Week 16

AP Biology

Homework bundle for this week

本周作业合集

exercises.lol

Contents 目录

6. Gene Expression and Regulation

Starter Quiz · 课前小测

AP Biology Name: _____ Score: _____

1. The two long sides of the DNA ladder are made of a repeating…
   - ☐ sugar-phosphate backbone
   - ☐ chain of amino acids
   - ☐ row of fatty acids
   - ☐ string of metals
2. Why must a cell copy its DNA before dividing?
   - ☐ so each daughter cell gets a full set of DNA
   - ☐ to make ATP
   - ☐ to break down glucose
   - ☐ to send a hormone
3. **Transcription** copies a gene from DNA into…
   - ☐ messenger RNA (mRNA)
   - ☐ a protein
   - ☐ ATP
   - ☐ a lipid
4. **Translation** builds a protein by reading…
   - ☐ the mRNA into a chain of amino acids
   - ☐ DNA into more DNA
   - ☐ glucose into ATP
   - ☐ a protein into DNA
5. **Gene expression** means…
   - ☐ a gene being switched on to make its product
   - ☐ a gene being deleted
   - ☐ copying all the DNA
   - ☐ a cell dividing
6. A cell keeps every one of its genes switched on all the time.

   ☐ True ☐ False

7. The repeating unit of a nucleic acid — a sugar, phosphate, and base — is a _____.

   _____
8. Because each new DNA keeps one old strand, replication is called _____-conservative.

   _____
9. The enzyme that builds the mRNA copy is RNA _____.

   _____
10. The molecule that carries an amino acid to the ribosome is called _____ RNA.

    _____

AP Biology

1. **sugar-phosphate backbone**

   Each strand's backbone is an alternating **sugar-phosphate** chain; the bases stick out from it.

2. **so each daughter cell gets a full set of DNA**

   Replication ensures both daughter cells receive a complete, identical copy of the DNA.

3. **messenger RNA (mRNA)**

   Transcription makes an **mRNA** copy of one gene, which can leave the nucleus.

4. **the mRNA into a chain of amino acids**

   Translation reads the mRNA message and builds the matching chain of amino acids — a protein.

5. **a gene being switched on to make its product**

   Gene expression is a gene being used — transcribed and translated to make its protein.

6. **False**

   A cell expresses only the genes it needs right now; the rest are switched off.

7. **nucleotide**

   Each **nucleotide** is one sugar + one phosphate + one base; many joined make a strand.

8. **semi**

   Replication is **semi-conservative**: each copy has one original strand and one new strand.

9. **polymerase**

   RNA polymerase reads the DNA template and joins RNA nucleotides into mRNA.

10. **transfer**

    Transfer RNA (tRNA) carries an amino acid and has an anticodon that matches the mRNA codon.

AP BIOLOGY • EXERCISE SHEET

6.1 DNA and RNA Structure

Name: _____ Class: _____ Date: _____ **Total: 11 marks**

KEY WORDS double helix 双螺旋 • complementary base pairing 互补配对 • antiparallel 反平行

Objective

Build the skills to answer exam questions on **DNA and RNA structure**.

You must be able to:

- describe the DNA **double helix** 双螺旋 and **complementary base pairing** 互补配对
- pair the bases (A–T, C–G; A–U in RNA)
- compare DNA and RNA structure

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 double helix

DNA is a **double helix** — two strands twisted together, held by hydrogen bonds between paired bases. The strands are **antiparallel** (run in opposite directions).

Base pairing

Bases pair specifically: **A–T** and **C–G** in DNA. This complementary pairing lets each strand act as a template to rebuild the other.

Reading a complementary strand

Given a strand 5′-ATGC-3′, its complement is 3′-TACG-5′ (A with T, C with G). In RNA, A pairs with **U** instead of T.

DNA vs RNA

- **DNA** — double-stranded, deoxyribose, bases A/T/C/G.
- **RNA** — single-stranded, ribose, bases A/U/C/G.

2 Practice

Now apply the methods above.

2.1 Which base pairs with adenine in DNA? [1]

2.2 Write the complementary DNA strand for 5′-AATGCC-3′. [2]

2.3 Which base replaces thymine in RNA? [1]

3 Exam-style questions

3.1 In DNA, cytosine pairs with [1]

- **A** adenine
- **B** thymine
- **C** guanine
- **D** uracil

3.2 A DNA strand reads 3′-TACGGA-5′.

(a) Write the complementary DNA strand. [2]

(b) Write the RNA sequence transcribed from the original strand. [2]

3.3 Explain how complementary base pairing allows DNA to be copied accurately. [2]

Solutions

2.1 Thymine.

2.2 3′-TTACGG-5′.

2.3 Uracil.

3.1 C — guanine.

3.2 (a) 5′-ATGCCT-3′. (b) RNA from 3′-TACGGA-5′: 5′-AUGCCU-3′.

3.3 Each base pairs only with its complement (A–T, C–G), so each strand acts as a template that specifies the exact sequence of the new strand.

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.

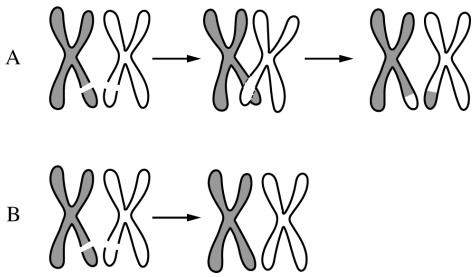


Figure 1. Double-strand breaks in chromatids are repaired with crossing over (A) or without crossing over (B).

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.

AP BIOLOGY • EXERCISE SHEET

6.2 DNA Replication

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS dna polymerase 聚合酶 • helicase 解旋酶 • semiconservative 半保留 • nucleotides 核苷酸 • complementary base pairing 互补配对

Objective

Build the skills to answer exam questions on **DNA replication**.

You must be able to:

- describe **semiconservative** 半保留 replication
- state the roles of **helicase** 解旋酶 and **DNA polymerase** 聚合酶
- explain why each new molecule has one old and one new strand

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.

■ Semiconservative replication

DNA replication is **semiconservative**: the two strands separate, and each acts as a template for a new strand. Each new DNA molecule has **one old** and **one new** strand.

■ Key enzymes

- **Helicase** unwinds and separates the two strands.
- **DNA polymerase** adds complementary nucleotides to each template strand, building the new strand.

■ The steps

1. Helicase unzips the helix. 2. Each strand is a template. 3. DNA polymerase adds matching bases (A–T, C–G). 4. Two identical double helices result.

■ A worked idea

If one template strand reads 3′-TACG-5′, DNA polymerase builds 5′-ATGC-3′ alongside it — an exact complement.

2 Practice

Now apply the methods above.

2.1 What does “semiconservative” mean for DNA replication? [1]

2.2 What does helicase do? [1]

2.3 What does DNA polymerase do? [1]

3 Exam-style questions

3.1 After replication, each new DNA molecule contains [1]

- **A** two new strands
- **B** two old strands
- **C** one old and one new strand
- **D** only RNA

3.2 A cell replicates its DNA.

(a) Describe the roles of helicase and DNA polymerase. [2]

(b) A template strand reads 3′-AATGCC-5′. Write the new strand. [2]

3.3 Explain why semiconservative replication ensures the two daughter molecules are identical to the original. [2]

Solutions

2.1 Each new molecule keeps one original strand and gains one new strand.

2.2 Unwinds and separates the two DNA strands.

2.3 Adds complementary nucleotides to build the new strand.

3.1 C — one old and one new strand.

3.2 (a) Helicase unwinds/separates the strands; DNA polymerase adds complementary bases to each template. (b) 5′-TTACGG-3′.

3.3 Each original strand acts as a template, and complementary base pairing forces the new strand to match exactly, so both daughter molecules are copies of the original.

AP BIOLOGY • EXERCISE SHEET

6.3 Transcription and RNA Processing

Name: _____ Class: _____ Date: _____ **Total: 11 marks**

KEY WORDS introns 内含子 • exons 外显子 • transcription 转录 • messenger rna 信使

Objective

Build the skills to answer exam questions on **transcription and RNA processing**.

You must be able to:

- describe **transcription** 转录 (DNA → mRNA) by RNA polymerase
- state the RNA processing steps (**cap, tail, splicing** 剪接)
- distinguish **introns** and **exons**

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.

Transcription

Transcription copies a gene from DNA into **messenger RNA (mRNA)**. **RNA polymerase** reads the DNA template and builds an mRNA strand with complementary bases (using **U** instead of T).

A worked transcript

Template 3′-TACGGA-5′ transcribes to mRNA 5′-AUGCCU-3′.

RNA processing (in eukaryotes)

Before leaving the nucleus, the mRNA is processed: a **cap** and a **poly-A tail** are added for stability, and **introns** are removed by **splicing**, joining the **exons**.

Introns and exons

- **Exons** — coding parts, kept in the final mRNA.
- **Introns** — non-coding parts, spliced out.

2 Practice

Now apply the methods above.

2.1 What enzyme carries out transcription? [1]

2.2 Transcribe the template 3′-TACG-5′ into mRNA. [2]

2.3 What is removed during splicing? [1]

3 Exam-style questions

3.1 During RNA processing, the parts removed from the pre-mRNA are the [1]

- **A** exons
- **B** introns
- **C** caps
- **D** tails

3.2 A gene is transcribed and processed.

(a) State two modifications made to the mRNA. [2]

(b) Distinguish introns from exons. [2]

3.3 Explain why processing is needed before the mRNA leaves the nucleus. [2]

Solutions

2.1 RNA polymerase.

2.2 mRNA 5′-AUGC-3′.

