

Question 6: Analyze Data**4 points**

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 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. **1 point**
- Modified cap II
- (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. **1 point**
- Accept one of the following:
- A longer mRNA half-life is associated with more protein.
 - There is a positive correlation/relationship.
- (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. **1 point**
- The data support their hypothesis because the half-lives of the two mRNAs are the same, but the amount of protein produced from the mRNA with modified cap I is more than (four times as much as) that produced from the mRNA with the normal

-
- (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. **1 point**

Accept one of the following:

- Protein production from the DNA requires (transcription) factors to initiate transcription.
 - Protein production from the mRNA does not depend on (correct posttranscriptional) processing of the pre-mRNA.
 - The cells may be unable to transcribe the DNA (while mRNA can be directly translated).
-

Total for question 6 4 points

Question 6: Analyze Data**4 points**

The small invertebrate krill species *Thysanoessa inermis* is adapted to cold (4°C) seawater. Over the past ten years, there has been a gradual increase in the water temperature of the krill's habitat. A sustained increase in water temperature may ultimately affect the ability of the krill to survive.

One effect of higher temperatures is protein misfolding within cells. Krill have several *hsp* genes that code for heat-shock proteins (HSPs). These proteins help prevent protein misfolding or help to refold proteins to their normal shapes.

Scientists conducted experiments on *T. inermis* to detect changes in the expression of *hsp* genes when the krill were exposed to temperatures above 4°C. An experimental group of krill was maintained in tanks with 4°C seawater and then placed into tanks with 10°C seawater for approximately three hours. The krill were then given a six-hour recovery period in the 4°C seawater tanks. A control group of krill was moved from a tank of 4°C seawater to another tank of 4°C seawater for approximately three hours and then returned to the original tank. The scientists analyzed *hsp* gene expression by measuring the concentrations of three mRNAs (I, II, III) transcribed from certain *hsp* genes in both the heat-shocked krill (Figure 1) and the control krill. For the control krill, no transcription of the *hsp* genes was detected throughout the test period (data not shown).

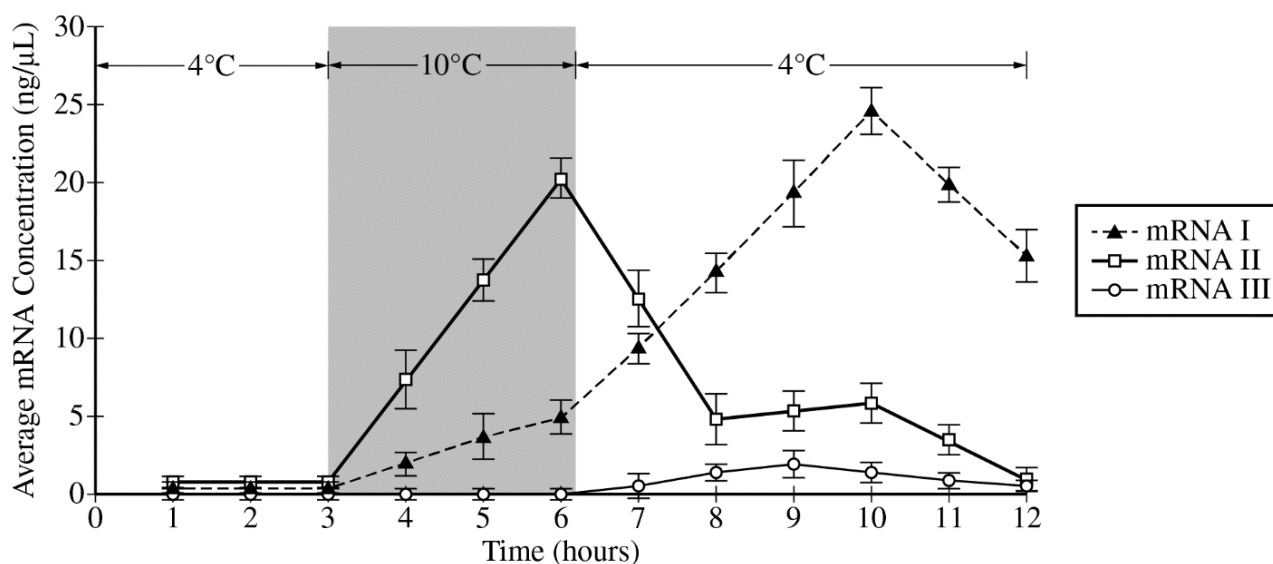


Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from *hsp* genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$.

- | | | |
|-----|---|----------------|
| (a) | Identify the <i>hsp</i> mRNA that has the slowest rate of concentration increase in response to heat-shock treatment. | 1 point |
| | <ul style="list-style-type: none"> (mRNA) III | |
| (b) | Describe the trend in the average concentration of mRNA I throughout the experiment. | 1 point |
| | <ul style="list-style-type: none"> (No change in concentration from 1 to 3 hours) increased concentration (slightly) between 3 and 6 hours/during the heat shock, increased concentration at a greater rate from 6 to 10 hours/for 4 hours after the heat shock, and then decreased concentration after hour 10. | |

-
- (c) The scientists hypothesized that the heat-shock protein (HSP) translated from mRNA I plays a greater role in refolding proteins than does the HSP translated from mRNA II. Use the data to **support** the hypothesis. **1 point**
- mRNA I is still expressed at a high level after the heat-shock period, while mRNA II levels decrease after the heat shock, when proteins would need to be refolded.
-

- (d) mRNAs I and II are transcribed from the same gene. **Explain** how a cell can produce two different mRNAs from the same gene. **1 point**

Accept one of the following:

- The cell expresses different exons/performs alternative splicing.
 - The cell uses different transcription termination sites (poly(A) sites).
 - The cell uses different promoters.
-

Total for question 6 4 points

2019

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2019 SCORING GUIDELINES

Question 1

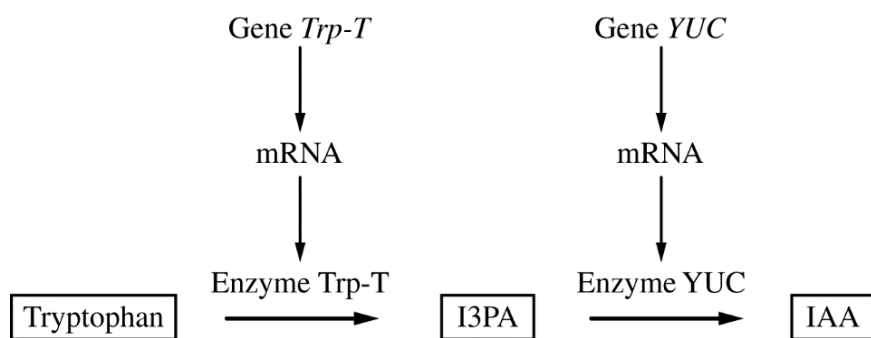


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

Auxins are plant hormones that coordinate several aspects of root growth and development. Indole-3-acetic acid (IAA) is an auxin that is usually synthesized from the amino acid tryptophan (Figure 1). Gene *Trp-T* encodes an enzyme that converts tryptophan to indole-3-pyruvic acid (I3PA), which is then converted to IAA by an enzyme encoded by the gene *YUC*.

