2023

AP® Biology

Scoring Guidelines

Question 1: Interpreting and Evaluating Experimental Results with Experimental Design — 9 points

In eukaryotic microorganisms, the PHO signaling pathway regulates the expression of certain genes. These genes, *Pho* target genes, encode proteins involved in regulating phosphate homeostasis. When the level of extracellular inorganic phosphate (Pi) is high, a transcriptional activator Pho4 is phosphorylated by a complex of two proteins, Pho80–Pho85. As a result, the *Pho* target genes are not expressed. When the level of extracellular Pi is low, the activity of the Pho80–Pho85 complex is inhibited by another protein, Pho81, enabling Pho4 to induce the expression of these target genes. A simplified model of this pathway is shown in Figure 1.

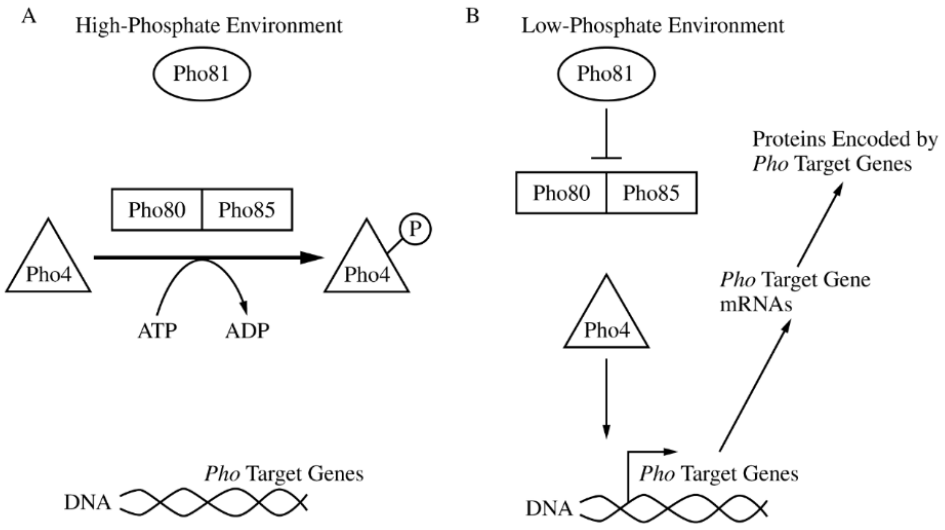


Figure 1. A simplified model of the regulation of expression of *Pho* target genes in (A) a high-phosphate (high-Pi) environment and (B) a low-phosphate (low-Pi) environment

To study the role of the different proteins in the PHO pathway, researchers used a wild-type strain of yeast to create a strain with a mutant form of Pho81 (*pho81mt*) and a strain with a mutated form of Pho4 (*pho4mt*). In each of these mutant strains, researchers measured the activity of a particular enzyme, APase, which removes phosphates from its substrates and is encoded by *PHO1*, a *Pho* target gene (Table 1). They then determined the level of *PHO1* mRNA relative to that of the wild-type yeast strain, which was set to 10.

TABLE 1. APase ACTIVITY AND RELATIVE AMOUNTS OF *PHO1* mRNA IN WILD-TYPE AND MUTANT STRAINS OF YEAST IN HIGH- AND LOW-PHOSPHATE ENVIRONMENTS

Yeast Strain	Mutation	APase Activity in High-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$	APase Activity in Low-Pi Environment (mU/mL/OD_{600}) $\pm 2SE_{\bar{x}}$	Relative Amounts of *PHO1* mRNA in High-Pi Environment $\pm 2SE_{\bar{x}}$	Relative Amounts of *PHO1* mRNA in Low-Pi Environment $\pm 2SE_{\bar{x}}$
Wild-type	None	0.5 ± 0.1	17.3 ± 0.9	0.1 ± 0.0	10 ± 2.0
pho81mt	Nonfunctional Pho81	0.4 ± 0.1	0.6 ± 0.1	0.7 ± 0.2	0.9 ± 0.8
pho4mt	Nonfunctional Pho4	0.5 ± 0.0	0.8 ± 0.2	0.6 ± 0.4	0.3 ± 0.1

(a) **Describe** the effect the addition of a charged phosphate group can have on a protein that would cause the protein to become inactive. **1 point**

- It changes the structure/shape of the protein.