2.3 Introns.

3.1 B — introns.

3.2 (a) Any two: adding a 5’ cap, adding a poly-A tail, splicing out introns. (b) Exons are the coding parts kept in the mRNA; introns are non-coding parts spliced out.

3.3 Processing (cap, tail, splicing) stabilizes the mRNA and removes non-coding introns, so the mature mRNA can be exported and correctly translated.

6. Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

   When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

5′ Cap Structure	mRNA Half-Life $\pm 2SE_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{x}}$ (relative to amount in normal cap)
No cap	1.41 ± 0.02	0.011 ± 0.000
Normal GTP cap	16.10 ± 1.83	1.000 ± 0.007
Modified cap I	15.50 ± 1.57	4.777 ± 0.042
Modified cap II	27.00 ± 2.85	13.094 ± 0.307
Modified cap III	18.09 ± 0.81	6.570 ± 0.075

(a) Based on the data, **identify** which cap structure is most likely to protect the end of the mRNAs from degradation.

(b) Based on the data for the mRNAs with modified caps, **describe** the relationship between the mRNA half-life and the total amount of protein produced.

(c) After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. **Evaluate** their hypothesis by comparing the data in Table 1.

(d) Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. **Explain** why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells.

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

STOP

END OF EXAM

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

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

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

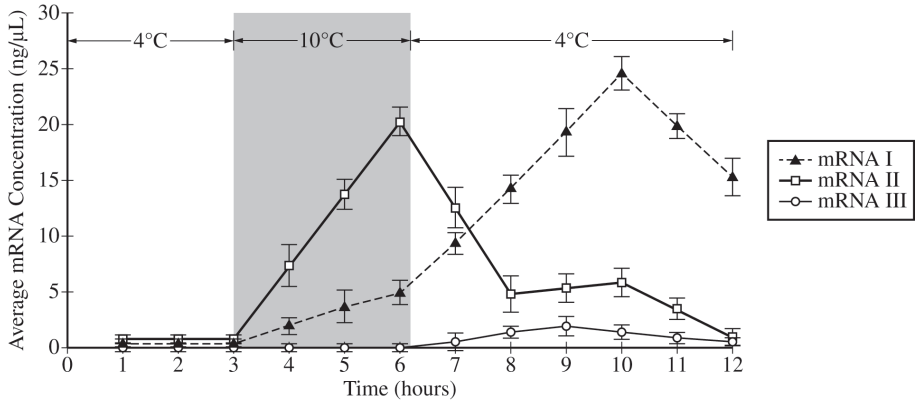


Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from *hsp* genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$.

(a) **Identify** the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment.

(b) **Describe** the trend in the average concentration of mRNA I throughout the experiment.

(c) The scientists hypothesized that the heat-shock protein (HSP) translated from mRNA I plays a greater role in refolding proteins than does the HSP translated from mRNA II. Use the data to **support** the hypothesis.

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

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

STOP

END OF EXAM

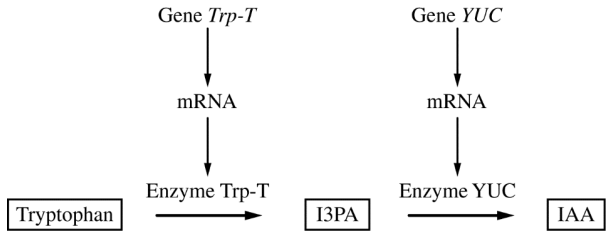


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

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*.

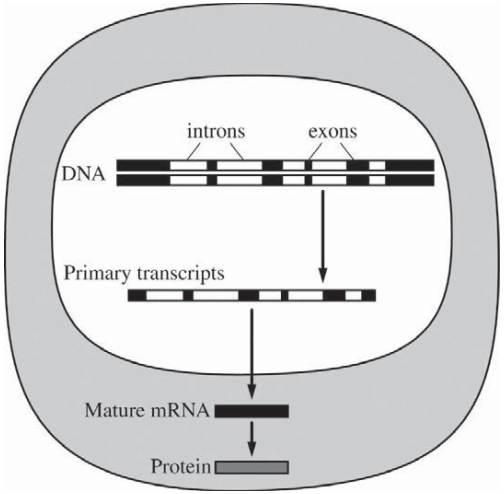
   (a) **Circle** ONE arrow that represents transcription on the template pathway. **Identify** the molecule that would be absent if enzyme YUC is nonfunctional.

   (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.



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

   (a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length. **Describe** the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs.

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

AP BIOLOGY • EXERCISE SHEET

6.4 Translation

Name: _____ Class: _____ Date: _____ **Total: 9 marks**

KEY WORDS translation 翻译 • ribosome 核糖体 • codons 密码子 • trna 转运 • dna polymerase 聚合酶

Objective

Build the skills to answer exam questions on **translation** — building a protein from mRNA.

You must be able to:

- read **codons** 密码子 from mRNA using the genetic code
- describe the roles of the **ribosome** and **tRNA** 转运 RNA
- translate a short mRNA sequence into amino acids

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.

Codons

Translation reads the mRNA in three-base groups called **codons**. Each codon specifies one amino acid (or a stop). Translation starts at the **start codon AUG** (methionine).

The players

- The **ribosome** reads the mRNA and joins amino acids.
- **tRNA** brings the correct amino acid; its **anticodon** pairs with the mRNA codon.

A worked translation

mRNA 5′-AUG-GCU-UAA-3′: AUG = Met (start), GCU = Ala, UAA = stop. So the chain is Met-Ala, then translation stops.

The genetic code

The code is (nearly) **universal** — the same codons mean the same amino acids in almost all organisms, which is why genes can be transferred between species.

2 Practice

Now apply the methods above.

2.1 How many bases make one codon? [1]

2.2 What is the start codon? [1]

2.3 What part of a tRNA pairs with the mRNA codon? [1]

3 Exam-style questions

3.1 During translation, the amino acids are joined by the [1]

- **A** nucleus
- **B** ribosome
- **C** mitochondrion
- **D** DNA polymerase

3.2 An mRNA reads 5′-AUG-CCU-GGA-UAA-3′ (AUG=Met, CCU=Pro, GGA=Gly, UAA=stop).

(a) Give the amino-acid sequence made. [2]

(b) Explain what happens at the UAA codon. [1]

3.3 Explain why the near-universal genetic code allows a human gene to be expressed in a bacterium. [2]

Solutions

2.1 Three.

2.2 AUG.

2.3 The anticodon.

3.1 **B** — the ribosome.

3.2 (a) Met-Pro-Gly. (b) UAA is a stop codon, so translation ends and the polypeptide is released.

3.3 Because the code is essentially universal, the bacterium's ribosomes read the same codons for the same amino acids, so a human gene is translated into the correct protein.

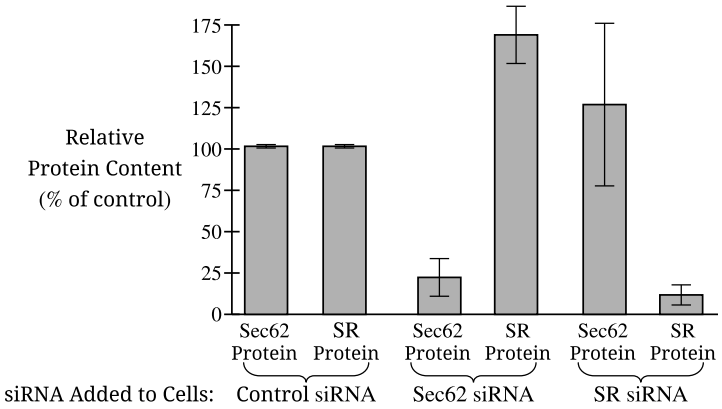
1. Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

A. Describe the function of ribosomes.

For proteins transported during translation, this process begins in the cytosol and pauses when a specific sequence of amino acids is translated. The translation complex is then transported to the surface of the ER where translation continues. Proteins that are transported after translation are translated entirely in the cytosol and then transported to the ER. In both instances, the translated proteins enter the ER through a protein channel in the membrane of the ER.

Researchers studying the two types of protein transport identified that the ER membrane protein SR is necessary for transport during translation, while the ER membrane protein Sec62 is necessary for transport after translation. To investigate which transport mechanism is used for different proteins, researchers first created small interfering RNAs (siRNAs) that reduce expression of either SR or Sec62. They then treated groups of cells with either the SR siRNA or the Sec62 siRNA and determined the relative amount of SR and Sec62 protein in each group of cells compared with cells treated with a control siRNA (Figure 1).

Figure 1. Average relative amounts of Sec62 and SR proteins in cells treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{x}}$.



B.

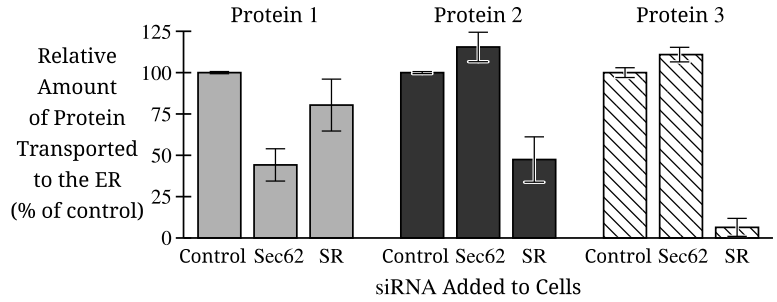
i. **Identify** the dependent variable in the experiments shown in Figure 1.

ii. **Justify** why the researchers included the control of measuring the relative amounts of both Sec62 and SR proteins in cells that were treated with Sec62 siRNA only (data shown in Figure 1).

iii. Based on Figure 1, **describe** the effect on the production of SR protein when cells are treated with Sec62 siRNA.

