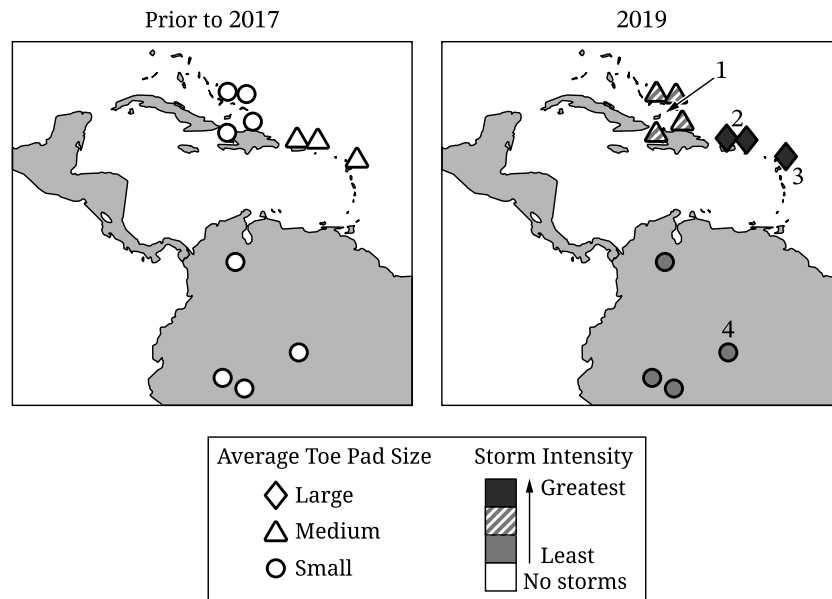


The following information applies to all parts.

5. Anole lizards throughout the Caribbean islands and Central and South America have pads of varying sizes on the bottom surfaces of their toes. The sizes of the toe pads are genetically determined and not the result of phenotypic plasticity. During storms with high winds, anoles cling to trees with the help of their toe pads. In recent years, an increase in both the number and intensity of storms has occurred across the range of anole habitats.

In 2017, two very intense storms occurred in the Caribbean islands within a month. In 2019, scientists investigated the relationship between the intense storms and the average toe pad size of the offspring of lizards that survived the storms. The scientists determined the average toe pad size of the surviving offspring and grouped their measurements into three categories: small, medium, and large toe pads. The scientists then compared the 2019 toe pad measurements with measurements recorded prior to 2017. Their data are represented in the figure.

A Map Representing Toe Pad Size Distributions Prior to 2017 and in 2019



Part A

Describe the role that changes in abiotic factors have in natural selection.

Part B

Based on the figure, **explain** the relationship between storm intensity and average toe pad size.

Part C

Identify the region on the 2019 map, by indicating the number, that experienced the least storm intensity.

Part D

Based on the information provided, **explain** how continued differences in storm intensity can apply different selective pressures on anole populations living on the Caribbean islands, eventually leading to speciation.

1. Crossing over in meiosis I is required for homologous chromosomes to properly align during metaphase and segregate during the first cell division.

(a)

- (i) **Describe** the function of S phase of interphase.

Some regions of a chromosome called hotspots display a higher frequency of crossing over than other regions do. Crossing over is suppressed in chromosomal regions near the centromeres. The centromere region of a duplicated chromosome includes a collection of proteins that form a structure called the kinetochore. Scientists hypothesized that one or more of these kinetochore proteins are responsible for suppressing crossing over around the centromere.

To investigate their hypothesis, scientists modified chromosome 8 in yeast such that, in each cell, one chromosome from the pair of homologous chromosome 8s contained the gene encoding red fluorescent protein (RFP), while the other chromosome from the pair contained the gene encoding green fluorescent protein (GFP). Cells expressing RFP emit (give off) red light, and cells expressing GFP emit green light. Models of the modified chromosome 8 both before and after crossing over are shown in Figure 1.

