2024

# AP® Biology

## Scoring Guidelines

## Question 1: Interpreting and Evaluating Experimental Results with Experimental Design — 9 points

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

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

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

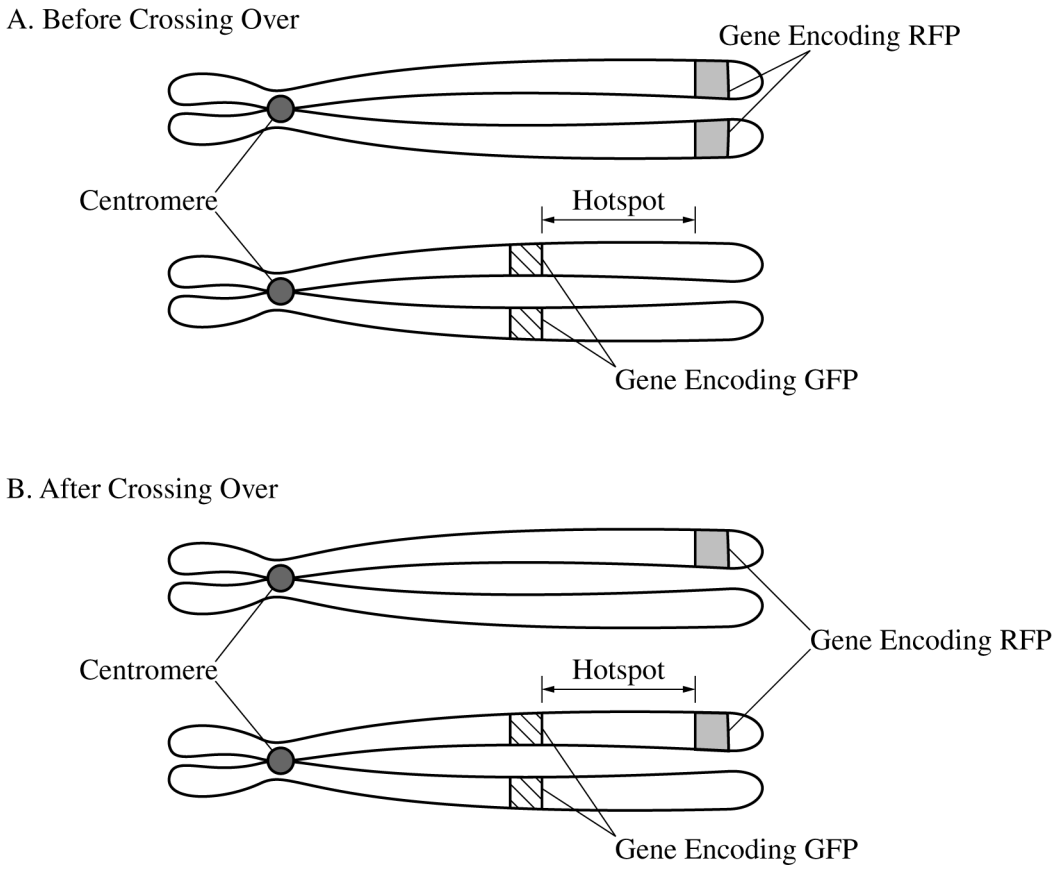



Figure 1. Models of modified chromosome 8 used in the experiment (A) before and (B) after crossing over occurs at the hotspot

The scientists then investigated whether attaching individual kinetochore proteins to a specific DNA sequence present in a known crossing-over hotspot on chromosome 8 affected the frequency of crossing

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

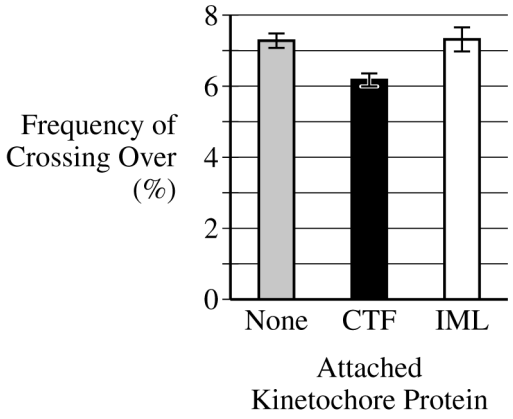



Figure 2. The frequency of crossing over in a hotspot on yeast chromosome 8 for cell groups treated with different kinetochore proteins. Error bars represent $\pm 2\mathrm{SE}_{\bar{X}}$.