The researchers then measured the amount of each of three different proteins that was transported to the ER in cells treated with Sec62 siRNA or SR siRNA. The researchers calculated the percent transported relative to the cells treated with control siRNA (Figure 2).

Figure 2. Average relative amounts of three proteins that were transported to the ER when treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{x}}$.



C.

i. **Identify** the independent variable in the researchers' second experiment (data shown in Figure 2).

ii. Based on Figure 2, **identify** the protein(s) that when treated with Sec62 siRNA showed an increase in percent transport to the ER compared with the control.

iii. Protein 1 is encoded by 234 nucleotides, while protein 2 is encoded by 495 nucleotides. Assuming all nucleotides for both proteins encode amino acids, **calculate** the difference in the number of amino acids between the two proteins.

D.

i. Researchers claim that protein 1 is the only tested protein that is transported to the ER following its complete translation in the cytosol. Using data from Figure 2, **support** the researchers' claim.

ii. For any protein that enters the ER, researchers claim that amino acids close to the protein's amino terminus determine how likely the protein is to pass through the protein channel within the ER membrane. **Justify** the researchers' claim based on your understanding of factors that affect the transport of proteins across membranes.

6. Scientists can quantify the rate of translation as ribosomes move along an mRNA from one codon to the next. Using a procedure called ribosome profiling, the scientists measured how long a ribosome remains stationary at each codon of each mRNA. They determined the average translation rate across all codons is 5.2 amino acids per second but that the average translation rate for specific codons in different mRNA sequences can vary widely. These variations in translation rates are thought to facilitate correct folding of the protein being produced. The rate at which three different codons were translated was measured in 100 different mRNAs. The scientists determined the distribution of rate (number of times each rate was recorded) for each of the three codons: GAC (Figure 1A), AUU (Figure 1B), and UGG (Figure 1C).

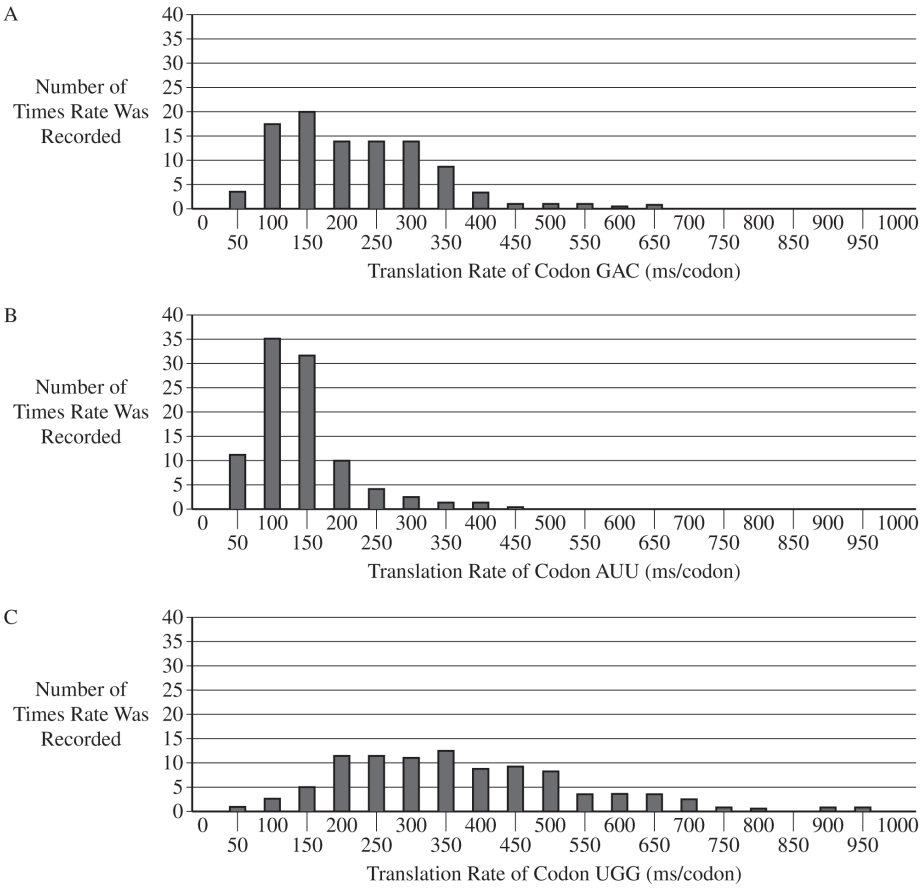


Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG

(a) Using the data in Figure 1, graph A, **identify** the rate (in ms/codon) that was recorded the greatest number of times for the GAC codon.

(b) Using the data in Figure 1, graphs B and C, **describe** the variation in translation rate of the AUU codon compared with that of the UGG codon.

(c) Scientists hypothesize that tRNA molecules that bind to UGG codons are available in lower abundance than are tRNAs that bind to AUU codons. **Support** the scientists' hypothesis using the data in Figure 1.

(d) Amino acids can be encoded by multiple codons. In many organisms, certain codons for the same amino acid occur more frequently in an mRNA than do other codons. Based on the data provided, **explain** why the use of one codon over another for the same amino acid might result in increased levels of protein production from a particular mRNA.

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.

STOP

END OF EXAM

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

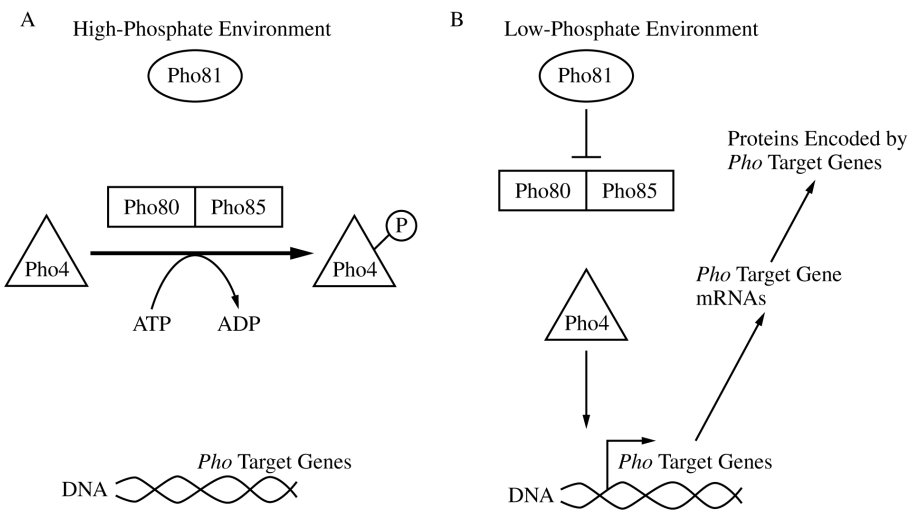


Figure 1. A simplified model of the regulation of expression of *Pho* target genes in (A) a high-phosphate (high-Pi) environment and (B) a low-phosphate (low-Pi) environment

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

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

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

(a) **Describe** the effect that the addition of a charged phosphate group can have on a protein that would cause the protein to become inactive. **Explain** how a signal can be amplified during signal transduction in a pathway such as the PHO signaling pathway.

(b) Based on Table 1, **identify** a dependent variable in the researchers' experiment. **Justify** the researchers' using the wild-type strain for the creation of the mutant strains. **Justify** the researchers' using mutant strains in which only a single component of the pathway was mutated in each strain.

(c) Based on the data in Table 1, **identify** the yeast strain and growth conditions that lead to the highest relative amount of *PHO1* mRNA. **Calculate** the percent change in APase activity in wild-type yeast cells in a high-Pi environment compared with that of wild-type cells in a low-Pi environment.

(d) In a follow-up experiment, researchers created a strain of yeast with a mutation that resulted in a nonfunctional Pho85 protein. Based on Figure 1, **predict** the effects of this mutation on *PHO1* expression in the mutant strain in a high-Pi environment. Provide reasoning to **justify** your prediction.

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

6. Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

   When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

5′ Cap Structure	mRNA Half-Life $\pm 2SE_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{x}}$ (relative to amount in normal cap)
No cap	1.41 ± 0.02	0.011 ± 0.000
Normal GTP cap	16.10 ± 1.83	1.000 ± 0.007
Modified cap I	15.50 ± 1.57	4.777 ± 0.042
Modified cap II	27.00 ± 2.85	13.094 ± 0.307
Modified cap III	18.09 ± 0.81	6.570 ± 0.075

(a) Based on the data, **identify** which cap structure is most likely to protect the end of the mRNAs from degradation.

(b) Based on the data for the mRNAs with modified caps, **describe** the relationship between the mRNA half-life and the total amount of protein produced.

(c) After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. **Evaluate** their hypothesis by comparing the data in Table 1.

(d) Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. **Explain** why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells.

