33.1 Gene expression: regulate products, not just genes

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS transcription factor • epigenetic modification

Objective

Gene expression: regulate products, not just genes. Original classroom practice for IB HL; not an official IB paper.

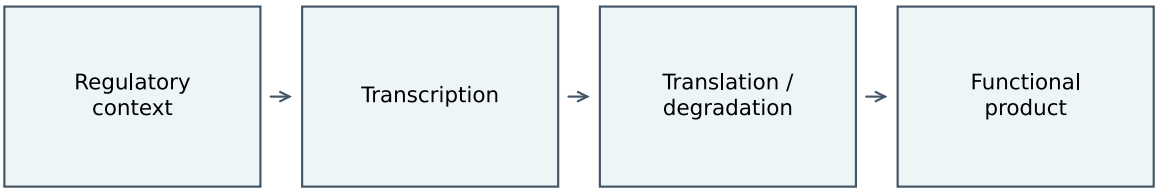
1 Key knowledge and worked examples

What would explain this observation?

- Two cells with the same genome make different proteins. Regulation changes which information is used and when.

Build the model

- Gene expression can be regulated at transcription and later stages.
- A **transcription factor** can affect transcription through interactions with DNA and other proteins.
- **Epigenetic modifications** can influence expression without changing the underlying DNA sequence.
- transcription factor: A protein that influences transcription.
- epigenetic modification: A change affecting expression without changing the DNA sequence.



Choose evidence that can test it

- Distinguish a measured mRNA change from a protein or functional change.
- Translation, degradation and protein modification can all intervene.
- Regulation is specific to a cell context and environmental conditions.

In the lab: Compare treated and control expression data after checking normalization and replicates. Use evidence from a supplied perturbation to discuss causal models, rather than equating every association with a direct mechanism.

Work from known quantities

- Known: normalized transcript abundance is 12 in treatment and 3 in control.
- Fold change = $12/3 = 4$.
- Equal normalized abundance does not require equal absolute cell counts in the two raw samples.

Your turn: Transcript abundance is 15 in treatment and 5 in control. Find fold change.

Check the conclusion and its limits

- An epigenetic change is not automatically a DNA-sequence mutation.
- More mRNA does not guarantee proportionally more active protein.

Not true: Every change in gene expression is a mutation. Expression changes are regulatory - the same DNA is read more or less often. A mutation is a change in the DNA sequence itself; most changes in expression involve no mutation at all.

Key:

- Gene expression can be regulated at transcription and later stages.
- Distinguish a measured mRNA change from a protein or functional change.
- Watch for: an epigenetic change is not automatically a DNA-sequence mutation.

■ **Write from a transcript fold change of 5**

- Normalized transcript abundance is 20 in the treatment and 4 in the control.
- Find the fold change. An mRNA change is not automatically a protein change.

2 Practice

2.1 What is justified by higher measured mRNA abundance? Choose one answer.

- **A** A guaranteed equal increase in protein activity
- **B** Proof that the gene sequence mutated
- **C** More of that transcript under the measured conditions [1]

2.2 Transcript abundance is 15 in treatment and 5 in control. Find fold change. Show the relation, substitution and units. [2]

2.3 Decide whether this claim is true and justify: Every change in gene expression is a mutation. [2]

2.4 A protein that influences transcription: write the technical term. [1]

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3 Exam-style questions

3.1 Normalized expression changes from 4 to 12 units. Distinguish fold change from percentage increase. What can be inferred about absolute transcript counts? [4]

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Solutions

2.1 C Higher mRNA abundance shows more of that transcript under the measured conditions - nothing more. Protein level also depends on translation and degradation, and an expression change says nothing about the DNA sequence.

2.2 fold change=treatment/control=15/5=3.

2.3 False. Expression changes are regulatory - the same DNA is read more or less often. A mutation is a change in the DNA sequence itself; most changes in expression involve no mutation at all.

2.4 transcription factor. transcription factor means A protein that influences transcription.

3.1 Fold change 3; increase$(12-4)/4\times100=200\%$. Absolute counts need normalization and sample-size information. Expression association alone does not demonstrate a causal regulatory mechanism.