| | | |
|---|---|---|
| **(a)** | **Describe** the function of S phase of interphase.<br>Accept one of the following:<br>• (The function of S phase is to) replicate/duplicate/synthesize the DNA/chromosomes.<br>• (The function of S phase is to) double the amount of DNA. | **1 point** |
| | **Explain** why some haploid cells formed after meiosis in this experiment will have only one fluorescent marker.<br>Accept one of the following:<br>• Some cells will receive a chromosome/(sister) chromatid that did not undergo crossing over/recombination (in the hotspot).<br>• Two (or a multiple of two) crossing-over events occurred (in the hotspot).<br>• Each daughter cell will receive one of the four sister chromatids. Two of the sister chromatids shown in Figure 1 have only one fluorescent protein gene.<br>• The two chromosomes that were not involved in crossing over will have only the RFP gene or the GFP gene. After meiosis II, a gamete with one of these chromosomes will have only the RFP or the GFP gene. | **1 point** |
| | | **Total for part (a) 2 points** |
| **(b)** | **Identify** the control group for the scientists' first experiment, shown in Figure 2.<br>Accept one of the following:<br>• Group 1<br>• (The group called) None<br>• Cells with no (kinetochore) protein (attached to the chromosome) | **1 point** |

| | | |
|---|---|---|
| | In a follow-up experiment, the scientists created a modified version of CTF in which the DNA-binding portion had been removed. They compared the frequency of crossing over in yeast cells in the presence and absence of unmodified CTF with that in yeast cells in the presence and absence of the modified CTF protein (data not shown). In the follow-up experiment, **justify** why the scientists used a modified CTF protein that is unable to bind to DNA as a control.<br>Accept one of the following:<br>• (Using a modified CTF enabled the scientists) to determine whether DNA binding of the CTF/kinetochore protein affects/inhibits crossing over/recombination.<br>• (Using a modified CTF enabled the scientists) to determine whether just the presence of the CTF/kinetochore protein is enough to affect/inhibit the crossing over/recombination frequency. | **1 point** |
| | **Identify** the independent variable in the follow-up experiment.<br>Accept one of the following:<br>• The type of CTF used<br>• The presence or absence of (modified/unmodified) CTF | **1 point** |
| | | **Total for part (b) 3 points** |
| **(c)** | Based on Figure 2, **describe** the effect on the frequency of crossing over when CTF is attached to the chromosome 8 hotspot compared with the effect when IML is attached to the hotspot.<br>Accept one of the following:<br>• CTF attachment results in a decreased/lower frequency of crossing over/recombination, (whereas IML had no effect).<br>• IML attachment results in an increased/a higher frequency of crossing over/recombination (compared with CTF attachment). | **1 point** |
| **(d)** | **Predict** the effect on the number of copies of chromosome 8 likely to be present in the resulting daughter cells when CTF is attached to the hotspot.<br>Accept one of the following:<br>• There will be zero/two (copies).<br>• There will be one less/one extra (copy). | **1 point** |
| | Provide reasoning to **justify** your prediction.<br>• Cells (with attached CTF molecules) undergo crossing over/recombination at a lower frequency, so it is more likely that nondisjunction would occur/chromosomes would not separate properly. | **1 point** |
| | **Explain** how the presence of hotspots (Figure 1) could increase the likelihood that a population will survive in the presence of selective pressures.<br>• Hotspots would increase genetic diversity; therefore, it would be more likely that some individuals would survive and reproduce. | **1 point** |
| | | **Total for part (d) 3 points** |
| | | **Total for question 1 9 points** |

## Question 2: Interpreting and Evaluating Experimental Results with Graphing — 9 points

To investigate how increases in environmental temperatures affect the metabolism of certain organisms, researchers incubated liver cells from toads at different temperatures and measured two markers of metabolic activity (Table 1): the rate of oxygen consumption and the rate of ATP synthesis.