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

STOP

END OF EXAM

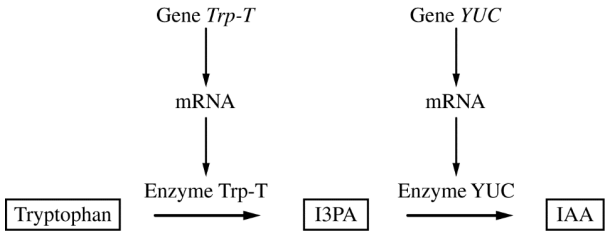


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

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.

3. Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydroxylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the *GA3H* gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F_1 generation are tall. When the F_1 plants are crossed with each other, 75 percent of the plants in the F_2 generation are tall and 25 percent of the plants are short.

Second Base in Codon

First Base in Codon	U	C	A	G	Third Base in Codon
U	UUU, UUC: Phe UUA, UUG: Leu	UCU, UCC, UCA, UCG: Ser	UAU, UAC: Tyr UAA: Stop UAG: Stop	UGU, UGC: Cys UGA: Stop UGG: Trp	U C A G
C	CUU, CUC, CUA, CUG: Leu	CCU, CCC, CCA, CCG: Pro	CAU, CAC: His CAA, CAG: Gln	CGU, CGC, CGA, CGG: Arg	U C A G
A	AUU, AUC, AUA: Ile AUG: Met or Start	ACU, ACC, ACA, ACG: Thr	AAU, AAC: Asn AAA, AAG: Lys	AGU, AGC: Ser AGA, AGG: Arg	U C A G
G	GUU, GUC, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U C A G

Figure 1. The universal genetic code

   (a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.

   (b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.

   (c) **Describe** how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype.

AP BIOLOGY • EXERCISE SHEET

6.5 Regulation of Gene Expression

Name: _____ Class: _____ Date: _____ **Total: 9 marks**

KEY WORDS promoters 启动子 • transcription 转录 • ribosome 核糖体

Objective

Build the skills to answer exam questions on the **regulation of gene expression**.

You must be able to:

- explain that cells control **which genes** are expressed and when
- describe regulation by **promoters** 启动子 and regulatory proteins
- give the example of an inducible/repressible operon idea

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.

■ Genes are switched on and off

A cell does not express all its genes at once. **Gene regulation** controls **which** genes are turned on, **when**, and **how much** — saving energy and allowing different cell types.

■ Promoters and regulatory proteins

RNA polymerase binds a gene's **promoter** to start transcription. **Regulatory proteins** can block or help this binding — acting as switches.

■ Turning genes on or off

- A **repressor** protein can bind and **block** transcription (off).
- An **activator** can **help** transcription (on).

Signals from the environment can control these proteins, so gene expression responds to conditions.

■ A worked idea

A bacterium turns on genes for digesting lactose only **when lactose is present**, saving resources when it is absent — efficient, controlled expression.

2 Practice

Now apply the methods above.

2.1 Does a cell express all its genes at once? [1]

2.2 Where does RNA polymerase bind to begin transcription? [1]

2.3 What does a repressor protein do? [1]

3 Exam-style questions

3.1 A protein that blocks transcription of a gene is a(n) [1]

- **A** activator
- **B** repressor
- **C** ribosome
- **D** polymerase

3.2 A bacterium expresses lactose-digesting genes only when lactose is present.

(a) Explain the advantage of this control. [2]

(b) State the general role of regulatory proteins in this. [1]

3.3 Explain why gene regulation is essential for a multicellular organism to have different cell types. [2]

Solutions

2.1 No.

2.2 At the gene's promoter.

2.3 Blocks transcription of a gene.

3.1 B — a repressor.

3.2 (a) The cell makes the digesting enzymes only when they are useful, saving energy and resources when lactose is absent. (b) Regulatory proteins switch the genes on or off in response to the lactose signal.

3.3 Different cell types express different sets of genes; regulation turns the right genes on in each cell, so the same genome can produce specialized cells.

The following information applies to all parts.

1. Molecules known as dinucleoside polyphosphates, a type of nucleotide, are signaling molecules that accumulate in plant cells during dry or stressful conditions.

Part A

Describe the three structural components of a nucleotide.

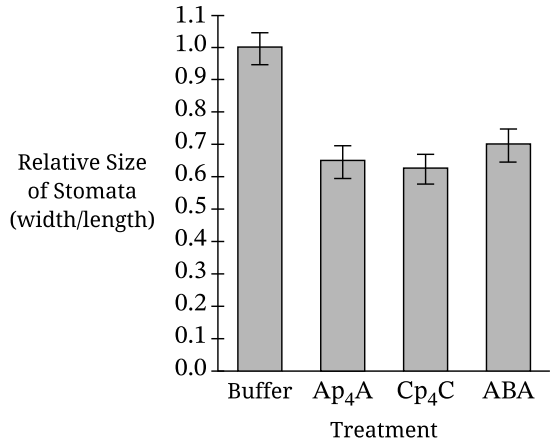
The following information applies to parts B, C, and D.

Stomata are pores on the surface of leaves that open when exposed to light and regulate the flow of carbon dioxide, oxygen, and water vapor in and out of a plant. In response to dry environmental conditions, many plants close their stomata, which reduces water loss.

Scientists hypothesized that the dinucleoside polyphosphates Ap_4A and Cp_4C bind to DORN1 receptors on the plasma membrane of plant cells and initiate signaling cascades that cause stomata to close. The scientists exposed plants to light to open the stomata and then placed samples of the leaves in buffer alone or in buffer containing one of three different compounds: Ap_4A, Cp_4C, or abscisic acid (ABA), a molecule that causes stomata to close.

The scientists measured the size of the stomata in each sample and calculated their sizes relative to the size of the stomata in the sample kept in buffer alone, as shown in Figure 1.

Figure 1. Effect of Ap_4A, Cp_4C, and ABA on Relative Stomatal Size (Error Bars Represent $\pm SE_{\bar{x}}$)



Part B

i. **Identify** the dependent variable in the scientists' first experiment.

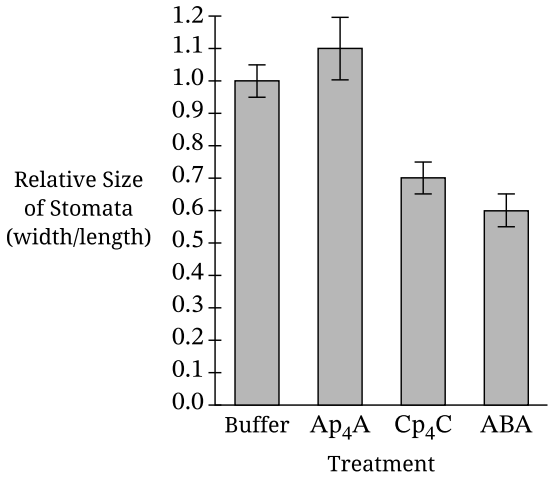
ii. Based on Figure 1, **describe** the relative size of the stomata in the Cp_4C treatment group as compared with the size of the stomata in the group treated with buffer alone.

iii. **Justify** the use of buffer alone as a control in the scientists' experiments.

Part C

In a second experiment, the scientists used plants that were identical to those in the first experiment except that the gene encoding the DORN1 receptor was mutated. The scientists repeated the procedure of the first experiment. Their results are shown in Figure 2.

Figure 2. Effect of Ap_4A, Cp_4C, and ABA on Relative Stomatal Size in DORN1 Mutants (Error Bars Represent $\pm SE_{\bar{x}}$)



i. **Justify** the scientists' treating one sample of leaves with ABA in the experiments.

ii. Based on Figure 2, **describe** the difference between the effects of Ap_4A and Cp_4C treatments on the size of stomata in plants with mutated DORN1 receptors.

iii. Activation of DORN1 receptors induces plant cells to produce certain molecules that cause the stomata to close. Based on the data in Figures 1 and 2 for cells treated with Ap_4A, **predict** the relative production of the molecules by DORN1-mutated cells in comparison to the production by nonmutated cells.

Part D

The DORN1 receptor transmits signals that result in an increase in the transcription of genes involved in plant defenses. The scientists then developed DORN1-mutant plants in which the DORN1 receptor lacked most of its intracellular domain.

i. In cells homozygous for this mutation, **predict** the effect of Ap_4A treatment on transcription of the genes involved in plant defenses relative to the effect of Ap_4A on nonmutated cells.

ii. **Justify** your prediction.

The following information applies to all parts.

---

2. Eukaryotic cells use small interfering RNA (siRNA) molecules that regulate the expression of certain genes by binding to complementary sequences in target mRNAs. This binding causes the protein AGO2 to cleave the target mRNAs. As a result of the cleavage, the mRNAs are not translated.

Part A

Describe one location where ribosomes are found in eukaryotic cells.

The following information applies to parts B, C, and D.

To investigate the role of AGO2 in the cleavage of mRNA transcribed from two genes, Gene *G* and Gene *H*, scientists determined the amount of Gene *G* and Gene *H* mRNA produced in cells with three different *AGO2* genotypes:

- Homozygous for the wild-type AGO2 protein ($AGO2^{+/+}$)
- Heterozygous for the allele encoding a nonfunctional AGO2 protein ($AGO2^{+/-}$)
- Homozygous for the allele encoding a nonfunctional AGO2 protein ($AGO2^{-/-}$)

The scientists then calculated the amount of Gene *G* and Gene *H* mRNA produced from cells of each genotype relative to that in $AGO2^{+/+}$ cells. These results are shown in the table.

