

2023



AP[®] Biology

Free-Response Questions

AP[®] BIOLOGY EQUATIONS AND FORMULAS

Statistical Analysis and Probability								
<u>Mean</u>			<u>Standard Deviation</u>					
$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$			$s = \sqrt{\frac{\sum (x_i - \bar{x})^2}{n - 1}}$					
<u>Standard Error of the Mean</u>			<u>Chi-Square</u>					
$SE_{\bar{x}} = \frac{s}{\sqrt{n}}$			$\chi^2 = \sum \frac{(o - e)^2}{e}$					
<u>Chi-Square Table</u>								
<i>p</i> value	Degrees of Freedom							
	1	2	3	4	5	6	7	8
	0.05	3.84	5.99	7.81	9.49	11.07	12.59	14.07
0.01	6.63	9.21	11.34	13.28	15.09	16.81	18.48	20.09
<u>Laws of Probability</u>								
If A and B are mutually exclusive, then:								
$P(A \text{ or } B) = P(A) + P(B)$								
If A and B are independent, then:								
$P(A \text{ and } B) = P(A) \times P(B)$								
<u>Hardy-Weinberg Equations</u>								
$p^2 + 2pq + q^2 = 1$			p = frequency of allele 1 in a population					
$p + q = 1$			q = frequency of allele 2 in a population					
<u>Metric Prefixes</u>								
<u>Factor</u>	<u>Prefix</u>		<u>Symbol</u>					
10 ⁹	giga		G					
10 ⁶	mega		M					
10 ³	kilo		k					
10 ⁻¹	deci		d					
10 ⁻²	centi		c					
10 ⁻³	milli		m					
10 ⁻⁶	micro		μ					
10 ⁻⁹	nano		n					
10 ⁻¹²	pico		p					
Mode = value that occurs most frequently in a data set								
Median = middle value that separates the greater and lesser halves of a data set								
Mean = sum of all data points divided by number of data points								
Range = value obtained by subtracting the smallest observation (sample minimum) from the greatest (sample maximum)								

BIOLOGY**SECTION II****Time—1 hour and 30 minutes****6 Questions**

Directions: Questions 1 and 2 are long free-response questions that require about 25 minutes each to answer. Questions 3 through 6 are short free-response questions that require about 10 minutes each to answer.

Read each question carefully and completely. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable.

You may plan your answers in this orange booklet, but no credit will be given for anything written in this booklet. **You will only earn credit for what you write in the separate Free Response booklet.**

Question 1 is on the following page.

Rate and Growth Rate $\frac{dY}{dt}$ dY = amount of change dt = change in time B = birth rate Population Growth $\frac{dN}{dt} = B - D$ D = death rate N = population size K = carrying capacity Exponential Growth $\frac{dN}{dt} = r_{\max} N$ $r_{\max}$ = maximum per capita growth rate of population Logistic Growth $\frac{dN}{dt} = r_{\max} N \left(\frac{K - N}{K} \right)$		Water Potential (Ψ) $\Psi = \Psi_p + \Psi_s$ Ψ_p = pressure potential Ψ_s = solute potential The water potential will be equal to the solute potential of a solution in an open container because the pressure potential of the solution in an open container is zero. The Solute Potential of a Solution $\Psi_s = -iCRT$ i = ionization constant (1.0 for sucrose because sucrose does not ionize in water) C = molar concentration R = pressure constant ($R = 0.0831$ liter bars/mole K) T = temperature in Kelvin ($^{\circ}\text{C} + 273$)
Simpson's Diversity Index Diversity Index = $1 - \sum \left(\frac{n}{N} \right)^2$ n = total number of organisms of a particular species N = total number of organisms of all species		pH = $-\log[\text{H}^+]$
Surface Area and Volume		
Surface Area of a Sphere $SA = 4\pi r^2$	Volume of a Sphere $V = \frac{4}{3}\pi r^3$	r = radius l = length
Surface Area of a Rectangular Solid $SA = 2lh + 2lw + 2wh$	Volume of a Rectangular Solid $V = lwh$	h = height w = width
Surface Area of a Cylinder $SA = 2\pi rh + 2\pi r^2$	Volume of a Cylinder $V = \pi r^2 h$	s = length of one side of a cube
Surface Area of a Cube $SA = 6s^2$	Volume of a Cube $V = s^3$	SA = surface area V = volume

1. 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.