TABLE 1. RATE OF OXYGEN CONSUMPTION AND ATP SYNTHESIS AT DIFFERENT TEMPERATURES

| Metabolic Marker | 20°C | 25°C | 30°C |
|---|---|---|---|
| Rate of Oxygen Consumption ( nmol/min/mg of mitochondrial protein $\pm 2SE_{\bar{X}}$ ) | $12.8 \pm 2.2$ | $16.5 \pm 2.0$ | $22.1 \pm 0.7$ |
| Rate of ATP Synthesis ( nmol/min/mg of mitochondrial protein $\pm 2SE_{\bar{X}}$ ) | $12.6 \pm 1.6$ | $16.8 \pm 2.0$ | $21.07 \pm 0.8$ |

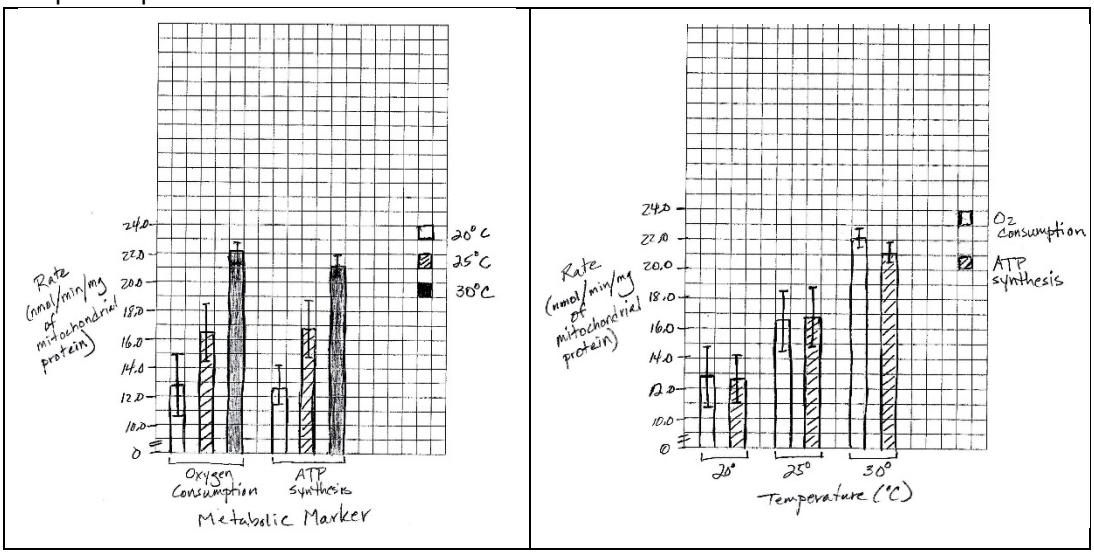
**(a)** **Describe** the role of water in the hydrolysis of ATP. **1 point**

Accept one of the following:

- Water is added in the process of cleaving/splitting (a phosphate from) ATP.
- Water breaks down/splits ATP.

**(b)** Using the template in the space provided for your response, **construct** a bar graph that represents the data shown in Table 1. Your graph should be appropriately plotted and labeled. **1 point**

Sample Responses:




- Data are represented in a bar graph.

Using the template in the space provided for your response, **construct** a bar graph that represents the data shown in Table 1. Your graph should be appropriately plotted and labeled. **1 point**

- Graph is appropriately labeled.

