

Past-paper walk-through

Biotechnology ■ 6.8

eXercise

Questions in this set

- 2022 Q6
- 2016 Q6

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.

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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 $\pm 2SE_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{x}}$ (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.

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(a)

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- 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).

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(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.

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(d)

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- 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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[Figure 1. Detectability of eDNA fragments of varying lengths. Bar graph with y-axis “Days that eDNA is Detectable after Shedding” from 0 to 5, x-axis “Amplified eDNA Fragment Length” with two categories: “Short” (bar height approximately 4.2 days) and “Long” (bar height approximately 2.7 days).]

[Figure 2. Map of the waterways that connect a nearby river system to Lake Michigan. A map showing a river system on the left connecting to Lake Michigan on the right, with numerous open circles (labeled “No silver carp eDNA detected”) scattered mostly within Lake Michigan and a few in the connecting rivers, and five filled/solid circles (labeled “Silver carp eDNA detected”) clustered along the connecting river/waterway near where it meets the lake, with one filled circle located just inside the lake boundary near the river mouth. Legend: filled circle = Silver carp eDNA detected; open circle = No silver carp eDNA detected; solid line = Rivers connected to Lake Michigan.]

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Living and dead organisms continuously shed DNA fragments, known as eDNA, into the environment. To detect eDNA fragments in the environment, the polymerase chain reaction (PCR) can be used to amplify specific eDNA fragments. eDNA fragments of different lengths persist in the environment for varying amounts of time before becoming undetectable (Figure 1).

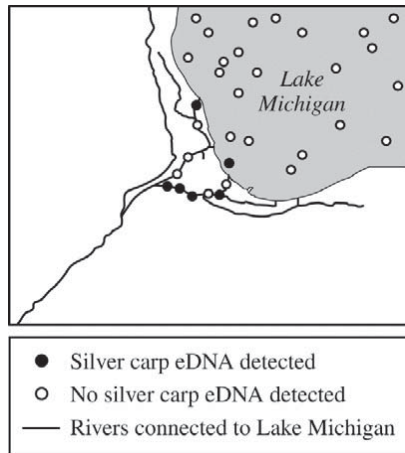
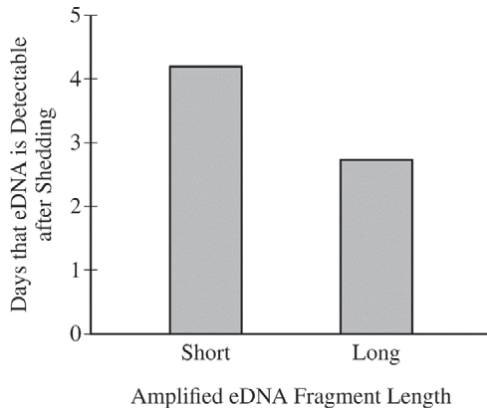
To investigate whether silver carp, an invasive fish, have moved from a nearby river system into Lake Michigan, researchers tested water samples for the presence of eDNA specific to silver carp (Figure 2).

(a) Justify the use of eDNA sampling as an appropriate technique for detecting the presence of silver carp in an environment where many different species of fish are found. **Propose** ONE advantage of identifying long eDNA fragments as opposed to short fragments for detecting silver carp.

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(b) The researchers tested a large number of water samples from Lake Michigan and found eDNA specific to silver carp in a single sample in the lake, as indicated in Figure 2. The researchers concluded that the single positive sample was a false positive and that no silver carp had entered Lake Michigan. **Provide reasoning** other than human error to support the researchers' claim.

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(a) Mark scheme

- Justify use of eDNA sampling (1 point): eDNA sampling allows detection of the fish's presence without needing to visually identify or physically catch the fish, and eDNA sequences can be matched specifically to silver carp even among a mixed community of many fish species. Proposed advantage of long fragments over short fragments (1 point, any one): longer eDNA fragments indicate a more recent presence of the fish (they degrade faster than persisting for long periods); longer fragments are more likely to contain a sequence that is uniquely specific to silver carp; OR longer sequences/more base pairs increase the accuracy/specificity/confidence that the eDNA truly comes from a silver carp rather than a related species.

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(b)

Mark scheme

- Reasoning other than human error (1 point): the silver-carp eDNA could have entered Lake Michigan by a means other than a live fish being present - e.g., carried in by river flow, transported on boats, or present in waste/feces from a predator that had eaten a silver carp elsewhere - so a positive eDNA sample does not necessarily mean a living silver carp is in the lake.