

Past-paper walk-through

Gene Expression and Cell Specialization ■ 6.6

eXercise

Questions in this set

- 2023 Q6
- 2019 Q7
- 2015 Q7

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

2023 ■ Q6

Housekeeping genes encode proteins involved in universally important processes such as transcription, translation, and glycolysis. Because these genes appear to be expressed in all cells at constant levels, the expression of housekeeping genes is often used as a control when comparing how the expression of other genes varies under different conditions.

Researchers studying the effect of pesticides on declining bee populations wanted to determine whether the expression of four housekeeping genes (*GAPDH*, *RPL32*, *RPS5*, and *TBP-AF*) was in fact constant in bees across different variables. The researchers collected samples of mRNA for each of the four genes and compared how their expression varied across the developmental stage of the bee, the sex of the bee, and the cell type from which the sample was taken. The mRNA from the samples was reverse transcribed to produce DNA copies of each gene. PCR was then used to

Question 6

amplify the DNA, and the Cq value was determined. The Cq value is the number of PCR cycles needed to produce a specified number of DNA copies. A high Cq value for a sample indicates the gene was expressed at a low level.

To analyze whether any of the examined variables affected expression of the housekeeping genes, researchers examined the range of Cq values for each gene in response to each variable. Genes with a wide range of Cq values were determined to be affected by the variable, while genes with a narrow range of Cq values were determined to be unaffected by the variable.

[Figure 1, a box-and-whisker plot with the y-axis labeled “Cq Value” ranging from 16 to 32 (gridlines at 16, 20, 24, 28, 32) and the x-axis labeled “Variable Examined”, divided by dashed vertical lines into three groups: “Developmental Stage”, “Sex”, and “Cell Types”. Each group contains four box plots, one per gene, per the legend: open square = *GAPDH*, filled black square = *RPL32*, gray square = *RPS5*,

Question 6

hatched/crosshatched square = *TBP-AF*. Developmental Stage group: *GAPDH* box spans roughly 15.5-19.5 (median ~17.5); *RPL32* box spans roughly 16.5-18.5 (median ~17.5); *RPS5* box spans roughly 15.5-18 (median ~16.5); *TBP-AF* box spans roughly 19.5-22 (median ~20.5). Sex group: *GAPDH* box spans roughly 17-18.5 (median ~17.5); *RPL32* box spans roughly 16.5-18.5 (median ~17.5); *RPS5* box spans roughly 15.5-17 (median ~16); *TBP-AF* box spans roughly 19.5-21.5 (median ~20.5). Cell Types group: *GAPDH* box spans roughly 17.5-31.5 (median ~20.5), the widest range of all boxes shown; *RPL32* box spans roughly 16.5-26 (median ~18.5); *RPS5* box spans roughly 16.5-25.5 (median ~18); *TBP-AF* box spans roughly 21-32 (median ~23).]

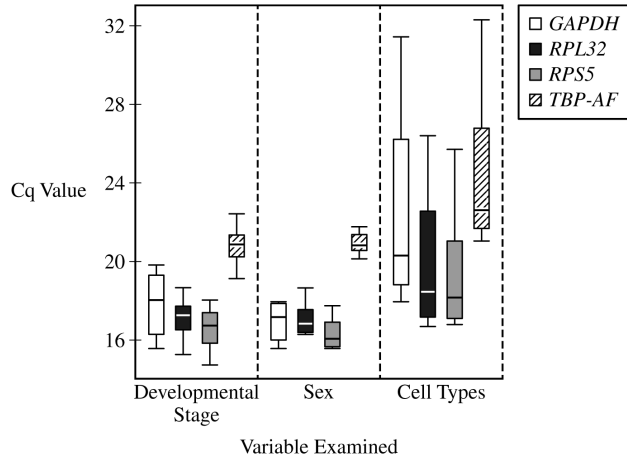
Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

(a) Based on the data in Figure 1, **identify** the gene that had the lowest median Cq value when bees of different developmental stages were compared.

Question 6

- (b) The Cq value is inversely proportional to the amount of mRNA from that gene in the starting sample. Based on the data in Figure 1, **identify** the gene that has the lowest level of gene expression regardless of variable.
- (c) The scientists investigated the effect of pesticides on the expression of other genes in one cell type of a group of bees containing males and females of the same developmental stage. They hypothesized that *TBP-AF* would serve as the best control gene for this experiment. Use the data to **evaluate** their hypothesis.
- (d) **Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee.

Question 6



Solution 6

(a)

Mark scheme

- RPS5 had the lowest median C_q value when bees of different developmental stages were compared (per the box plot in Figure 1).

Solution 6

(b)

Mark scheme

- TBP-AF has the lowest level of gene expression regardless of variable. Because Cq value is inversely proportional to the amount of starting mRNA, and TBP-AF shows the highest Cq values across all three variables examined (developmental stage, sex, and cell type) in Figure 1, it corresponds to the lowest mRNA/expression level overall.

Solution 6

(c)

Mark scheme

- The hypothesis that TBP-AF is the best control gene for this experiment (comparing males vs. females within one cell type/developmental stage) is supported: in the "Sex" panel of Figure 1, TBP-AF has the smallest (narrowest) range of Cq values / most constant expression when comparing sexes, meaning its expression is unaffected by the sex variable — the property required of a good control gene.

