point]

Question 1

2018 ■ Q1

Question 1

[Figure 1: Phylogenetic tree (cladogram) representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons. The tree branches, from top to bottom: Black Bears, European Brown Bears, Polar Bears, Western North American Brown Bears, Asian Brown Bears. European Brown Bears and Polar Bears share a node; that node and (Western North American Brown Bears + Asian Brown Bears, which share their own node) share a deeper node; that node and Black Bears share the deepest node shown. Below the tree is a time axis labeled “Hundreds of Thousands of Years Ago” with tick marks at 50, 40, then a break (squiggle) then 4, 3, 2, 1, with the deepest node aligning near 40-50 and shallower nodes aligning at successively smaller values toward 1. Caption: “Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons.”]

Question 1

Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their evolutionary relatedness (Figure 1).

Question 1

A researcher studying adaptation in bears sequenced the nuclear gene encoding a lysosomal trafficking protein (LYST) in polar bears, brown bears, black bears, and panda bears. There are seven inferred amino acid substitutions that are found only in polar bears. Mutations that cause similar substitutions in the human LYST protein are associated with Chediak-Higashi syndrome, an autosomal recessive condition in which pigment is absent from the hair and eyes. The researcher used the inferred amino acid sequences to build the distance matrix shown in Table 1.

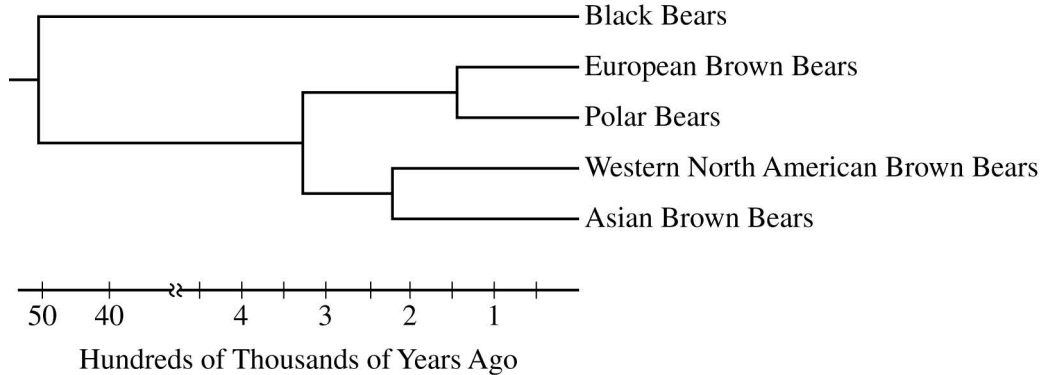
TABLE 1. AMINO ACID DIFFERENCES IN THE LYST PROTEIN AMONG BEAR SPECIES

	Panda	Black	Brown	Polar
Panda	–			
Black	33	–		
Brown	34	1	–	
Polar	40	7	8	–

Question 1

(a) Use the phylogenetic tree in Figure 1 to **estimate** the age in hundreds of thousands of years of the most recent common ancestor of all brown bears. **Identify** the population of brown bears to which polar bears are most closely related based on the mitochondrial DNA sequence comparison. **Identify** two populations whose positions could be switched without affecting the relationships illustrated in the phylogenetic tree.

Question 1

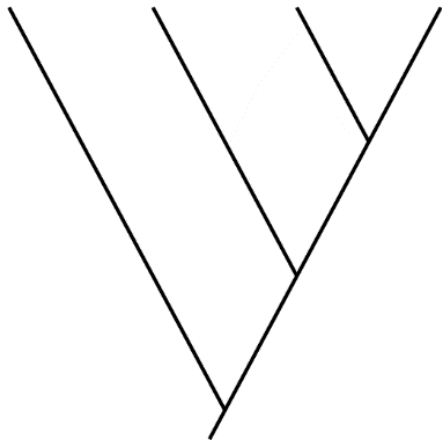


Question 1

DATA FROM THE FOLLOWING TABLE

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Question 1



Question 1

2018 ■ Q1

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