| | | |
|---|---|---|
| | Using the template in the space provided for your response, **construct** a bar graph that represents the data shown in Table 1. Your graph should be appropriately plotted and labeled.<br>• Data points and error bars are correctly plotted. | **1 point** |
| | Based on the data provided, **determine** the temperature in $°C$ at which the rate of oxygen consumption is different from the rate of oxygen consumption at $25°C$.<br>• 30 | **1 point** |
| | | **Total for part (b) 4 points** |
| **(c)** | Based on the data in Table 1, **describe** the effect of temperature on the rate of ATP synthesis in liver cells from toads.<br>Accept one of the following:<br>• As the temperature increases, the rate of ATP synthesis also increases.<br>• There is a positive relationship (between temperature and ATP synthesis).<br>• Temperature and ATP synthesis are directly correlated. | **1 point** |
| | Based on the data in Table 1**, calculate** the average amount of oxygen consumed, in $nmol$, for 10 $mg$ of mitochondrial protein after 10 minutes at $25°C$.<br>1,650 [$16.5\ nmol/min/mg \times 10\ mg \times 10\ min$] | **1 point** |
| | | **Total for part (c) 2 points** |
| **(d)** | Oligomycin is a compound that can block the channel protein function of ATP synthase. **Predict** the effects of using oligomycin on the proton gradient across the inner mitochondrial membrane.<br>Accept one of the following:<br>• (The proton gradient) will increase/become steeper (and may eventually plateau).<br>• The difference in the concentration of protons/pH (across the inner mitochondrial membrane) will increase.<br>• There will be an increase in the concentration of protons/a decrease in pH in the intermembrane space relative to that found within the mitochondrial matrix. | **1 point** |
| | **Justify** your prediction.<br>Accept one of the following:<br>• (Without protons being able to flow back into the matrix through ATP synthase), more protons will accumulate in the intermembrane space/between the two mitochondrial membranes.<br>• (Without protons being able to flow back into the matrix through ATP synthase), there will be a lower pH in the intermembrane space/between the two mitochondrial membranes.<br>• Protons will not be able to flow across the membrane (through ATP synthase), but the electron transport chain will still pump protons into the intermembrane space. | **1 point** |
| | | **Total for part (d) 2 points** |
| | | **Total for question 2 9 points** |

## Question 3: Scientific Investigation — 4 points

To investigate whether red blood cells of animals lose the ability to take in glucose from their environment as they age, scientists collected red blood cells from guinea pigs that ranged in age from one day old to seven months old. Scientists incubated an equal number of red blood cells in separate culture dishes that contained a $300\ \text{nM}$ solution of radioactively labeled glucose. The amount of radioactively labeled glucose present inside the red blood cells of each group was measured over time.

**(a)** **Describe** a difference between passive transport and active transport. **1 point**

Accept one of the following:

- Active transport requires energy/ATP (while passive transport does not).
- Passive transport does not require energy/ATP (while active transport does).
- In passive transport, substances move from a high concentration to a low concentration, (while in active transport substances move from a low concentration to a high concentration).
- In active transport, substances move from a low concentration to a high concentration (while in passive transport substances move from a high concentration to a low concentration).

**(b)** **Justify** why the scientists used an equal number of red blood cells in each culture dish as a control. **1 point**

Accept one of the following:

- (Scientists used an equal number of cells) to attribute differences in results/glucose transport to guinea pig age, (rather than to the number of cells used in the experiment).
- (Scientists used an equal number of cells) to compare results from the different dishes (containing cells from guinea pigs of different ages).
- (Scientists used an equal number of cells) to eliminate the number of cells as a variable (that might affect the amount of glucose in each group).
- (Scientists used an equal number of cells) because the number of cells used might affect the results/amount of glucose (present inside the red blood cells).

**(c)** Glucose transporters are required for the facilitated diffusion of glucose into red blood cells. The scientists claim that the expression of the gene encoding these transporters decreases as guinea pigs age. If the scientists' claim is supported by experimental data, **predict** the effect of increased age on the amount of radioactively labeled glucose present inside the cells of each group. **1 point**

- (As guinea pig age increases) the amount of glucose (inside the cells) decreases.

**(d)** **Justify** your prediction in part (c). **1 point**

- With fewer transporters, fewer glucose molecules will be moved into the cells.

**Total for question 3** **4 points**

## Question 4: Conceptual Analysis — 4 points

The common wild oat is native to regions of Europe and Asia but is an invasive species in central California grasslands. In California, the common wild oat has almost completely replaced some species of native bunchgrass. Researchers found that aphids, a type of small insect that often carries plant viruses, have a much higher reproductive rate in grasslands that include the common wild oat than in grasslands composed of only native bunchgrass species. Additionally, the viruses carried by the aphids appear to affect only the native bunchgrasses and not the common wild oat. Native bunchgrasses infected by the virus have much higher death rates than do native bunchgrasses that are not infected.

