

Week 23

AP Biology

Homework bundle for this week

本周作业合集

exercises.lol

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AP Biology

Name: _____ Score: _____

1. Natural selection needs **variation** in a population, which means...
 - ☐ individuals differ from one another
 - ☐ every individual is identical
 - ☐ there is only one individual
 - ☐ no one reproduces
2. In biology, an organism's **fitness** measures its...
 - ☐ reproductive success — how many offspring it leaves
 - ☐ physical strength only
 - ☐ running speed
 - ☐ body size
3. In **artificial selection**, who decides which individuals reproduce?
 - ☐ humans
 - ☐ the environment
 - ☐ predators
 - ☐ no one
4. A **gene pool** is...
 - ☐ all the alleles present in a population
 - ☐ a single gene
 - ☐ a type of cell
 - ☐ a pool of water
5. A population in **Hardy-Weinberg equilibrium** is one that is...
 - ☐ not evolving — its allele frequencies stay constant
 - ☐ evolving very quickly
 - ☐ about to go extinct
 - ☐ made of one individual
6. Artificial and natural selection use the same basic mechanism — differences in who reproduces.
 - ☐ True ☐ False

7. A feature that helps an organism survive in its environment is an _____.

8. At the population level, evolution is a change in allele _____ over generations.

9. If $q^2 = 0.09$, what is the recessive allele frequency q ?

10. A body part that has lost most of its original function, like the human tailbone, is a _____ structure.

AP Biology

1. **individuals differ from one another**

Variation means individuals differ; selection can only act if there are differences to choose between.

2. **reproductive success — how many offspring it leaves**

Fitness is reproductive success — leaving more surviving offspring — not just physical strength.

3. **humans**

In **artificial selection**, humans choose which individuals breed — also called **selective breeding**.

4. **all the alleles present in a population**

A **gene pool** is the whole collection of alleles in a **population** at a given time.

5. **not evolving — its allele frequencies stay constant**

In **Hardy-Weinberg equilibrium**, allele frequencies do not change — the population is *not* evolving.

6. **True**

Both work by some individuals reproducing more than others; only the selector differs.

7. **adaptation**

An **adaptation** is a helpful feature that natural selection has favoured over generations.

8. **frequency**

Evolution is defined as a change in **allele frequency** in a population over time.

9. **0.3**

$q = \sqrt{0.09} = 0.3$. Then $p = 1 - q = 0.7$.

10. **vestigial**

A **vestigial structure** is a reduced leftover from an ancestor that once used it fully.

7.1 Introduction to Natural Selection

Name: _____ Class: _____ Date: _____

Total: 11 marks

KEY WORDS natural selection 自然选择 • variation 变异 • fitness 适合度 • evolution 进化

Objective

Build the skills to answer exam questions on **natural selection** — the core idea.

You must be able to:

- state the conditions for **natural selection** 自然选择 (variation, heritability, overproduction, differential survival)
- explain **fitness** 适合度 as reproductive success
- link selection to changes in a population

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ The conditions for natural selection

Natural selection requires:

1. **Variation** — individuals differ.
2. **Heritability** — some variation is inherited.
3. **Overproduction** — more offspring are made than can survive.
4. **Differential survival/reproduction** — those better suited survive and reproduce more.

■ Fitness

Fitness is an organism's **reproductive success** — how many surviving offspring it produces, not its strength or size. High-fitness traits become more common.

■ How the population changes

Individuals with advantageous heritable traits leave more offspring, so those alleles increase in the population over generations — the population **adapts**.

■ A worked example

In a population of beetles, darker ones are better camouflaged, survive more, and reproduce more; over generations the dark allele becomes more common.

2 Practice

Now apply the methods above.

2.1 State two of the conditions required for natural selection. [2]

2.2 Define fitness in evolutionary terms. [1]

2.3 Why must the variation be heritable for selection to change a population? [1]

3 Exam-style questions

3.1 In evolutionary terms, fitness means an organism's [1]

- **A** physical strength
- **B** reproductive success
- **C** body size
- **D** lifespan only

3.2 Dark beetles survive better than light ones on dark soil.

(a) Explain how natural selection changes the population over generations. [3]

(b) State the condition that ensures the change is passed on. [1]

3.3 Explain why overproduction of offspring is important for natural selection. [2]

Solutions

2.1 Any two: variation, heritability, overproduction, differential survival/reproduction.

2.2 An organism's reproductive success (number of surviving offspring).

2.3 Only heritable traits can be passed to offspring, so only they can change the population's makeup over generations.

3.1 B — reproductive success.

3.2 (a) Dark beetles are better camouflaged, so more survive; survivors reproduce more, passing on the dark allele; over generations the dark allele becomes more common. (b) The trait (color) is heritable.

3.3 More offspring are produced than can survive, so there is competition; this lets the better-suited individuals survive and reproduce, driving selection.

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.

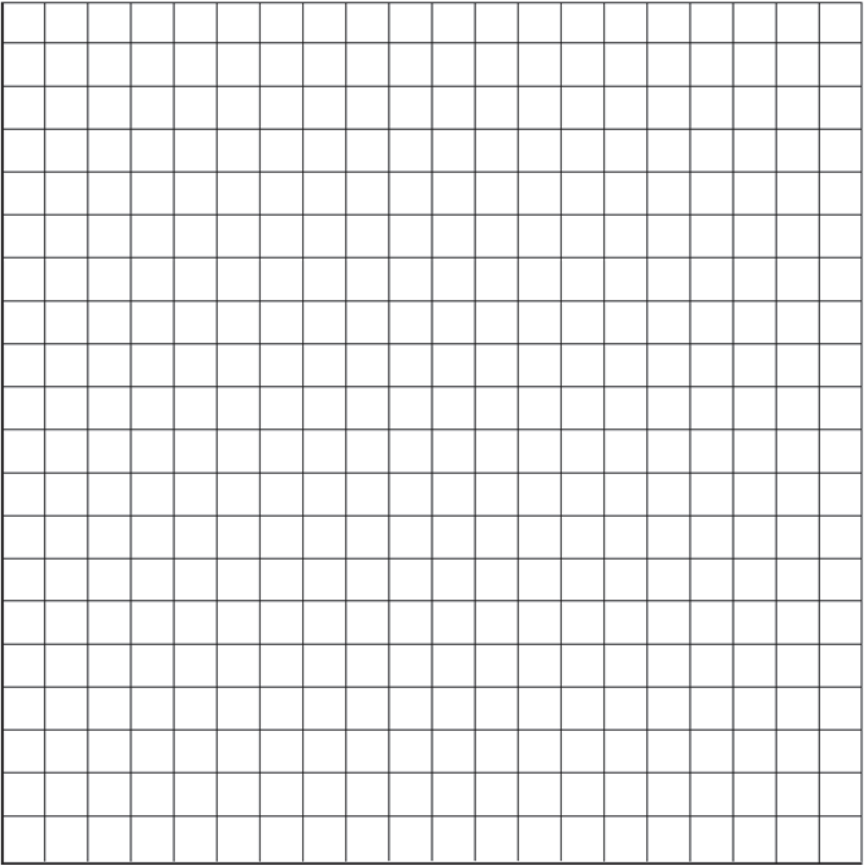
1. Trichomes are hairlike outgrowths of the epidermis of plants that are thought to provide protection against being eaten by herbivores (herbivory). In a certain plant species, stem trichome density is genetically determined.

To investigate variation in stem trichome density within the plant species, a student counted the number of trichomes on the stems of six plants in each of three different populations. The student used the data to calculate the mean trichome density (numbers of hairs per square centimeter) for each population. The results are provided in the table below.

TRICHOME DENSITY IN THREE PLANT POPULATIONS (number of trichomes/cm²)

Population	Plant 1	Plant 2	Plant 3	Plant 4	Plant 5	Plant 6	Mean	Standard Error of the Mean (SEM)
I	8	11	9	10	8	6	9	1
II	12	6	15	9	13	8	11	1
III	13	17	9	14	12	16	14	1

- (a) On the axes provided, **create** an appropriately labeled graph to illustrate the sample means of the three populations to within 95% confidence (i.e., sample mean $\pm$ 2 SEM).
- (b) Based on the sample means and standard errors of the means, **identify** the two populations that are most likely to have statistically significant differences in the mean stem trichome densities. **Justify** your response.
- (c) **Describe** the independent and dependent variables and a control treatment for an experiment to test the hypothesis that higher trichome density in plants is selected for in the presence of herbivores. **Identify** an appropriate duration of the experiment to ensure that natural selection is measured, and **predict** the experimental results that would support the hypothesis.



7.2 Natural Selection

Name: _____ Class: _____ Date: _____

Total: 9 marks

KEY WORDS disruptive 分裂 • directional 定向 • stabilizing 稳定 • natural selection 自然选择 • variation 变异

Objective

Build the skills to answer exam questions on **types of natural selection**.

You must be able to:

- distinguish **directional** 定向, **stabilizing** 稳定, and **disruptive** 分裂 selection
- match each to its effect on a trait distribution
- give an example of each

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Three patterns of selection

- **Directional** — favors one **extreme**; the average shifts that way (e.g. larger beak size in a drought).
- **Stabilizing** — favors the **middle**; extremes are selected against (e.g. average human birth weight).
- **Disruptive** — favors **both extremes** over the middle; can split a population.

■ Reading a distribution graph

- Directional: the peak **moves** left or right.
- Stabilizing: the peak gets **taller and narrower** (less variation).
- Disruptive: **two peaks** appear.

■ A worked identification

If small and large individuals both survive better than medium ones, that is **disruptive** selection (two favored extremes).

■ Why it matters

Each pattern changes the population's trait distribution differently, shaping how a species adapts over time.

2 Practice

Now apply the methods above.

2.1 Which type of selection favors the average trait? [1]

2.2 Which type shifts the average toward one extreme? [1]

2.3 What happens to a distribution under disruptive selection? [1]

3 Exam-style questions

3.1 Selection that favors both extremes over the middle is [1]

- **A** directional
 - **B** stabilizing
 - **C** disruptive
 - **D** artificial
-

3.2 In a drought, only birds with large beaks can crack the remaining hard seeds.

(a) Name the type of selection. [1]

(b) Describe how the beak-size distribution changes over generations. [2]

3.3 Human birth weight clusters near an average, with very small and very large babies less likely to survive. Name and explain the type of selection. [2]

Solutions

2.1 Stabilizing selection.

2.2 Directional selection.

2.3 It splits toward both extremes (two peaks).

3.1 C — disruptive.

3.2 (a) Directional. (b) Large-beaked birds survive and reproduce more, so average beak size increases over generations (the distribution shifts toward large).

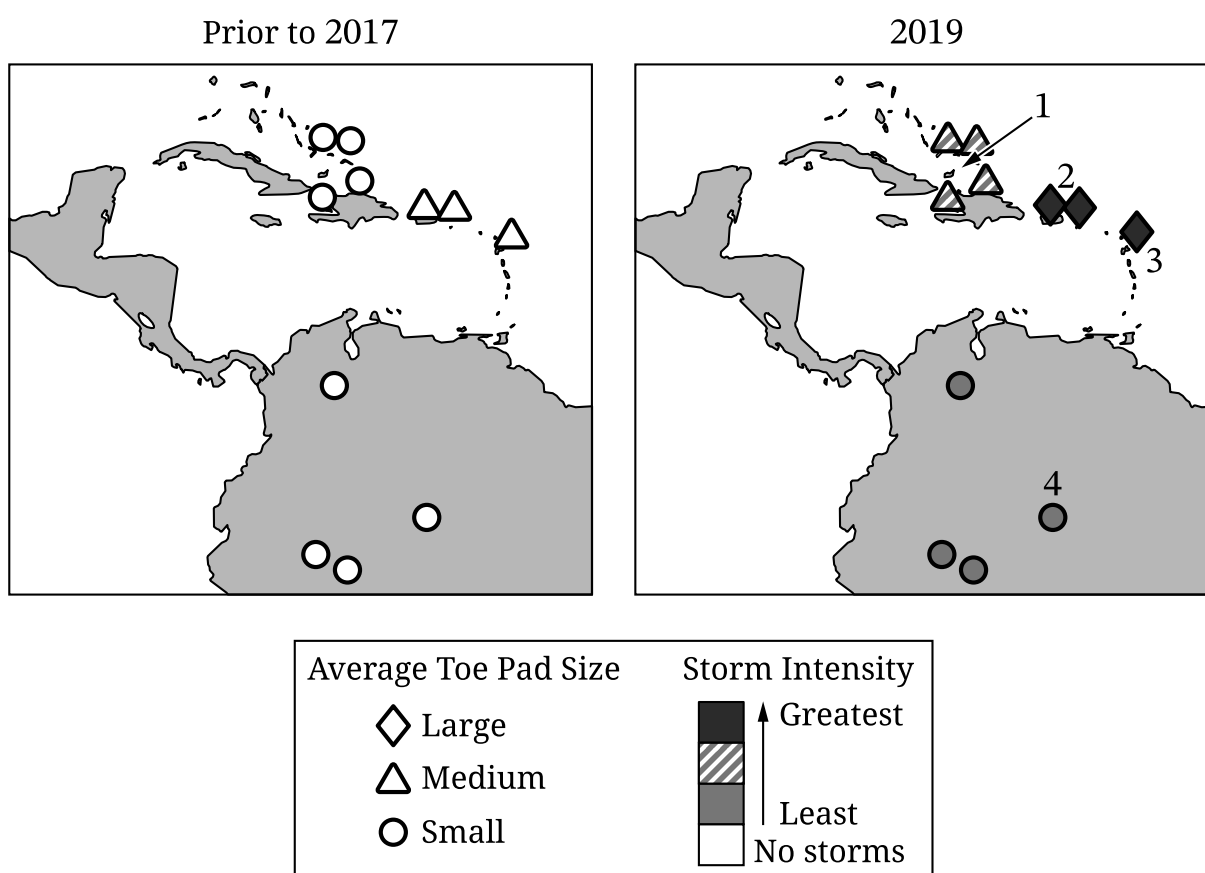
3.3 Stabilizing selection — the average birth weight is favored while both extremes are selected against, narrowing the distribution around the mean.

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.

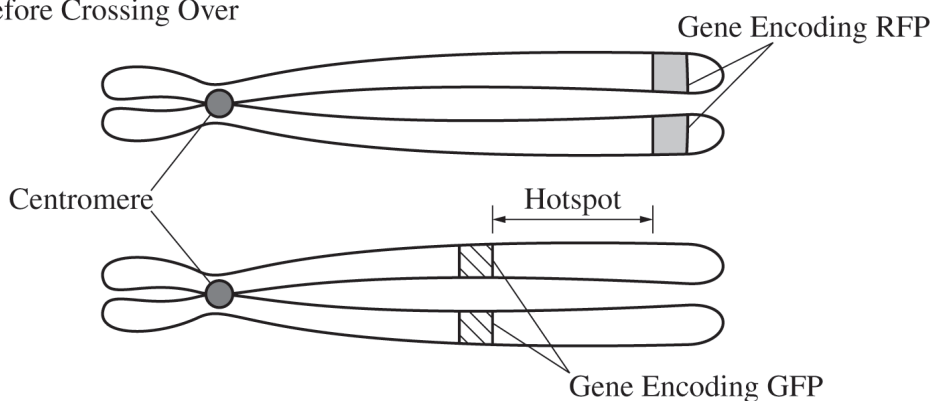
(a)

- (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.

A. Before Crossing Over



B. After Crossing Over

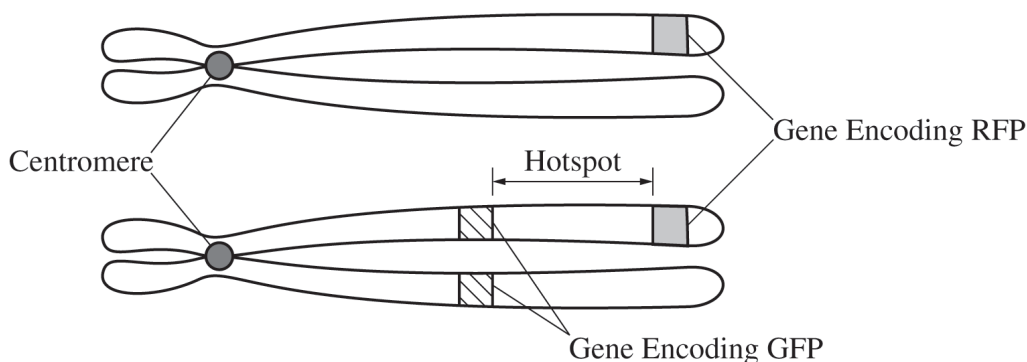


Figure 1. Models of modified chromosome 8 used in the experiment (A) before and (B) after crossing over occurs at the hotspot

- (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).

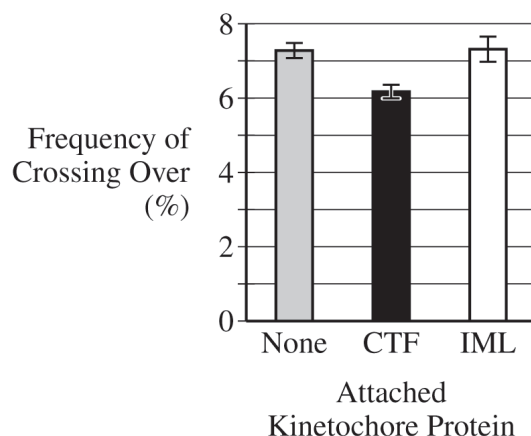


Figure 2. The frequency of crossing over in a hotspot on yeast chromosome 8 for cell groups treated with different kinetochore proteins. Error bars represent $\pm 2SE_{\bar{x}}$.