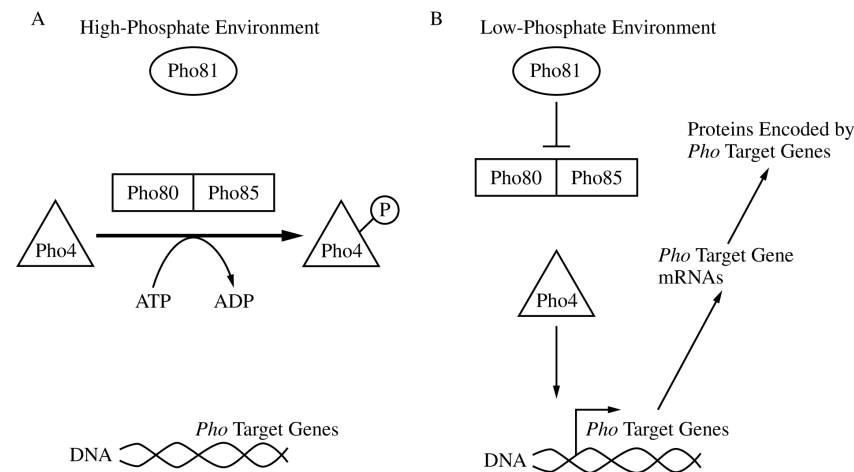


Figure 1. A simplified model of the regulation of expression of *Pho* target genes in (A) a high-phosphate (high-Pi) environment and (B) a low-phosphate (low-Pi) environment

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 mutant 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) ±2SE _{$\bar{x}$}	APase Activity in Low-Pi Environment (mU/mL/OD ₆₀₀) ±2SE _{$\bar{x}$}	Relative Amounts of <i>PHO1</i> mRNA in High-Pi Environment ±2SE _{$\bar{x}$}	Relative Amounts of <i>PHO1</i> mRNA in Low-Pi Environment ±2SE _{$\bar{x}$}
Wild-type	None	0.5 ± 0.1	17.3 ± 0.9	0.1 ± 0.0	10 ± 2.0
<i>pho81mt</i>	Nonfunctional Pho81	0.4 ± 0.1	0.6 ± 0.1	0.7 ± 0.2	0.9 ± 0.8
<i>pho4mt</i>	Nonfunctional Pho4	0.5 ± 0.0	0.8 ± 0.2	0.6 ± 0.4	0.3 ± 0.1

- (a) **Describe** the effect that the addition of a charged phosphate group can have on a protein that would cause the protein to become inactive. **Explain** how a signal can be amplified during signal transduction in a pathway such as the PHO signaling pathway.
- (b) Based on Table 1, **identify** a dependent variable in the researchers’ experiment. **Justify** the researchers’ using the wild-type strain for the creation of the mutant strains. **Justify** the researchers’ using mutant strains in which only a single component of the pathway was mutated in each strain.
- (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. **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.
- (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. Provide reasoning to **justify** your prediction.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

2. Elevated levels of CO₂ 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 CO₂, there is an increase in the number of chloroplasts per cell. To investigate whether the elevated levels of CO₂ 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 CO₂ (Table 1).

TABLE 1. AVERAGE NUMBER OF MITOCHONDRIA IN PLANTS EXPOSED TO NORMAL AND ELEVATED LEVELS OF CO₂

Species	Mitochondria at Normal CO ₂ (per 100 μm ² of cell area) ±2SE _{<i>x</i>}	Mitochondria at Elevated CO ₂ (per 100 μm ² of cell area) ±2SE _{<i>x</i>}
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.
- (b) Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1. **Determine** which species show(s) a difference in the number of mitochondria between normal and elevated levels of CO₂.
- (c) Based on the data in Table 1, **describe** the relationship between the level of CO₂ and the average number of mitochondria per unit area of a cell.
- (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. Provide reasoning to **justify** your prediction. **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 CO₂.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

3. 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 CO₂ levels associated with climate change.

Sand lance embryos typically develop and mature into adult fish at low temperatures (approximately 5°C) and stable, low CO₂ 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 CO₂ maintained at 400 μatm, 1,000 μatm, and 2,100 μatm for each temperature.