| | | |
|---|---|---|
| **(a)** | **Describe** the change in the resilience of an ecosystem when there is a decrease in the number of species.<br>• (The resilience of the ecosystem) will decrease. | **1 point** |
| **(b)** | **Explain** how the addition of the common wild oat affects the number of native bunchgrass plants that can be supported by the California grasslands ecosystem.<br>Accept one of the following:<br>• (The addition of the wild oat) limits the resources available (to the native plants), resulting in a decrease (in the population size).<br>• (The addition of the wild oat) <u>enables the aphid population to increase</u>/<u>increases the exposure to viruses</u>, resulting in a decrease (in the population size of the native bunchgrass). | **1 point** |
| **(c)** | Researchers suggest adding ladybugs, predators of aphids, to the California grasslands. **Predict** the effect of adding ladybugs on the abundance of the native bunchgrass population.<br>• (The native bunchgrass population) will increase (in abundance). | **1 point** |
| **(d)** | **Justify** your prediction in part (c).<br>• (Adding ladybugs) will decrease the number of aphids, which will cause a decrease in the <u>transmission of</u>/<u>infection by</u> plant viruses. | **1 point** |
| | **Total for question 4** | **4 points** |

## Question 5: Analyze Model or Visual Representation of a Biological Concept or Process — 4 points

Researchers study mechanisms that enable or prevent speciation.

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

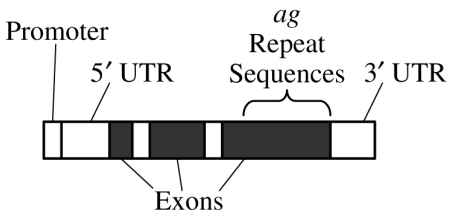
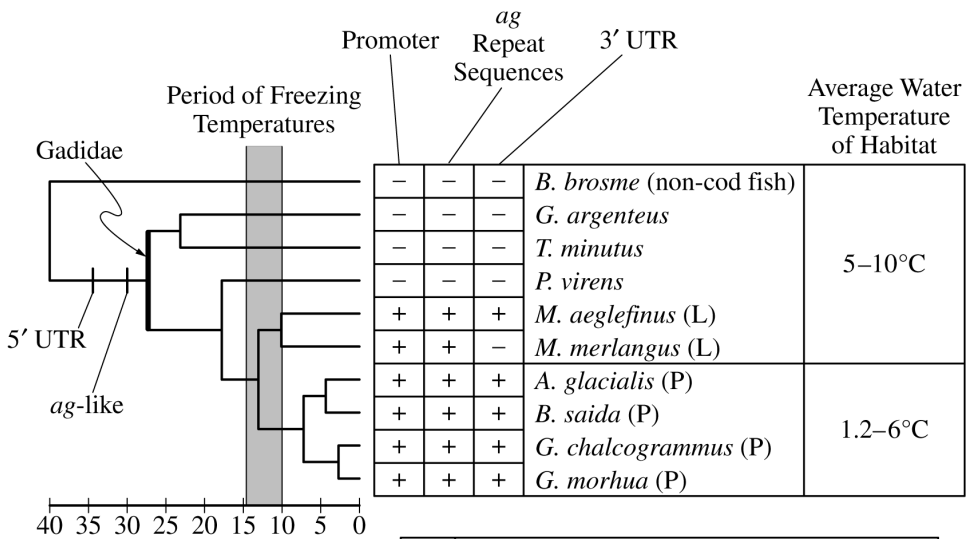



Figure 1. Basic structure of a functional *ag* gene

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




| | | | | |
|---|---|---|---|---|
| – | – | – | *B. brosme* (non-cod fish) | 5–10°C |
| – | – | – | *G. argenteus* | |
| – | – | – | *T. minutus* | |
| – | – | – | *P. virens* | |
| + | + | + | *M. aeglefinus* (L) | |
| + | + | – | *M. merlangus* (L) | |
| + | + | + | *A. glacialis* (P) | 1.2–6°C |
| + | + | + | *B. saida* (P) | |
| + | + | + | *G. chalcogrammus* (P) | |
| + | + | + | *G. morhua* (P) | |

| | |
|---|---|
| – | Element is absent. |
| + | Element is present. |
| L | Functional *ag* genes are lost. |
| P | Functional *ag*-encoded proteins are present. |