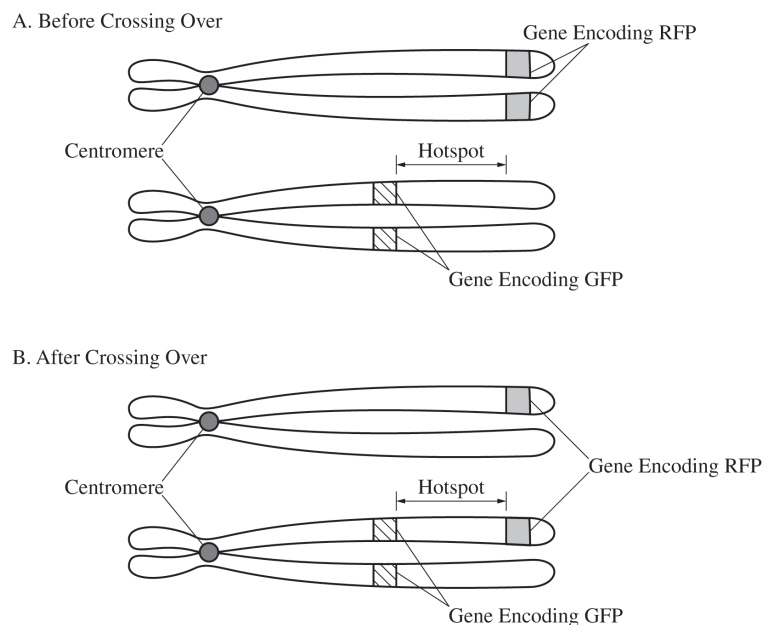


Figure 1. Models of modified chromosome 8 used in the experiment (A) before and (B) after crossing over occurs at the hotspot

- (ii) **Explain** why some haploid cells formed after meiosis in this experiment will have only one fluorescent marker.

The scientists then investigated whether attaching individual kinetochore proteins to a specific DNA sequence present in a known crossing-over hotspot on chromosome 8 affected the frequency of crossing over at this location. In their first experiment, they examined three groups of yeast cells containing the modified chromosome 8. Group 1 contained no kinetochore proteins attached to the hotspot, group 2 contained the kinetochore protein CTF attached to the hotspot, and group 3 contained the kinetochore protein IML attached to the hotspot. For each group, the scientists determined the frequency of crossing over between the RFP and GFP genes. To determine the frequency, the scientists added the number of cells emitting both red and green light to the number of cells that emitted no light and divided by the total number of cells (Figure 2).

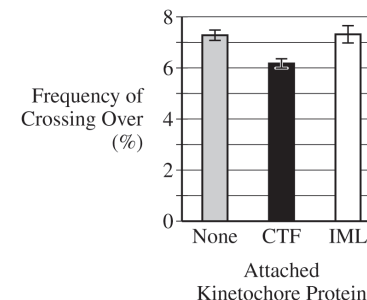


Figure 2. The frequency of crossing over in a hotspot on yeast chromosome 8 for cell groups treated with different kinetochore proteins. Error bars represent $\pm 2SE_{\bar{x}}$.

(b)

- (i) **Identify** the control group for the scientists' first experiment, shown in Figure 2.
- (ii) In a follow-up experiment, the scientists created a modified version of CTF in which the DNA-binding portion had been removed. They compared the frequency of crossing over in yeast cells in the presence and absence of unmodified CTF with that in yeast cells in the presence and absence of the modified CTF protein (data not shown). In the follow-up experiment, **justify** why the scientists used a modified CTF protein that is unable to bind to DNA as a control.
- (iii) **Identify** the independent variable in the follow-up experiment.
- (c) Based on Figure 2, **describe** the effect on the frequency of crossing over when CTF is attached to the chromosome 8 hotspot compared with the effect when IML is attached to the hotspot.
- (d)
- (i) **Predict** the effect on the number of copies of chromosome 8 likely to be present in the resulting daughter cells when CTF is attached to the hotspot.
- (ii) Provide reasoning to **justify** your prediction.
- (iii) **Explain** how the presence of hotspots (Figure 1) could increase the likelihood that a population will survive in the presence of selective pressures.

