Past-paper walk-through

Transcription and RNA Processing ▪ 6.3

eXercise

Questions in this set

- 2022 Q6
- 2021 Q6
- 2019 Q1
- 2016 Q4

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 6

2022 ▪ Q6

Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the

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normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

5' Cap Structure	mRNA Half-Life $\pm 2\text{SE}_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2\text{SE}_{\bar{x}}$ (relative to amount in normal cap)
No cap	1.41 ± 0.02	0.011 ± 0.000
Normal GTP cap	16.10 ± 1.83	1.000 ± 0.007
Modified cap I	15.50 ± 1.57	4.777 ± 0.042
Modified cap II	27.00 ± 2.85	13.094 ± 0.307
Modified cap III	18.09 ± 0.81	6.570 ± 0.075

(a) Based on the data, identify which cap structure is most likely to protect the end of the mRNAs from degradation.

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(b) Based on the data for the mRNAs with modified caps, describe the relationship between the mRNA half-life and the total amount of protein produced.
(c) After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. Evaluate their hypothesis by comparing the data in Table 1.
(d) Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. Explain why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells.

Solution 6

(a)

Mark scheme

- Modified cap II is most likely to protect the end of the mRNAs from degradation, since it has the longest mRNA half-life in Table 1 (27.00 +/- 2.85 hours).

Solution 6

(b)

Mark scheme

- For the mRNAs with modified caps, a longer mRNA half-life is associated with a greater total amount of protein produced - i.e. there is a positive correlation/relationship between mRNA half-life and the amount of protein produced.

Solution 6

(c)

Mark scheme

- The data support the researchers' hypothesis: the half-lives of the modified-cap-I mRNA (15.50 hours) and the normal-GTP-cap mRNA (16.10 hours) are essentially the same, but the amount of protein produced from the modified-cap-I mRNA (4.777, relative units) is more than four times that produced from the normal-cap mRNA (1.000) - so, with roughly equal amounts of mRNA available for translation over a similar timeframe, each modified-cap-I mRNA molecule must have been translated more frequently than each normal-cap mRNA molecule.

Solution 6

(d)

Mark scheme

- Production of a foreign protein is more likely from introduced mRNA than DNA because protein production from DNA first requires transcription (and transcription factors to initiate it), whereas an introduced mRNA can be translated directly; also, protein production from mRNA does not depend on correct posttranscriptional processing of a pre-mRNA, and the cell may be unable to transcribe the foreign DNA at all, whereas the mRNA can still be directly translated.

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2021 ▪ Q6

The small invertebrate krill species *Thysanoessa inermis* is adapted to cold (4°C) seawater. Over the past ten years, there has been a gradual increase in the water temperature of the krill's habitat. A sustained increase in water temperature may ultimately affect the ability of the krill to survive.

One effect of higher temperatures is protein misfolding within cells. Krill have several *hsp* genes that code for heat-shock proteins (HSPs). These proteins help prevent protein misfolding or help to refold proteins to their normal shapes.

Scientists conducted experiments on *T. inermis* to detect changes in the expression of *hsp* genes when the krill were exposed to temperatures above 4°C. An experimental group of krill was maintained in tanks with 4°C seawater and then placed into tanks with 10°C seawater for approximately three hours. The krill were then given a six-hour recovery period in the 4°C seawater tanks. A control group of krill was moved from a

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tank of 4°C seawater to another tank of 4°C seawater for approximately three hours and then returned to the original tank. The scientists analyzed *hsp* gene expression by measuring the concentrations of three mRNAs (I, II, III) transcribed from certain *hsp* genes in both the heat-shocked krill (Figure 1) and the control krill. For the control krill, no transcription of the *hsp* genes was detected throughout the test period (data not shown).