Explain how a signal can be amplified during signal transduction in a pathway such as the PHO signaling pathway. **1 point**

- Each enzyme (in a signal transduction pathway) can act on many copies of a protein.

Total for part (a) 2 points

(b) Based on Table 1, **identify** a dependent variable in the researchers' experiment. **1 point**

Accept one of the following:

- APase activity
- (Relative) amount of *PHO1* (mRNA)

Justify the researchers' using the wild-type strain for the creation of the mutant strains. **1 point**

Accept one of the following:

- It ensures that any observed differences (in experimental results) between the strains are due to the introduced mutations (and not to other genetic differences between the yeast strains).
- It ensures that the strains are genetically identical except for the introduced mutations.

Justify the researchers' using mutant strains in which only a single component of the pathway was mutated in each strain. **1 point**

Accept one of the following:

- It allows them to test the effect of each mutation separately.
- It allows them to (better) determine which component is responsible for any observed differences.

Total for part (b) 3 points

(c)	Based on the data in Table 1, **identify** the yeast strain and growth conditions that lead to the highest relative amount of *PHO1* mRNA. • Wild-type yeast in a low-Pi environment	**1 point**
	Calculate the percent change in APase activity in wild-type yeast cells in a high-Pi environment compared with that of wild-type cells in a low-Pi environment. Accept one of the following: • 3,360% [(17.3–0.5)/0.5 × 100%] • -97% [(0.5–17.3)/17.3 × 100%]	**1 point**
	Total for part (c)	**2 points**
(d)	In a follow-up experiment, researchers created a strain of yeast with a mutation that resulted in a nonfunctional Pho85 protein. Based on Figure 1, **predict** the effects of this mutation on *PHO1* expression in the mutant strain in a high-Pi environment. • It/*PHO1*/Target genes will be expressed.	**1 point**
	Provide reasoning to **justify** your prediction. • (In a high-Pi environment) a nonfunctional Pho85 will be unable to phosphorylate/inhibit Pho4.	**1 point**
	Total for part (d)	**2 points**
	Total for question 1	**9 points**

Question 2: Interpreting and Evaluating Experimental Results with Graphing — 9 points

Elevated levels of CO_2 increase the rate of photosynthesis and growth in plants. Scientists studying the mechanisms involved in these increases examined a variety of species and found that when plants are exposed to elevated levels of CO_2, there is an increase in the number of chloroplasts per cell. To investigate whether the elevated levels of CO_2 have a similar effect on the number of mitochondria in plant cells, the scientists then selected six of these species to quantify the number of mitochondria per cell when the plants were exposed to both normal and elevated levels of CO_2 (Table 1).

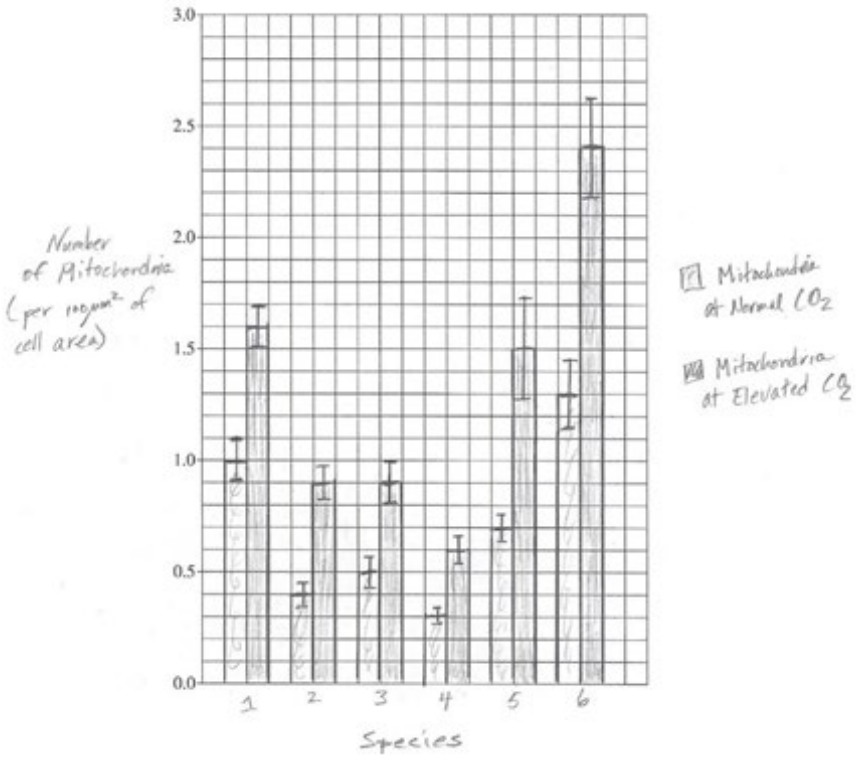
TABLE 1. AVERAGE NUMBER OF MITOCHONDRIA IN PLANTS EXPOSED TO NORMAL AND ELEVATED LEVELS OF CO_2