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

If there are multiple parts to this question, write the part letter with your response.

5. Researchers study mechanisms that enable or prevent speciation.

(a) **Describe** a post-zygotic mechanism that prevents gene flow and thus enables speciation.

New genes can evolve from noncoding regions of DNA. It is not until certain regulatory elements are present in the DNA that a noncoding region becomes a new, functional gene that encodes a protein. These regulatory elements include a promoter, a 5' untranslated region (UTR) followed by a start codon, and a 3' UTR following a stop codon (Figure 1).

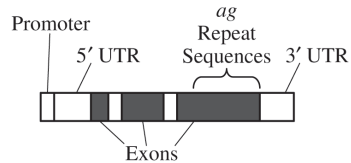


Figure 1. Basic structure of a functional *ag* gene

Researchers studied the evolution of the family of antifreeze-glycoprotein (AG) encoding genes in Gadidae, a family of marine fish known as cods. When present in the fish, these glycoproteins reduce the freezing temperature of the fish. The researchers compared genomic sequences in nine cod species and one non-cod fish species, *B. brosme*. They recorded the presence or absence of the elements of functional *ag* genes as well as *ag*-like sequences that are similar to a functional gene but have undergone mutation and do not contain all the elements required to enable protein production (Figure 2).

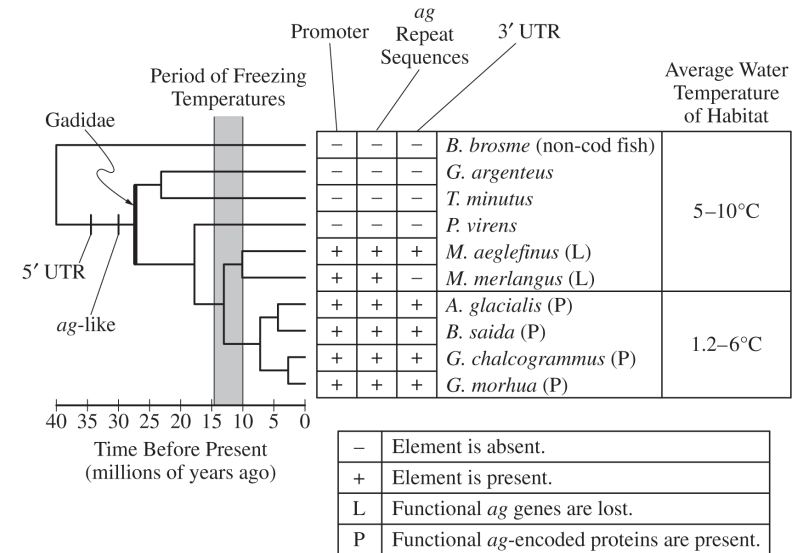


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

- (b) Based on the data in Figure 2, **explain** how changes to the genome enabled cods to survive and reproduce after a period of freezing temperatures between 10 and 15 million years ago.
- (c) Using the template in the space provided for your response, place an “X” on the phylogenetic tree to **represent** the origin of the functional *ag* gene.
- (d) Based on Figure 2, **explain** how genetic differences among the species in the Gadidae family determine the habitats in which they can survive.

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

If there are multiple parts to this question, write the part letter with your response.

4. Existing isolated brook trout populations in Newfoundland, Canada, were once part of a larger population that was fragmented at the end of the most recent glaciation period about 10,000 to 12,000 years ago. Researchers investigated 14 naturally separated stream populations of brook trout. They found that the populations are all genetically distinct and show differences in morphology.