- (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).

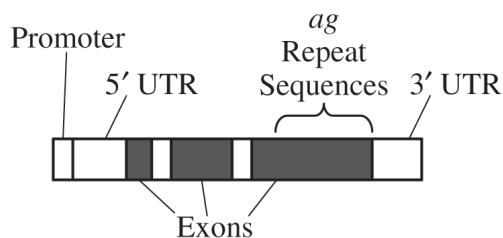


Figure 1. Basic structure of a functional *ag* gene

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).

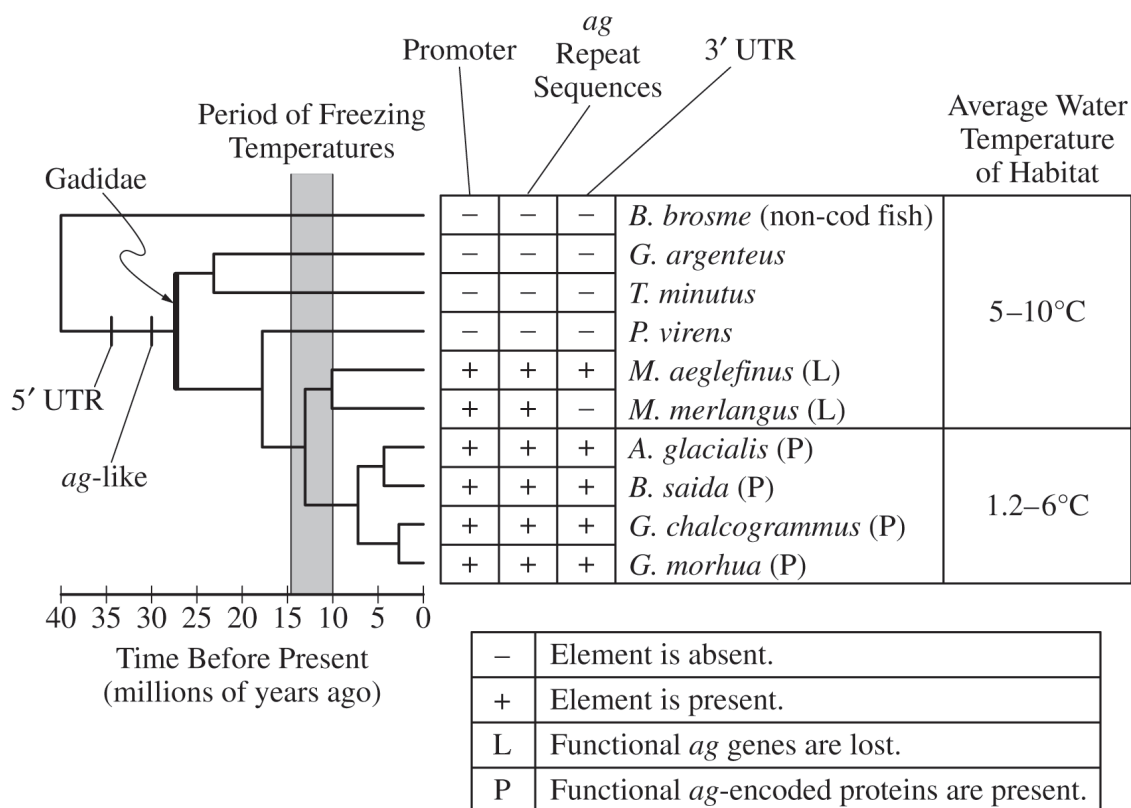


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

- (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.
- (a) **Describe** the prezygotic barrier that results in these genetically distinct populations.
- (b) 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.
- (c) If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, **predict** the likely impact on both populations.
- (d) 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 F₁ 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.

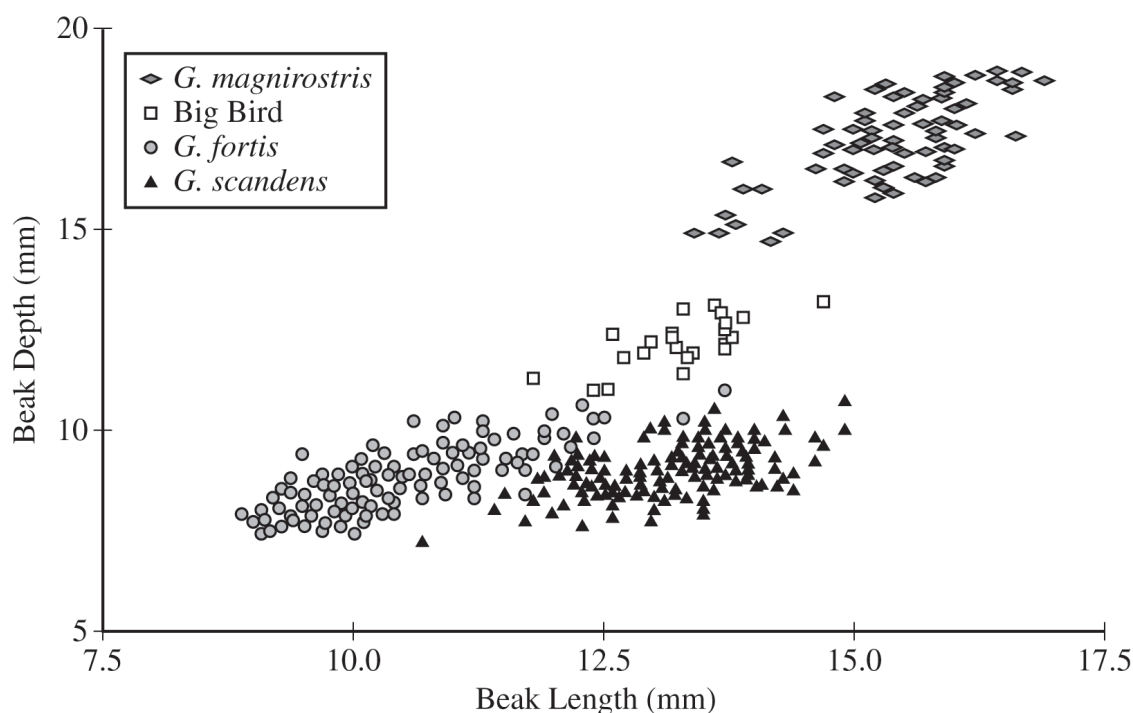


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

- (a) 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*.
- (b) Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.
- (c) 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.
- (d) 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.

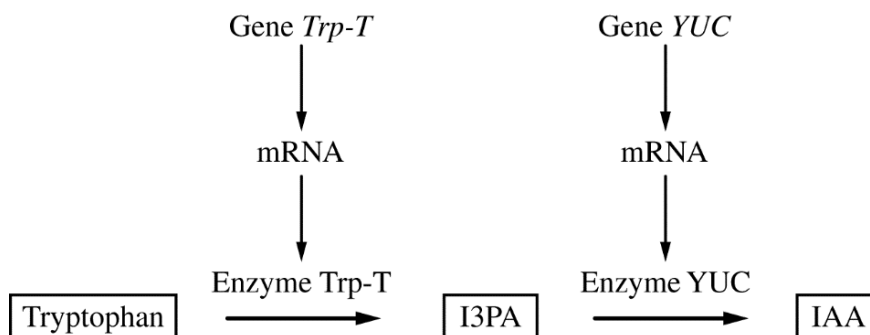


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

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.

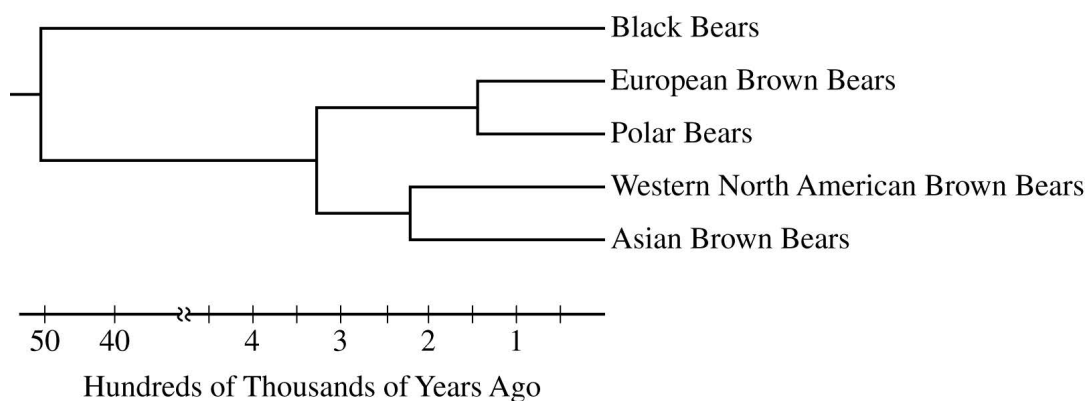


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

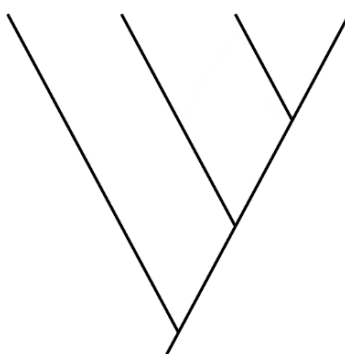
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their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

- (a) 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.
- (b) **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.
- (c) 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.
- (d) 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.
- (e) **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.



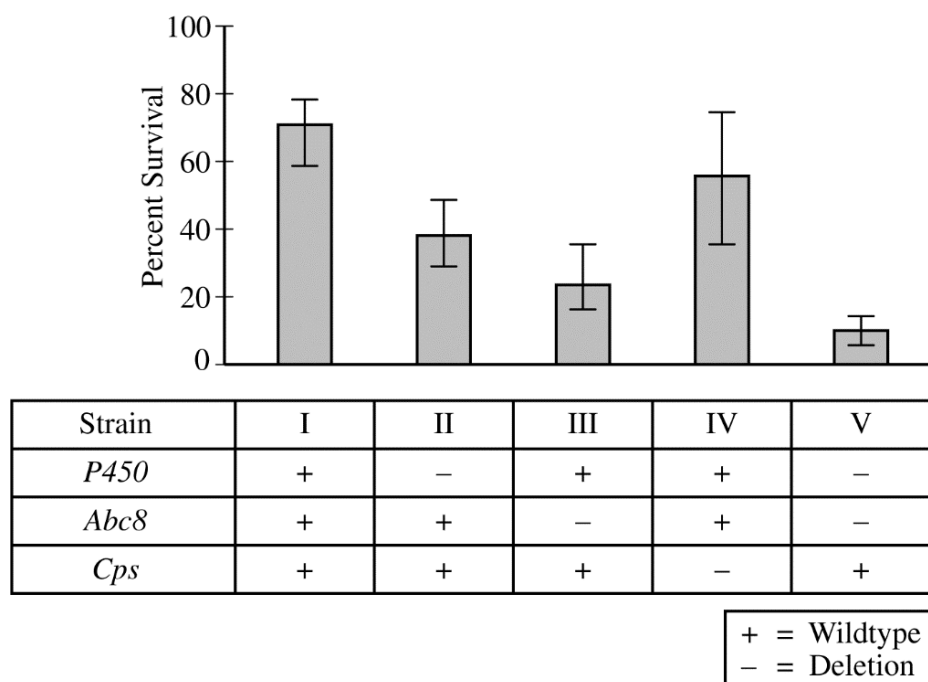


Figure 1. Percent survival of five strains of bedbugs treated with beta-cyfluthrin. A (+) indicates the gene is present; a (–) indicates the gene is deleted. Error bars represent the 95% confidence interval.

4. 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.
- (a) **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.
- (b) *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.

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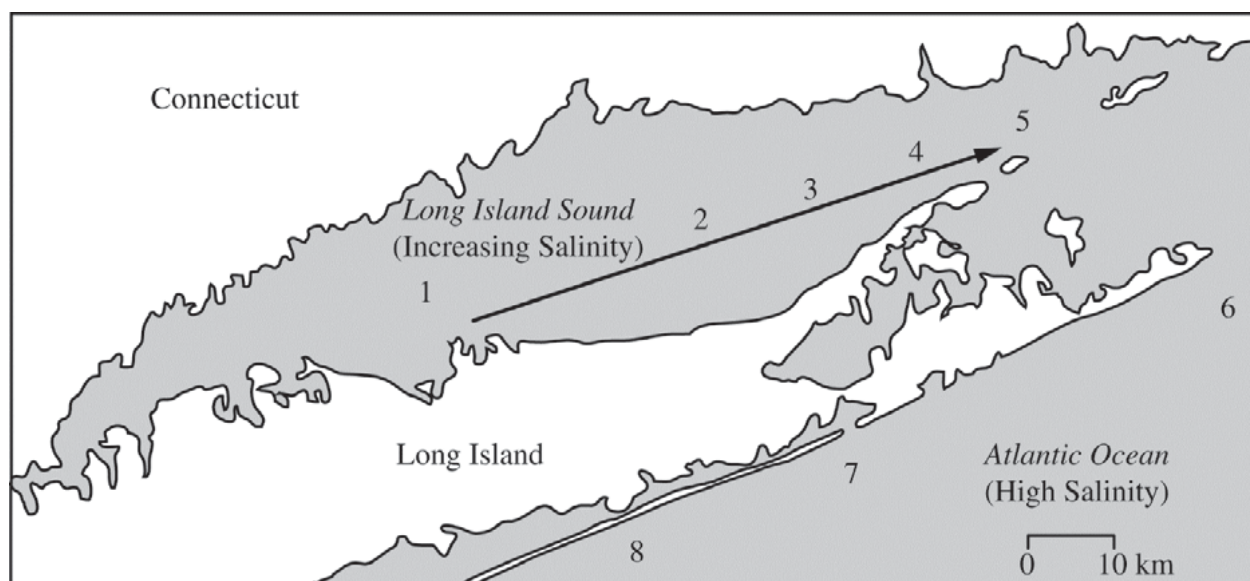
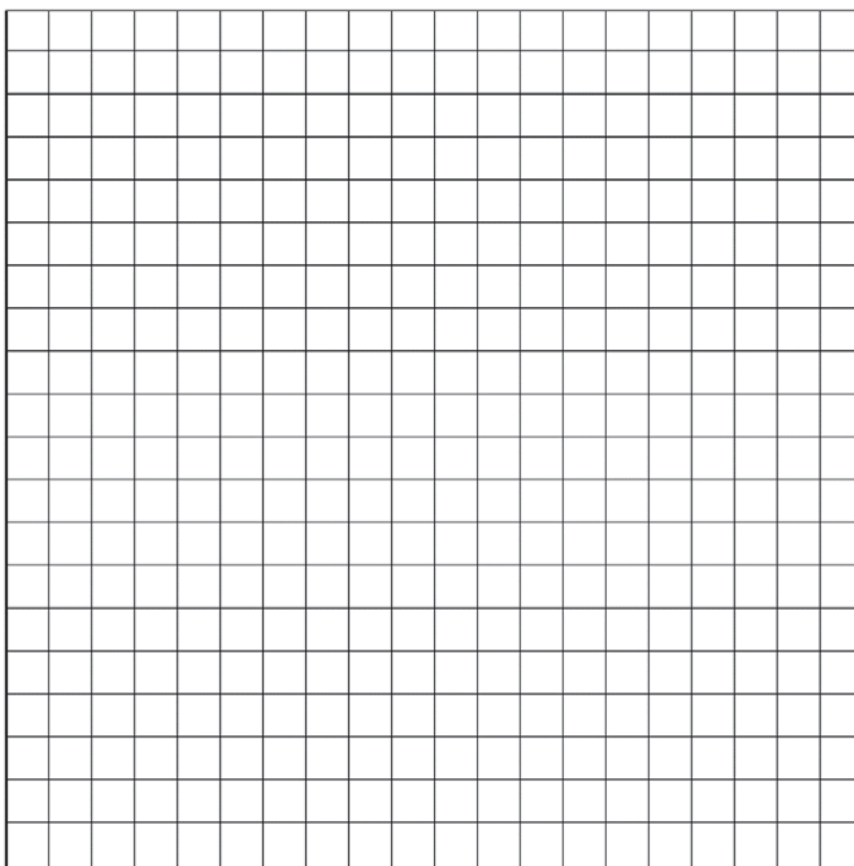


Figure 1. Sampling sites of marine mussels at various locations (1–8) in Long Island Sound and the Atlantic Ocean

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		

1. 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).
- (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.
- (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.
- (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.
- (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.