Relative Average Amounts of Gene *G* and Gene *H* mRNA in Cells with Different *AGO2* Genotypes

	mRNA in $AGO2^{+/+}$ Cells $\pm$ $SE_{\bar{x}}$	mRNA in $AGO2^{+/-}$ Cells $\pm$ $SE_{\bar{x}}$	mRNA in $AGO2^{-/-}$ Cells $\pm$ $SE_{\bar{x}}$
Gene *G*	1.0 ± 0.1	0.9 ± 0.4	1.5 ± 0.5
Gene *H*	1.0 ± 0.1	2.0 ± 0.1	3.0 ± 0.4

Part B

i. Using the template in the space provided for your response, **construct** a bar graph that represents the data in the table. Your graph should be appropriately plotted and labeled.

ii. Based on the table, **determine** all the cells in which the amount of Gene *G* mRNA produced is statistically the same as the amount in the cells with the $AGO2^{+/+}$ genotype.

Part C

i. Based on the table, **describe** the relationship between the number of wild-type copies of the *AGO2* gene and the amount of Gene *H* mRNA in the cells.

ii. Based on the data in the table for Gene *H*, **calculate** the percent by which the average amount of mRNA in $AGO2^{-/-}$ cells increases compared with that in $AGO2^{+/-}$ cells.

Part D

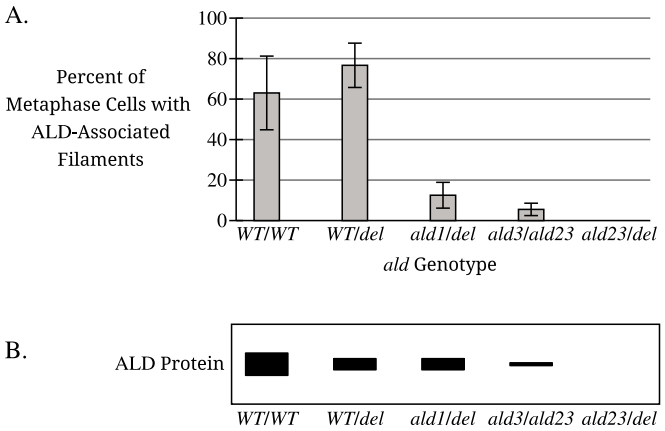
i. The scientists claim that siRNA binding and AGO2 cleavage of mRNAs play a greater role in the regulation of Gene *H* expression than in the regulation of Gene *G* expression. Based on the table, **support** the scientists' claim.

ii. Anaphase I of meiosis is blocked in mice with the $AGO2^{-/-}$ genotype. Scientists hypothesize that the block in meiosis occurs because the continued presence of a spindle-fiber stabilizing protein prevents the chromosomes from separating. Based on the table, **explain** how the $AGO2^{-/-}$ genotype could cause this effect on the dividing cells.

6. The *ald* gene of fruit flies encodes the ALD protein, which is associated with both the centromeres of chromosomes and protein filaments produced during meiosis. In the absence of functional ALD proteins, gamete-producing cells enter anaphase I before homologous chromosomes are correctly aligned. As a result, the gametes produced do not contain the correct numbers of chromosomes.

Scientists generated four mutations in the *ald* gene: *ald1*, *ald3*, *ald23*, and *del*, which was a deletion of the gene. To study the role of the ALD protein in meiosis, scientists used gameteforming metaphase cells from groups of flies with different *ald* genotypes. Some of the flies were homozygous for the wild-type allele of *ald*: *WT/WT*. Other flies were heterozygous for different *ald* alleles: *WT/del*; *ald1/del*; *ald3/ald23*; *ald23/del*. The scientists measured the percent of metaphase cells that contained ALD-associated filaments (Figure 1A) and the amount of ALD protein produced by each of the cell types (Figure 1B).

Figure 1. (A) The average percent of gamete-forming metaphase cells that contained filaments associated with ALD and (B) the amount of ALD protein produced by each cell type. A thicker band indicates a greater amount of ALD protein.



A. Based on Figure 1A, **identify** the fly genotype in which the average percent of metaphase cells with ALD-associated filaments is close to 12%.

B. Based on Figure 1B, **describe** the difference in ALD protein production between gamete-forming metaphase cells of flies with the genotype *ald3/ald23* and flies with the genotype *ald23/del*.

C. Scientists hypothesize that gamete-forming metaphase cells can produce a normal amount of ALD-associated filaments even when they produce about half as much ALD protein as the wild-type cells produce. Use the data in Figures 1A and 1B to **support** the scientists' hypothesis.

D. For gamete-forming metaphase cells of the *WT/del* and *ald1/del* flies, **explain** why the phenotypes observed in Figure 1A differ even though the amount of ALD protein produced (Figure 1B) does not.

STOP

END OF EXAM

6. Scientists can quantify the rate of translation as ribosomes move along an mRNA from one codon to the next. Using a procedure called ribosome profiling, the scientists measured how long a ribosome remains stationary at each codon of each mRNA. They determined the average translation rate across all codons is 5.2 amino acids per second but that the average translation rate for specific codons in different mRNA sequences can vary widely. These variations in translation rates are thought to facilitate correct folding of the protein being produced. The rate at which three different codons were translated was measured in 100 different mRNAs. The scientists determined the distribution of rate (number of times each rate was recorded) for each of the three codons: GAC (Figure 1A), AUU (Figure 1B), and UGG (Figure 1C).

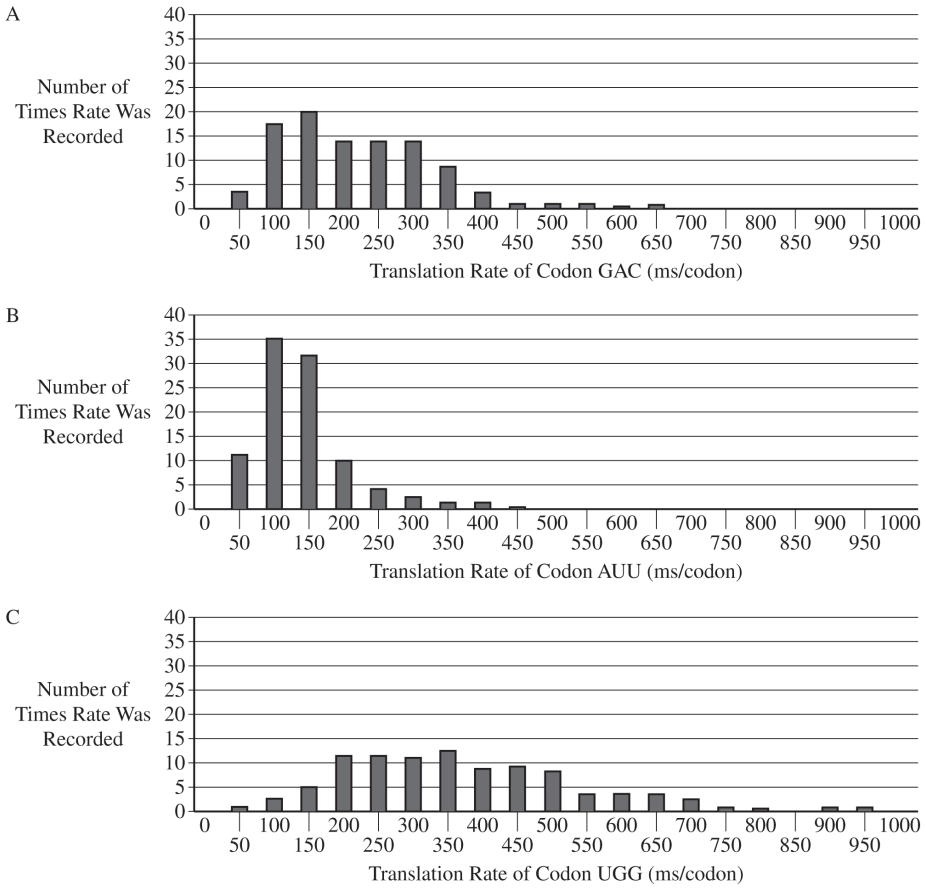


Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG

(a) Using the data in Figure 1, graph A, **identify** the rate (in ms/codon) that was recorded the greatest number of times for the GAC codon.

(b) Using the data in Figure 1, graphs B and C, **describe** the variation in translation rate of the AUU codon compared with that of the UGG codon.

(c) Scientists hypothesize that tRNA molecules that bind to UGG codons are available in lower abundance than are tRNAs that bind to AUU codons. **Support** the scientists' hypothesis using the data in Figure 1.

(d) Amino acids can be encoded by multiple codons. In many organisms, certain codons for the same amino acid occur more frequently in an mRNA than do other codons. Based on the data provided, **explain** why the use of one codon over another for the same amino acid might result in increased levels of protein production from a particular mRNA.

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.

STOP

END OF EXAM

6. Housekeeping genes encode proteins involved in universally important processes such as transcription, translation, and glycolysis. Because these genes appear to be expressed in all cells at constant levels, the expression of housekeeping genes is often used as a control when comparing how the expression of other genes varies under different conditions.

   Researchers studying the effect of pesticides on declining bee populations wanted to determine whether the expression of four housekeeping genes (*GAPDH*, *RPL32*, *RPS5*, and *TBP-AF*) was in fact constant in bees across different variables. The researchers collected samples of mRNA for each of the four genes and compared how their expression varied across the developmental stage of the bee, the sex of the bee, and the cell type from which the sample was taken. The mRNA from the samples was reverse transcribed to produce DNA copies of each gene. PCR was then used to amplify the DNA, and the Cq value was determined. The Cq value is the number of PCR cycles needed to produce a specified number of DNA copies. A high Cq value for a sample indicates the gene was expressed at a low level.

