

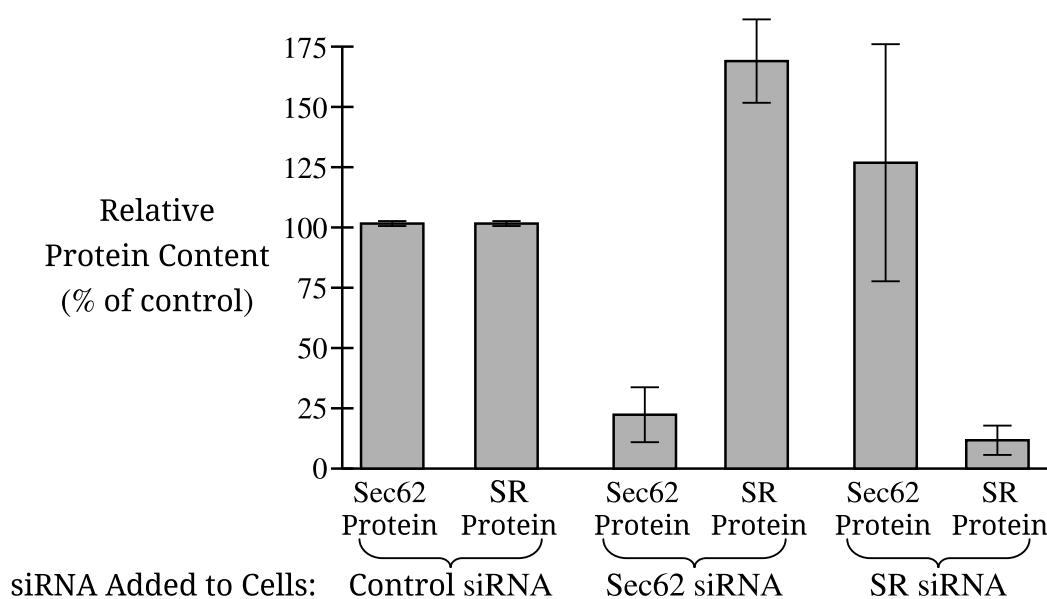
1. Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

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 $\pm SE_{\bar{x}}$.

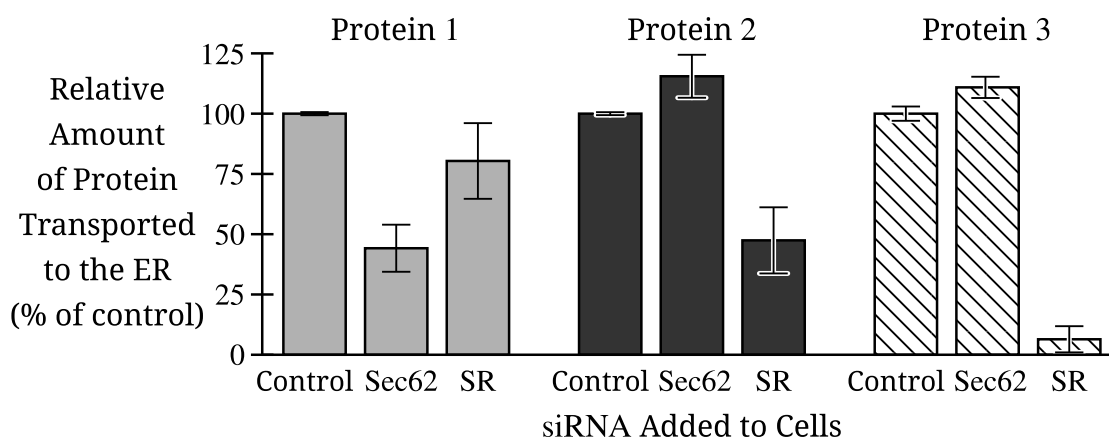


B.

- Identify** the dependent variable in the experiments shown in Figure 1.
- 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).
- 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.

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

- 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.
- 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).