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

**(a)** **Describe** a post-zygotic mechanism that prevents gene flow and thus enables speciation. **1 point**

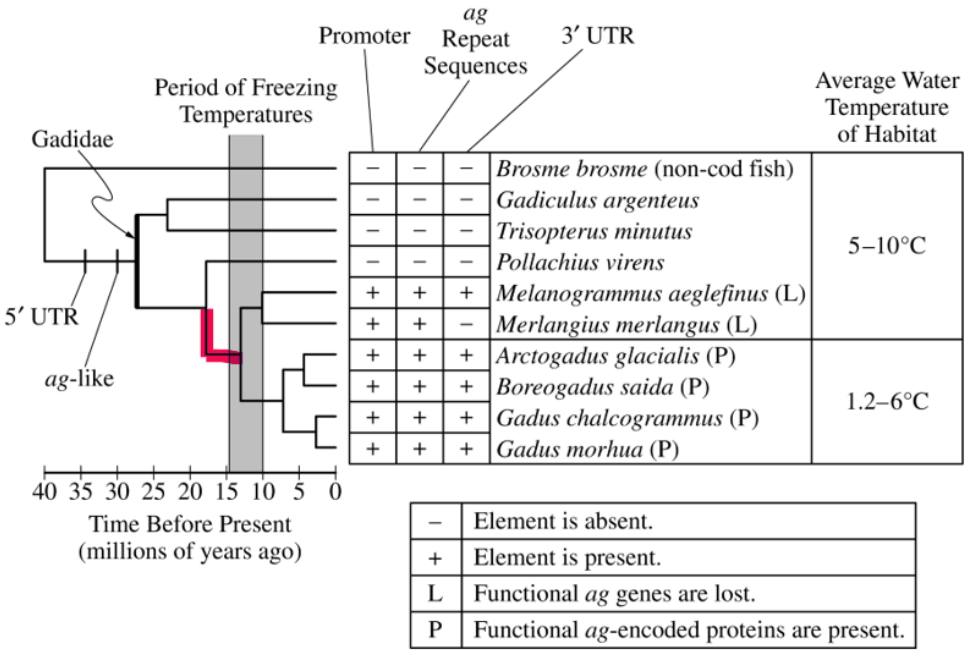
- The offspring do not survive (long enough to reproduce)/cannot (successfully) reproduce.

**(b)** Based on the data in Figure 2, **explain** how changes to the genome enabled cods to survive and reproduce after a period of freezing temperatures between 10 and 15 million years ago. **1 point**

- (Over time) the addition of the promoter/*ag* repeat sequences/3′ UTR/regulatory elements led to emergence of new genes/*ag* genes/functional gene products (that prevent freezing).

**(c)** Using the template in the space provided for your response, place an "X" on the phylogenetic tree to **represent** the origin of the functional *ag* gene. **1 point**

- An X is placed anywhere along the colored L-shaped line in the figure.




| | | | | |
|---|---|---|---|---|
| – | – | – | *Brosme brosme* (non-cod fish) | 5–10°C |
| – | – | – | *Gadiculus argenteus* | |
| – | – | – | *Trisopterus minutus* | |
| – | – | – | *Pollachius virens* | |
| + | + | + | *Melanogrammus aeglefinus* (L) | |
| + | + | – | *Merlangius merlangus* (L) | |
| + | + | + | *Arctogadus glacialis* (P) | 1.2–6°C |
| + | + | + | *Boreogadus saida* (P) | |
| + | + | + | *Gadus chalcogrammus* (P) | |
| + | + | + | *Gadus morhua* (P) | |

| | |
|---|---|
| – | Element is absent. |
| + | Element is present. |
| L | Functional *ag* genes are lost. |
| P | Functional *ag*-encoded proteins are present. |

**(d)** Based on Figure 2, **explain** how genetic differences among the species in the Gadidae family determine the habitats in which they can survive. **1 point**

- Species with the functional *ag* gene/antifreeze glycoprotein are able to live in colder water/lower temperatures (than are species without the functional gene).

**Total for question 5** **4 points**

## Question 6: Analyze Data — 4 points

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).