- (a) **Circle** ONE arrow that represents transcription on the template pathway. **Identify** the molecule that would be absent if enzyme YUC is nonfunctional.

Circle (1 point)

- Circle around either arrow pointing from a gene (*Trp-T* or *YUC*) to mRNA

Identification (1 point)

- IAA

- (b) **Predict** how the deletion of one base pair in the fourth codon of the coding region of gene *Trp-T* would most likely affect the production of IAA. **Justify** your prediction.

Prediction (1 point)

- Reduction in IAA production OR No production of IAA

Justification (1 point)

- The mutation will result in the translation of an inactive/nonfunctional Trp-T enzyme.
- The mutation will result in no translation of the Trp-T enzyme.
- The mutation will result in no/reduced production of I3PA.

- (c) **Explain** one feedback mechanism by which a cell could prevent production of too much IAA without limiting I3PA production.

Explanation (2 points)

- Negative feedback/feedback inhibition/increasing amounts of IAA inhibits the pathway.
- Production of YUC enzyme is inhibited OR YUC enzyme activity is inhibited.

2019 SCORING GUIDELINES**Question 1 (continued)**

- (d) Rhizobacteria are a group of bacteria that live in nodules on plant roots. Rhizobacteria can produce IAA and convert atmospheric nitrogen into forms that can be used by plants. Plants release carbon-containing molecules into the nodules. Based on this information, **identify** the most likely ecological relationship between plants and rhizobacteria. **Describe** ONE advantage to the bacteria of producing IAA.

Identification (1 point)

- Mutualism

Description (1 point)

- Increases habitat/number of nodules for the rhizobacteria.
- The bacteria receive carbon/carbon-containing molecules (as a result of increased plant growth).

- (e) A researcher removed a plant nodule and identified several “cheater” rhizobacteria that do not produce IAA or fix nitrogen. **Describe** the evolutionary advantage of being a bacterial cheater in a population composed predominantly of noncheater bacteria. Plants can adjust the amount of carbon-containing molecules released into nodules in response to the amount of nitrogen fixed in the nodule. **Predict** the change in the bacterial population that would cause the plant to reduce the amount of carbon-containing molecules provided to the nodule.

Description (1 point)

- Cheaters/bacteria that benefit without producing IAA/fixing nitrogen have more energy for reproduction.

Prediction (1 point)

- Decrease in the nitrogen-fixing/noncheater bacteria
- Decrease in the amount of nitrogen fixed (by bacteria)

2019 SCORING GUIDELINES**Question 2**

A student studying two different aquatic, plant-eating, unicellular protist species (species A and B) designed an experiment to investigate the ecological relationship between the two species (Table 1).

TABLE 1. EXPERIMENTAL TREATMENT GROUPS

Group I.	Species A and B are each grown in separate containers.
Group II.	Species A and B are grown together in the same container.

In treatment group I, the student placed 10 individuals of species A into a container with liquid growth medium and 10 individuals of species B into a separate container with an equal amount of the same liquid growth medium. In treatment group II, the student placed 5 individuals of each species into a single container with the liquid growth medium. The student then maintained the containers under the same environmental conditions and recorded the number of individuals in each population at various time points. The results are shown in Table 2.

TABLE 2. NUMBER OF INDIVIDUALS IN EACH PROTIST POPULATION IN BOTH TREATMENT GROUPS

Time (h)	Group I. Grown Separately		Group II. Grown Together	
	Species A	Species B	Species A	Species B
0	10	10	5	5
10	100	50	45	20
20	400	200	100	50
30	1100	500	250	25
40	1400	650	525	20
50	1500	700	900	10
60	1500	700	1250	0
70	1500	700	1400	0

(a) The growth curves for species B in group I and for species A in group II (shaded columns) have been plotted on the template. Use the template to **complete** an appropriately labeled line graph to illustrate the growth of species A in treatment group I and species B in treatment group II (unshaded columns).

Completion (3 points)

- Correctly plotted lines for remaining two treatments
- Correctly labeled axes including units
- Correctly labeled data lines

2019 SCORING GUIDELINES**Question 2 (continued)**

(b) As shown in the table, the researcher established treatment group II with 5 individuals of each species. **Provide reasoning** for the reduced initial population sizes.

Reasoning (1 point)

- Reduced initial population sizes keep the total number of organisms the same in all containers.
- Reduced initial population sizes serve as a control for population density.

(c) The student claims that species A and B compete for the same food source. **Provide TWO pieces of evidence** from the data that support the student's claim.

Evidence (1 point per row; 2 points max.)

Comparison of Groups	Evidence
I-A to II-A	• Growth rate is faster in I/slower in II
I-A to II-A	• Grows to a higher population density in I/lower population density in II
I-B to II-B	• Growth rate is faster in I/slower in II
I-B to II-B	• Grows to a higher population density in I/lower population density in II/ II dies out/II goes to zero

(d) **Predict** TWO factors that most likely limit the population growth of species A in treatment group I.

Prediction (2 points)

Acceptable factors include:

- Food
- Space
- Metabolic waste
- Dissolved oxygen

(e) Many protists contain an organelle called a contractile vacuole that pumps water out of the cell. The student repeated the experiment using a growth medium with a lower solute concentration. **Predict** how the activity of the contractile vacuole will change under the new experimental conditions. **Justify** your prediction.

Prediction (1 point)

- The contractile vacuole will be more active.

Justification (1 point)

- The environment is hypotonic with respect to the cell.
- The cell is hypertonic with respect to environment.
- Water has entered the cell (which could cause lysis).
- The cell has lower water potential than the environment/the environment has higher water potential than the cell.

2019 SCORING GUIDELINES**Question 3**

The pyruvate dehydrogenase complex (PDC) catalyzes the conversion of pyruvate to acetyl-CoA, a substrate for the Krebs (citric acid) cycle. The rate of pyruvate conversion is greatly reduced in individuals with PDC deficiency, a rare disorder.