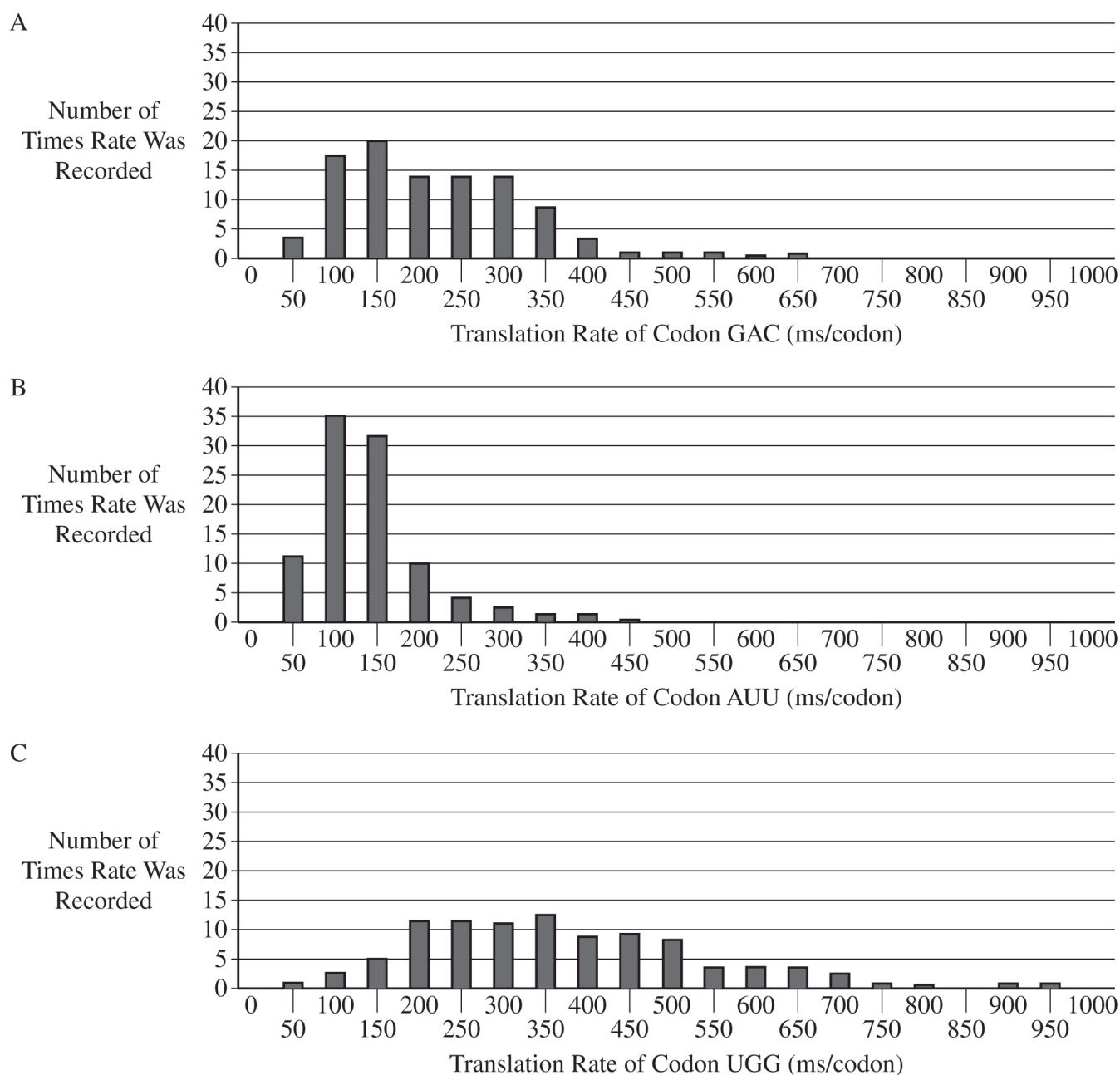


Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG

- (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.