- Describe** the prezygotic barrier that results in these genetically distinct populations.
- Brook trout with longer fins are able to swim faster than brook trout with shorter fins. In one of the Newfoundland streams, the main prey of the brook trout evolved to move faster. For brook trout living in this stream, **explain** the difference in fitness between longer-finned individuals and shorter-finned individuals.
- If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, **predict** the likely impact on both populations.
- Researchers claim that there are more genetic differences between any two current brook trout populations than there are between any single current population and the ancestral brook trout population from which all the trout are descended. Provide reasoning to **justify** their claim.

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

4. In 1981 a single immature male *Geospiza conirostris* finch flew more than 100 kilometers from the Galápagos island of Española to the Galápagos island of Daphne Major, where no *G. conirostris* finches were living. The immigrant finch bred with a female *G. fortis*, a species of finch common on Daphne Major. The F_1 finches and later generations interbred only within their lineage. By 2012 scientists counted 23 individuals, including eight breeding pairs, within this hybrid lineage on Daphne Major. The hybrid lineage became known as Big Bird.

Birds with different beak shapes and sizes eat different types of food. The dimensions of the Big Bird beaks relative to the beaks of the major competitor finch species on Daphne Major are shown in Figure 1.

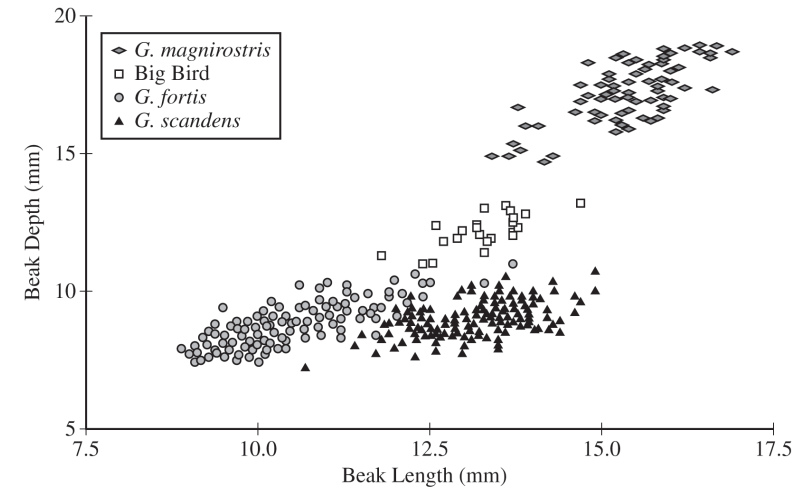


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

- The Big Bird lineage became reproductively isolated from *G. fortis*. **Describe** one prezygotic mechanism that likely contributed to the reproductive isolation of the Big Bird lineage from *G. fortis*.
- Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.
- A virus infects and kills all *G. magnirostris* on Daphne Major but does not affect the other finch species. Assuming food type and availability stay the same, **predict** the most likely change in the beak phenotype of the Big Bird population after six more generations.
- Provide reasoning to **justify** your prediction in part (c).

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

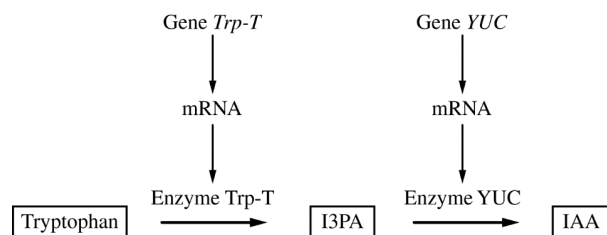


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

1. 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.
 - (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.
 - (c) **Explain** one feedback mechanism by which a cell could prevent production of too much IAA without limiting I3PA production.
 - (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.
 - (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.