(a) **Identify** the cellular location where PDC is most active.

Identification (1 point)

- Mitochondria
- Mitochondrial matrix

(b) **Make a claim** about how PDC deficiency affects the amount of NADH produced by glycolysis AND the amount of NADH produced by the Krebs (citric acid) cycle in a cell. **Provide reasoning** to support your claims based on the position of the PDC-catalyzed reaction in the sequence of the cellular respiration pathway.

(1 point per row; 2 points max.)

	Claim	Reasoning
Glycolysis	No change	• Glycolysis continues; PDC is not needed. • Glycolysis occurs before conversion of pyruvate to acetyl-CoA.
Krebs cycle	Decrease	• The Krebs cycle is greatly reduced/slowed down if there is no/less acetyl-CoA. • The Krebs cycle occurs after conversion of pyruvate to acetyl-CoA.

(c) PDC deficiency is caused by mutations in the *PDHA1* gene, which is located on the X chromosome. A male with PDC deficiency and a homozygous female with no family history of PDC deficiency have a male offspring. **Calculate** the probability that the male offspring will have PDC deficiency.

Calculation (1 point)

- The probability of inheritance is 0.
- The offspring cannot/will not have PDC deficiency.

2019 SCORING GUIDELINES

Question 4

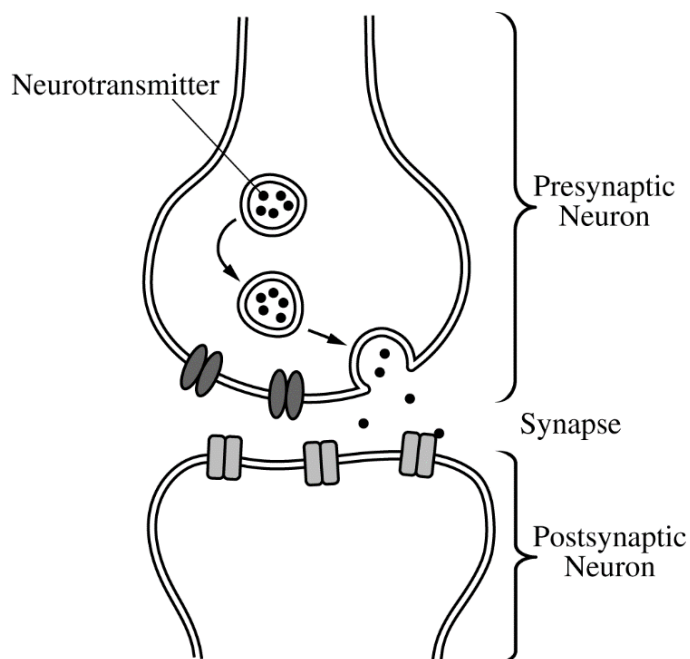


Figure 1. Release of neurotransmitters into the synapse in response to an action potential

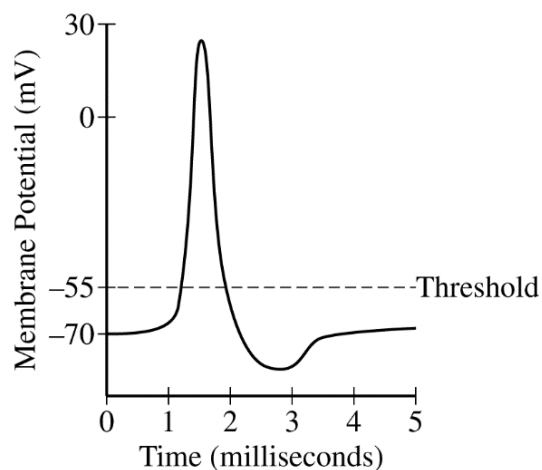


Figure 2. Model of a typical action potential in a neuron

Acetylcholine is a neurotransmitter that can activate an action potential in a postsynaptic neuron (Figures 1 and 2). A researcher is investigating the effect of a particular neurotoxin that causes the amount of acetylcholine released from presynaptic neurons to increase.

(a) **Describe** the immediate effect of the neurotoxin on the number of action potentials in a postsynaptic neuron. **Predict** whether the maximum membrane potential of the postsynaptic neuron will increase, decrease, or stay the same.

Description (1 point)

- It will increase the number of action potentials.

Prediction (1 point)

- It will stay the same.

(b) The researcher proposes two models, A and B, for using acetylcholinesterase (AChE), an enzyme that degrades acetylcholine, to prevent the effect of the neurotoxin. In model A, AChE is added to the synapse. In model B, AChE is added to the cytoplasm of the postsynaptic cell. **Predict** the effectiveness of EACH proposed model. **Provide reasoning** to support your predictions.

(1 point per row; 2 points max.)

	Prediction	Reasoning
Model A	Effective	Acetylcholine is in the synapse.
Model B	Not effective	Acetylcholine is not in the cytoplasm of the postsynaptic cell.

2019 SCORING GUIDELINES

Question 5

TABLE 1. DIVERGENCE (IN PERCENT) OF MITOCHONDRIAL DNA SEQUENCES AMONG FIVE PRIMATE SPECIES

	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

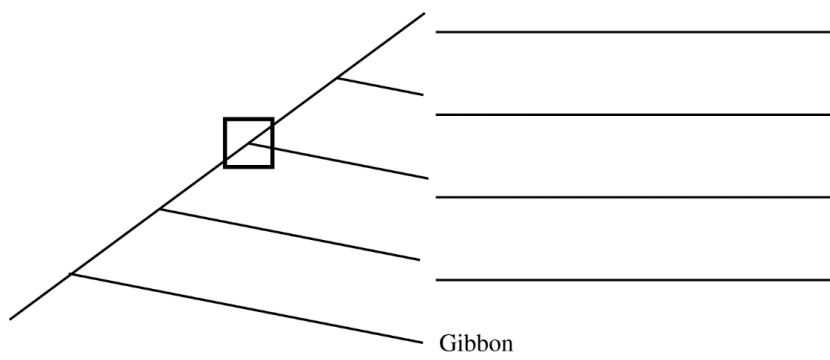
A researcher studying the evolutionary relationship among five primate species obtained data from a sequence of mitochondrial DNA (mtDNA) from a representative individual of each species. The researcher then calculated the percent divergence in the sequences between each pair of primate species (Table 1).

(a) Based on fossil data, the researcher estimates that humans and their most closely related species in the data set diverged approximately seven million years ago. Using these data, **calculate** the rate of mtDNA percent divergence per million years between humans and their most closely related species in the data set. Round your answer to two decimal places.