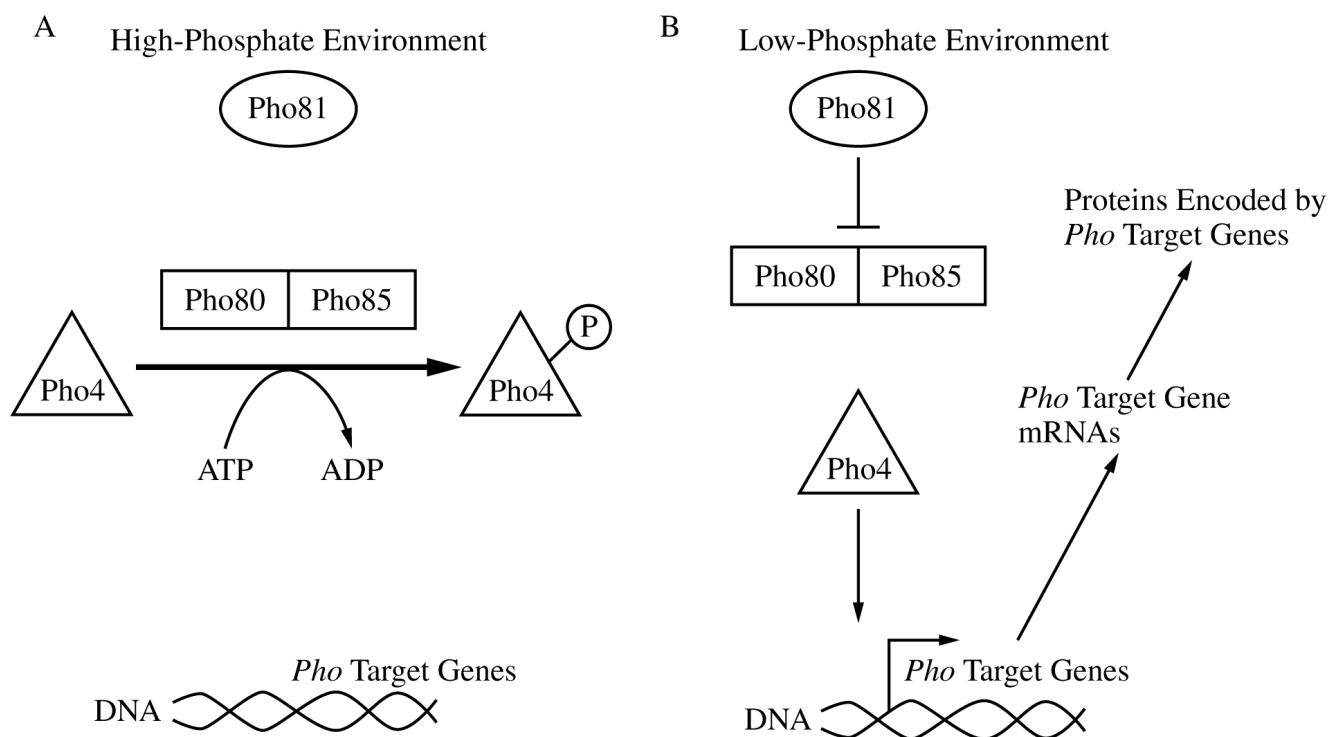


Figure 1. A simplified model of the regulation of expression of *Pho* target genes in (A) a high-phosphate (high-Pi) environment and (B) a low-phosphate (low-Pi) environment

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 <i>PHO1</i> mRNA in High-Pi Environment $\pm 2SE_{\bar{x}}$	Relative Amounts of <i>PHO1</i> 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
<i>pho81mt</i>	Nonfunctional Pho81	0.4 ± 0.1	0.6 ± 0.1	0.7 ± 0.2	0.9 ± 0.8
<i>pho4mt</i>	Nonfunctional Pho4	0.5 ± 0.0	0.8 ± 0.2	0.6 ± 0.4	0.3 ± 0.1

- (a) **Describe** the effect that the addition of a charged phosphate group can have on a protein that would cause the protein to become inactive. **Explain** how a signal can be amplified during signal transduction in a pathway such as the PHO signaling pathway.
- (b) Based on Table 1, **identify** a dependent variable in the researchers' experiment. **Justify** the researchers' using the wild-type strain for the creation of the mutant strains. **Justify** the researchers' using mutant strains in which only a single component of the pathway was mutated in each strain.
- (c) Based on the data in Table 1, **identify** the yeast strain and growth conditions that lead to the highest relative amount of *PHO1* mRNA. **Calculate** the percent change in APase activity in wild-type yeast cells in a high-Pi environment compared with that of wild-type cells in a low-Pi environment.
- (d) In a follow-up experiment, researchers created a strain of yeast with a mutation that resulted in a nonfunctional Pho85 protein. Based on Figure 1, **predict** the effects of this mutation on *PHO1* expression in the mutant strain in a high-Pi environment. Provide reasoning to **justify** your prediction.

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

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.

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END OF EXAM

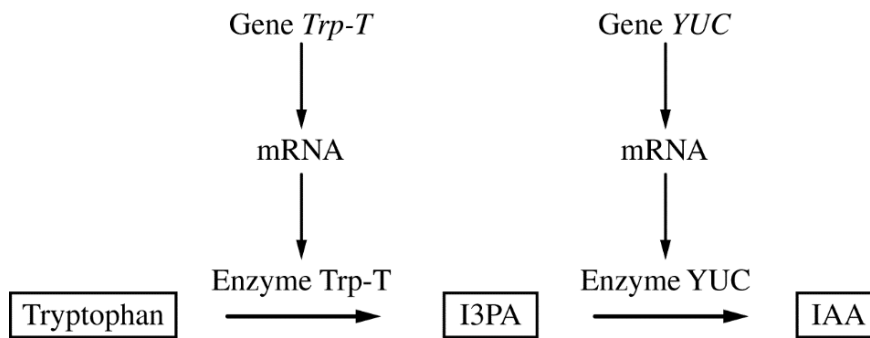


Figure 1. Model of two-step enzymatic plant pathway for synthesis of IAA from tryptophan

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 F₁ generation are tall. When the F₁ plants are crossed with each other, 75 percent of the plants in the F₂ generation are tall and 25 percent of the plants are short.

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