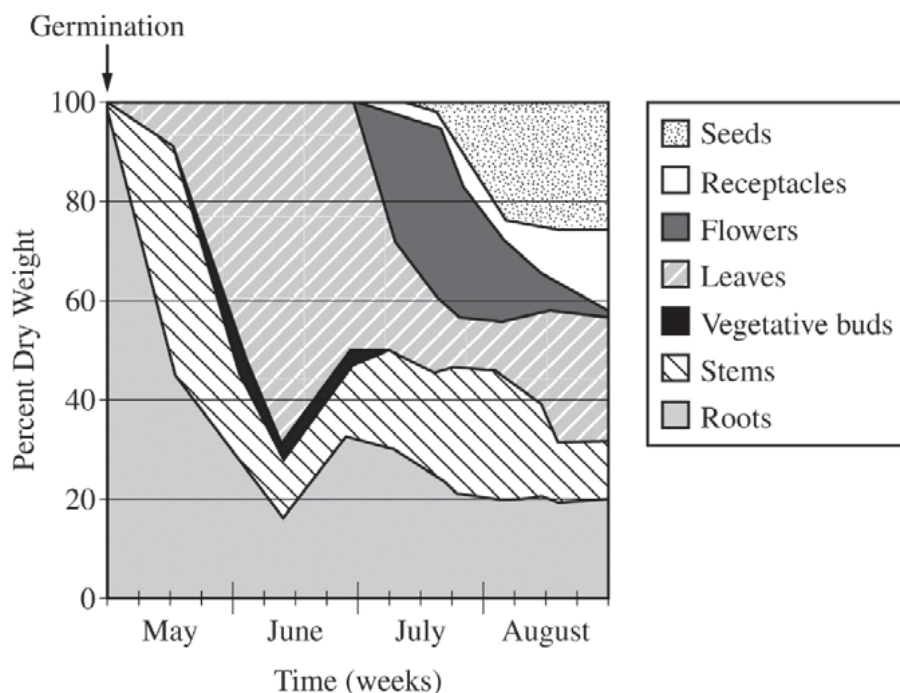


Figure 1. Percent dry weight of different plant structures during the growing season for an annual plant

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.

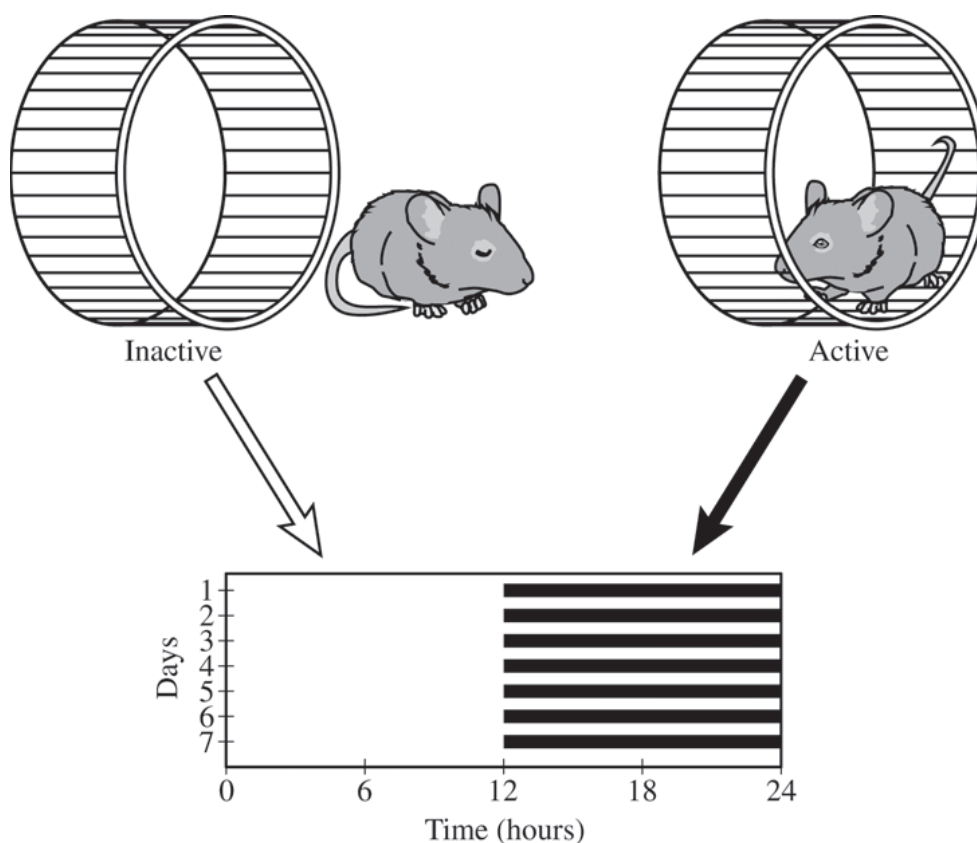


Figure 1. Strategy for recording mouse activity data. When a mouse is active on the running wheel, the activity is recorded as a dark horizontal line on an actogram. When the mouse is inactive, no dark line is recorded.

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.

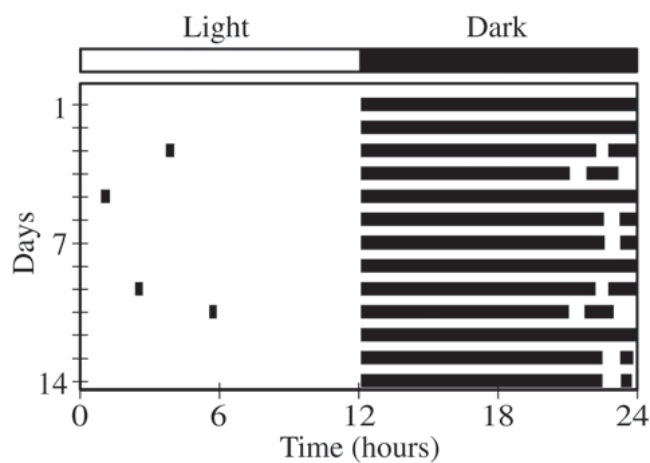


Figure 2. Actogram of mouse activity under L12:D12 conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

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.

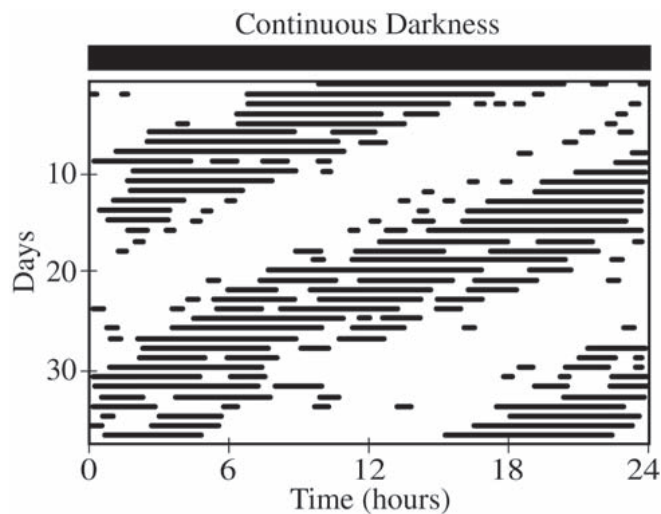


Figure 3. Actogram of mouse activity under DD conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

- (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

7.3 Artificial Selection

Name: _____ Class: _____ Date: _____

Total: 10 marks**KEY WORDS** artificial selection 人工选择 • natural selection 自然选择 • variation 变异 • evolution 进化

Objective

Build the skills to answer exam questions on **artificial selection**.

You must be able to:

- describe **artificial selection** 人工选择 (selective breeding by humans)
- contrast it with natural selection
- give examples (crops, dogs)

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Artificial selection

In **artificial selection**, **humans** choose which individuals reproduce, based on traits they want. Over generations the chosen traits become more common.

■ Contrast with natural selection

- **Natural** — the **environment** selects; traits that aid survival/reproduction spread.
- **Artificial** — **humans** select; traits humans prefer spread (even if not survival-useful).

Both work on **heritable variation**, but the selecting agent differs.

■ Examples

Crops bred for larger fruit; dogs bred from wolves into many breeds; cows bred for more milk. All show rapid change from human choice.

■ Evidence for evolution

Artificial selection's fast, visible changes show that selection on heritable variation can reshape a population — supporting how natural selection works over longer times.

2 Practice

Now apply the methods above.

2.1 Who does the selecting in artificial selection? [1]

2.2 Give one example of artificial selection. [1]

2.3 What do artificial and natural selection have in common? [1]

3 Exam-style questions

3.1 In artificial selection, traits become common because they [1]

- **A** aid survival in the wild
 - **B** are chosen by humans for breeding
 - **C** appear randomly
 - **D** are never inherited
-

3.2 A farmer breeds only the cows that produce the most milk.

(a) Name the process. [1]

(b) Explain how milk yield increases over generations. [2]

3.3 Explain the key difference between natural and artificial selection, and one similarity. [3]

Solutions

2.1 Humans.

2.2 Any one: crops for larger fruit, dog breeds, high-milk cows.

2.3 Both act on heritable variation, increasing chosen/favored traits over generations.

3.1 B — chosen by humans for breeding.

3.2 (a) Artificial selection (selective breeding). (b) Only the highest-yielding cows reproduce, passing on their milk-yield alleles; over generations the average yield rises.

3.3 Difference: the selecting agent — the environment (natural) vs humans (artificial); similarity: both act on heritable variation to change the population.

2. During meiosis, double-strand breaks occur in chromatids. The breaks are either repaired by the exchange of genetic material between homologous nonsister chromatids, which is the process known as crossing over (Figure 1A), or they are simply repaired without any crossing over (Figure 1B). Plant breeders developing new varieties of corn are interested in determining whether, in corn, a correlation exists between the number of meiotic double-strand chromatid breaks and the number of crossovers.

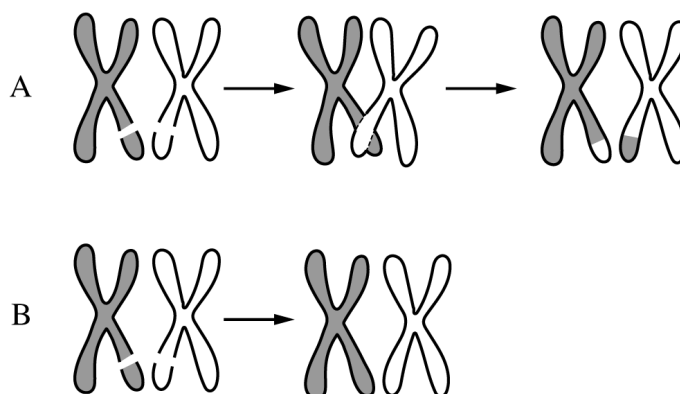


Figure 1. Double-strand breaks in chromatids are repaired with crossing over (A) or without crossing over (B).

Using specialized staining and microscopy techniques, scientists counted the number of double-strand chromatid breaks and the number of crossovers in the same number of meiotic gamete-forming cells of six inbred strains of corn (Table 1).

TABLE 1. NUMBER OF CHROMATID DOUBLE-STRAND BREAKS AND AVERAGE NUMBER OF CROSSOVERS IN INBRED STRAINS OF CORN

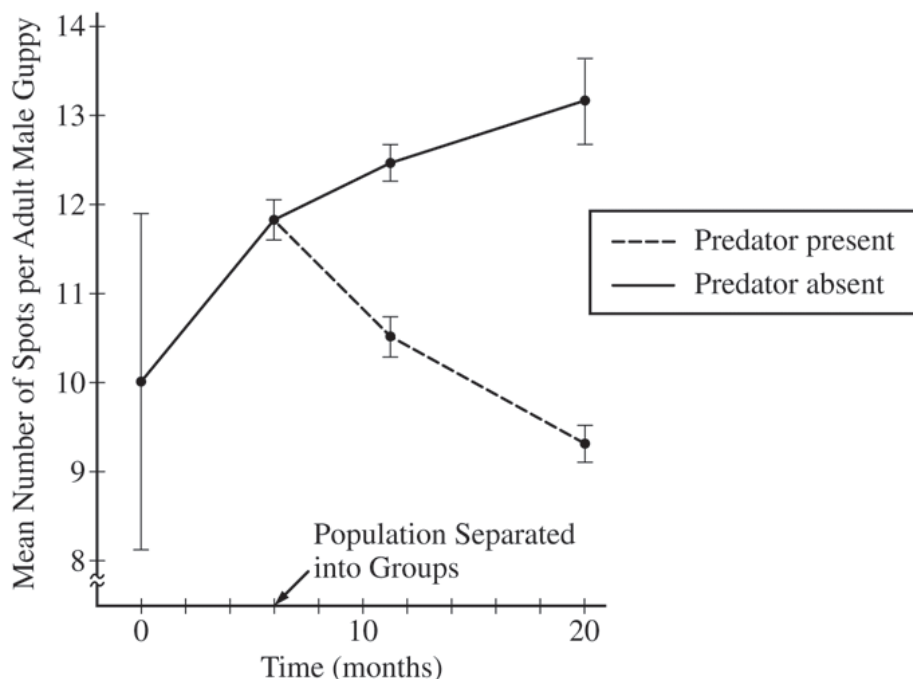
Strain of Corn	Number of Double-Strand Breaks	Average Number of Crossovers ($\pm 2SE_{\bar{x}}$)
I	710	19.5 ± 0.5
II	650	18.0 ± 0.7
III	600	17.5 ± 1.0
IV	510	16.0 ± 1.0
V	425	14.0 ± 0.5
VI	325	11.0 ± 1.5

- (a) The double-strand breaks occur along the DNA backbone. **Describe** the process by which the breaks occur.
- (b) Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1 and allows examination of a possible correlation between double-strand breaks and crossovers. Based on the data, **determine** whether corn strains I, II, and III differ in their average number of crossovers.
- (c) Based on the data, **describe** the relationship between the average number of double-strand breaks and the average number of crossovers in the strains of corn analyzed in the experiment.
- (d) Crossing over (Figure 1A) creates physical connections that are required for proper separation of homologous chromosomes during meiosis. A diploid cell with four pairs of homologous chromosomes undergoes meiosis to produce four haploid cells. Crossing over occurs between only three of the pairs. **Predict** the number of chromosomes most likely present in each of the four haploid cells. Provide reasoning to **justify** your prediction. **Explain** how plant breeders can use the information in Table 1 to help develop new varieties of corn.

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

4. Adult male guppies (*Poecilia reticulata*) exhibit genetically determined spots, while juvenile and adult female guppies lack spots. In a study of selection, male and female guppies from genetically diverse populations were collected from different mountain streams and placed together in an isolated environment containing no predators.

The study population was maintained for several generations in the isolated area before being separated into two groups. One group was moved to an artificial pond containing a fish predator, while a second group was moved to an artificial pond containing no predators. The two groups went through several generations in their new environments. At different times during the experiment, the mean number of spots per adult male guppy was determined as shown in the figure below. Vertical bars in the figure represent two standard errors of the mean (SEM).



- (a) **Describe** the change in genetic variation in the population between 0 and 6 months and **provide** reasoning for your description based on the means and SEM.
- (b) **Propose** ONE type of mating behavior that could have resulted in the observed change in the number of spots per adult male guppy between 6 and 20 months in the absence of the predator.
- (c) **Propose** an evolutionary mechanism that explains the change in average number of spots between 6 and 20 months in the presence of the predator.

7.4 Population Genetics

Name: _____ Class: _____ Date: _____

Total: 11 marks

KEY WORDS allele frequencies 等位基因频率 • genetic drift 遗传漂变 • gene flow 基因流 • population genetics 群体遗传学
• evolution 进化

Objective

Build the skills to answer exam questions on **population genetics** — allele and genotype frequencies.

You must be able to:

- calculate **allele frequencies** 等位基因频率 from genotype counts
- describe how frequencies change with evolution
- name the causes of allele-frequency change

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Allele frequency

An **allele frequency** is the fraction of all copies of a gene that are a given allele. Count alleles: each individual has **two**.

■ A worked frequency

In 100 individuals: 36 *AA*, 48 *Aa*, 16 *aa* (200 alleles total). *A* count = $2(36) + 48 = 120$; frequency of *A* = $120/200 = 0.6$. So *a* = 0.4.

■ Evolution = change in frequencies

Evolution at the population level is a **change in allele frequencies** over generations. If frequencies stay constant, the population is not evolving.

■ Causes of change

Allele frequencies change due to **natural selection**, **mutation**, **gene flow** (migration), **genetic drift** (chance, strong in small populations), and **non-random mating**.

2 Practice

Now apply the methods above.

2.1 How many alleles for a gene does each individual carry? [1]

2.2 In a population, allele A has frequency 0.7. What is the frequency of a ? [1]

2.3 Name two causes of allele-frequency change. [2]

3 Exam-style questions

3.1 Evolution at the population level is defined as a change in [1]

- **A** an individual's genes
 - **B** allele frequencies over generations
 - **C** the environment
 - **D** the number of species
-

3.2 A population of 50 has 18 BB , 24 Bb , and 8 bb .

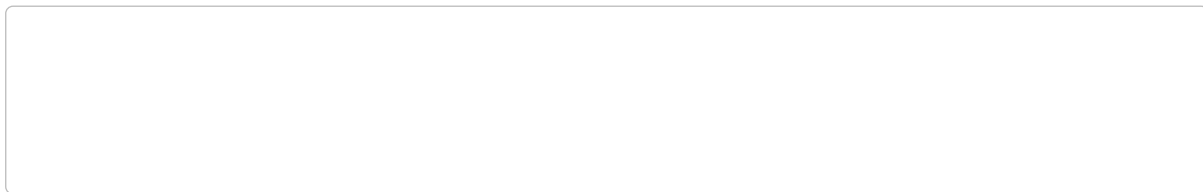
(a) Find the total number of alleles. [1]

(b) Calculate the frequency of the B allele. [3]

3.3 Explain why genetic drift changes allele frequencies more in a small population than

a large one.