Calculation (1 point)

- 1.25 OR 1.26

(b) Using the data in the table, **construct** a cladogram on the template provided. **Provide reasoning** for the placement of gibbons as the outgroup on the cladogram.

**Construction (1 point)**

- From top to bottom: Human/Chimpanzee (interchangeable), Gorilla, Orangutan

Reasoning (1 point)

- Gibbon mtDNA is the least similar (to all of the other species)/most different (from all of the other species).
- Gibbon mtDNA is the most divergent (from all of the other species).

2019 SCORING GUIDELINES**Question 5 (continued)**

(c) On the cladogram, **draw** a circle around all of the species that are descended from the species indicated by the node within the square.

Circle (1 point)

- Circle species 1, 2, and 3, as numbered from the top.

2019 SCORING GUIDELINES

Question 6

	MEDIUM	STRAINS		
		Wild Type	Mutant 1	Mutant 2
Treatment I	All amino acids present	+	+	+
Treatment II	No amino acids present	+	–	–
Treatment III	All amino acids present EXCEPT methionine	+	–	+
Treatment IV	All amino acids present EXCEPT leucine	+	+	–

Table 1. The data show the growth of haploid *Saccharomyces cerevisiae* yeast strains on media that differ in amino acid content. A plus sign (+) indicates that the yeast strains grow, and a minus sign (–) indicates that the strains do not grow.

The yeast *Saccharomyces cerevisiae* is a single-celled organism. Amino acid synthesis in yeast cells occurs through metabolic pathways, and enzymes in the synthesis pathways are encoded by different genes. The synthesis of a particular amino acid can be prevented by mutation of a gene encoding an enzyme in the required pathway.

A researcher conducted an experiment to determine the ability of yeast to grow on media that differ in amino acid content. Yeast can grow as both haploid and diploid cells. The researcher tested two different haploid yeast strains (Mutant 1 and Mutant 2), each of which has a single recessive mutation, and a haploid wild-type strain. The resulting data are shown in Table 1.

(a) **Identify** the role of treatment I in the experiment.

Identification (1 point)

- (Positive) control (for yeast growth).
- To test the viability of all yeast strains.
- Treatment I allows the researcher to be confident that changes in experimental outcome are due to differences in treatments.

(b) **Provide reasoning** to explain how Mutant 1 can grow on treatment I medium but cannot grow on treatment III medium.

Reasoning (1 point)

- Mutant 1 can use methionine when it is present in the medium, but Mutant 1 cannot synthesize methionine.

(c) Yeast mate by fusing two haploid cells to make a diploid cell. In a second experiment, the researcher mates the Mutant 1 and Mutant 2 haploid strains to produce diploid cells. Using the table provided, **predict** whether the diploid cells will grow on each of the four media. Use a plus sign (+) to indicate growth and a minus sign (–) to indicate no growth.

Prediction (1 Point)

- There will be growth (+) in all four cells of the fourth column.

2019 SCORING GUIDELINES

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.

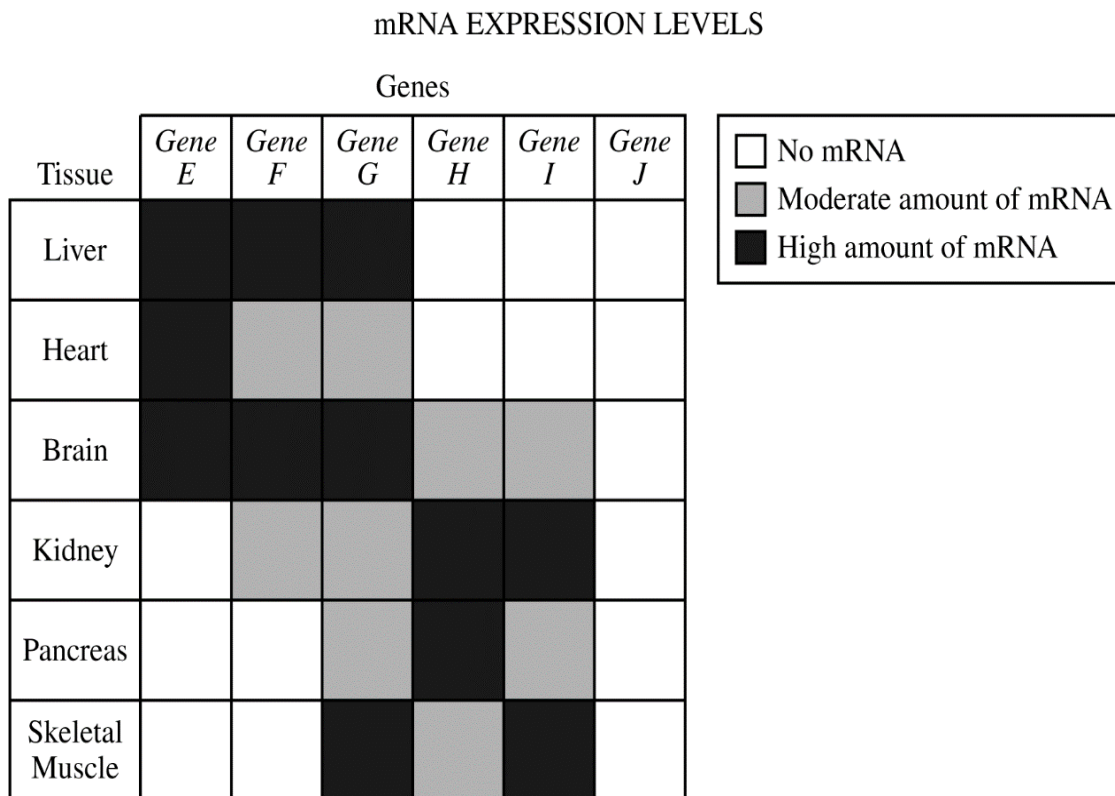


Figure 1. mRNA expression levels of six genes

(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.

Identification (1 point)

- *Gene G*

Reasoning (1 point)

- (*Gene G*) is the only gene expressed in all (six) tissues, AND glycolysis occurs in all (six) tissues.
- (*Gene G*) mRNA is the only mRNA present in all (six) tissues, AND glycolysis occurs in all (six) tissues.

(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.