- Describe** the effect of increased biodiversity on the resilience of an ecosystem in a changing environment.
- Justify** the scientists' selecting 5°C as the lowest temperature and 400 μatm as the lowest CO₂ level in their study of sand lance embryo survival.
- State** a null hypothesis for the experiment.
- 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.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

4. 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).

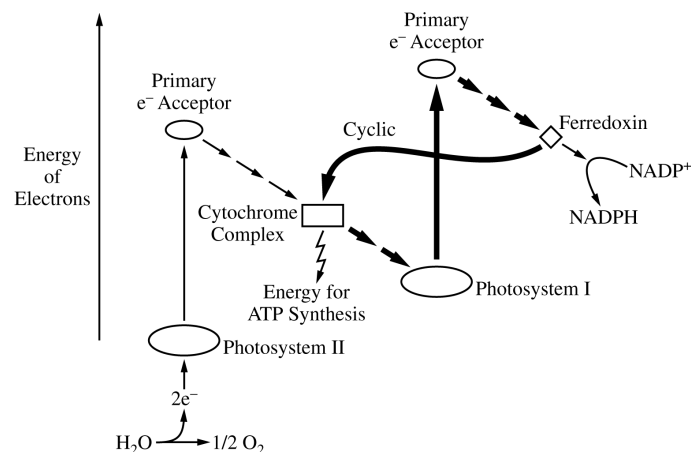


Figure 1. The pathways of noncyclic and cyclic (heavy arrows) electron flow. The cytochrome complex is a component of the electron transport chain between the two photosystems.

- Describe** the role of chlorophyll in the photosystems of plant cells.
- 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.
- 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.
- Justify** your prediction in part (c).

Write your responses to this question only on the designated pages in the separate Free Response booklet.

5. 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.

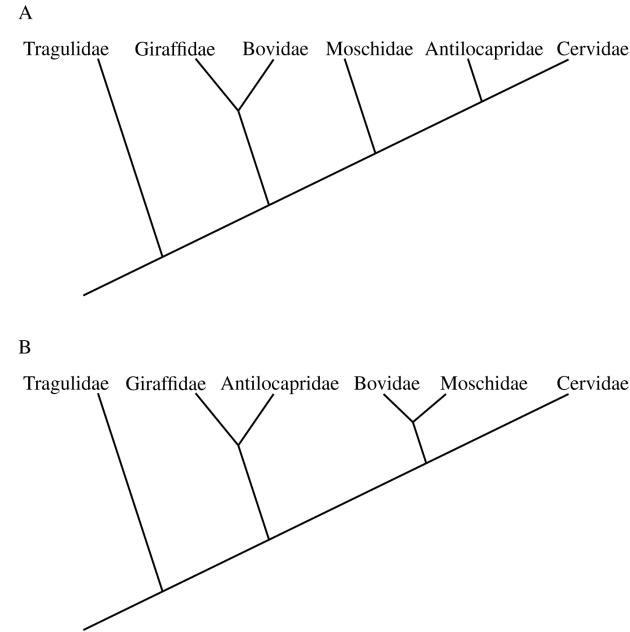


Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

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.
- (b) Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
- (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).
- (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.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

6. 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. 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.

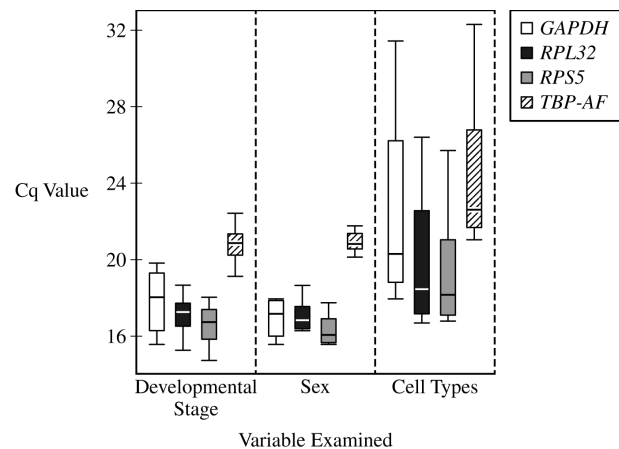


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

- (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.
- (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.

Write your responses to this question only on the designated pages in the separate Free Response booklet.

STOP

END OF EXAM