[2]



Solutions

2.1 Two.

2.2 $1 - 0.7 = 0.3$.

2.3 Any two: natural selection, mutation, gene flow, genetic drift, non-random mating.

3.1 B — allele frequencies over generations.

3.2 (a) $50 \times 2 = 100$ alleles. (b) B count = $2(18) + 24 = 60$; frequency = $60/100 = 0.6$.

3.3 In a small population, chance events (which few individuals happen to reproduce) have a large effect on frequencies; in a large population these random effects average out.

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.
- (a) **Describe** the prezygotic barrier that results in these genetically distinct populations.
- (b) 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.
- (c) If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, **predict** the likely impact on both populations.
- (d) 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.

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.

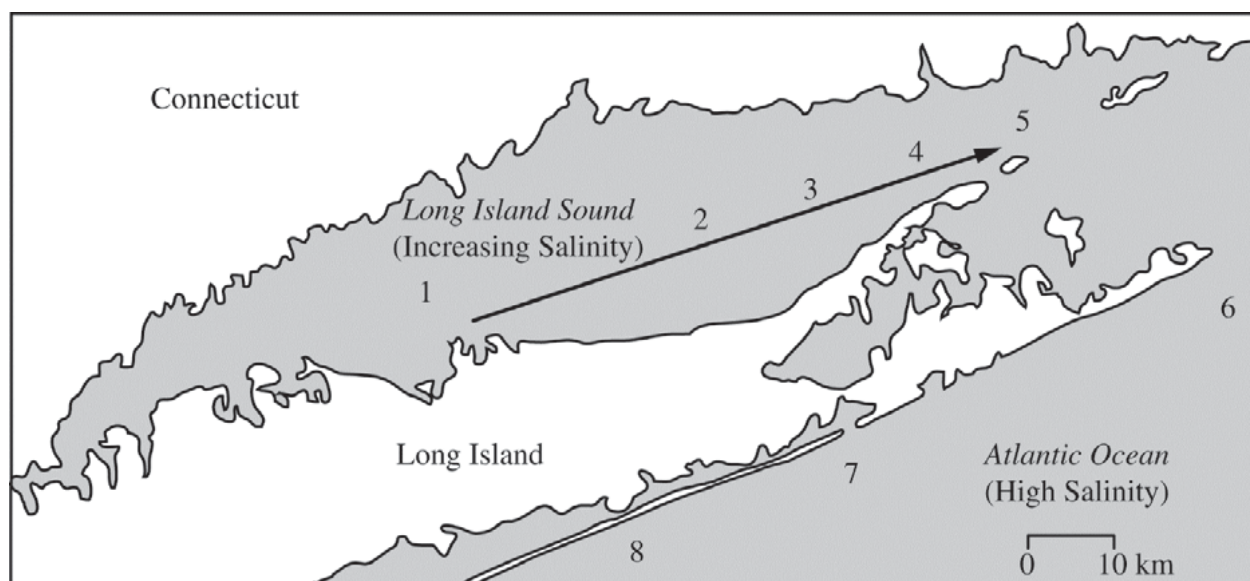
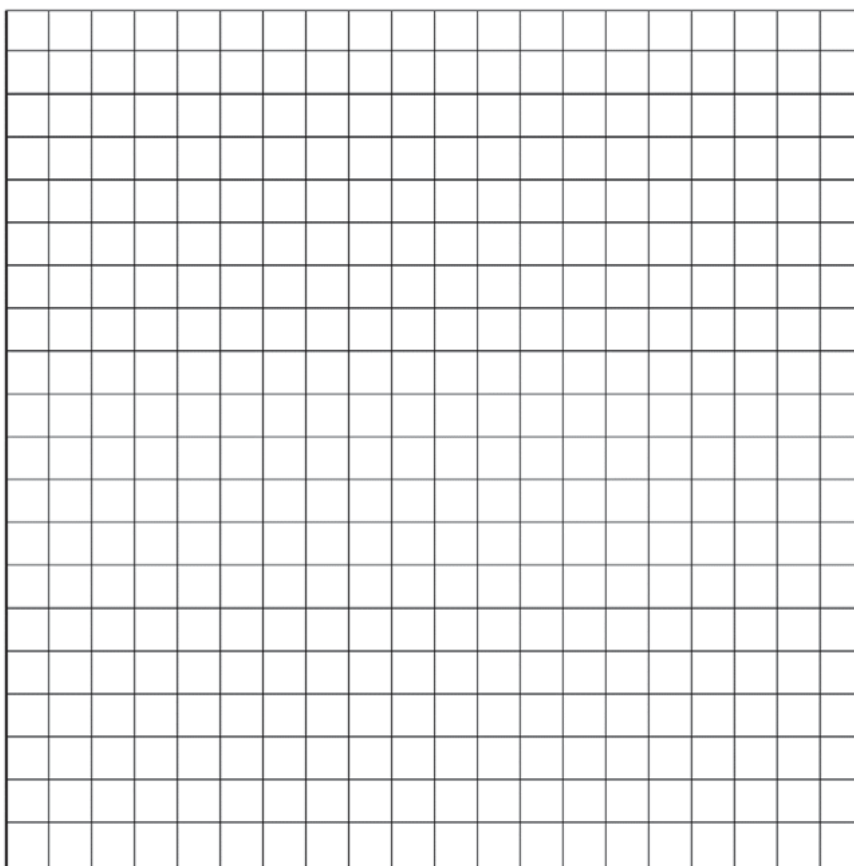


Figure 1. Sampling sites of marine mussels at various locations (1–8) in Long Island Sound and the Atlantic Ocean

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

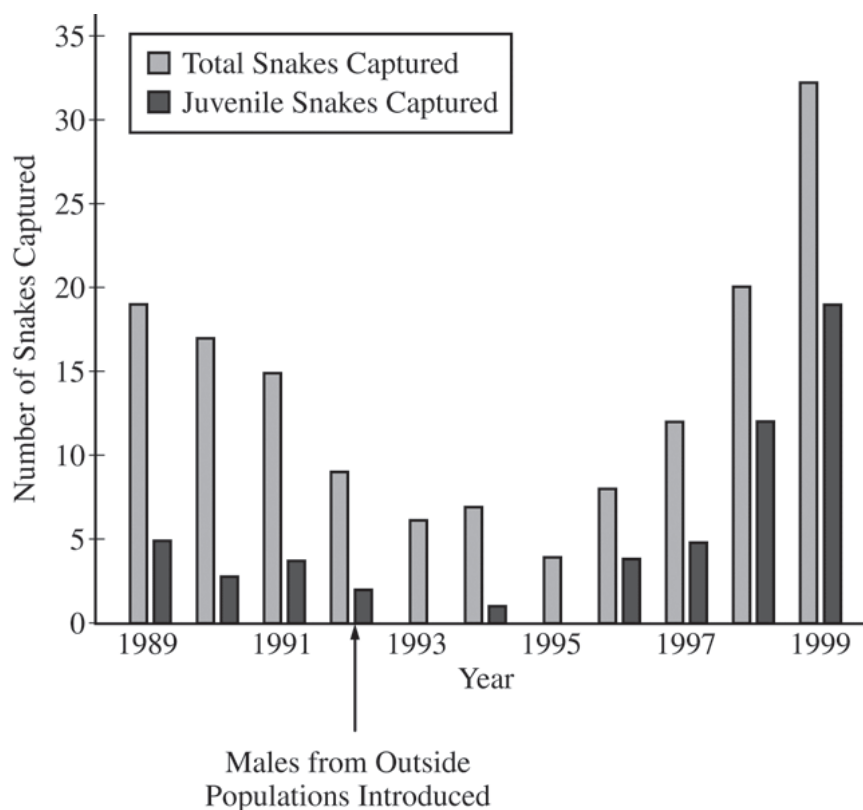
	Long Island Sound					Atlantic Ocean		
Site	1	2	3	4	5	6	7	8
<i>lap</i> ⁹⁴ frequency (%)	13	16	25	37	55	59	59	59
Salinity	Low $\longrightarrow$ High					High		

1. 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).
- (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.
- (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.
- (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.
- (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.



6. In an attempt to rescue a small isolated population of snakes from decline, a few male snakes from several larger populations of the same species were introduced into the population in 1992. The snakes reproduce sexually, and there are abundant resources in the environment.

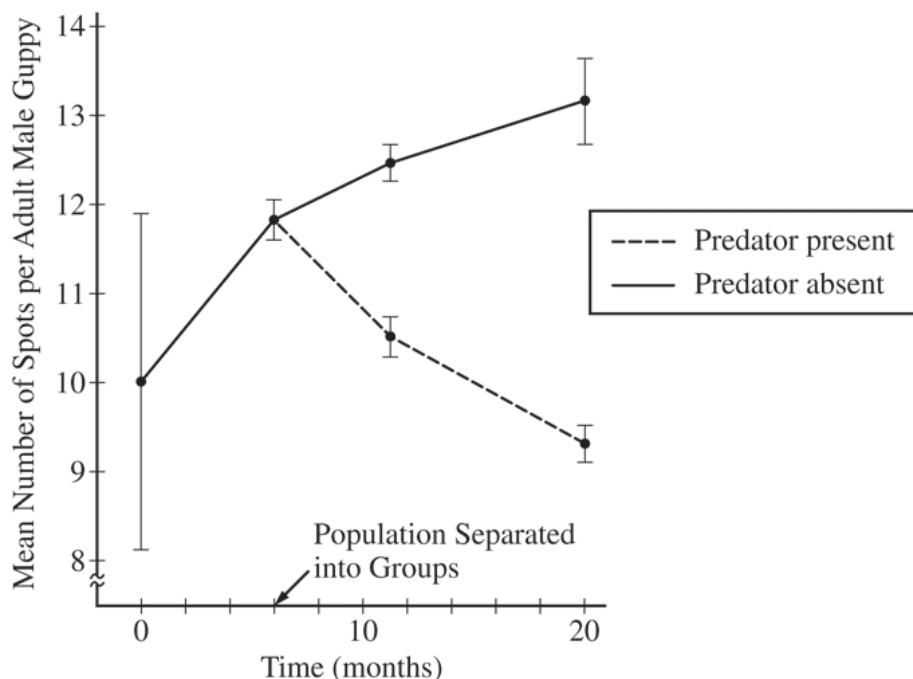
The figure below shows the results of a study of the snake population both before and after the introduction of the outside males. In the study, the numbers of captured snakes indicate the overall population size.



- (a) **Describe** ONE characteristic of the original population that may have led to the population's decline in size between 1989 and 1993.
- (b) **Propose** ONE reason that the introduction of the outside males rescued the snake population from decline.
- (c) **Describe** how the data support the statement that there are abundant resources in the environment.

4. Adult male guppies (*Poecilia reticulata*) exhibit genetically determined spots, while juvenile and adult female guppies lack spots. In a study of selection, male and female guppies from genetically diverse populations were collected from different mountain streams and placed together in an isolated environment containing no predators.

The study population was maintained for several generations in the isolated area before being separated into two groups. One group was moved to an artificial pond containing a fish predator, while a second group was moved to an artificial pond containing no predators. The two groups went through several generations in their new environments. At different times during the experiment, the mean number of spots per adult male guppy was determined as shown in the figure below. Vertical bars in the figure represent two standard errors of the mean (SEM).



- (a) **Describe** the change in genetic variation in the population between 0 and 6 months and **provide** reasoning for your description based on the means and SEM.
- (b) **Propose** ONE type of mating behavior that could have resulted in the observed change in the number of spots per adult male guppy between 6 and 20 months in the absence of the predator.
- (c) **Propose** an evolutionary mechanism that explains the change in average number of spots between 6 and 20 months in the presence of the predator.

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

7.5 Hardy-Weinberg Equilibrium

Name: _____ Class: _____ Date: _____

Total: 12 marks

KEY WORDS gene flow 基因流 • natural selection 自然选择 • evolution 进化

Objective

Build the skills to answer exam questions on **Hardy-Weinberg equilibrium**.**You must be able to:**

- use $p + q = 1$ and $p^2 + 2pq + q^2 = 1$
- find allele and genotype frequencies
- state the conditions for equilibrium

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ The two equations

For a gene with alleles of frequency p and q :

$$p + q = 1, \quad p^2 + 2pq + q^2 = 1,$$

where p^2 = homozygous dominant, $2pq$ = heterozygous, q^2 = homozygous recessive.

■ Working from the recessive phenotype

The recessive phenotype's frequency is q^2 . So $q = \sqrt{q^2}$, then $p = 1 - q$.

■ A worked calculation

If 16% (0.16) show the recessive trait: $q^2 = 0.16$, so $q = 0.4$, $p = 0.6$. Heterozygotes = $2pq = 2(0.6)(0.4) = 0.48$ (48%).

■ The conditions

A population is in equilibrium (**not** evolving) only if: no selection, no mutation, no gene flow, random mating, and a very large population. Real deviations signal evolution.

2 Practice

Now apply the methods above.

2.1 Write the two Hardy-Weinberg equations. [2]

2.2 If $q = 0.3$, find p . [1]

2.3 What genotype does q^2 represent? [1]

3 Exam-style questions

3.1 In Hardy-Weinberg, the frequency of heterozygotes is [1]

- A p^2
 - B q^2
 - C $2pq$
 - D $p + q$
-

3.2 In a population, 9% of individuals show a recessive trait.

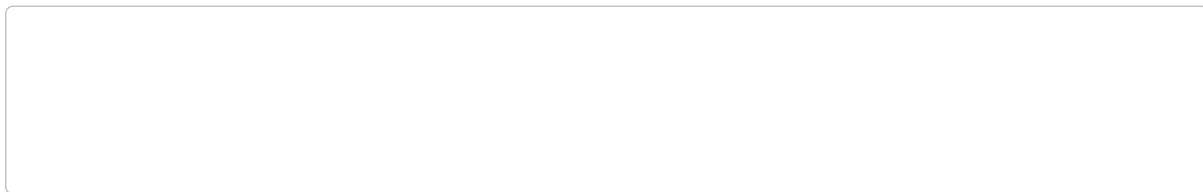
(a) Find q and p . [3]

(b) Find the frequency of heterozygotes. [2]

3.3 State two conditions that must hold for a population to stay in Hardy-Weinberg

equilibrium.

[2]



Solutions

2.1 $p + q = 1$ and $p^2 + 2pq + q^2 = 1$.

2.2 $p = 1 - 0.3 = 0.7$.

2.3 Homozygous recessive.

3.1 $C = 2pq$.

3.2 (a) $q^2 = 0.09$, so $q = 0.3$; $p = 1 - 0.3 = 0.7$. (b) $2pq = 2(0.7)(0.3) = 0.42$ (42%).

3.3 Any two: no natural selection, no mutation, no gene flow (migration), random mating, very large population.

7.6 Evidence of Evolution

Name: _____ Class: _____ Date: _____

Total: 9 marks**KEY WORDS** homologous structures 同源结构 • analogous 同功 • fossils 化石 • evolution 进化 • common ancestor

Objective

Build the skills to answer exam questions on the **evidence of evolution**.

You must be able to:

- describe evidence from **fossils** 化石, **homologous structures** 同源结构, and **molecular** data
- distinguish homologous from **analogous** 同功 structures
- explain how each supports common descent

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Fossil evidence

Fossils show that life has changed over time, and reveal **transitional forms** linking older and newer groups.

■ Homologous structures

Homologous structures have the **same basic plan** but different functions (e.g. the bones of a human arm, whale flipper, and bat wing). They suggest a **common ancestor**.

■ Analogous structures

Analogous structures have the **same function** but **different** underlying structure (e.g. bird wing vs insect wing). They arise from **convergent evolution**, not close common ancestry.

■ Molecular evidence

Similar **DNA and protein sequences** between species indicate how closely related they are — the more similar, the more recent the common ancestor.

2 Practice

Now apply the methods above.

2.1 What do homologous structures suggest? [1]

2.2 Give one type of molecular evidence for evolution. [1]

2.3 What are transitional fossils? [1]

3 Exam-style questions

3.1 The similar bone arrangement in a human arm and a whale flipper is an example of [1]

- **A** analogous structures
 - **B** homologous structures
 - **C** vestigial organs
 - **D** convergent evolution
-

3.2 A bird's wing and an insect's wing both allow flight but have very different structures.

(a) State whether they are homologous or analogous. [1]

(b) Explain what this tells you about their evolutionary relationship. [2]

3.3 Explain how comparing DNA sequences can show how closely two species are related. [2]

Solutions

2.1 A common ancestor (shared ancestry).

2.2 Similar DNA or protein sequences between species.

2.3 Fossils showing features intermediate between older and newer groups.

3.1 B — homologous structures.

3.2 (a) Analogous. (b) They evolved independently (convergent evolution) for the same function, so they do **not** indicate a close common ancestor.

3.3 The more similar two species' DNA sequences are, the fewer changes have accumulated since they diverged, so the more recently they shared a common ancestor.