BIOLOGY

Section II

Total Time—1 hour and 30 minutes

Reading Period—10 minutes

Writing Period—1 hour and 20 minutes

8 Questions

Directions: Questions 1 and 2 are long free-response questions that require about 22 minutes each to answer and are worth 10 points each. Questions 3–8 are short free-response questions that require about 6 minutes each to answer. Questions 3–5 are worth 4 points each and questions 6–8 are worth 3 points each. Read each question carefully and completely. You are advised to spend the 10-minute reading period planning your answers. You may begin writing your responses before the reading period is over. Write your response in the space provided for each question. Only material written in the space provided will be scored. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable.

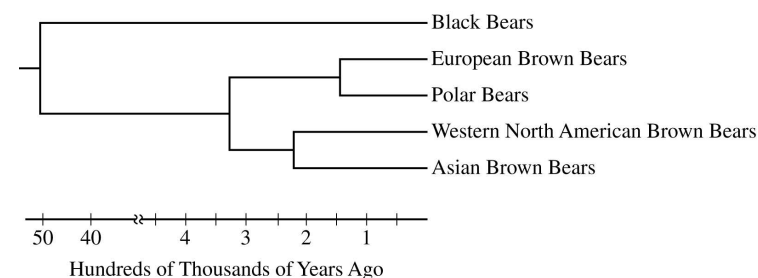


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

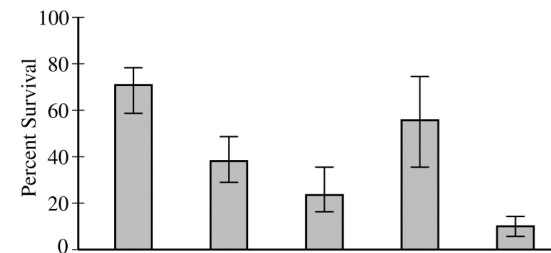
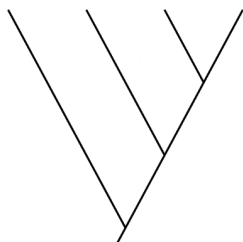
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their evolutionary relatedness (Figure 1).

A researcher studying adaptation in bears sequenced the nuclear gene encoding a lysosomal trafficking protein (LYST) in polar bears, brown bears, black bears, and panda bears. There are seven inferred amino acid substitutions that are found only in polar bears. Mutations that cause similar substitutions in the human LYST protein are associated with Chediak-Higashi syndrome, an autosomal recessive condition in which pigment is absent from the hair and eyes. The researcher used the inferred amino acid sequences to build the distance matrix shown in Table 1.

TABLE 1. AMINO ACID DIFFERENCES IN THE LYST PROTEIN AMONG BEAR SPECIES

	Panda	Black	Brown	Polar
Panda	—			
Black	33	—		
Brown	34	1	—	
Polar	40	7	8	—

- Use the phylogenetic tree in Figure 1 to **estimate** the age in hundreds of thousands of years of the most recent common ancestor of all brown bears. **Identify** the population of brown bears to which polar bears are most closely related based on the mitochondrial DNA sequence comparison. **Identify** two populations whose positions could be switched without affecting the relationships illustrated in the phylogenetic tree.
- Construct** a cladogram on the template to represent a model of the evolutionary relatedness among the bear species based on the differences in LYST protein sequences (Table 1). **Circle** the position on the cladogram that represents the out-group.
- A student claims that mitochondrial DNA sequence comparisons provide a more accurate phylogeny of bear species than do LYST protein sequence comparisons. **Provide ONE piece of reasoning** to support the student's claim.
- A researcher genetically engineers a mouse strain by deleting the mouse *lyst* gene and replacing it with the polar bear *lyst* gene. **Predict** the most likely difference in phenotype of the transgenic mouse strain compared to the wild-type mouse strain. **Justify** your prediction.
- Describe** how the mutation in the *lyst* gene became common in the polar bear population. If the *lyst* gene were the only determinant of fur color, **predict** the percent of white offspring produced by a mating between a polar bear and a brown bear.