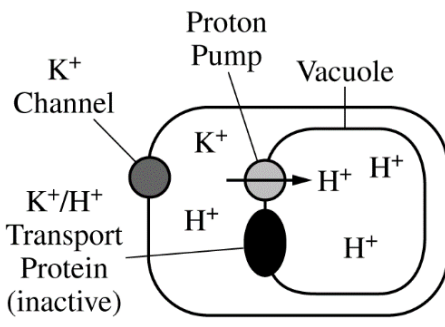
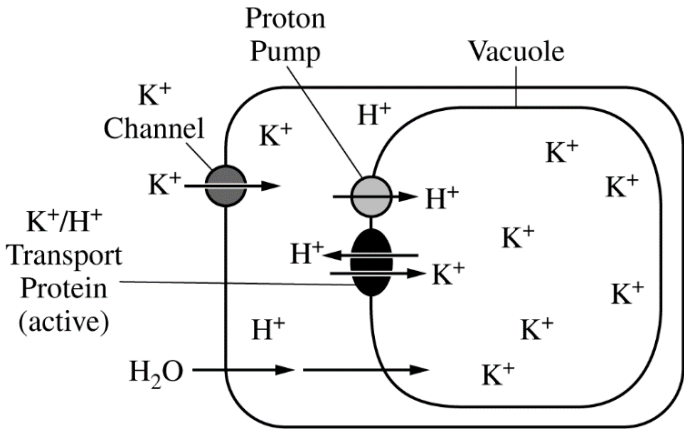
Reasoning (1 point)

- The mRNA is not exported from the nucleus.
- *Gene H* mRNA is not translated/RNA interference prevent(s) translation.
- Post-transcriptional modifications.

2019 SCORING GUIDELINES

Question 8

TABLE 1. CHANGES IN MORNING GLORY PETAL CELLS DURING FLOWER OPENING

	BUD	OPEN FLOWER
		
Vacuole pH	6.6	7.7
Flower Color	Red	Blue
Cell Volume	Small	Large

The petal color of the Mexican morning glory (*Ipomoea tricolor*) changes from red to blue, and the petal cells swell during flower opening. The pigment heavenly blue anthocyanin is found in the vacuole of petal cells. Petal color is determined by the pH of the vacuole. A model of a morning glory petal cell before and after flower opening is shown in Table 1.

(a) **Identify** the cellular component in the model that is responsible for the increase in the pH of the vacuole during flower opening AND **describe** the component's role in changing the pH of the vacuole.

Identification (1 point)

- (K^+ / H^+) transport protein

Description (1 point)

- It moves H^+ out of the vacuole.

(b) A researcher claims that the activation of the K^+ / H^+ transport protein causes the vacuole to swell with water. **Provide reasoning** to support the researcher's claim.

Reasoning (1 point)

- The concentration of solute (K^+) is increasing inside the vacuole.
- The solute (K^+) is moving into the vacuole, making it hypertonic/hyperosmotic/lowering water potential.

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2016 SCORING GUIDELINES

Question 1

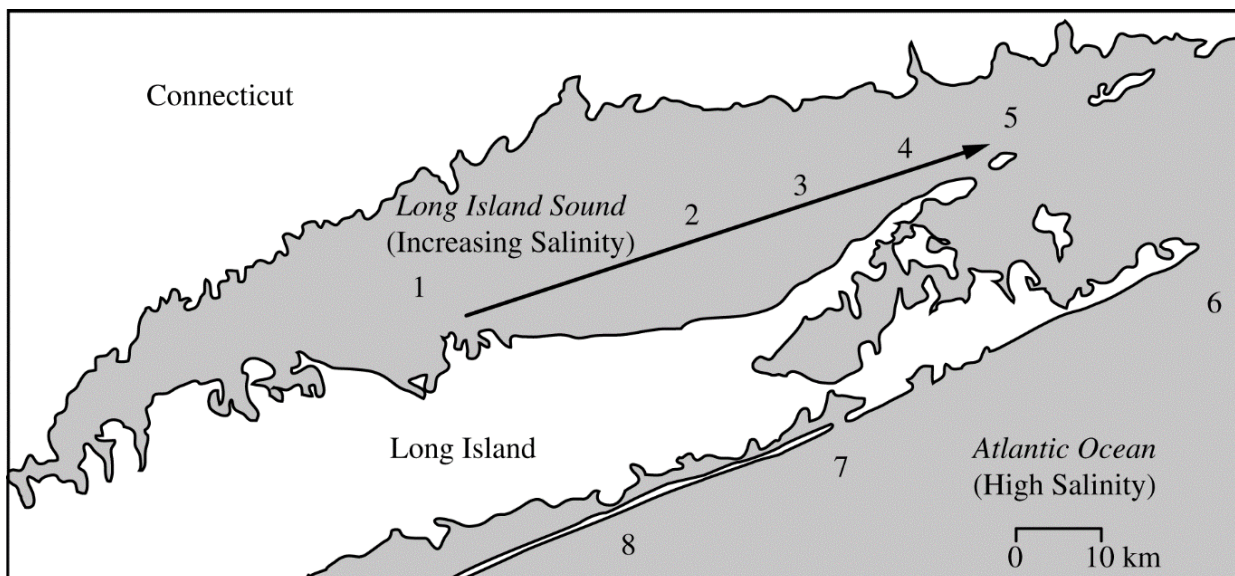


Figure 1. Sampling sites of marine mussels at various locations (1-8) in Long Island Sound and the Atlantic Ocean

TABLE 1. PERCENT OF INDIVIDUALS POSSESSING *lap*⁹⁴ ALLELE

	Long Island Sound					Atlantic Ocean		
Site	1	2	3	4	5	6	7	8
<i>lap</i> ⁹⁴ frequency (%)	13	16	25	37	55	59	59	59
Salinity	Low $\longrightarrow$ High					High		

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1).

2016 SCORING GUIDELINES

Question 1 (continued)

- (a) On the axes provided, **construct** an appropriately labeled bar graph to illustrate the observed frequencies of the *lap*⁹⁴ allele in the study populations. **(3 points)**

Construct graph (3 points)

- Correctly plotted bar graph that accurately represents the trend
- Correct axis labeling
- Correct scale and units

- (b) Based on the data, **describe** the most likely effect of salinity on the frequency of the *lap*⁹⁴ allele in the marine mussel populations in Long Island Sound. **Predict** the likely *lap*⁹⁴ allele frequency at a sampling site between site 1 and site 2 in Long Island Sound. **(2 points)**

Description (1 point)	Prediction (1 point)
• As salinity increases <i>lap</i>⁹⁴ frequency increases • As salinity decreases <i>lap</i>⁹⁴ frequency decreases	Between 13 and 16 percent (or a selected value between 13 and 16 percent)

- (c) **Describe** the most likely effect of LAP⁹⁴ activity on the osmolarity of the cytosol. **Describe** the function of LAP⁹⁴ in maintaining water balance in the mussels living in the Atlantic Ocean. **(2 points)**