Species	Mitochondria at Normal CO_2 (per 100 µm^2 of cell area) $\pm 2SE_{\bar{x}}$	Mitochondria at Elevated CO_2 (per 100 µm^2 of cell area) $\pm 2SE_{\bar{x}}$
1	1.0 ± 0.10	1.6 ± 0.10
2	0.4 ± 0.05	0.9 ± 0.08
3	0.5 ± 0.07	0.9 ± 0.10
4	0.3 ± 0.03	0.6 ± 0.06
5	0.7 ± 0.06	1.5 ± 0.22
6	1.3 ± 0.15	2.4 ± 0.22

(a) **Describe** the role of the inner mitochondrial membrane in cellular respiration. **1 point**

Accept one of the following:

- It provides the location for the components of the electron transport chain/ATP synthase/oxidative phosphorylation.
- It separates (reactions in) the intermembrane space from (reactions in) the matrix.
- It allows the establishment of a proton gradient.

(b)	Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1. Sample response:  • Appropriate labelling	**1 point**
	Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1. • Data are represented in a bar/modified bar graph.	**1 point**
	Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1. • Data points and error bars are correctly plotted.	**1 point**
	Determine which species show(s) a difference in the number of mitochondria between normal and elevated levels of CO_2. • All of the species	**1 point**
		Total for part (b) 4 points
(c)	Based on the data in Table 1, **describe** the relationship between the level of CO_2 and the average number of mitochondria per unit area of a cell. Accept one of the following: • The number of mitochondria is greater under conditions of elevated CO_2 (than under normal CO_2). • It is a positive relationship/correlation.	**1 point**

(d)	The leaves of a particular plant species are typically green, but scientists notice a plant in which the leaves have white stripes. They determine that the stripes result from a mutation in mitochondrial DNA that interferes with the development of chloroplasts. The scientists crossed plants using pollen from the plant with white-striped leaves and ovules from a plant with green leaves. **Predict** the phenotype(s) of the leaves of offspring produced from this cross. • The leaves will be (all) green/not have white stripes.	**1 point**
	Provide reasoning to **justify** your prediction. • (All offspring will have the same leaf phenotype as the ovule-producing plant because) mitochondria are maternally inherited/transferred by the ovule.	**1 point**
	Explain why plants with the same genotype are able to differ in the structure and/or number of certain organelles in response to changes in atmospheric levels of CO_2. • (Plants have different phenotypes because) changes in CO_2 levels/the environment affect the expression of certain genes.	**1 point**
	Total for part (d)	**3 points**
	Total for question 2	**9 points**

Question 3: Scientific Investigation — 4 points

Sand lances of the genus *Ammodytes* are small fish that function as keystone organisms in several coastal ecosystems. These sand lances are prey fish that support organisms at higher trophic levels. Scientists performed experiments to examine how sand lance populations are likely to be affected by the rising temperatures and CO_2 levels associated with climate change.

Sand lance embryos typically develop and mature into adult fish at low temperatures (approximately 5°C) and stable, low CO_2 levels (approximately 400 µatm). Over the course of two years, the scientists measured the survival rate of sand lance embryos allowed to develop and mature in a laboratory at three different temperatures, 5°C, 7°C, and 10°C, with the level of CO_2 maintained at 400 µatm, 1,000 µatm, and 2,100 µatm for each temperature.