[Figure 1: Line graph, "Average mRNA Concentration (ng/μL)" (y-axis, 0 to 30) vs. "Time (hours)" (x-axis, 0 to 12), with a shaded region from hour 3 to hour 6 marking the 10°C exposure period (labeled "4°C" from 0-3, "10°C" from 3-6 shaded grey, "4°C" from 6-12). Three curves: mRNA I (filled triangles, dashed line) stays near 0 from hours 0-3, rises slowly to ~2 at hour 4, ~3.5 at hour 5, ~5 at hour 6, then rises steeply to ~9.5 at hour 7, ~14.5 at hour 8, ~19.5 at hour 9, peaks at ~25 at hour 10, declines to ~20 at hour 11, ~15.5 at hour 12; mRNA II (open squares, solid line) stays

Question 6

near 0 from hours 0-2, rises to ~2 at hour 3, ~7.5 at hour 4, ~13.5 at hour 5, peaks at ~20 at hour 6, then declines to ~12.5 at hour 7, ~5 at hour 8, ~5.5 at hour 9, ~6 at hour 10, ~3.5 at hour 11, ~1 at hour 12; mRNA III (open circles, solid line) stays near 0 throughout hours 0-7, rises slightly to ~1 at hour 8, ~2 at hour 9, ~1.5 at hour 10, ~1 at hour 11, back to ~0 at hour 12. Error bars represent $\pm 2SE_{\bar{x}}$ on all curves. Caption: "Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from hsp genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$."]

(a) Identify the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment.

(b) Describe the trend in the average concentration of mRNA I throughout the experiment.

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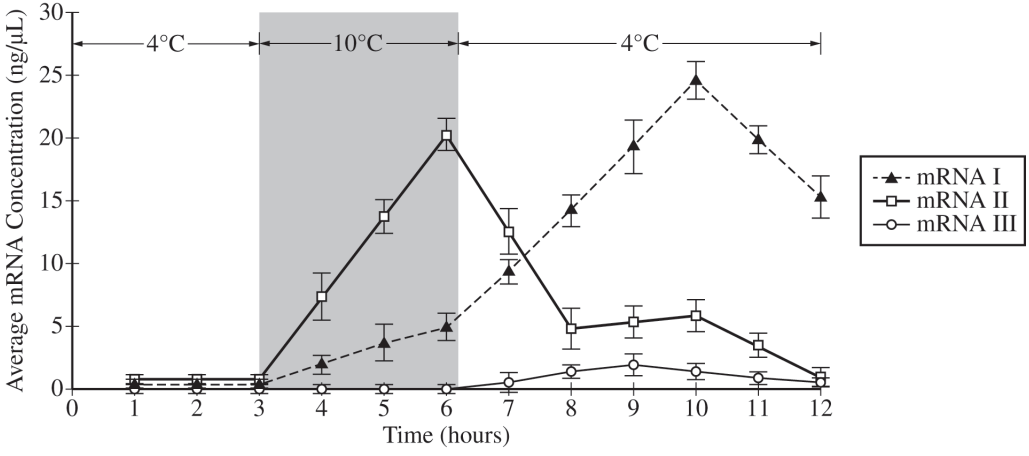
(c) The scientists hypothesized that the heat-shock protein (HSP) translated from mRNA I plays a greater role in refolding proteins than does the HSP translated from mRNA II. Use the data to **support** the hypothesis.
(d) mRNAs I and II are transcribed from the same gene. **Explain** how a cell can produce two different mRNAs from the same gene.

Question 6


4°C
10°C
4°C
Average mRNA Concentration (ng/μL)
Time (hours)
0
1
2
3
4
5
6
7
8
9
10
11
12
0
5
10
15
20
25
30
mRNA I
mRNA II
mRNA III

Solution 6

(a)

Mark scheme

- The hsp mRNA with the slowest rate of concentration increase in response to heat-shock treatment is mRNA III.

Solution 6

(b)

Mark scheme

- Trend in average concentration of mRNA I throughout the experiment: no change in concentration from hour 1 to 3; concentration increased (slightly) between hours 3 and 6 (during the heat shock); concentration increased at a greater rate from hours 6 to 10 (for about 4 hours after the heat shock ended); concentration then decreased after hour 10.

Solution 6

(c)

Mark scheme

- Data supporting the hypothesis that the HSP from mRNA I plays a greater role in refolding proteins than the HSP from mRNA II: mRNA I is still expressed at a high level after the heat-shock period (peaking around hour 10, well after the 10°C exposure ends at hour 6), while mRNA II levels decrease after the heat shock — i.e., right when misfolded proteins would need to be refolded, mRNA I (and its protein) remains elevated while mRNA II does not.

Solution 6

(d)

Mark scheme

- How a cell can produce two different mRNAs (I and II) from the same gene (accept any): the cell expresses different exons/performs alternative splicing; the cell uses different transcription termination sites (poly(A) sites); or the cell uses different promoters.