Describe effect of LAP ⁹⁴ activity (1 point)	Describe function of LAP ⁹⁴ in maintaining water balance (1 point)
• LAP⁹⁴ increases osmolarity/solute concentration of the cytosol • LAP⁹⁴ decreases water potential of the cytosol	Prevents water loss to the environment

- (d) Marine mussel larvae are evenly dispersed throughout the study area by water movement. As larvae mature, they attach to the rocks in the water. **Explain** the differences in *lap*⁹⁴ allele frequency among adult mussel populations at the sample sites despite the dispersal of larvae throughout the entire study area. **Predict** the likely effect on distribution of mussels in Long Island Sound if the *lap*⁹⁴ allele was found in all of the mussels in the population. **Justify** your prediction. **(3 points)**

Explanation (1 point)	Prediction (1 point)	Justification (1 point)
• Mussels with <i>lap</i>⁹⁴ allele are more likely to survive in high salinity/less likely to survive in low salinity. • Mussels without <i>lap</i>⁹⁴ allele are less likely to survive in high salinity/more likely to survive in low salinity.	• Mussel population will increase in high salinity. • Mussel population will decline in low salinity.	• Mussels in high salinity with <i>lap</i>⁹⁴ allele will osmoregulate. • Mussels in low salinity with <i>lap</i>⁹⁴ allele will not osmoregulate.

2016 SCORING GUIDELINES

Question 2

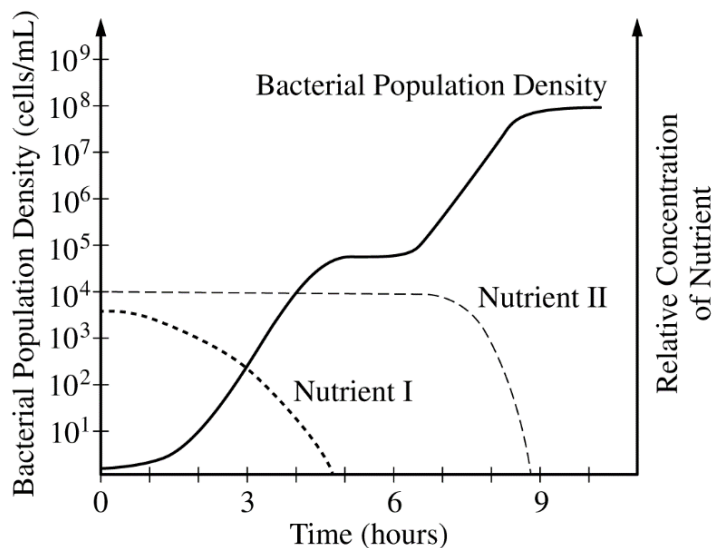


Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II)

Bacteria can be cultured in media with carefully controlled nutrient composition. The graph above shows the growth of a bacterial population in a medium with limiting amounts of two nutrients, I and II.

- (a) **Estimate** the maximum population density in $\frac{\text{cells}}{\text{mL}}$ for the culture. Using the data, **describe** what prevents further growth of the bacterial population in the culture. **(2 points)**

Estimate (1 point)

- 10^8

Description (1 point)

- When both nutrients are depleted

- (b) Using the data, **calculate** the growth rate in $\frac{\text{cells}}{\text{mL} \times \text{hour}}$ of the bacterial population between hours 2 and 4. **(1 point)**.

Calculation (1 point)

- 4,995

2016 SCORING GUIDELINES**Question 2 (continued)**

- (c) **Identify** the preferred nutrient source of the bacteria in the culture over the course of the experiment. Use the graph to **justify** your response. **Propose** ONE advantage of the nutrient preference for an individual bacterium. **(3 points)**

Identification (1 point)

- Nutrient I is the preferred nutrient.

Justification (1 point)

- When both nutrients are present in the growth medium, only nutrient I is used.
- Nutrient II is only used after nutrient I is depleted.

Proposed advantage (1 point)

- Do not spend energy making enzymes/proteins that the cell doesn't need.
- Do not have to express all metabolic genes at once.
- The preferred nutrient provides more energy.

- (d) **Describe** how nutrient I most likely regulates the genes for metabolism of nutrient I and the genes for metabolism of nutrient II. **Provide** TWO reasons that the population does not grow between hours 5 and 6. **(4 points)**

Description (2 points)

- Nutrient I promotes expression of genes required for metabolism of nutrient I.
- Nutrient I represses expression of genes required for metabolism of nutrient II.

Reasoning (2 points)

- Nutrient I is depleted from the growth medium OR neither nutrient is being consumed.
- Takes time to produce proteins/enzymes required to metabolize nutrient II.

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Question 3

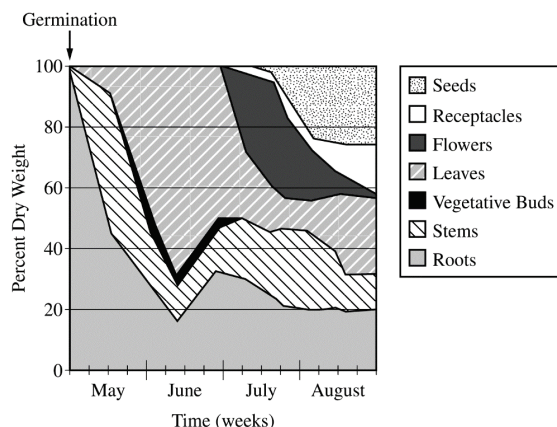


Figure 1. Percent dry weight of different plant structures during the growing season for an annual plant

The graph above illustrates the percent dry weight of different parts of a particular annual plant (plants that live less than one year) from early May to late August. The percent dry weight can be used to estimate the amount of energy a plant uses to produce its leaves, vegetative buds, stems, roots, and reproductive parts (seeds, receptacles, and flowers).