(a) **Describe** the effect of increased biodiversity on the resilience of an ecosystem in a changing environment. **1 point**

- (Ecosystem) resilience/it will be greater (with increased biodiversity).

(b) **Justify** the scientists' selecting 5°C as the lowest temperature and 400 µatm as the lowest CO_2 level in their study of sand lance embryo survival. **1 point**

Accept one of the following:

- These are the normal/current conditions at which the embryos develop and were used as a basis for comparison.
- These (current) conditions were used as a basis to compare the effects of changes in environmental conditions/increases in temperature and CO_2.

(c) **State** a null hypothesis for the experiment. **1 point**

Accept one of the following:

- Climate change will have no effect on sand lance (embryo) survival/sand lance development/the size of sand lance populations.
- (Increases in) temperature/CO_2 levels will have no effect on sand lance (embryo) survival/sand lance development /the size of sand lance populations.
- There will be no difference in the sand lance (embryo) survival rates/sand lance development/the size of sand lance populations measured at all/different temperatures and CO_2 levels.

(d) The scientists claim that a reduction in the population size of the *Ammodytes* sand lances will affect the stability of the entire coastal ecosystem. Provide reasoning to **support** the scientists' claim. **1 point**

Accept one of the following:

- There will be a negative effect on other trophic levels because the sand lance provides food for many other species.
- There will be a negative effect on other trophic levels because there will be reduced energy to transfer (to higher trophic levels).

Total for question 3 — 4 points

Question 4: Conceptual Analysis — 4 points

Noncyclic electron flow and cyclic electron flow are two major pathways of the light-dependent reactions of photosynthesis. In noncyclic electron flow, electrons pass through photosystem II, then components of a chloroplast electron transport chain, and then photosystem I before finally reducing $NADP^+$ to NADPH. In cyclic electron flow, electrons cycle through photosystem I and some components of the electron transport chain (Figure 1).

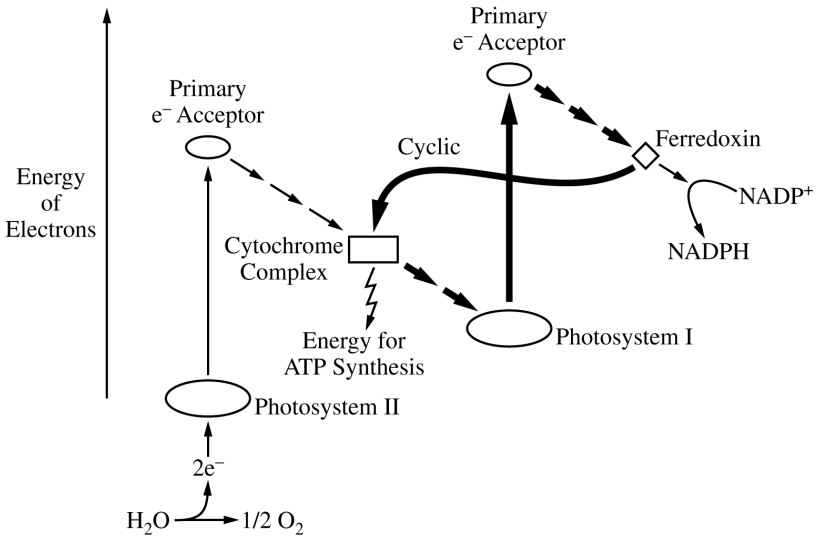


Figure 1. The pathways of noncyclic and cyclic (heavy arrows) electron flow. The cytochrome complex is a component of the electron transport chain between the two photosystems.