4. Twenty million years ago the Caribbean Sea and Pacific Ocean were connected, and water flowed freely between the two bodies of water. Many of the same marine species were found in both areas. Over millions of years, the land referred to as the Isthmus of Panama formed, eventually closing off the connection between the Caribbean Sea and Pacific Ocean and creating two separate bodies of water. The ecology of these two marine habitats was dramatically altered by this land formation. The warmer Caribbean water could no longer flow west, so the Pacific water cooled and became more nutrient-rich, while the Caribbean water became warmer.

A. Describe the genetic evidence that evolution is occurring in a population.

B. Explain how the isolation of marine species by the formation of a land barrier can lead to divergent evolution of those species.

The formation of the Isthmus of Panama connected two continents, North America and South America. Many North American land animal species migrated to South America after the formation of the isthmus and occupied similar niches as South American species.

C. Predict the effect the formation of the isthmus had on resource availability for South American species.

D. Justify your prediction in part C.

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.

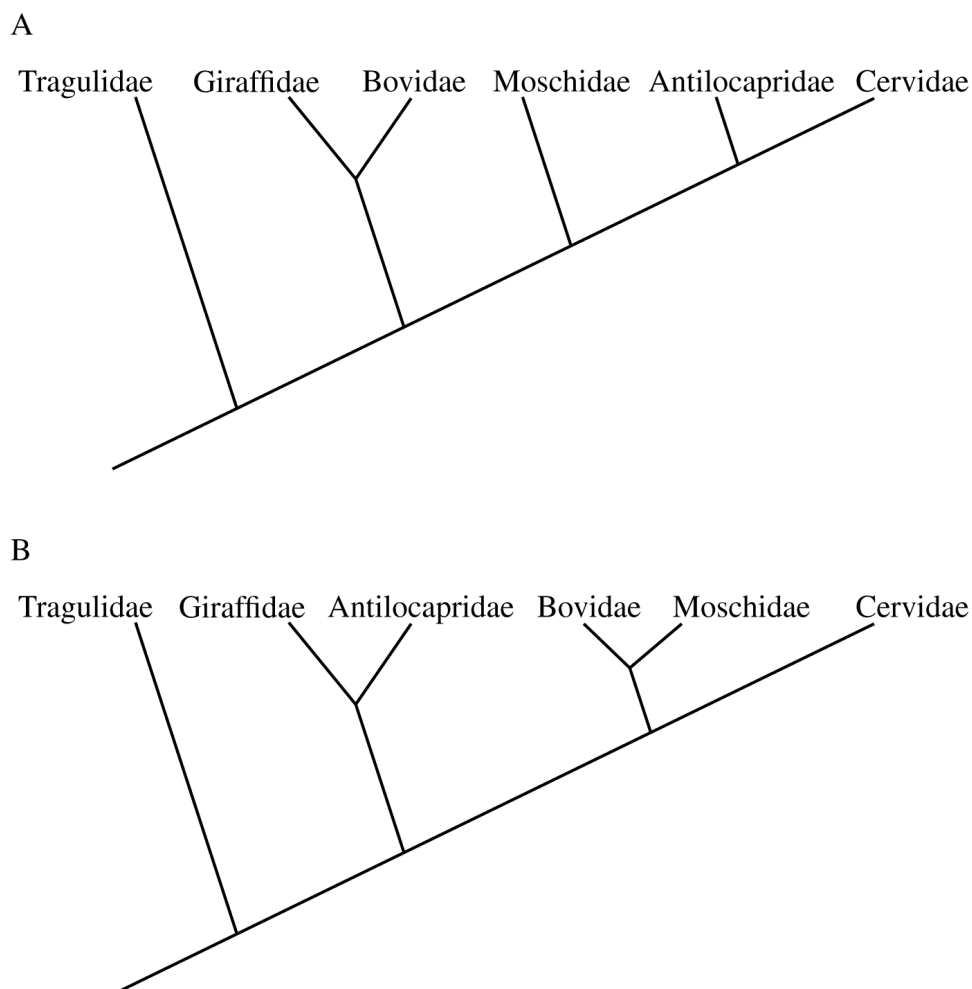


Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

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

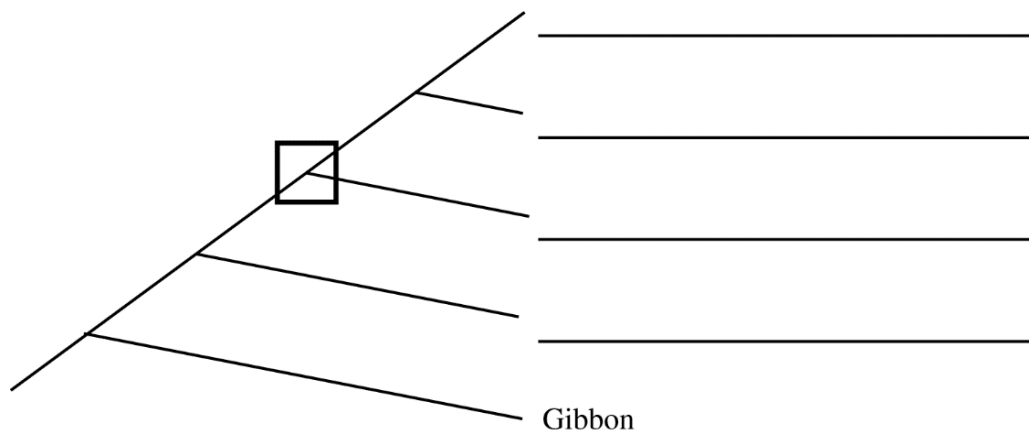
- (a) **Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
- (b) Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
- (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.

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					-

5. 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.
- (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.
- (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.



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.

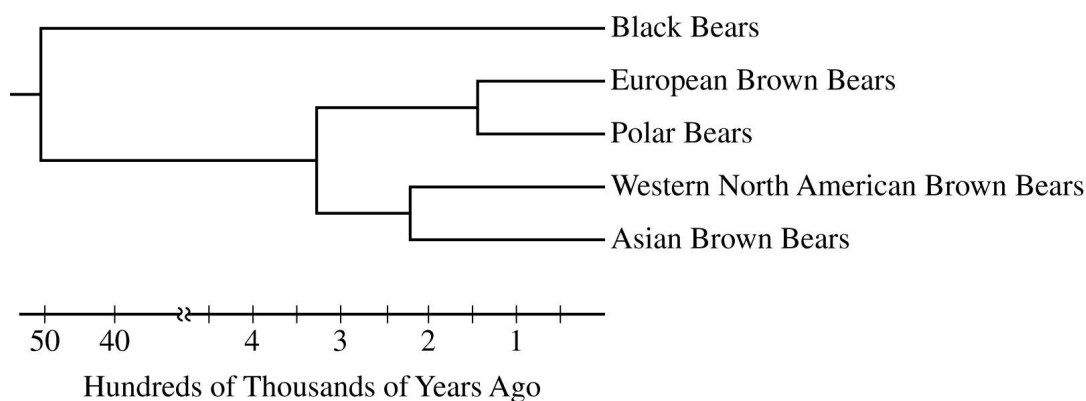


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

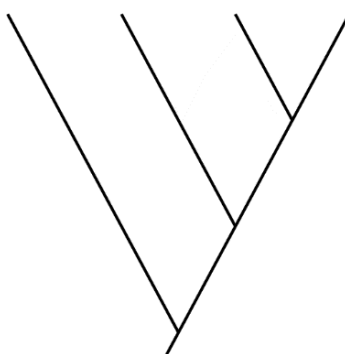
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their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

- (a) 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.
- (b) **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.
- (c) 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.
- (d) 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.
- (e) **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.

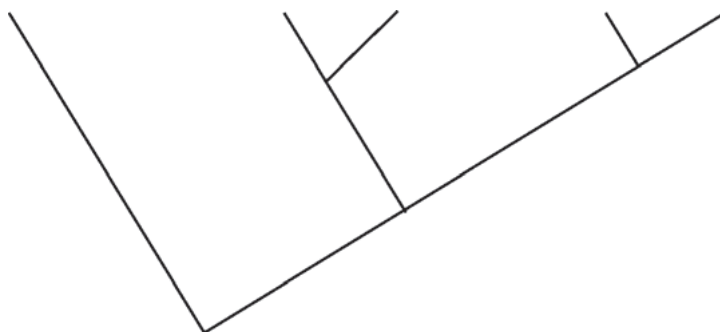


3. The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

THE NUMBER OF AMINO ACID DIFFERENCES
IN CYTOCHROME *c* AMONG FIVE SPECIES

	<i>E. ferus</i>	<i>D. polylepis</i>	<i>G. gallus</i>	<i>A. forsteri</i>	<i>E. africanus</i>
<i>E. ferus</i>	0	21	11	13	1
<i>D. polylepis</i>		0	18	17	20
<i>G. gallus</i>			0	3	10
<i>A. forsteri</i>				0	12
<i>E. africanus</i>					0

- (a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.
- (b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.



7.7 Common Ancestry

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS common ancestor 共同祖先

Objective

Build the skills to answer exam questions on **common ancestry**.

You must be able to:

- explain evidence for a **common ancestor** 共同祖先 of all life
- cite shared features (DNA, ribosomes, ATP, the genetic code)
- interpret shared traits as descent from a common ancestor

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Shared core features

All living things share fundamental features, pointing to a **common ancestor**:

- **DNA/RNA** as genetic material;
- the **same genetic code** (codons);
- **ribosomes** that make proteins;
- **ATP** as energy currency.

■ Why this is evidence

It would be a huge coincidence for unrelated origins to share the **same code** and machinery. The simplest explanation is that all life **descended** from a shared ancestor that already had them.

■ Nested similarities

More closely related groups share **more** features (and more similar DNA), forming a nested pattern that maps onto a tree of descent.

■ A worked reasoning

Because a bacterium and a human both use the same genetic code and ribosomes, they most likely inherited these from a distant common ancestor.

2 Practice

Now apply the methods above.

2.1 Name two features shared by all living things. [2]

2.2 What does sharing the same genetic code suggest? [1]

2.3 Do more closely related species share more or fewer features? [1]

3 Exam-style questions

3.1 The universal genetic code is evidence that all organisms [1]

- **A** evolved separately
- **B** share a common ancestor
- **C** are identical
- **D** cannot be related

3.2 A student notes that bacteria and humans both use ATP and ribosomes.

(a) Explain how this supports common ancestry. [2]

(b) State one other shared feature. [1]

3.3 Explain why the pattern of “more related organisms share more features” fits descent from common ancestors. [2]

Solutions

2.1 Any two: DNA/RNA, the same genetic code, ribosomes, ATP.

2.2 That all organisms share a common ancestor.

2.3 More features.

3.1 B — share a common ancestor.

3.2 (a) Both features are complex and identical in function; the simplest explanation is that both inherited them from a shared ancestor rather than evolving them independently.

(b) The same genetic code (or DNA as genetic material).

3.3 Closely related species diverged more recently, so they have had less time to accumulate differences and retain more shared inherited features — exactly what a branching tree of descent predicts.

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.

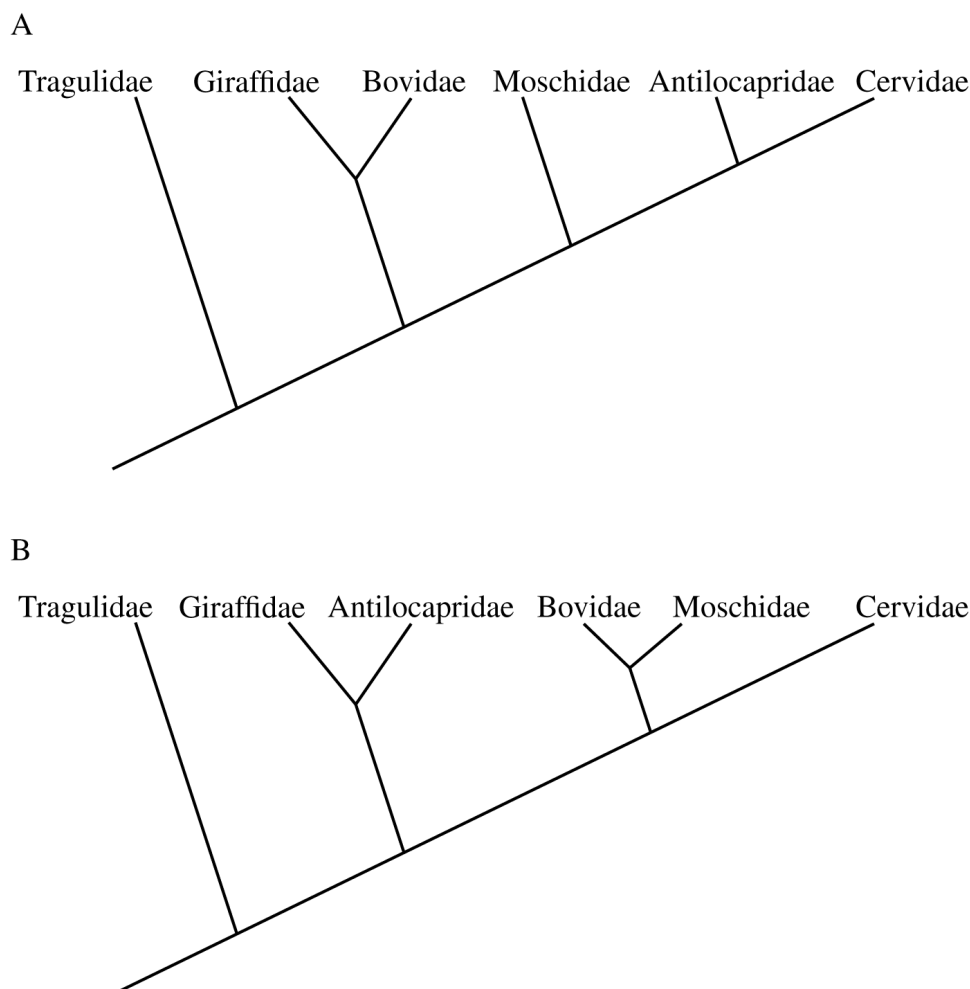


Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

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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.
-

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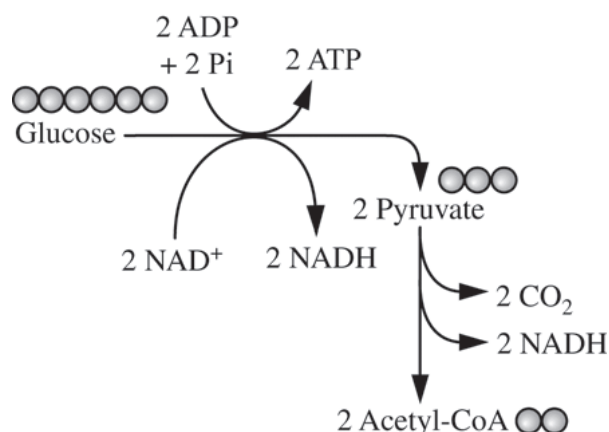


Figure 1. Glycolysis and pyruvate oxidation

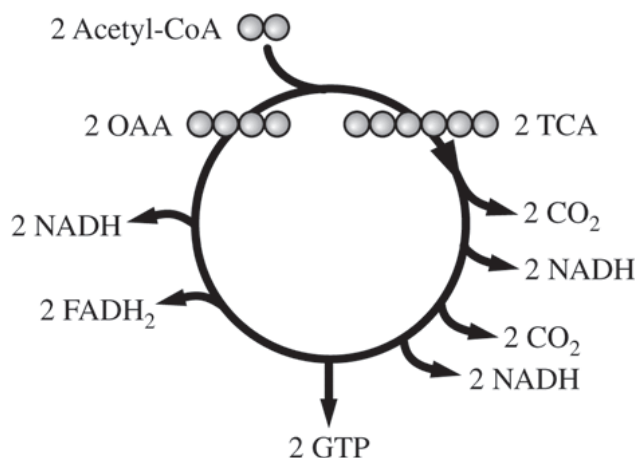


Figure 2. Krebs cycle

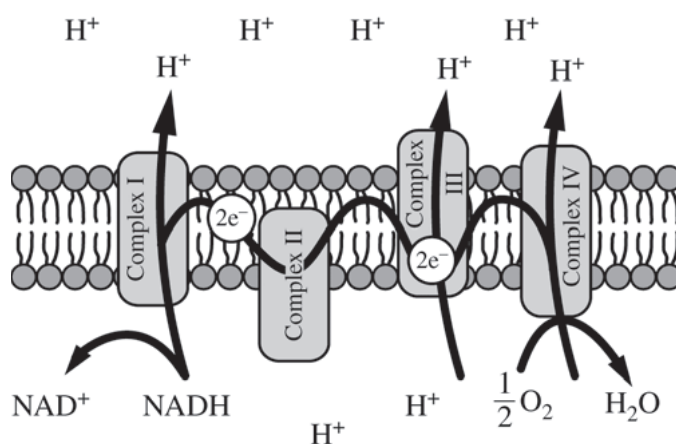


Figure 3. Electron transport chain

2. Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.
- (a) Using the information above, **describe** ONE contribution of each of the following in ATP synthesis.
- Catabolism of glucose in glycolysis and pyruvate oxidation
 - Oxidation of intermediates in the Krebs cycle
 - Formation of a proton gradient by the electron transport chain
- (b) Use each of the following observations to **justify** the claim that glycolysis first occurred in a common ancestor of all living organisms.
- Nearly all existing organisms perform glycolysis.
 - Glycolysis occurs under anaerobic conditions.
 - Glycolysis occurs only in the cytosol.