- (a) **Identify** the direct source of the energy used for plant growth during the first week of May, and **identify** the part of the plant that grew the most during the same period. **(2 points)**

Identify direct source of energy (1 point)

- Seed
- Stored organic nutrients/carbohydrates

Identify plant part (1 point)

- Roots

- (b) Based on the data on the graph, **estimate** the percent of the total energy that the plant has allocated to the growth of leaves on the first day of July. **(1 point)**

Identification (1 point)

- Any value between 45-55 percent

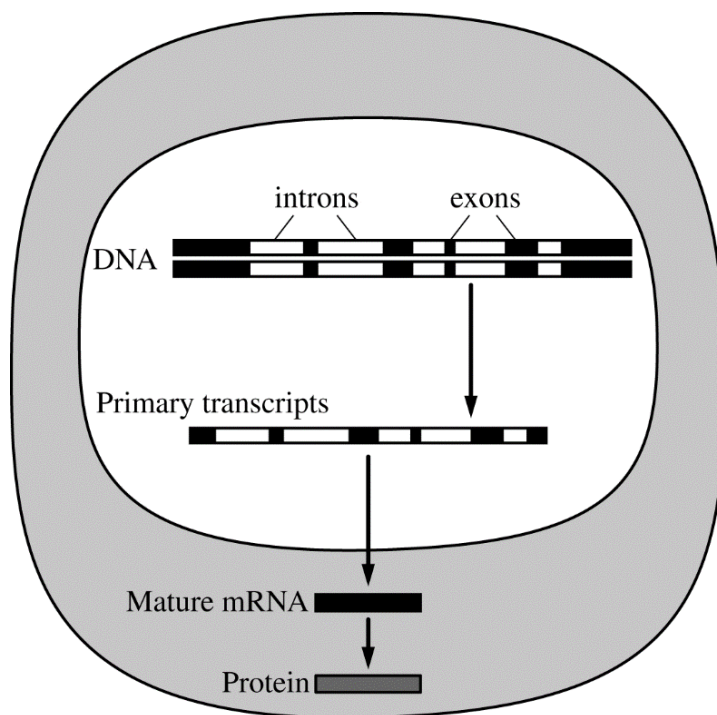
- (c) Compared with perennials (plants that live more than two years), annual plants often allocate a much greater percentage of their total energy to growth of their reproductive parts in any given year. **Propose** ONE evolutionary advantage of the energy allocation strategy in annual plants compared with that in perennial plants. **(1 point)**

Proposed advantage (1 point)

- Increased chance of reproduction before the plants die.
- If the plants do not use the strategy, they decrease the likelihood they will ever reproduce.

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Question 4



The figure represents the process of expression of gene *X* in a eukaryotic cell.

- (a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length.

Describe the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs.

(2 points)

Describe process (1 point)

- Removal of introns
- RNA processing

Identification (1 point)

- Nucleus

- (b) **Predict** the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction. (2 points)

Prediction (1 point)

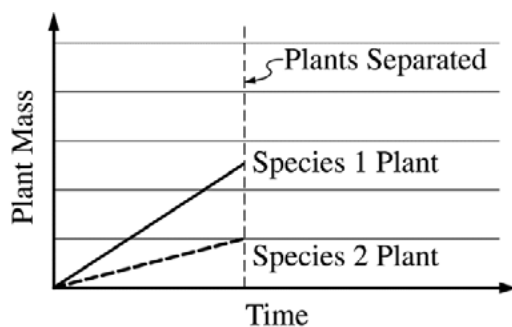
- 15 kb
- Longer than the mature mRNA in the eukaryote

Justification (1 point)

- mRNA processing typically does not occur in prokaryotes

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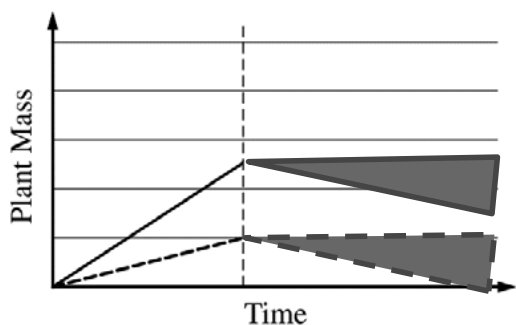
Question 5



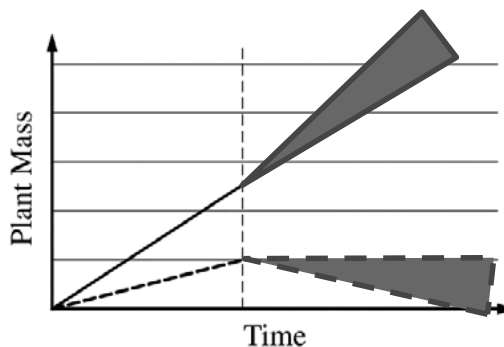
The graph above shows the mass of plants from two different species over time. The plants grew while attached to each other. The plants were separated at the time indicated by the vertical line in the graph.

Using template 1, **graph** the predicted shape of the plant-mass lines after separation of the two plants if the plants were in an obligate mutualistic relationship. On template 2, **graph** the predicted shape of the plant-mass lines if the species 2 plant was a parasite of the species 1 plant. **Justify** each of your predictions. (4 points)

TEMPLATE 1: OBLIGATE MUTUALISM



TEMPLATE 2: PARASITISM



	Graph characteristics (1 point each graph; 2 points maximum)	Justification (1 point each box; 2 points maximum)
Obligate Mutualism	Both of the growth curves level off or decline.	- Each species depends on the other for survival. - Without the relationship, both species are harmed.
Parasitism	Species 1 continues to increase while species 2 levels off or declines.	- The parasite requires an association with the host to survive but harms the host. - Without the relationship, the parasite cannot survive while the host continues to grow.

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Question 6

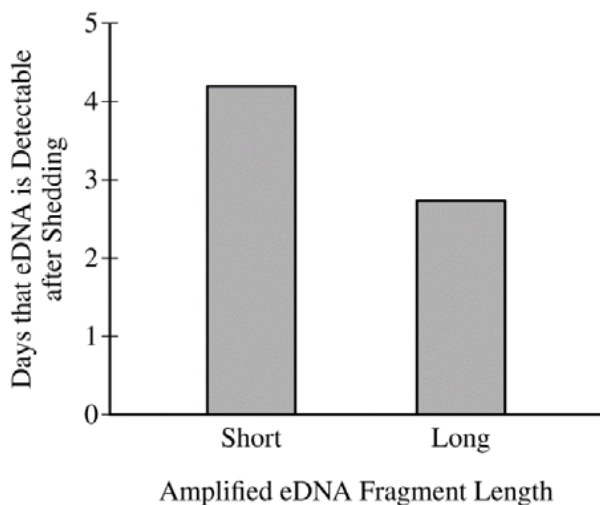


Figure 1. Detectability of eDNA fragments of varying lengths

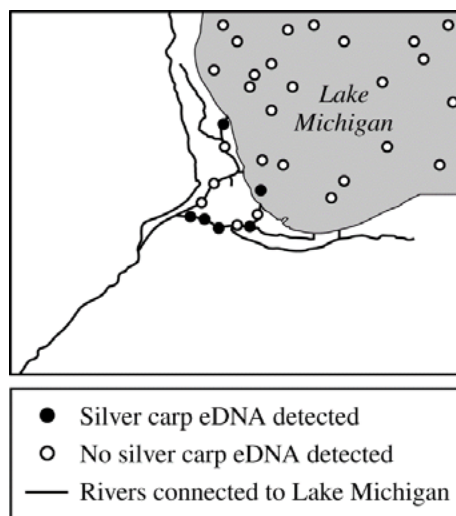


Figure 2. Map of the waterways that connect a nearby river system to Lake Michigan

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. **(2 points)**

Justify (1 point)

- eDNA allows detection of the fish without visual identification/catching the fish.