   To analyze whether any of the examined variables affected expression of the housekeeping genes, researchers examined the range of Cq values for each gene in response to each variable. Genes with a wide range of Cq values were determined to be affected by the variable, while genes with a narrow range of Cq values were determined to be unaffected by the variable.

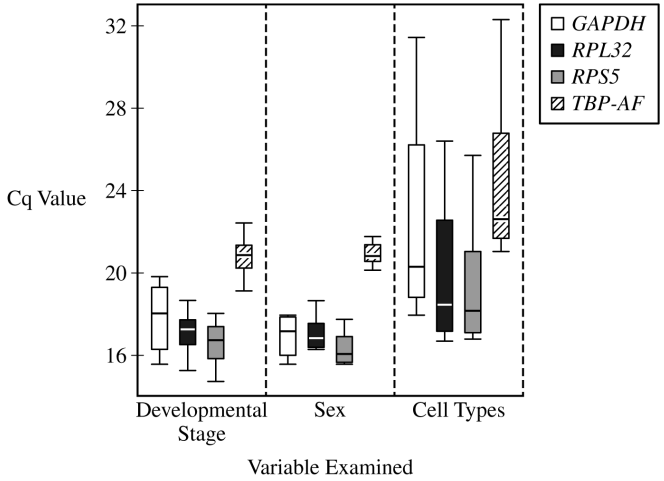


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

(a) Based on the data in Figure 1, **identify** the gene that had the lowest median Cq value when bees of different developmental stages were compared.

(b) The Cq value is inversely proportional to the amount of mRNA from that gene in the starting sample. Based on the data in Figure 1, **identify** the gene that has the lowest level of gene expression regardless of variable.

(c) The scientists investigated the effect of pesticides on the expression of other genes in one cell type of a group of bees containing males and females of the same developmental stage. They hypothesized that *TBP-AF* would serve as the best control gene for this experiment. Use the data to **evaluate** their hypothesis.

(d) **Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee.

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

STOP

END OF EXAM

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

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

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

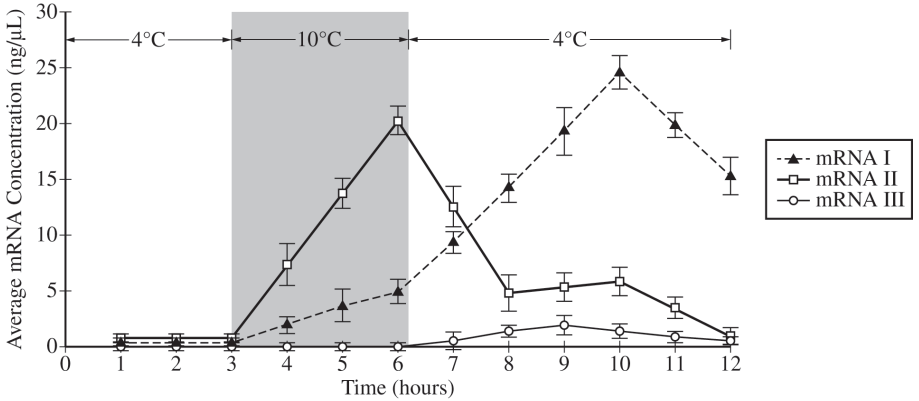


Figure 1. Average concentration of three mRNAs (I, II, III) transcribed from *hsp* genes in krill heat shocked at 10°C. Error bars represent $\pm 2SE_{\bar{x}}$.

(a) **Identify** the *hsp* mRNA that has the slowest rate of concentration increase in response to heat-shock treatment.

(b) **Describe** the trend in the average concentration of mRNA I throughout the experiment.

(c) The scientists hypothesized that the heat-shock protein (HSP) translated from mRNA I plays a greater role in refolding proteins than does the HSP translated from mRNA II. Use the data to **support** the hypothesis.

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

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

STOP

END OF EXAM

7. A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

mRNA EXPRESSION LEVELS

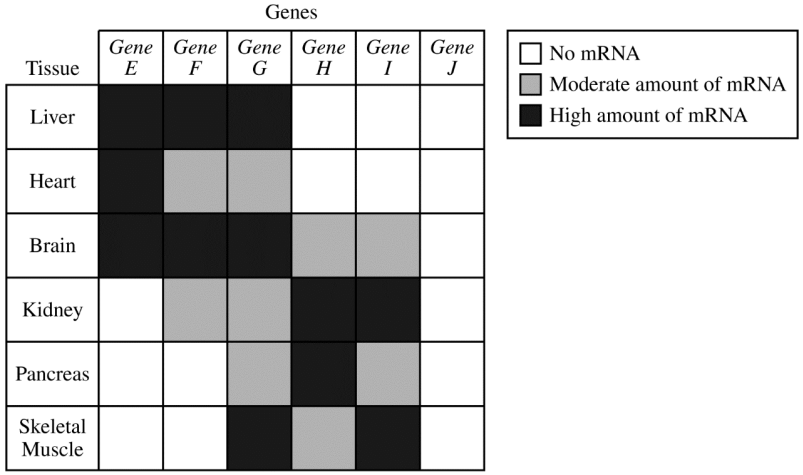


Figure 1. mRNA expression levels of six genes

(a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.

(b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.

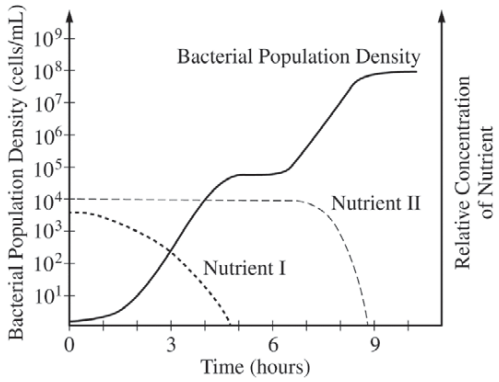


Figure 1. Bacterial population growth in the presence of two nutrients (nutrient I and nutrient II)

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

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

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

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

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

AP Biology: **2015**

7. Smell perception in mammals involves the interactions of airborne odorant molecules from the environment with receptor proteins on the olfactory neurons in the nasal cavity. The binding of odorant molecules to the receptor proteins triggers action potentials in the olfactory neurons and results in transmission of information to the brain. Mammalian genomes typically have approximately 1,000 functional odorant-receptor genes, each encoding a unique odorant receptor.

(a) **Describe** how the signal is transmitted across the synapse from an activated olfactory sensory neuron to the interneuron that transmits the information to the brain.

(b) **Explain** how the expression of a limited number of odorant receptor genes can lead to the perception of thousands of odors. Use the evidence about the number of odorant receptor genes to **support** your answer.

AP BIOLOGY • EXERCISE SHEET

6.6 Gene Expression and Cell Specialization

Name: _____ Class: _____ Date: _____ **Total: 9 marks**

KEY WORDS differentiation 分化 • ribosome 核糖体

Objective

Build the skills to answer exam questions on **gene expression and cell specialization**.

You must be able to:

- explain that specialized cells express **different genes** from the same genome
- describe **differentiation** 分化
- link expressed genes to a cell's structure and function

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.

■ Same genome, different genes on

Every body cell has the **same DNA**, yet a nerve cell and a muscle cell look and act differently. This is because they express **different subsets** of genes.

■ Differentiation

Differentiation is the process by which an unspecialized cell becomes specialized, by switching on the genes for that cell type and switching off others.

■ Genes shape structure and function

A muscle cell expresses genes for contractile proteins; a pancreatic cell expresses the insulin gene. The **genes turned on** determine the cell's proteins, structure, and job.

■ A worked example

A red blood cell expresses the hemoglobin gene strongly (to carry oxygen); a skin cell does not — same DNA, different expression.

2 Practice

Now apply the methods above.

2.1 Do specialized cells in one body have the same or different DNA? [1]

2.2 What is differentiation? [1]

2.3 Why does a muscle cell differ from a nerve cell? [1]

3 Exam-style questions

3.1 Two cells in the same organism differ mainly because they [1]

- **A** have different DNA
- **B** express different genes
- **C** have no genes
- **D** lack ribosomes

3.2 A stem cell becomes a specialized muscle cell.

(a) Name this process. [1]

(b) Explain how the same genome produces a specialized cell. [2]

3.3 Explain why a pancreatic cell makes insulin but a skin cell does not, even though both have the insulin gene. [2]

Solutions

2.1 The same DNA.

2.2 The process by which an unspecialized cell becomes specialized.

2.3 They express different genes.

3.1 B — express different genes.

3.2 (a) Differentiation. (b) The cell switches on the genes needed for the muscle-cell type and switches off others, so the same DNA yields a specialized cell.

3.3 Both have the gene, but only the pancreatic cell expresses (transcribes and translates) it; in the skin cell the insulin gene is switched off.

6. Housekeeping genes encode proteins involved in universally important processes such as transcription, translation, and glycolysis. Because these genes appear to be expressed in all cells at constant levels, the expression of housekeeping genes is often used as a control when comparing how the expression of other genes varies under different conditions.