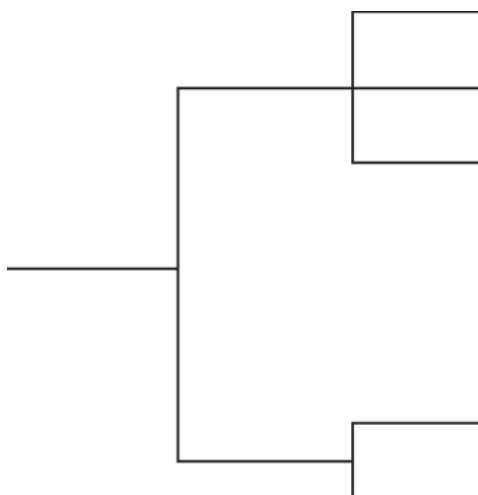
- (c) A researcher estimates that, in a certain organism, the complete metabolism of glucose produces 30 molecules of ATP for each molecule of glucose. The energy released from the total oxidation of glucose under standard conditions is 686 kcal/mol. The energy released from the hydrolysis of ATP to ADP and inorganic phosphate under standard conditions is 7.3 kcal/mol. **Calculate** the amount of energy available from the hydrolysis of 30 moles of ATP. **Calculate** the efficiency of total ATP production from 1 mole of glucose in the organism. **Describe** what happens to the excess energy that is released from the metabolism of glucose.
- (d) The enzymes of the Krebs cycle function in the cytosol of bacteria, but among eukaryotes the enzymes function mostly in the mitochondria. **Pose** a scientific question that connects the subcellular location of the enzymes in the Krebs cycle to the evolution of eukaryotes.

2. Mammalian milk contains antibodies that are produced by the mother's immune system and passed to offspring during feeding. Mammalian milk also contains a sugar (lactose) and may contain proteins (protein A, protein B, and casein), as indicated in the table.

MILK COMPONENTS IN DIFFERENT MAMMALS

Character	Cat	Cow	Horse	Human	Pig
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	–	+	+	–	+
Casein	–	+	+	–	+
+ indicates the presence of the character, and – indicates the absence of the character					

- (a) Using the data in the table, **construct** a cladogram on the template provided to indicate the most likely evolutionary relationships among the different mammals. **Indicate** on the cladogram where each of the characters most likely arose in the evolutionary process, and **justify** the placement of the characters on the cladogram.
- (b) **Describe** FOUR steps in the activation of the mother's specific immune response following exposure to a bacterial pathogen. **Predict** how the mother's immune response would differ upon a second exposure to the same bacterial pathogen a year later.
- (c) **Predict** the most likely consequence for a nursing infant who is exposed to an intestinal bacterial pathogen (e.g., *Salmonella*) to which the mother was exposed three months earlier. **Justify** your prediction.



7.8 Continuing Evolution

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS antibiotic resistance 抗生素抗性 • evolution 进化 • variation 变异

Objective

Build the skills to answer exam questions on **continuing evolution**.

You must be able to:

- give evidence that evolution is **ongoing** (antibiotic and pesticide resistance)
- explain how resistance evolves by selection
- link the process to public-health concerns

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Evolution happens now

Evolution is **ongoing**, not just in the past. Fast examples: bacteria evolving **antibiotic resistance** 抗生素抗性 and insects evolving **pesticide resistance**.

■ How resistance evolves

1. A population has **variation** — a few individuals carry a resistance allele.
2. The antibiotic/pesticide **kills the susceptible** ones.
3. The **resistant** survivors reproduce.
4. Over generations the resistance allele becomes common.

■ The antibiotic does not create resistance

The drug does not **cause** the mutation; the resistant allele was already present. The drug only **selects** for it by removing the non-resistant individuals.

■ Public-health link

Overusing antibiotics speeds this selection, producing hard-to-treat “superbugs” — which is why doctors limit antibiotic use.

2 Practice

Now apply the methods above.

2.1 Give one example that shows evolution is ongoing. [1]

2.2 Does an antibiotic create the resistance allele? [1]

2.3 Which individuals survive antibiotic treatment? [1]

3 Exam-style questions

3.1 Antibiotic resistance spreads in a bacterial population because the antibiotic [1]

- **A** creates the resistance gene
 - **B** selects for pre-existing resistant bacteria
 - **C** kills all bacteria equally
 - **D** stops reproduction
-

3.2 A bacterial population is repeatedly treated with an antibiotic.

(a) Describe how the population becomes resistant over time. [3]

(b) Explain why overusing antibiotics is a public-health concern. [1]

3.3 Explain why the resistance allele must already exist in the population for resistance to evolve. [2]

Solutions

2.1 Antibiotic resistance in bacteria (or pesticide resistance in insects).

2.2 No.

2.3 The resistant individuals.

3.1 B — selects for pre-existing resistant bacteria.

3.2 (a) A few bacteria already carry a resistance allele; the antibiotic kills the susceptible ones; the resistant survivors reproduce; over generations resistance becomes common. (b) It selects for hard-to-treat resistant “superbugs”.

3.3 Selection can only act on existing variation — it favors the resistant allele but cannot create it; if no bacterium carried it, none would survive to reproduce.

7.9 Phylogeny

Name: _____ Class: _____ Date: _____

Total: 9 marks**KEY WORDS** phylogenetic tree 系统发生树 • evolution 进化 • common ancestor 共同祖先

Objective

Build the skills to answer exam questions on **phylogeny** — reading evolutionary trees.

You must be able to:

- read a **phylogenetic tree** 系统发生树 (branches, nodes, common ancestors)
- identify the **most recent common ancestor** of two species
- interpret shared derived traits

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ What a tree shows

A **phylogenetic tree** shows how species are related by descent. **Tips** are species; **nodes** (branch points) are **common ancestors**; the closer two tips branch, the more closely related.

■ Most recent common ancestor

The **most recent common ancestor** of two species is the node where their lines last join — trace each back until the branches meet.

■ Reading relatedness

Two species that share a **more recent** node are **more closely related** than either is to a species that branches off earlier.

■ Shared derived traits

A trait shared by all descendants of a node (and not by outgroups) marks that branch — used to build and read the tree.

2 Practice

Now apply the methods above.

2.1 What does a node (branch point) on a tree represent? [1]

2.2 How do you find the most recent common ancestor of two species? [1]

2.3 Are two species that branch off close together more or less related? [1]

3 Exam-style questions

3.1 On a phylogenetic tree, the tips represent [1]

- **A** common ancestors
 - **B** species (or groups)
 - **C** mutations
 - **D** fossils only
-

3.2 On a tree, species A and B branch from one node; species C branches off earlier.

(a) Which two species are most closely related? [1]

(b) Explain your reasoning using the tree. [2]

3.3 Explain how shared derived traits are used to group species on a tree. [2]

Solutions

2.1 A common ancestor.

2.2 Trace both species' lines back until they meet at a shared node.

2.3 More related.

3.1 B — species (or groups).

3.2 (a) A and B. (b) A and B share a more recent common ancestor (node) than either shares with C, which branched off earlier, so A and B are most closely related.

3.3 A trait shared by all descendants of a node (but not by earlier-branching groups) marks that branch, grouping those species together as sharing that derived feature from their common ancestor.

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).

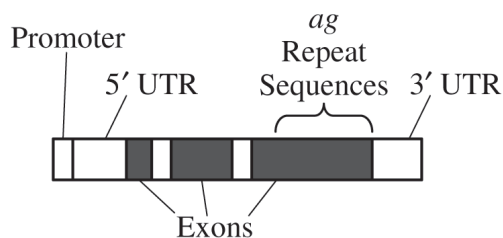


Figure 1. Basic structure of a functional *ag* gene

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).

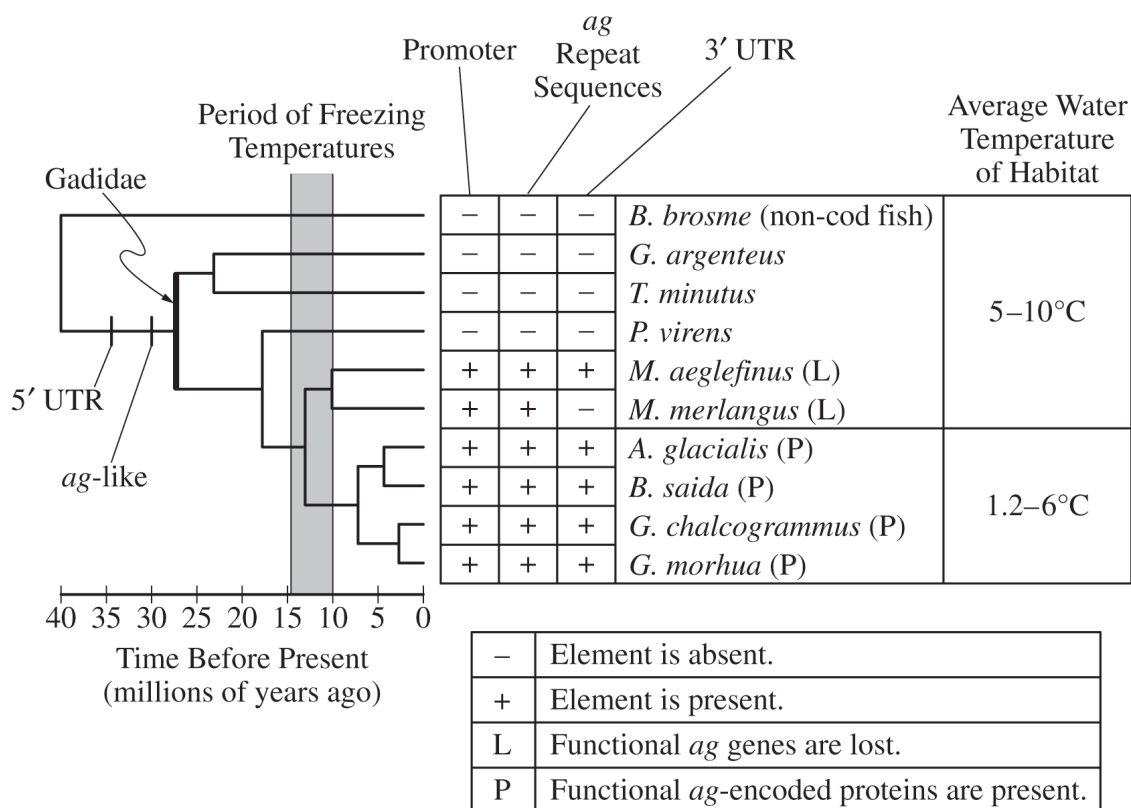


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

- (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.

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.

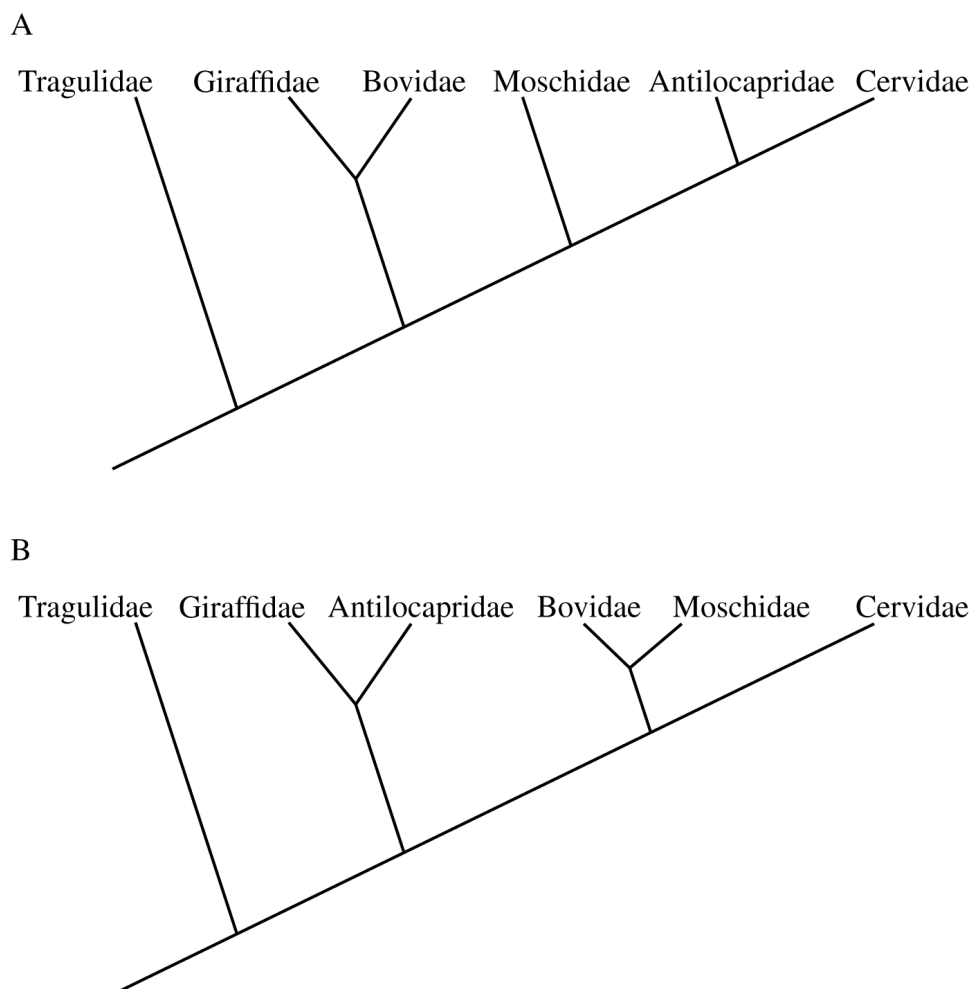


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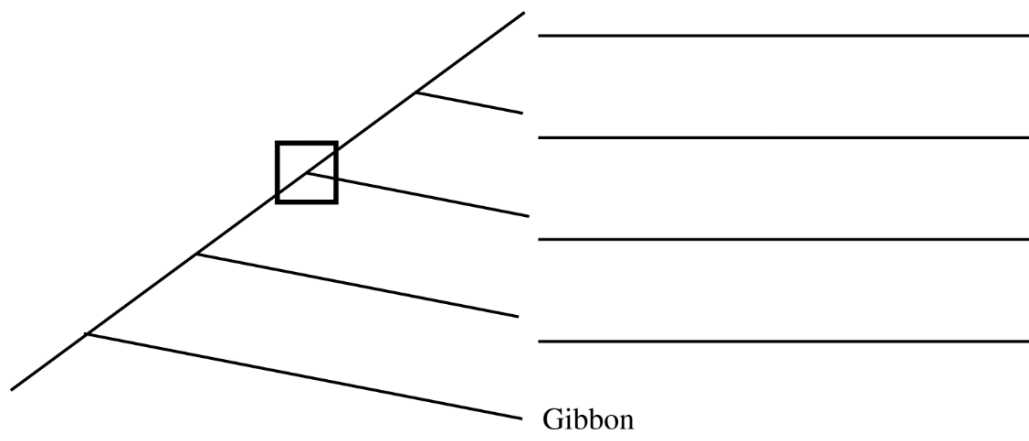
- (a) **Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
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Chimpanzee					-

5. 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.
- (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.
- (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.



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.

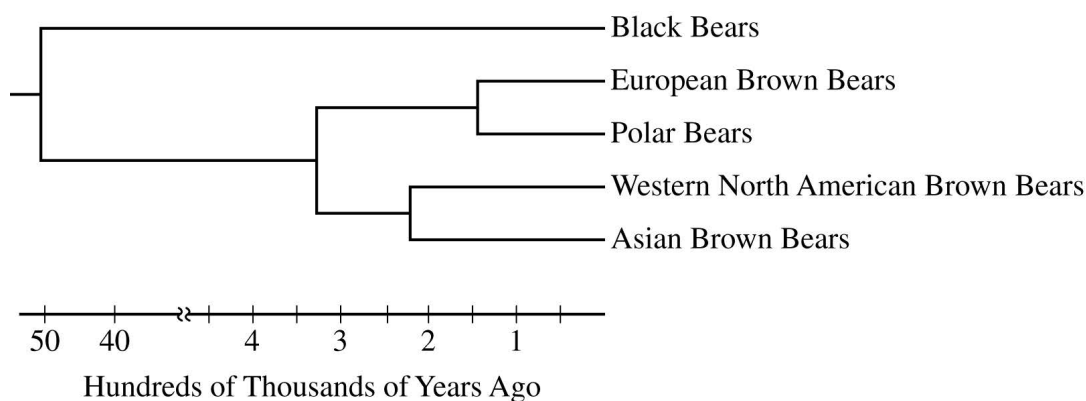


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

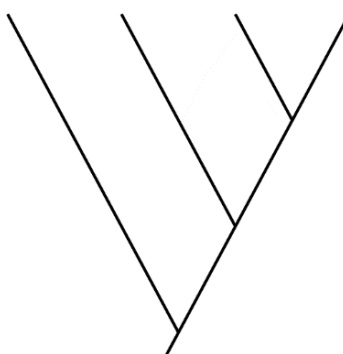
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their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

- (a) 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.
- (b) **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.
- (c) 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.
- (d) 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.
- (e) **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.