Solution 6

(d)

Mark scheme

- Expression of a gene such as GAPDH can differ between cell types within the same bee because different cell types contain different levels/types of transcription factors, which bind regulatory DNA sequences differently in each cell type and therefore regulate (activate or repress) the expression of genes like GAPDH differently from one cell type to another, even though all cells share the same genome.

Question 7

2019 ■ Q7

mRNA EXPRESSION LEVELS

[Figure 1. mRNA expression levels of six genes — a table with rows Liver, Heart, Brain, Kidney, Pancreas, Skeletal Muscle and columns Gene E, Gene F, Gene G, Gene H, Gene I, Gene J; each cell is shaded white (No mRNA), gray (Moderate amount of mRNA), or black (High amount of mRNA), as follows:

Tissue	Gene E	Gene F	Gene G	Gene H	Gene I	Gene J
Liver	High	High	High	No	No	No
Heart	High	Moderate	Moderate	No	No	No
Brain	High	High	High	Moderate	Moderate	No
Kidney	No	Moderate	Moderate	High	High	No
Pancreas	No	No	Moderate	High	Moderate	No
Skeletal Muscle	No	No	High	Moderate	High	No

Question 7

A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

(a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.

(b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.

Question 7

mRNA EXPRESSION LEVELS

		Genes					
Tissue		<i>Gene E</i>	<i>Gene F</i>	<i>Gene G</i>	<i>Gene H</i>	<i>Gene I</i>	<i>Gene J</i>
Liver		High amount of mRNA	High amount of mRNA	High amount of mRNA	No mRNA	No mRNA	No mRNA
Heart		High amount of mRNA	Moderate amount of mRNA	Moderate amount of mRNA	No mRNA	No mRNA	No mRNA
Brain		High amount of mRNA	High amount of mRNA	High amount of mRNA	Moderate amount of mRNA	Moderate amount of mRNA	No mRNA
Kidney		No mRNA	Moderate amount of mRNA	Moderate amount of mRNA	High amount of mRNA	High amount of mRNA	No mRNA
Pancreas		No mRNA	No mRNA	Moderate amount of mRNA	High amount of mRNA	Moderate amount of mRNA	No mRNA
Skeletal Muscle		No mRNA	No mRNA	High amount of mRNA	Moderate amount of mRNA	High amount of mRNA	No mRNA

□ No mRNA

■ Moderate amount of mRNA

■ High amount of mRNA

Solution 7

(a)

Mark scheme

- Identification: Gene G is most likely to encode a protein that is an essential component of glycolysis. [1 point] Reasoning: Gene G's mRNA is the only one of the six genes expressed (present, whether moderate or high) in all six tissues examined (liver, heart, brain, kidney, pancreas, skeletal muscle); since glycolysis is a metabolic pathway that occurs in essentially all cells/tissues (all six tissues), a gene essential for glycolysis would be expected to be expressed everywhere, matching Gene G's universal expression pattern. [1 point]

Solution 7

(b)

Mark scheme

- A tissue can have high gene H mRNA levels but no gene H protein because gene expression is regulated beyond transcription — for example: the mRNA may fail to be exported from the nucleus into the cytoplasm where translation occurs; the mRNA may not be translated at all (e.g., translation is blocked by RNA interference/a regulatory microRNA); or the protein could undergo post-transcriptional/post-translational regulation (e.g., rapid degradation) that prevents functional, detectable protein from accumulating even though the mRNA is present.

Question 7

2015 ■ Q7

Smell perception in mammals involves the interactions of airborne odorant molecules from the environment with receptor proteins on the olfactory neurons in the nasal cavity. The binding of odorant molecules to the receptor proteins triggers action potentials in the olfactory neurons and results in transmission of information to the brain. Mammalian genomes typically have approximately 1,000 functional odorant-receptor genes, each encoding a unique odorant receptor.

(a) Describe how the signal is transmitted across the synapse from an activated olfactory sensory neuron to the interneuron that transmits the information to the brain.

(b) Explain how the expression of a limited number of odorant receptor genes can lead to the perception of thousands of odors. Use the evidence about the number of odorant receptor genes to **support** your answer.

Solution 7

(a)

Mark scheme

- 1 point. Neurotransmitters are released from the (presynaptic) olfactory sensory neuron and bind to receptors on the (postsynaptic) interneuron, which transmits the signal onward toward the brain.

Solution 7

(b) Mark scheme

- 2 points maximum, credited from only ONE of the following rows (explanation 1 pt + matching support 1 pt). Molecular: Explanation — one odorant molecule can be recognized by more than one odorant receptor, and/or one odorant receptor can bind more than one odorant molecule; Support — the resulting mathematical combinations of receptor activation greatly expand the number of distinguishable odors despite a limited number of receptor genes. CNS Control: Explanation — signals from different receptors are integrated in the brain; Support — multiple interactions among neurons in the brain. Genetic: Explanation — alternate processing/splicing of the pre-mRNA/primary transcript; Support — multiple different receptor proteins can be produced from a single gene.