(a)	**Describe** the role of chlorophyll in the photosystems of plant cells. Accept one of the following: • Chlorophyll captures/absorbs light (energy). • Chlorophyll receives electrons (from water)/receives electrons (from an electron transport chain)/transfers electrons (to an electron transport chain).	**1 point**
(b)	Based on Figure 1, **explain** why an increase in the ratio of NADPH to $NADP^+$ will cause an increase in the flow of electrons through the cyclic pathway. • There is less/no $NADP^+$ to accept the electrons, so the electrons pass (instead) to the cyclic pathway/from ferredoxin to the cytochrome complex.	**1 point**
(c)	Using rice plants, scientists examined the effect of a mutation that results in the loss of the protein CRR6. CRR6 is a part of the photosystem I complex, and its absence reduces the activity of photosystem I. **Predict** the effect of the mutation on the rate of biomass (dry weight) accumulation. • The rate (of biomass accumulation)/Biomass/It will be lower (in comparison with plants without the mutation).	**1 point**
(d)	**Justify** your prediction in part (c). • There will be insufficient ATP/NADPH produced for the synthesis of carbohydrates/the Calvin cycle.	**1 point**
	Total for question 4	**4 points**

Question 5: Analyze Model or Visual Representation of a Biological Concept or Process — 4 points

Ruminants are hoofed animals, including cattle and sheep, that have a unique four-chambered stomach specialized to digest tough, fiber-filled grasses. Researchers studying ruminants are investigating the morphological and molecular characteristics of different ruminant families in order to determine the evolutionary relationships among the families. Cladograms of several ruminant families were constructed based on morphological data (Figure 1A) and molecular data (Figure 1B). Table 1 shows a sample of the morphological characteristics present in each family used to construct the cladogram in Figure 1A.

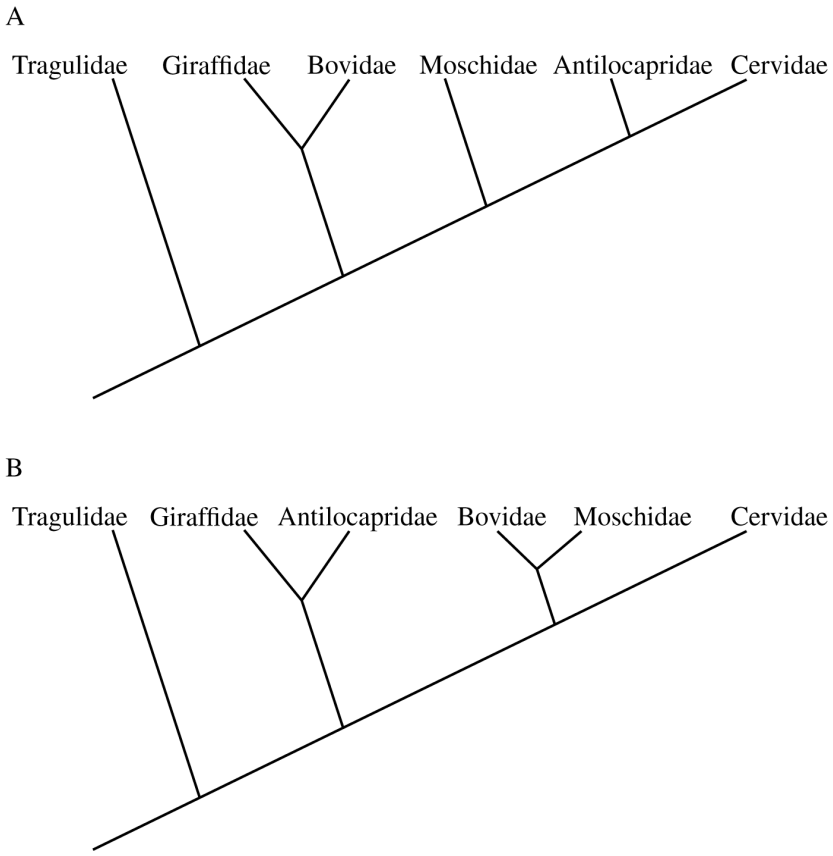
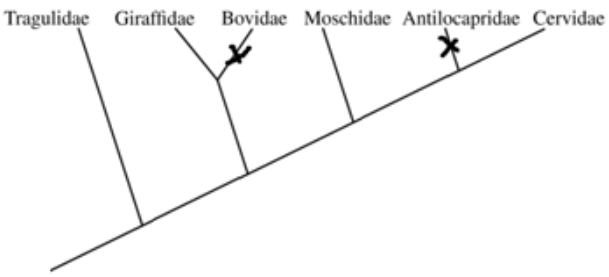


Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

TABLE 1. MORPHOLOGICAL CHARACTERISTICS FOUND IN EACH RUMINANT FAMILY

Characteristic Number	Morphological Characteristic	Tragulidae	Giraffidae	Bovidae	Moschidae	Antilocapridae	Cervidae
1	Extra tooth material			X		X	
2	Third stomach		X	X	X	X	X
3	Double opening for tear ducts					X	X

(a)	**Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms. • The (DNA) sequences of organisms that are more closely related are more similar (than those of organisms that are less closely related).	**1 point**
(b)	Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae. Accept one of the following: • (The molecular data/Figure 1B support(s) this relationship, and) molecular data are more reliable (than are morphological data). • (The molecular data/Figure 1B support(s) this relationship.) Morphological similarities may not reliably indicate evolutionary relatedness.	**1 point**
(c)	Using the template in the space provided for your response, **represent** the point(s) at which characteristic 1, listed in Table 1, evolved by marking "X" on the line(s) of the cladogram in the correct location(s). Sample Response:  • Response must show an X placed on the line leading to Bovidae and an X placed on the line leading to Antilocapridae.	**1 point**
(d)	Based on Figure 1A, **explain** why a characteristic found only in the Cervidae and Bovidae families is more likely evidence of convergent evolution than it is of common ancestry. Accept one of the following: • There are other families that have the same common ancestor as the Bovidae and Cervidae families but do not have the characteristic. • It is more likely that the characteristic arose independently in Cervidae and Bovidae than it arose in their common ancestor and was lost in Giraffidae, Moschidae, and Antilocapridae.	**1 point**
	Total for question 5	**4 points**

Question 6: Analyze Data — 4 points

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 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 (Figure 1). 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.

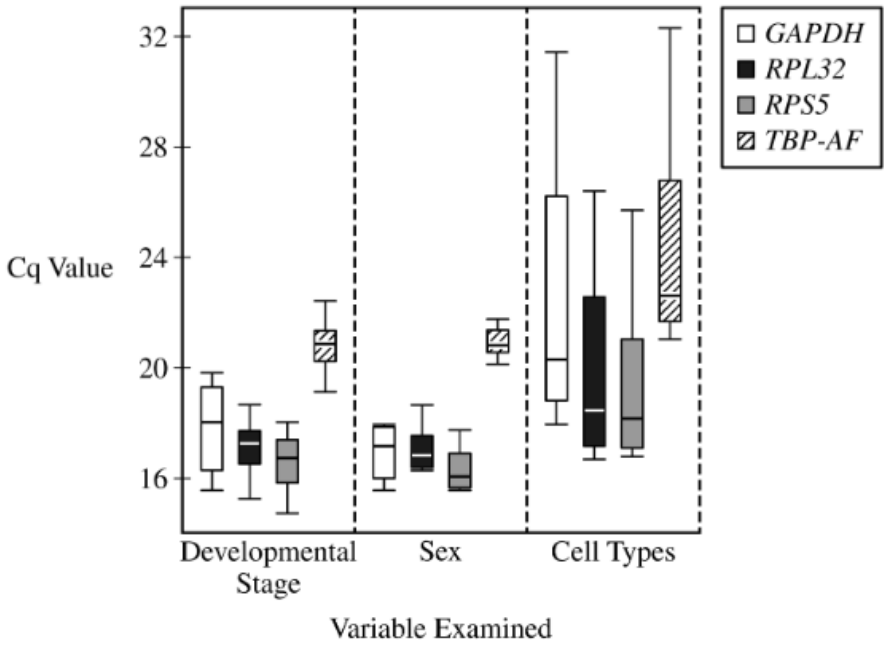


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

(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. • *RPS5*	**1 point**
(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. • *TBP-AF*	**1 point**
(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. • Their hypothesis is supported because *TBP-AF* has the smallest Cq range/most constant expression (when comparing sexes).	**1 point**
(d)	**Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee. • Different cell types contain different levels of/different transcription factors, and therefore regulate the expression of genes in different ways.	**1 point**
	Total for question 6	**4 points**