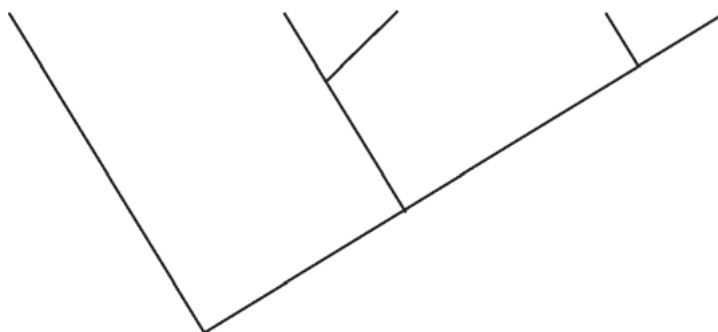


3. The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

THE NUMBER OF AMINO ACID DIFFERENCES
IN CYTOCHROME *c* AMONG FIVE SPECIES

	<i>E. ferus</i>	<i>D. polylepis</i>	<i>G. gallus</i>	<i>A. forsteri</i>	<i>E. africanus</i>
<i>E. ferus</i>	0	21	11	13	1
<i>D. polylepis</i>		0	18	17	20
<i>G. gallus</i>			0	3	10
<i>A. forsteri</i>				0	12
<i>E. africanus</i>					0

- (a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.
- (b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.

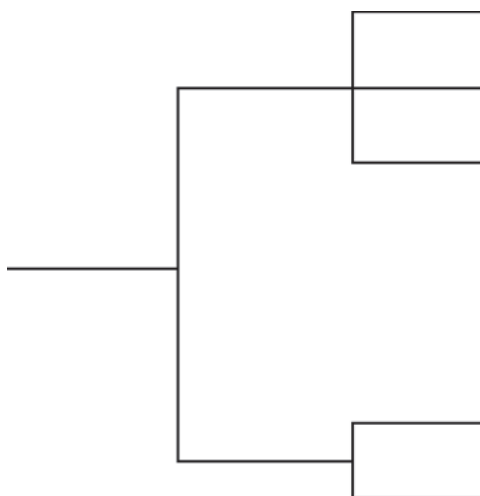


2. Mammalian milk contains antibodies that are produced by the mother's immune system and passed to offspring during feeding. Mammalian milk also contains a sugar (lactose) and may contain proteins (protein A, protein B, and casein), as indicated in the table.

MILK COMPONENTS IN DIFFERENT MAMMALS

Character	Cat	Cow	Horse	Human	Pig
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	–	+	+	–	+
Casein	–	+	+	–	+
+ indicates the presence of the character, and – indicates the absence of the character					

- (a) Using the data in the table, **construct** a cladogram on the template provided to indicate the most likely evolutionary relationships among the different mammals. **Indicate** on the cladogram where each of the characters most likely arose in the evolutionary process, and **justify** the placement of the characters on the cladogram.
- (b) **Describe** FOUR steps in the activation of the mother's specific immune response following exposure to a bacterial pathogen. **Predict** how the mother's immune response would differ upon a second exposure to the same bacterial pathogen a year later.
- (c) **Predict** the most likely consequence for a nursing infant who is exposed to an intestinal bacterial pathogen (e.g., *Salmonella*) to which the mother was exposed three months earlier. **Justify** your prediction.



7.10 Speciation

Name: _____ Class: _____ Date: _____

Total: 10 marks

KEY WORDS speciation 物种形成 • reproductively isolated 生殖隔离 • allopatric 异域 • sympatric 同域
 • gene flow 基因流

Objective

Build the skills to answer exam questions on **speciation**.

You must be able to:

- define a **species** by the biological species concept
- distinguish **allopatric** 异域 and **sympatric** 同域 speciation
- explain the role of **reproductive isolation** 生殖隔离

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ What a species is

By the **biological species concept**, a species is a group that can **interbreed and produce fertile offspring**. Two groups that can no longer do so are separate species.

■ Speciation needs isolation

New species form when populations become **reproductively isolated** — gene flow between them stops — and then diverge until they cannot interbreed.

■ Allopatric vs sympatric

- **Allopatric** — a **geographic barrier** (mountain, river) separates populations, which diverge.
- **Sympatric** — populations diverge **without** physical separation (e.g. differences in mating time or habitat).

■ A worked example

A river splits a population; the two sides evolve differently and eventually cannot interbreed — **allopatric** speciation.

2 Practice

Now apply the methods above.

2.1 Define a species (biological species concept). [1]

2.2 What must happen for speciation to occur? [1]

2.3 Which type of speciation involves a geographic barrier? [1]

3 Exam-style questions

3.1 Speciation requires that populations become [1]

- **A** larger
 - **B** reproductively isolated
 - **C** identical
 - **D** extinct
-

3.2 A mountain range separates one population into two, which evolve differently.

(a) Name this type of speciation. [1]

(b) Explain how two species can form from one. [3]

3.3 Explain how sympatric speciation can occur without a physical barrier. [2]

Solutions

2.1 A group that can interbreed and produce fertile offspring.

2.2 The populations must become reproductively isolated (gene flow stops).

2.3 Allopatric speciation.

3.1 B — reproductively isolated.

3.2 (a) Allopatric speciation. (b) The barrier stops gene flow between the two groups; each accumulates different mutations and adaptations; eventually they diverge so much they can no longer interbreed — two species.

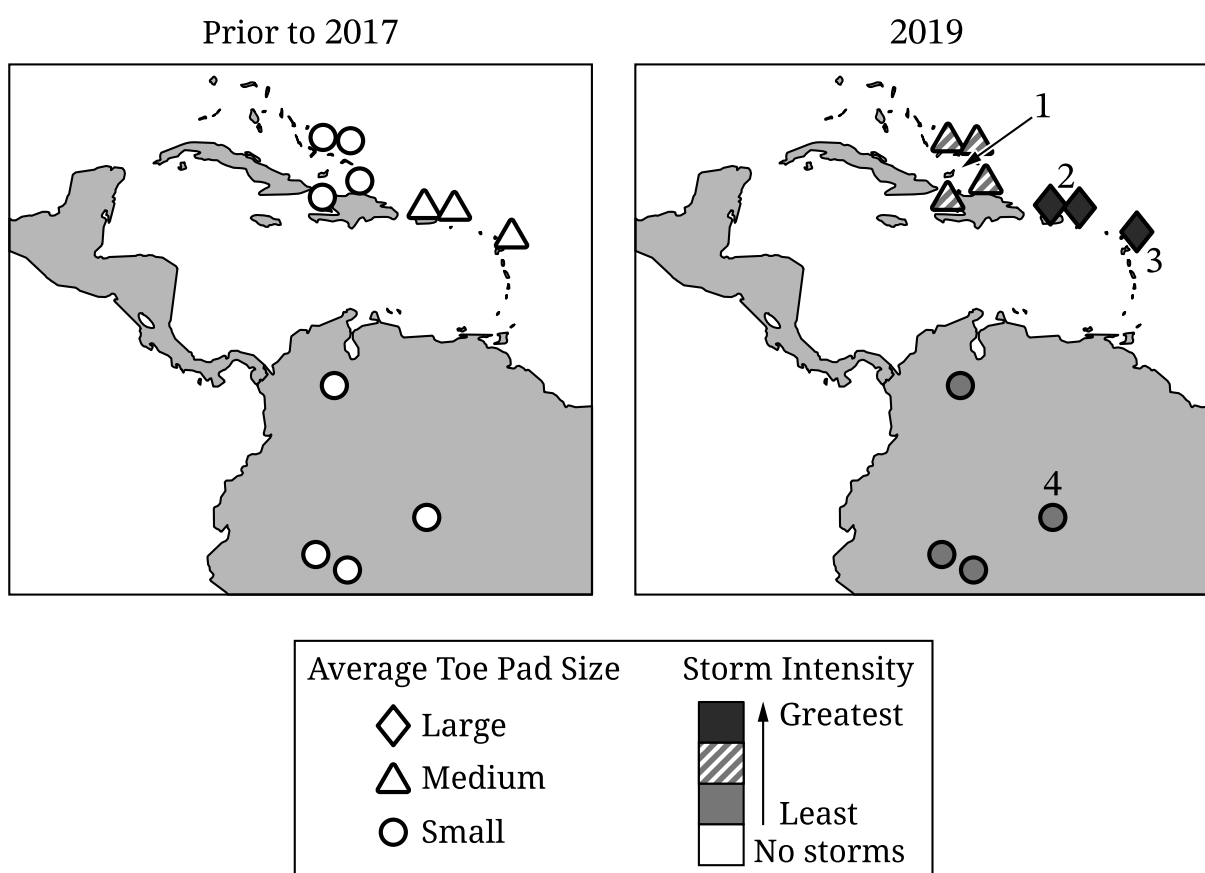
3.3 Populations in the same area can be isolated by differences in mating time, habitat, or behavior, so they stop interbreeding and diverge without a physical barrier.

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.

4. Twenty million years ago the Caribbean Sea and Pacific Ocean were connected, and water flowed freely between the two bodies of water. Many of the same marine species were found in both areas. Over millions of years, the land referred to as the Isthmus of Panama formed, eventually closing off the connection between the Caribbean Sea and Pacific Ocean and creating two separate bodies of water. The ecology of these two marine habitats was dramatically altered by this land formation. The warmer Caribbean water could no longer flow west, so the Pacific water cooled and became more nutrient-rich, while the Caribbean water became warmer.

- A. Describe** the genetic evidence that evolution is occurring in a population.
B. Explain how the isolation of marine species by the formation of a land barrier can lead to divergent evolution of those species.

The formation of the Isthmus of Panama connected two continents, North America and South America. Many North American land animal species migrated to South America after the formation of the isthmus and occupied similar niches as South American species.

- C. Predict** the effect the formation of the isthmus had on resource availability for South American species.
D. Justify your prediction in part C.

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).

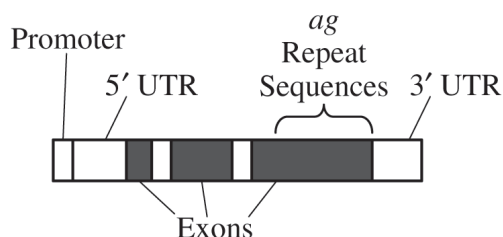


Figure 1. Basic structure of a functional *ag* gene

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).

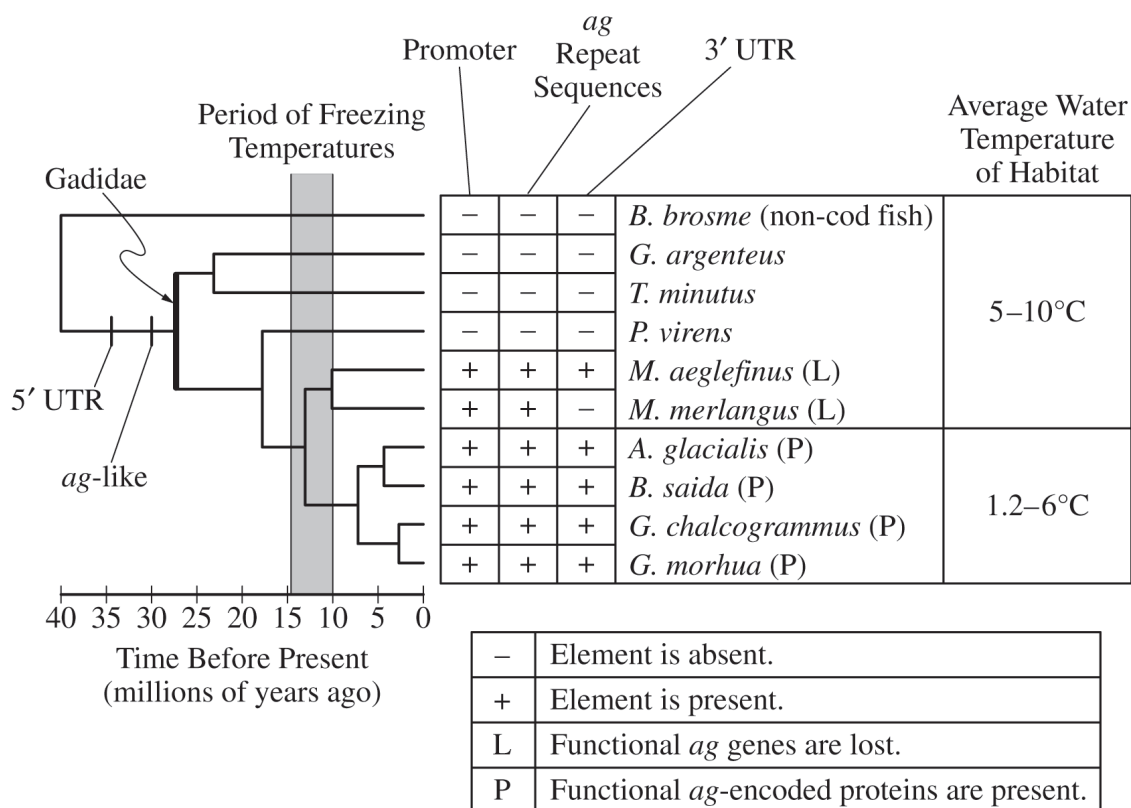


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

- (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.
- (a) **Describe** the prezygotic barrier that results in these genetically distinct populations.
- (b) 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.
- (c) If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, **predict** the likely impact on both populations.
- (d) 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.

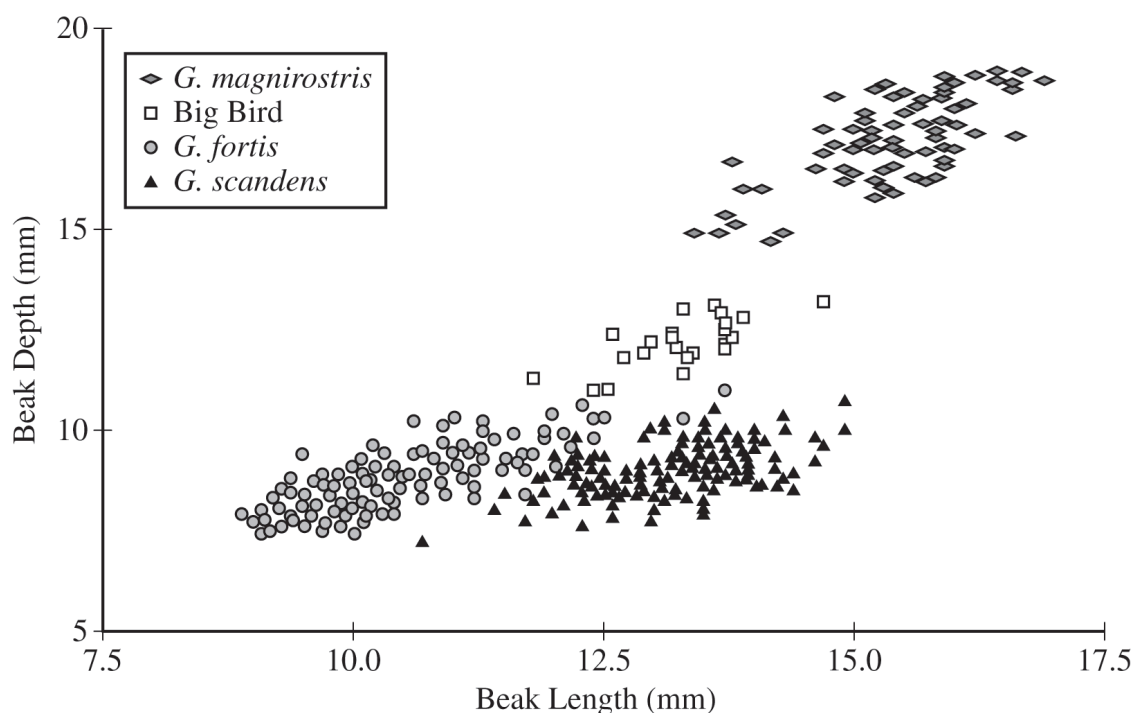


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

- (a) 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*.
- (b) Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.
- (c) 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.
- (d) 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.

7.11 Variations in Populations

Name: _____ Class: _____ Date: _____

Total: 9 marks

KEY WORDS diversity 多样性 • genetic diversity 遗传多样性 • variation 变异

Objective

Build the skills to answer exam questions on **variation in populations**.

You must be able to:

- explain why **genetic diversity** 遗传多样性 helps a population survive change
- link low diversity to extinction risk
- describe how variation arises and is maintained

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ Variation is raw material

A population with more **genetic variation** has more different traits, so it is **more likely** that some individuals can survive a new challenge (disease, climate change).

■ Low diversity is risky

A population with **low** genetic diversity (e.g. after a bottleneck) may have **no** individuals able to survive a new threat, raising the **extinction risk**.

■ Sources of variation

Variation comes from **mutation** (new alleles) and **sexual reproduction** (crossing over, independent assortment, random fertilization mixing alleles).

■ A worked example

A genetically diverse crop is more likely to include disease-resistant plants; a genetically uniform (monoculture) crop can be wiped out by one disease.

2 Practice

Now apply the methods above.