   Researchers studying the effect of pesticides on declining bee populations wanted to determine whether the expression of four housekeeping genes (*GAPDH*, *RPL32*, *RPS5*, and *TBP-AF*) was in fact constant in bees across different variables. The researchers collected samples of mRNA for each of the four genes and compared how their expression varied across the developmental stage of the bee, the sex of the bee, and the cell type from which the sample was taken. The mRNA from the samples was reverse transcribed to produce DNA copies of each gene. PCR was then used to amplify the DNA, and the Cq value was determined. The Cq value is the number of PCR cycles needed to produce a specified number of DNA copies. A high Cq value for a sample indicates the gene was expressed at a low level.

   To analyze whether any of the examined variables affected expression of the housekeeping genes, researchers examined the range of Cq values for each gene in response to each variable. Genes with a wide range of Cq values were determined to be affected by the variable, while genes with a narrow range of Cq values were determined to be unaffected by the variable.

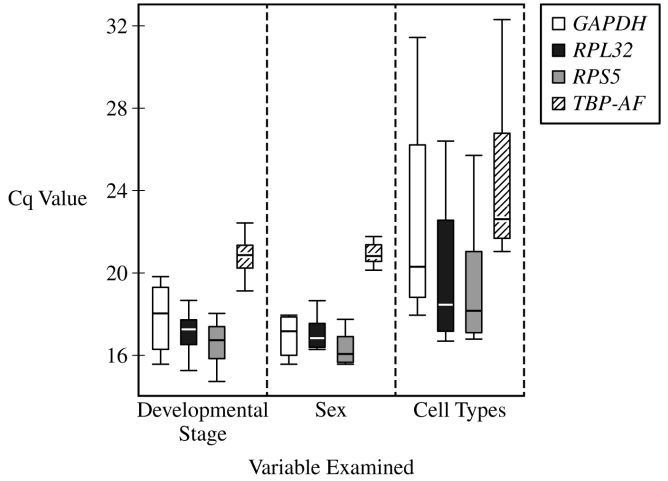


Figure 1. The effect of developmental stage, sex, and cell type on the Cq value of four housekeeping genes

(a) Based on the data in Figure 1, **identify** the gene that had the lowest median Cq value when bees of different developmental stages were compared.

(b) The Cq value is inversely proportional to the amount of mRNA from that gene in the starting sample. Based on the data in Figure 1, **identify** the gene that has the lowest level of gene expression regardless of variable.

(c) The scientists investigated the effect of pesticides on the expression of other genes in one cell type of a group of bees containing males and females of the same developmental stage. They hypothesized that *TBP-AF* would serve as the best control gene for this experiment. Use the data to **evaluate** their hypothesis.

(d) **Explain** how expression of a gene such as *GAPDH* can vary from one cell type to another within the same bee.

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

STOP

END OF EXAM

7. A researcher is studying patterns of gene expression in mice. The researcher collected samples from six different tissues in a healthy mouse and measured the amount of mRNA from six genes. The data are shown in Figure 1.

mRNA EXPRESSION LEVELS

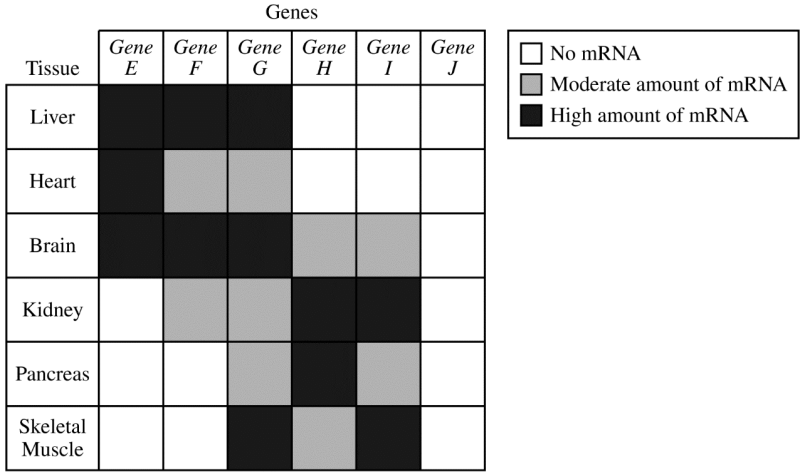


Figure 1. mRNA expression levels of six genes

(a) Based on the data provided, **identify** the gene that is most likely to encode a protein that is an essential component of glycolysis. **Provide reasoning** to support your identification.

(b) The researcher observed that tissues with a high level of *gene H* mRNA did not always have gene H protein. **Provide reasoning** to explain how tissues with high *gene H* mRNA levels can have no gene H protein.

7. Smell perception in mammals involves the interactions of airborne odorant molecules from the environment with receptor proteins on the olfactory neurons in the nasal cavity. The binding of odorant molecules to the receptor proteins triggers action potentials in the olfactory neurons and results in transmission of information to the brain. Mammalian genomes typically have approximately 1,000 functional odorant-receptor genes, each encoding a unique odorant receptor.

   (a) **Describe** how the signal is transmitted across the synapse from an activated olfactory sensory neuron to the interneuron that transmits the information to the brain.

   (b) **Explain** how the expression of a limited number of odorant receptor genes can lead to the perception of thousands of odors. Use the evidence about the number of odorant receptor genes to **support** your answer.

AP BIOLOGY • EXERCISE SHEET

6.7 Mutations

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS mutation 突变 • frameshift 移码 • point mutations 点突变 • codons 密码子

Objective

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

You must be able to:

- describe **point mutations** 点突变 (substitution) and **frameshift** 移码 (insertion/deletion)
- explain silent, missense, and nonsense effects
- link mutations to variation and disease

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.

Types of mutation

A **mutation** is a change in the DNA sequence:

- **Substitution** (point) — one base is swapped.
- **Insertion / deletion** — bases are added or removed, causing a **frameshift** that changes every codon after it.

Effects of a substitution

- **Silent** — the codon still codes for the same amino acid (no change).
- **Missense** — a different amino acid is used (protein may work worse).
- **Nonsense** — a stop codon appears early, cutting the protein short.

Frameshift is severe

An insertion or deletion (not a multiple of three) shifts the **reading frame**, so all downstream codons change — usually ruining the protein.

Consequences

Mutations create **variation** (raw material for evolution) but can also cause disease (e.g. sickle-cell from a single substitution).

2 Practice

Now apply the methods above.

2.1 What is a point mutation? [1]

2.2 What kind of mutation shifts the reading frame? [1]

2.3 What is a silent mutation? [1]

3 Exam-style questions

3.1 A substitution that creates an early stop codon is a [1]

- **A** silent mutation
- **B** missense mutation
- **C** nonsense mutation
- **D** frameshift

3.2 A single base is deleted near the start of a gene.

(a) Name the type of mutation and its effect on the reading frame. [2]

(b) Explain why this is usually more damaging than a single substitution. [2]

3.3 Explain how mutations can be both harmful and a source of useful variation. [2]

Solutions

2.1 A change in a single DNA base (substitution).

2.2 An insertion or deletion (frameshift).

2.3 A base change that does not change the amino acid coded.

3.1 C — a nonsense mutation.

3.2 (a) A frameshift (deletion); it shifts the reading frame so all following codons change. (b) A substitution changes at most one amino acid, but a frameshift changes every downstream codon, usually ruining the whole rest of the protein.

3.3 Harmful mutations can disrupt a protein and cause disease, but mutations also create new alleles (variation) that natural selection can act on, sometimes benefiting the organism.

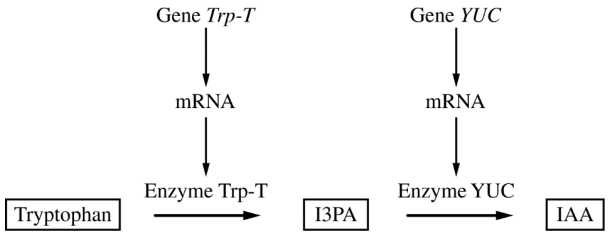


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

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.

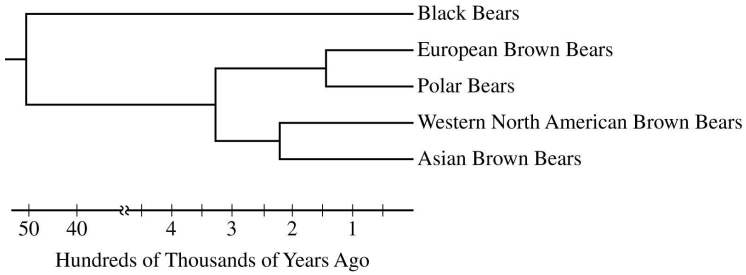


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

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	–

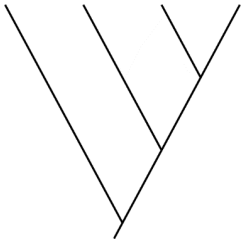
(a) Use the phylogenetic tree in Figure 1 to **estimate** the age in hundreds of thousands of years of the most recent common ancestor of all brown bears. **Identify** the population of brown bears to which polar bears are most closely related based on the mitochondrial DNA sequence comparison. **Identify** 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.