Strain	I	II	III	IV	V
<i>P450</i>	+	—	+	+	—
<i>Abc8</i>	+	+	—	+	—
<i>Cps</i>	+	+	+	—	+

+ = Wildtype
— = Deletion

Figure 1. Percent survival of five strains of bedbugs treated with beta-cyfluthrin. A (+) indicates the gene is present; a (—) indicates the gene is deleted. Error bars represent the 95% confidence interval.

- The common bedbug (*Cimex lectularius*) is a species of insect that is becoming increasingly resistant to insecticides. Bedbugs possess several genes suspected of contributing to the resistance, including *P450*, *Abc8*, and *Cps*. To investigate the role of these genes in insecticide resistance, researchers deleted one or more of these genes in different strains of bedbugs, as indicated in Figure 1, and treated the strains with the insecticide beta-cyfluthrin. Each strain was genetically identical except for the deleted gene(s) and was equally fit in the absence of beta-cyfluthrin. The percent survival of each strain following beta-cyfluthrin treatment is shown in Figure 1.
 - Identify** the control strain in the experiment. Use the means and confidence intervals in Figure 1 to **justify** the claim that *Abc8* is effective at providing resistance to beta-cyfluthrin.
 - P450* encodes an enzyme that detoxifies insecticides. *Abc8* encodes a transporter protein that pumps insecticides out of cells. *Cps* encodes an external structural protein located in the exoskeleton that greatly reduces the absorption of insecticides. Based on this information and the data in Figure 1, **explain** how a deletion of both *P450* and *Abc8* results in lower survival in bedbugs compared with a deletion of *Cps* only.

BIOLOGY
Section II
8 Questions

Total Time—90 minutes

Reading Period—10 minutes

Writing Period—80 minutes

Directions: Questions 1 and 2 are long free-response questions that require about 22 minutes each to answer and are worth 10 points each. Questions 3–8 are short free-response questions that require about 6 minutes each to answer. Questions 3–5 are worth 4 points each and questions 6–8 are worth 3 points each.

Read each question carefully and completely. You are advised to spend the 10-minute reading period planning your answers. You may begin writing your responses before the reading period is over. Write your response in the space provided for each question. Only material written in the space provided will be scored. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable.

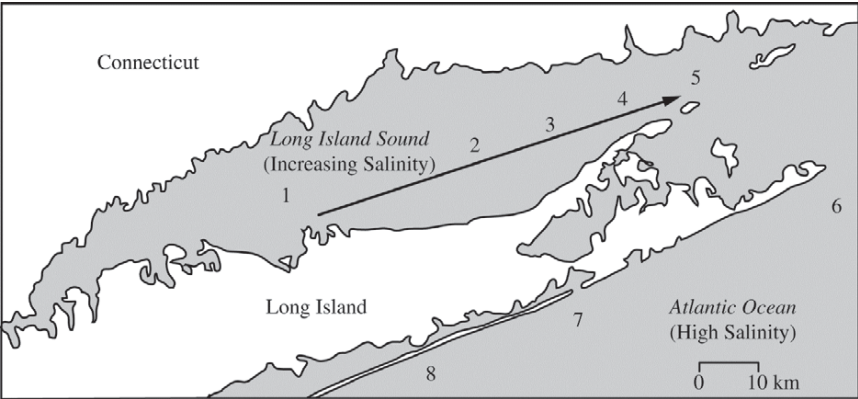
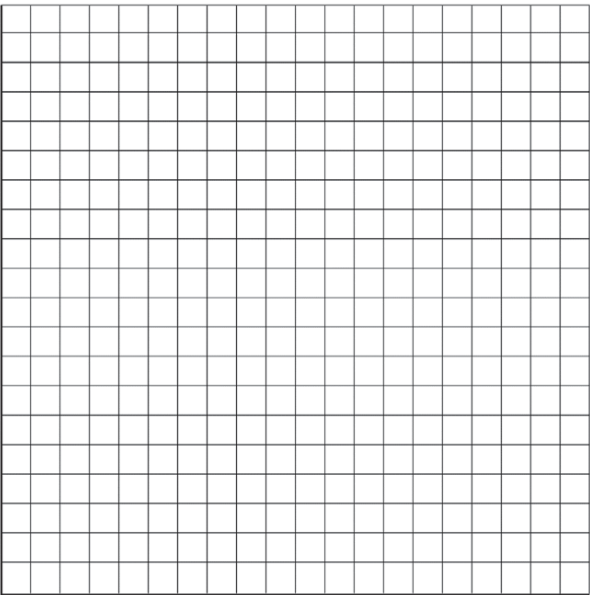