2.1 Why is genetic diversity useful when the environment changes? [1]

2.2 State one source of genetic variation. [1]

2.3 What is the risk of low genetic diversity? [1]

3 Exam-style questions

3.1 A population with high genetic diversity is more likely to [1]

- **A** go extinct
 - **B** survive an environmental change
 - **C** stop reproducing
 - **D** have identical individuals
-

3.2 A new disease spreads through two populations of the same species.

(a) Explain why the more genetically diverse population is more likely to survive. [2]

(b) State one source of the genetic variation. [1]

3.3 Explain why a monoculture crop is vulnerable to being destroyed by a single disease. [2]

Solutions

2.1 It makes it more likely some individuals have traits that let them survive the change.

2.2 Mutation (or sexual reproduction).

2.3 A higher risk of extinction if no individuals can survive a new threat.

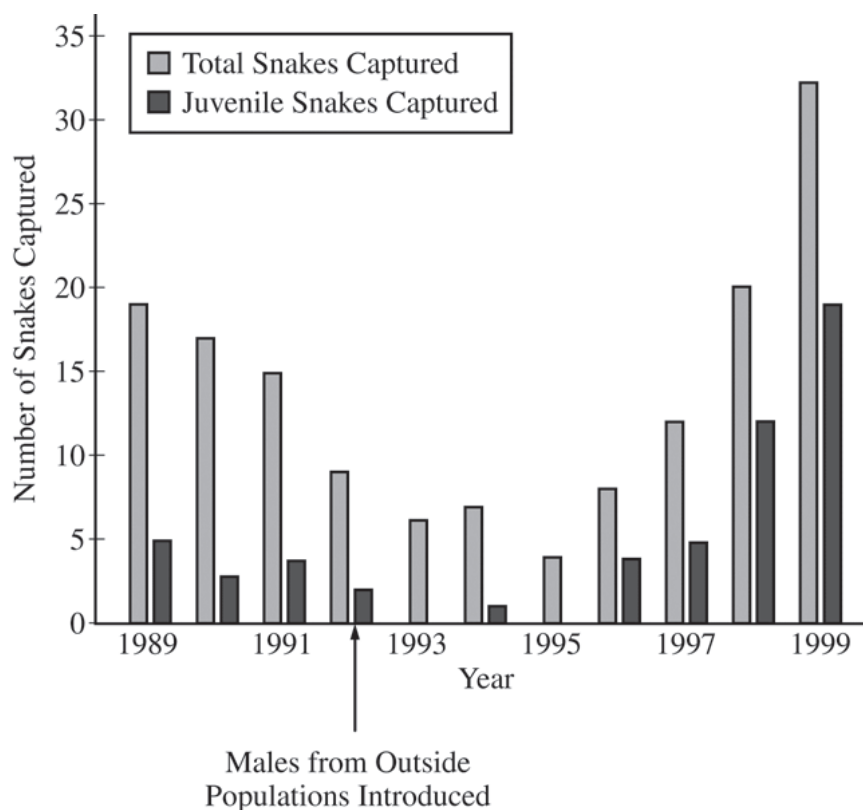
3.1 B — survive an environmental change.

3.2 (a) A diverse population is more likely to include individuals with resistance to the disease, so some survive and reproduce. (b) Mutation (or sexual reproduction).

3.3 A monoculture has almost identical genes, so if the disease can kill one plant it can kill them all — there are no resistant variants to survive.

6. In an attempt to rescue a small isolated population of snakes from decline, a few male snakes from several larger populations of the same species were introduced into the population in 1992. The snakes reproduce sexually, and there are abundant resources in the environment.

The figure below shows the results of a study of the snake population both before and after the introduction of the outside males. In the study, the numbers of captured snakes indicate the overall population size.



- (a) **Describe** ONE characteristic of the original population that may have led to the population's decline in size between 1989 and 1993.
- (b) **Propose** ONE reason that the introduction of the outside males rescued the snake population from decline.
- (c) **Describe** how the data support the statement that there are abundant resources in the environment.

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.

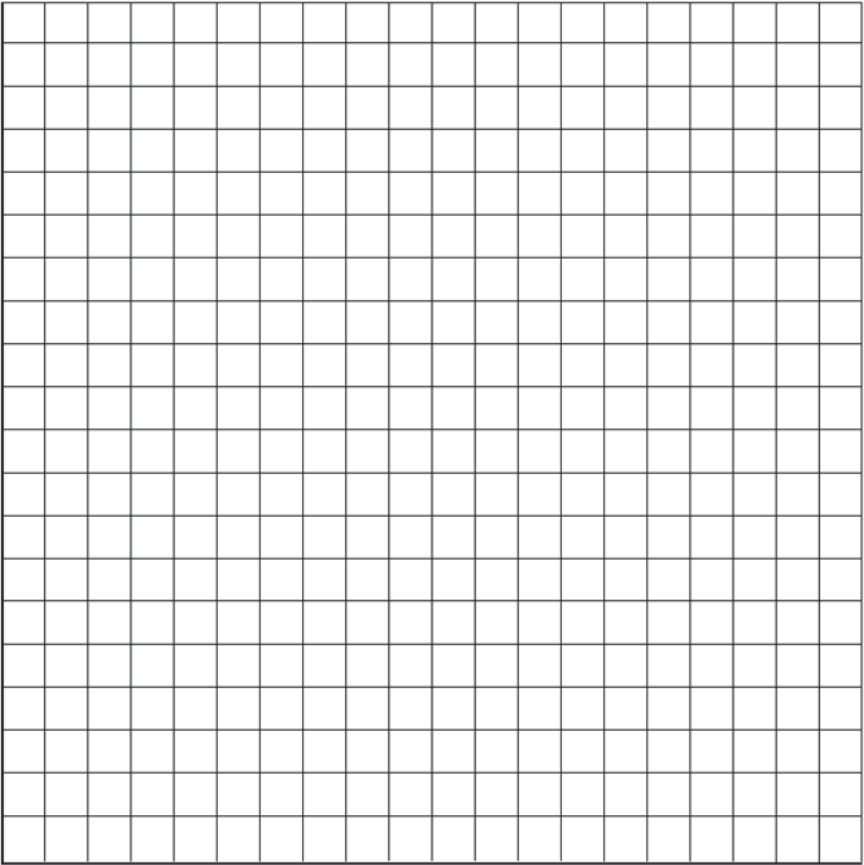
1. Trichomes are hairlike outgrowths of the epidermis of plants that are thought to provide protection against being eaten by herbivores (herbivory). In a certain plant species, stem trichome density is genetically determined.

To investigate variation in stem trichome density within the plant species, a student counted the number of trichomes on the stems of six plants in each of three different populations. The student used the data to calculate the mean trichome density (numbers of hairs per square centimeter) for each population. The results are provided in the table below.

TRICHOME DENSITY IN THREE PLANT POPULATIONS (number of trichomes/cm²)

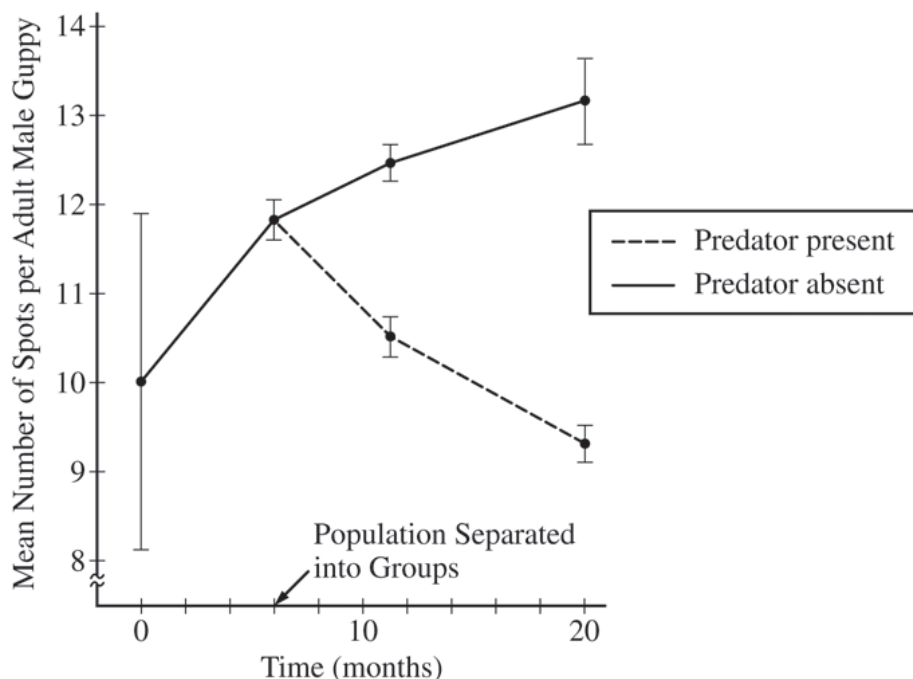
Population	Plant 1	Plant 2	Plant 3	Plant 4	Plant 5	Plant 6	Mean	Standard Error of the Mean (SEM)
I	8	11	9	10	8	6	9	1
II	12	6	15	9	13	8	11	1
III	13	17	9	14	12	16	14	1

- (a) On the axes provided, **create** an appropriately labeled graph to illustrate the sample means of the three populations to within 95% confidence (i.e., sample mean $\pm$ 2 SEM).
- (b) Based on the sample means and standard errors of the means, **identify** the two populations that are most likely to have statistically significant differences in the mean stem trichome densities. **Justify** your response.
- (c) **Describe** the independent and dependent variables and a control treatment for an experiment to test the hypothesis that higher trichome density in plants is selected for in the presence of herbivores. **Identify** an appropriate duration of the experiment to ensure that natural selection is measured, and **predict** the experimental results that would support the hypothesis.



4. Adult male guppies (*Poecilia reticulata*) exhibit genetically determined spots, while juvenile and adult female guppies lack spots. In a study of selection, male and female guppies from genetically diverse populations were collected from different mountain streams and placed together in an isolated environment containing no predators.

The study population was maintained for several generations in the isolated area before being separated into two groups. One group was moved to an artificial pond containing a fish predator, while a second group was moved to an artificial pond containing no predators. The two groups went through several generations in their new environments. At different times during the experiment, the mean number of spots per adult male guppy was determined as shown in the figure below. Vertical bars in the figure represent two standard errors of the mean (SEM).



- (a) **Describe** the change in genetic variation in the population between 0 and 6 months and **provide** reasoning for your description based on the means and SEM.
- (b) **Propose** ONE type of mating behavior that could have resulted in the observed change in the number of spots per adult male guppy between 6 and 20 months in the absence of the predator.
- (c) **Propose** an evolutionary mechanism that explains the change in average number of spots between 6 and 20 months in the presence of the predator.

7.12 Origins of Life on Earth

Name: _____ Class: _____ Date: _____

Total: 8 marks

KEY WORDS evolution 进化 • variation 变异

Objective

Build the skills to answer exam questions on the **origins of life on Earth**.

You must be able to:

- outline the main hypothesis (simple molecules → polymers → protocells)
- describe the evidence (Miller-Urey, RNA world)
- put the key steps in order

1 Worked examples

Study these first. Each one shows the method for a question type used later — follow the steps and you can do the Practice and Exam-style questions yourself.

■ The proposed sequence

A leading hypothesis for life's origin:

1. **Simple organic molecules** (amino acids, nucleotides) formed from inorganic ones on early Earth.
2. These joined into **polymers**.
3. Polymers became enclosed in membrane droplets (**protocells**).
4. Molecules that could **self-replicate** allowed heredity and evolution to begin.

■ Miller-Urey evidence

The **Miller-Urey experiment** showed that amino acids can form from simple gases and energy (simulating early Earth), supporting step 1.

■ The RNA world

RNA can both store information **and** act as a catalyst, so it may have been the first self-replicating molecule — the “**RNA world**” idea.

■ A worked ordering

Order: inorganic molecules → organic monomers → polymers → protocells → self-replicating systems → early cells.

2 Practice

Now apply the methods above.

2.1 What did the Miller-Urey experiment produce? [1]

2.2 Why is RNA proposed as the first self-replicating molecule? [1]

2.3 What is a protocell? [1]

3 Exam-style questions

3.1 The Miller-Urey experiment supported the idea that [1]

- **A** cells arose fully formed
 - **B** organic molecules can form from inorganic ones
 - **C** DNA came before RNA
 - **D** life came from space only
-

3.2 Put these steps of life's origin in order: polymers, protocells, simple organic monomers, self-replicating molecules. [2]

3.3 Explain why the ability to self-replicate was a key step for evolution to begin. [2]

Solutions

2.1 Amino acids (organic molecules) from simple gases and energy.

2.2 RNA can both store information and act as a catalyst (enzyme).

2.3 A membrane-enclosed droplet containing molecules — a precursor to a cell.

3.1 B — organic molecules can form from inorganic ones.

3.2 Simple organic monomers → polymers → protocells → self-replicating molecules.

3.3 Self-replication allowed information to be copied and passed on (heredity); variation in the copies could then be selected, so evolution could begin.

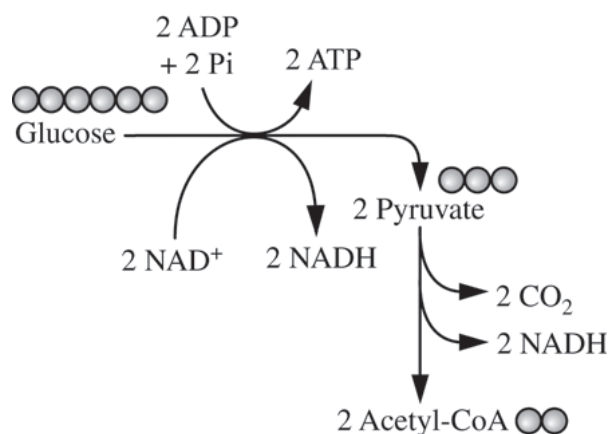


Figure 1. Glycolysis and pyruvate oxidation

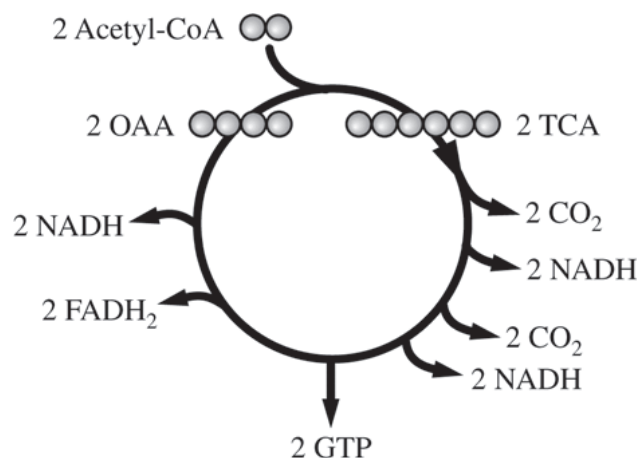


Figure 2. Krebs cycle

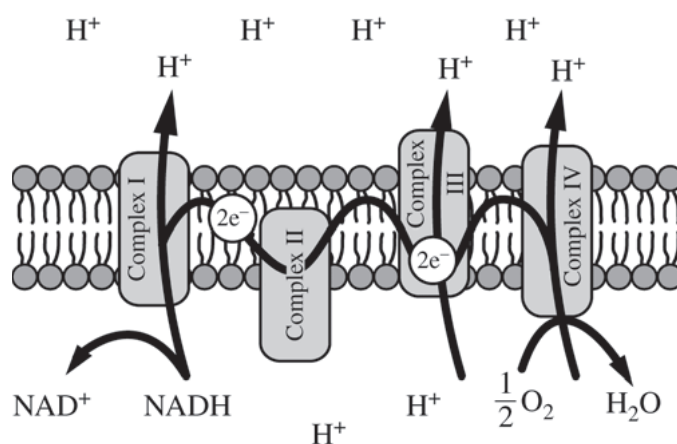


Figure 3. Electron transport chain

2. Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.
- (a) Using the information above, **describe** ONE contribution of each of the following in ATP synthesis.
- Catabolism of glucose in glycolysis and pyruvate oxidation
 - Oxidation of intermediates in the Krebs cycle
 - Formation of a proton gradient by the electron transport chain
- (b) Use each of the following observations to **justify** the claim that glycolysis first occurred in a common ancestor of all living organisms.
- Nearly all existing organisms perform glycolysis.
 - Glycolysis occurs under anaerobic conditions.
 - Glycolysis occurs only in the cytosol.

- (c) A researcher estimates that, in a certain organism, the complete metabolism of glucose produces 30 molecules of ATP for each molecule of glucose. The energy released from the total oxidation of glucose under standard conditions is 686 kcal/mol. The energy released from the hydrolysis of ATP to ADP and inorganic phosphate under standard conditions is 7.3 kcal/mol. **Calculate** the amount of energy available from the hydrolysis of 30 moles of ATP. **Calculate** the efficiency of total ATP production from 1 mole of glucose in the organism. **Describe** what happens to the excess energy that is released from the metabolism of glucose.
- (d) The enzymes of the Krebs cycle function in the cytosol of bacteria, but among eukaryotes the enzymes function mostly in the mitochondria. **Pose** a scientific question that connects the subcellular location of the enzymes in the Krebs cycle to the evolution of eukaryotes.