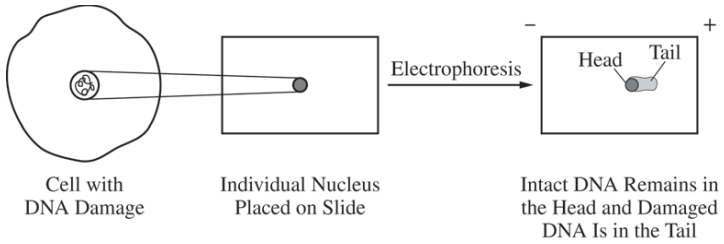


Figure 1. Comet assay to detect double-stranded breaks in DNA

6. A comet assay is a technique used to determine the amount of double-strand breaks in DNA (DNA damage) in cells. The nucleus of an individual cell is placed on a microscope slide coated with an agarose gel. An electric current is applied to the gel that causes DNA to move (electrophoresis), and the DNA is stained with a fluorescent dye. When viewed using a microscope, undamaged DNA from the nucleus appears as a round shape (the head), and the fragments of damaged DNA extend out from the head (the tail). The length of the tail corresponds to the amount of the damage in the DNA (see Figure 1).

   (a) To explain the movement of DNA fragments in the comet assay, **identify** one property of DNA and **provide reasoning** to support how the property contributes to the movement during the comet assay technique.

   (b) In a different experiment, cells are treated with a chemical mutagen that causes only nucleotide substitutions in DNA. **Predict** the likely results of a comet assay for this treatment.

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.

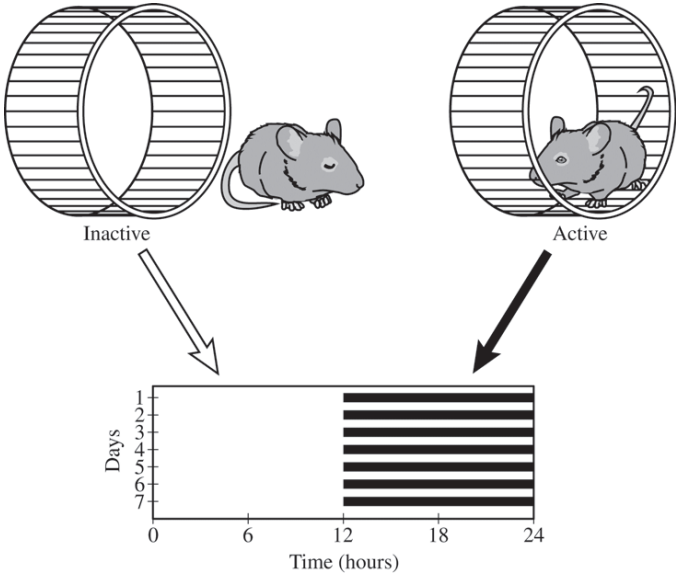


Figure 1. Strategy for recording mouse activity data. When a mouse is active on the running wheel, the activity is recorded as a dark horizontal line on an actogram. When the mouse is inactive, no dark line is recorded.

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.

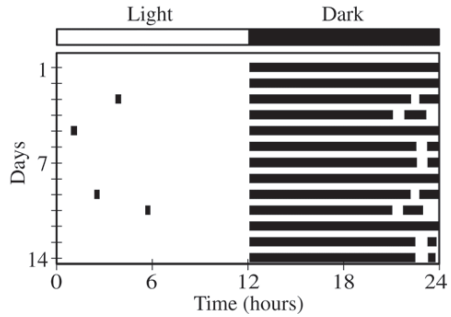


Figure 2. Actogram of mouse activity under L12:D12 conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

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.

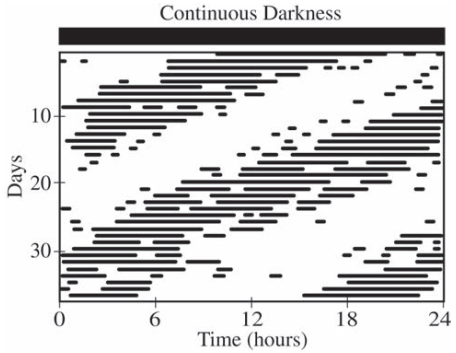


Figure 3. Actogram of mouse activity under DD conditions. Each row represents a 24-hour period, and the dark horizontal lines represent activity on the running wheel.

(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.

AP Biology: **2014**

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

AP BIOLOGY • EXERCISE SHEET

6.8 Biotechnology

Name: _____ Class: _____ Date: _____ **Total: 10 marks**

KEY WORDS pcr 聚合酶链式反应 • gel electrophoresis 凝胶电泳 • genetic engineering 基因工程 • biotechnology 生物技术 • codons 密码子

Objective

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

You must be able to:

- describe **PCR** 聚合酶链式反应, **gel electrophoresis** 凝胶电泳, and **genetic engineering** 基因工程
- state what each technique is used for
- interpret a simple gel result

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.

■ PCR

PCR (polymerase chain reaction) makes **many copies** of a DNA segment. Cycles of heating and cooling with a polymerase double the DNA each cycle — useful when only a tiny sample exists.

■ Gel electrophoresis

Gel electrophoresis separates DNA fragments by **size**. An electric field pulls the negatively charged DNA through a gel; **smaller** fragments move **farther**. It produces a pattern of bands.

■ Reading a gel

Bands nearer the far end are smaller fragments; matching band patterns between samples suggest a match (used in DNA fingerprinting/forensics).

■ Genetic engineering

Genetic engineering inserts a gene from one organism into another (using a vector like a plasmid), e.g. putting the human insulin gene into bacteria so they make insulin.

2 Practice

Now apply the methods above.

2.1 What does PCR do? [1]

2.2 What property separates DNA in gel electrophoresis? [1]

2.3 Which fragments travel farther in a gel? [1]

3 Exam-style questions

3.1 Gel electrophoresis separates DNA fragments according to their [1]

- **A** color
- **B** size
- **C** base sequence only
- **D** temperature

3.2 Bacteria are engineered to produce human insulin.

(a) Name the technique used to insert the human gene. [1]

(b) Explain why bacteria can make a human protein from this gene. [2]

3.3 A crime-scene DNA sample is tiny. Explain how PCR and gel electrophoresis together could help identify a suspect. [3]

Solutions

2.1 Makes many copies of a DNA segment.

2.2 Size (length) of the fragments.

2.3 The smaller fragments.

3.1 B — size.

3.2 (a) Genetic engineering (using a plasmid/vector). (b) The genetic code is universal, so the bacterium's ribosomes read the human gene's codons and translate it into human insulin.

3.3 PCR amplifies the tiny sample into many copies; gel electrophoresis separates the DNA into a band pattern; matching the pattern to a suspect's DNA can identify them.

6. Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

   When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

5′ Cap Structure	mRNA Half-Life $\pm 2SE_{\bar{x}}$ (hours after introduction into cells)	Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{x}}$ (relative to amount in normal cap)
No cap	1.41 ± 0.02	0.011 ± 0.000
Normal GTP cap	16.10 ± 1.83	1.000 ± 0.007
Modified cap I	15.50 ± 1.57	4.777 ± 0.042
Modified cap II	27.00 ± 2.85	13.094 ± 0.307
Modified cap III	18.09 ± 0.81	6.570 ± 0.075

(a) Based on the data, **identify** which cap structure is most likely to protect the end of the mRNAs from degradation.

(b) Based on the data for the mRNAs with modified caps, **describe** the relationship between the mRNA half-life and the total amount of protein produced.

(c) After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. **Evaluate** their hypothesis by comparing the data in Table 1.

(d) Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. **Explain** why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells.

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

STOP

END OF EXAM

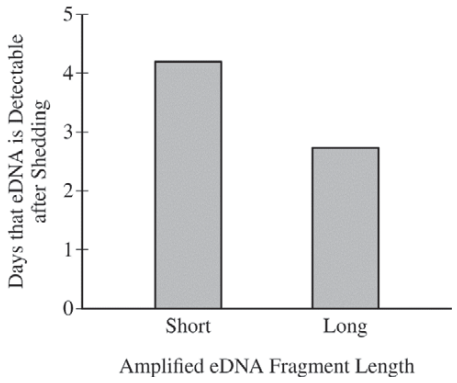


Figure 1. Detectability of eDNA fragments of varying lengths

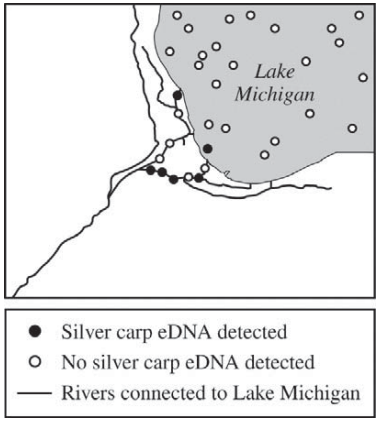


Figure 2. Map of the waterways that connect a nearby river system to Lake Michigan

6. Living and dead organisms continuously shed DNA fragments, known as eDNA, into the environment. To detect eDNA fragments in the environment, the polymerase chain reaction (PCR) can be used to amplify specific eDNA fragments. eDNA fragments of different lengths persist in the environment for varying amounts of time before becoming undetectable (Figure 1).

   To investigate whether silver carp, an invasive fish, have moved from a nearby river system into Lake Michigan, researchers tested water samples for the presence of eDNA specific to silver carp (Figure 2).

   (a) **Justify** the use of eDNA sampling as an appropriate technique for detecting the presence of silver carp in an environment where many different species of fish are found. **Propose** ONE advantage of identifying long eDNA fragments as opposed to short fragments for detecting silver carp.

   (b) The researchers tested a large number of water samples from Lake Michigan and found eDNA specific to silver carp in a single sample in the lake, as indicated in Figure 2. The researchers concluded that the single positive sample was a false positive and that no silver carp had entered Lake Michigan. **Provide reasoning** other than human error to support the researchers' claim.