Figure 1. Sampling sites of marine mussels at various locations (1–8) in Long Island Sound and the Atlantic Ocean

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



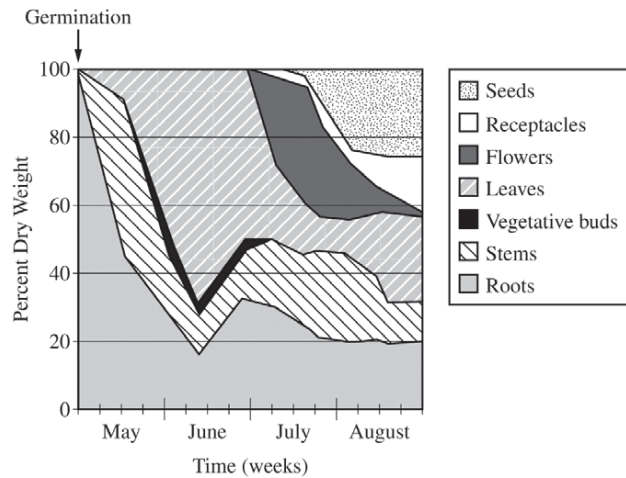


Figure 1. Percent dry weight of different plant structures during the growing season for an annual plant

3. 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).
- 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.
 - 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.
 - 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.

BIOLOGY

Section II

8 Questions

Planning Time—10 minutes

Writing Time—80 minutes

Directions: Questions 1 and 2 are long free-response questions that require about 22 minutes each to answer and are worth 10 points each. Questions 3–8 are short free-response questions that require about 6 minutes each to answer. Questions 3–5 are worth 4 points each and questions 6–8 are worth 3 points each.

Read each question carefully and completely. Write your response in the space provided for each question. Only material written in the space provided will be scored. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable.

1. Many species have circadian rhythms that exhibit an approximately 24-hour cycle. Circadian rhythms are controlled by both genetics and environmental conditions, including light.

Researchers investigated the effect of light on mouse behavior by using a running wheel with a motion sensor to record activity on actograms, as shown in Figure 1.

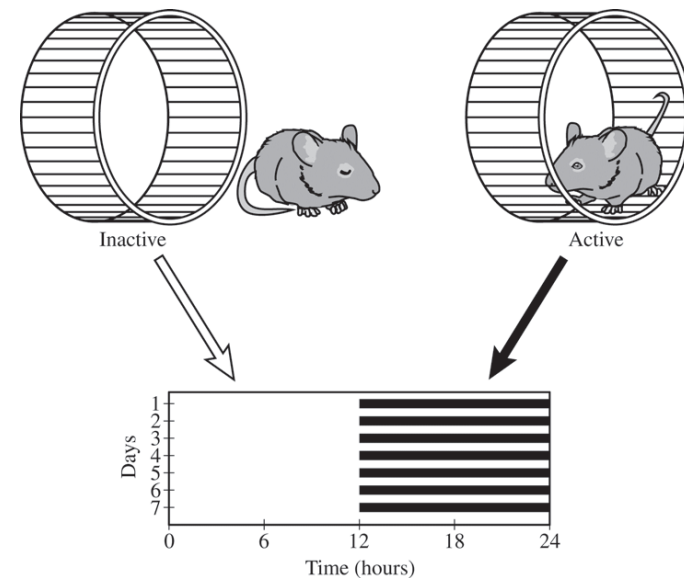


Figure 1. Strategy for recording mouse activity data. When a mouse is active on the running wheel, the activity is recorded as a dark horizontal line on an actogram. When the mouse is inactive, no dark line is recorded.