Question 1

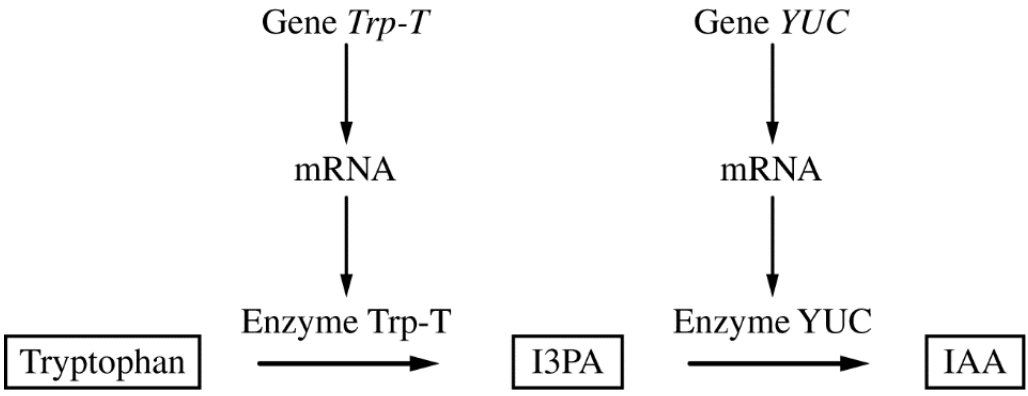
2019 ▪ Q1

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(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


Gene *Trp-T*
mRNA
Enzyme Trp-T
Tryptophan
I3PA
Gene *YUC*
mRNA
Enzyme YUC
IAA

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

[Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan: Gene Trp-T -> (arrow down) mRNA -> (arrow down) Enzyme Trp-T; Tryptophan –(Enzyme Trp-T)–> I3PA. Gene YUC -> (arrow down) mRNA -> (arrow down) Enzyme YUC; I3PA –(Enzyme YUC)–> IAA.]

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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 (I3PA $\rightarrow$ 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 4

2016 ▪ Q4

[Figure showing gene expression in a eukaryotic cell (nucleus enclosed within the cell membrane). A DNA strand is shown with alternating black and white segments labeled "introns" (white segments) and "exons" (black segments) at the top, inside the nucleus. An arrow points down from the DNA to a shorter bar labeled "Primary transcripts," which still has alternating black/white (intron/exon) segments. A second arrow points from the primary transcript down through the nuclear envelope to a solid black bar labeled "Mature mRNA" (now containing only the exon segments, introns removed) in the cytoplasm. A third arrow points from the mature mRNA down to a shorter gray bar labeled "Protein."]

The figure represents the process of expression of gene X in a eukaryotic cell.

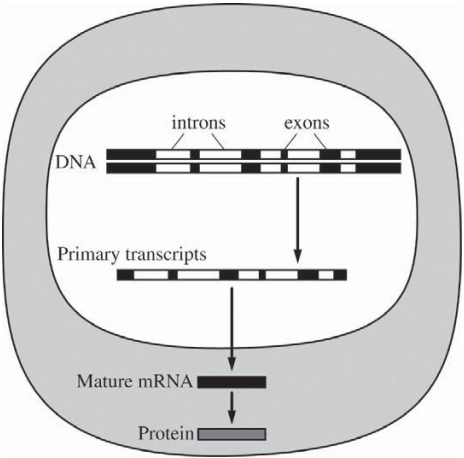
(a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length. **Describe** the modification that most likely resulted in the 8

Question 4

kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs.

(b) Predict the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction.

Question 4


introns
exons
DNA
Primary transcripts
Mature mRNA
Protein

Solution 4

(a)

Mark scheme

- Describe the modification (1 point): removal of introns from the primary transcript (RNA splicing/RNA processing) accounts for the 8 kb difference between the 15 kb primary transcript and the 7 kb mature mRNA. Identify the cellular location (1 point): the nucleus.

Solution 4

(b)

Mark scheme

- Prediction (1 point): the mature gene X mRNA would be 15 kb long if the full-length gene were introduced and expressed in prokaryotic cells - i.e., longer than the 7 kb mature mRNA produced in the eukaryote. Justification (1 point): mRNA processing (intron splicing) typically does not occur in prokaryotic cells, so the primary (unspliced) transcript itself would serve as the mature mRNA, retaining the introns and thus the full 15 kb length.