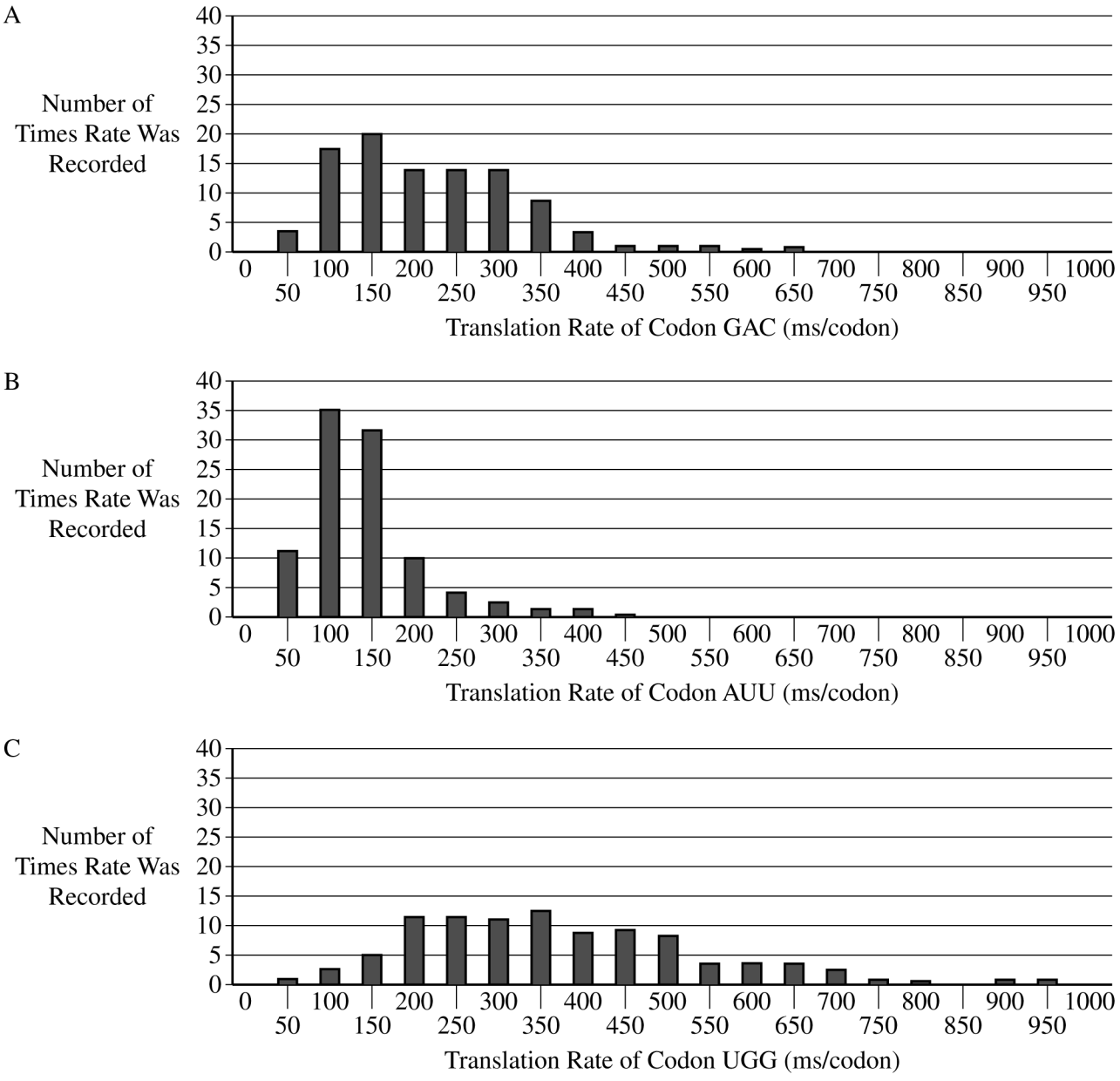



Figure 1. The distribution of translation rates for three different codons (A) GAC, (B) AUU, and (C) UGG

| | | |
|---|---|---|
| **(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.<br>• 150 | **1 point** |
| **(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.<br>Accept one of the following:<br>• There is greater variation in (the translation rate of) UGG codons (than in the translation rate of AUU codons).<br>• (The translation rate of) UGG ranges from 50 (ms/codon) to 950 (ms/codon), while (the translation rate of) AUU ranges from 50 (ms/codon) to 450 (ms/codon). | **1 point** |
| **(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.<br>Accept one of the following:<br>• The (average) translation rate of UGG is slower (than that of AUU).<br>• Translation of UGG takes longer (per codon than does translation of AUU).<br>• More of the UGG codons were translated at slower rates (than AUU codons were). | **1 point** |
| **(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.<br>• Certain codons are translated at faster rates than are others (and result in increased levels of protein production from a particular mRNA). | **1 point** |
| | **Total for question 6** | **4 points** |