For the investigation, adult male mice were individually housed in cages in a soundproof room at 25°C. Each mouse was provided with adequate food, water, bedding material, and a running wheel. The mice were exposed to daily periods of 12 hours of light (L) and 12 hours of dark (D) (L12:D12) for 14 days, and their activity was continuously monitored. The activity data are shown in Figure 2.

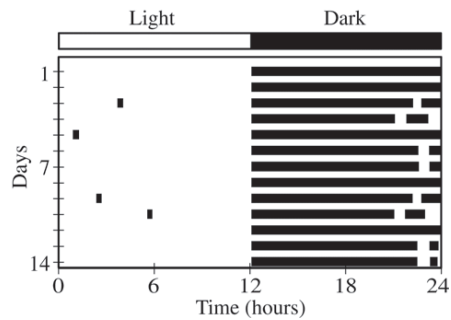


Figure 2. Actogram of mouse activity under L12:D12 conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

After 14 days in L12:D12, the mice were placed in continuous darkness (DD), and their activity on the running wheel was recorded as before. The activity data under DD conditions are shown in Figure 3.

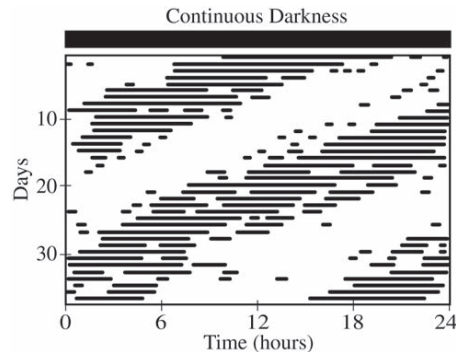


Figure 3. Actogram of mouse activity under DD conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

- (a) The nervous system plays a role in coordinating the observed activity pattern of the mice in response to light-dark stimuli. **Describe** ONE role of each of the following anatomical structures in responding to light-dark stimuli.
 - A photoreceptor in the retina of the eye
 - The brain
 - A motor neuron
- (b) Based on an analysis of the data in Figure 2, **describe** the activity pattern of the mice during the light and dark periods of the L12:D12 cycle.
- (c) The researchers claim that the genetically controlled circadian rhythm in the mice does not follow a 24-hour cycle. **Describe** ONE difference between the daily pattern of activity under L12:D12 conditions (Figure 2) and under DD conditions (Figure 3), and use the data to **support** the researchers' claim.
- (d) To investigate the claim that exposure to light overrides the genetically controlled circadian rhythm, the researchers plan to repeat the experiment with mutant mice lacking a gene that controls the circadian rhythm. **Predict** the observed activity pattern of the mutant mice under L12:D12 conditions and under DD conditions that would support the claim that light overrides the genetically controlled circadian rhythm.
- (e) In nature, mice are potential prey for some predatory birds that hunt during the day. **Describe** TWO features of a model that represents how the predator-prey relationship between the birds and the mice may have resulted in the evolution of the observed activity pattern of the mice.

8. A research team has genetically engineered a strain of fruit flies to eliminate errors during DNA replication. The team claims that this will eliminate genetic variation in the engineered flies. A second research team claims that eliminating errors during DNA replication will not entirely eliminate genetic variation in the engineered flies.
 - (a) **Provide** ONE piece of evidence that would indicate new genetic variation has occurred in the engineered flies.
 - (b) **Describe** ONE mechanism that could lead to genetic variation in the engineered strain of flies.
 - (c) **Describe** how genetic variation in a population contributes to the process of evolution in the population.

STOP

END OF EXAM