Proposed advantage (1 point)

- Longer fragments indicate more recent presence of fish.
- Longer fragments are more likely to contain a sequence that is specific to silver carp.
- Longer sequences/more base pairs may increase accuracy/specificity/confidence that the eDNA is from a silver carp and not a related species.

- (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.

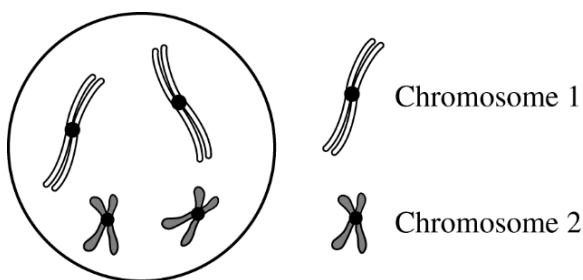
Provide reasoning other than human error to support the researchers' claim. **(1 point)**

Reasoning (1 point)

- eDNA entered the lake by means other than the fish (e.g., river flow, boats, waste from predators).

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Question 7

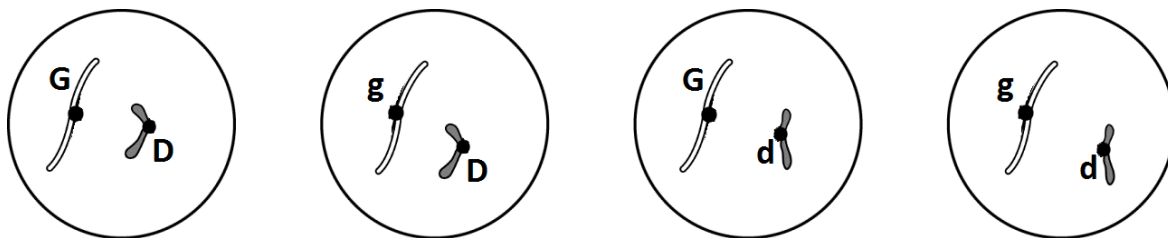


In a certain species of plant, the diploid number of chromosomes is 4 ($2n = 4$). Flower color is controlled by a single gene in which the green allele (G) is dominant to the purple allele (g). Plant height is controlled by a different gene in which the dwarf allele (D) is dominant to the tall allele (d). Individuals of the parental (P) generation with the genotypes $GGDD$ and $ggdd$ were crossed to produce F_1 progeny.

- (a) **Construct** a diagram below to depict the four possible normal products of meiosis that would be produced by the F_1 progeny. Show the chromosomes and the allele(s) they carry. Assume the genes are located on different chromosomes and the gene for flower color is on chromosome 1. **(1 point)**

Construct diagram (1 point)

- Diagram must include all of the following:
 - Each cell has one unduplicated chromosome 1 (with G or g).
 - Each cell has one unduplicated chromosome 2 (with D or d).
 - Genotype combinations should be: GD , Gd , gD , gd .



- (b) **Predict** the possible phenotypes and their ratios in the offspring of a testcross between an F_1 individual and a $ggdd$ individual. **(1 point)**

Prediction (1 point)

- 1 green dwarf: 1 green tall: 1 purple dwarf: 1 purple tall

- (c) If the two genes were genetically linked, **describe** how the proportions of phenotypes of the resulting offspring would most likely differ from those of the testcross between an F_1 individual and a $ggdd$ individual. **(1 point)**

Identify difference (1 point)

- The majority/greater than 50 percent would have the parental plant phenotypes
- Greater than 25 percent would be green dwarf plants and greater than 25 percent would be purple tall plants
- Less than 25 percent would be green tall plants and less than 25 percent would be purple dwarf plants

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Question 8

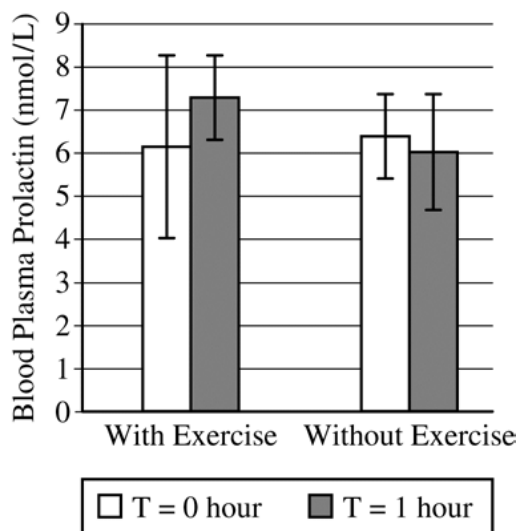


Figure 1. Effect of exercise on blood prolactin levels in adult males. The data represent the mean $\pm 2SE_{\bar{x}}$.

Researchers conducted a study to investigate the effect of exercise on the release of prolactin into the blood. The researchers measured the concentration of prolactin in the blood of eight adult males before (T = 0 hour) and after one hour (T = 1 hour) of vigorous exercise. As a control, the researchers measured the concentration of blood prolactin in the same group of individuals at the same times of day one week later, but without having them exercise. The results are shown in Figure 1.

- (a) **Justify** the use of the without-exercise treatment as the control in the study design. **(1 point)**

Justification (1 point)

- Attribute changes in the concentration of blood prolactin to exercise only
- Rule out normal fluctuations in prolactin release/levels

- (b) Using evidence from the specific treatments, **determine** whether prolactin release changes after exercise. **Justify** your answer. **(2 points)**

Determination (1 point)

- Exercise does not affect prolactin release

Justification (1 point)

- The T=1 hour with-exercise mean and the T=1 hour without-exercise mean are within $\pm 2SE_{\bar{x}}$.
- The $\pm 2SE_{\bar{x}}$ error bars for the T=1 hour with-exercise time point and the T=1 hour time without-exercise point overlap.
- The $\pm 2SE_{\bar{x}}$ error bars for the T=0 and T=1 hour with-exercise time points overlap.
- The T=0 hour with-exercise mean and the T=1 hour with exercise-mean are within $\pm 2SE_{\bar{x}}$.