

5. Researchers study mechanisms that enable or prevent speciation.

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

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

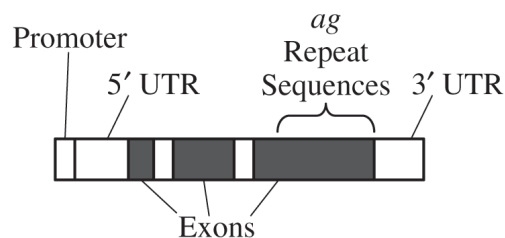


Figure 1. Basic structure of a functional *ag* gene

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

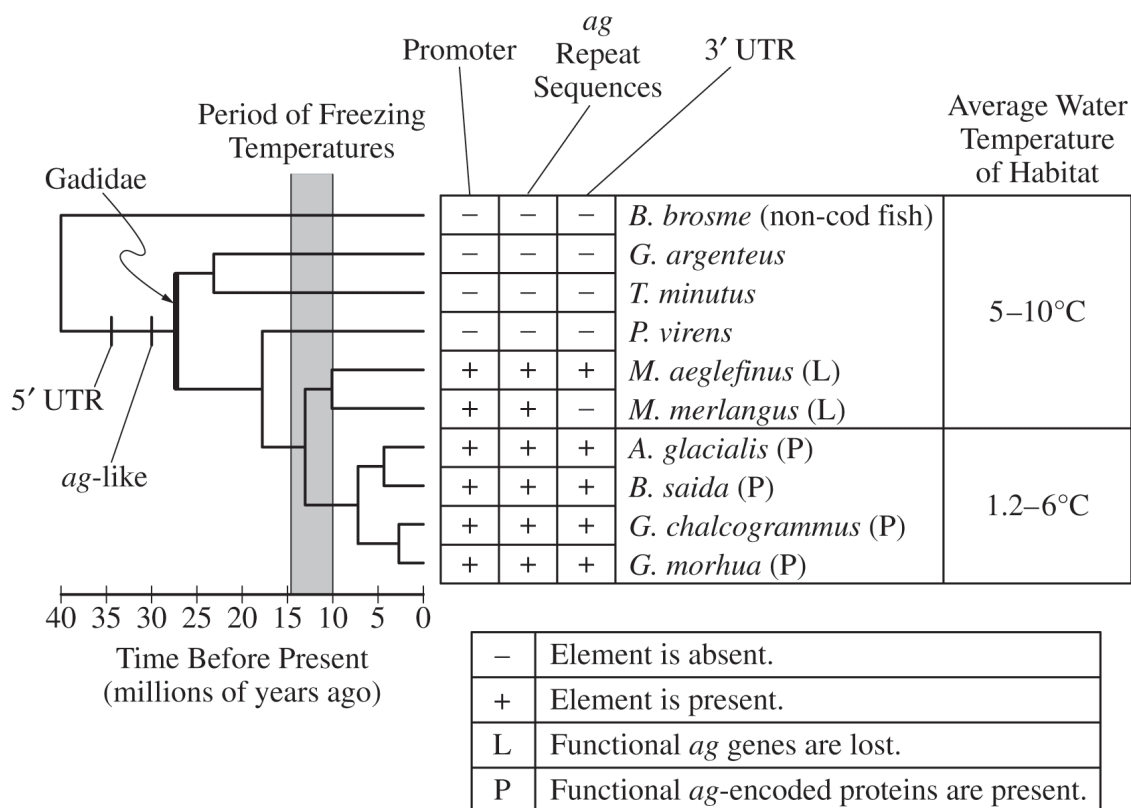


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

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

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

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

5. Ruminants are hoofed animals, including cattle and sheep, that have a unique four-chambered stomach specialized to digest tough, fiber-filled grasses. Researchers studying ruminants are investigating the morphological and molecular characteristics of different ruminant families in order to determine the evolutionary relationships among the families. Cladograms of several ruminant families were constructed based on morphological data (Figure 1A) and molecular data (Figure 1B). Table 1 shows a sample of the morphological characteristics present in each family used to construct the cladogram in Figure 1A.

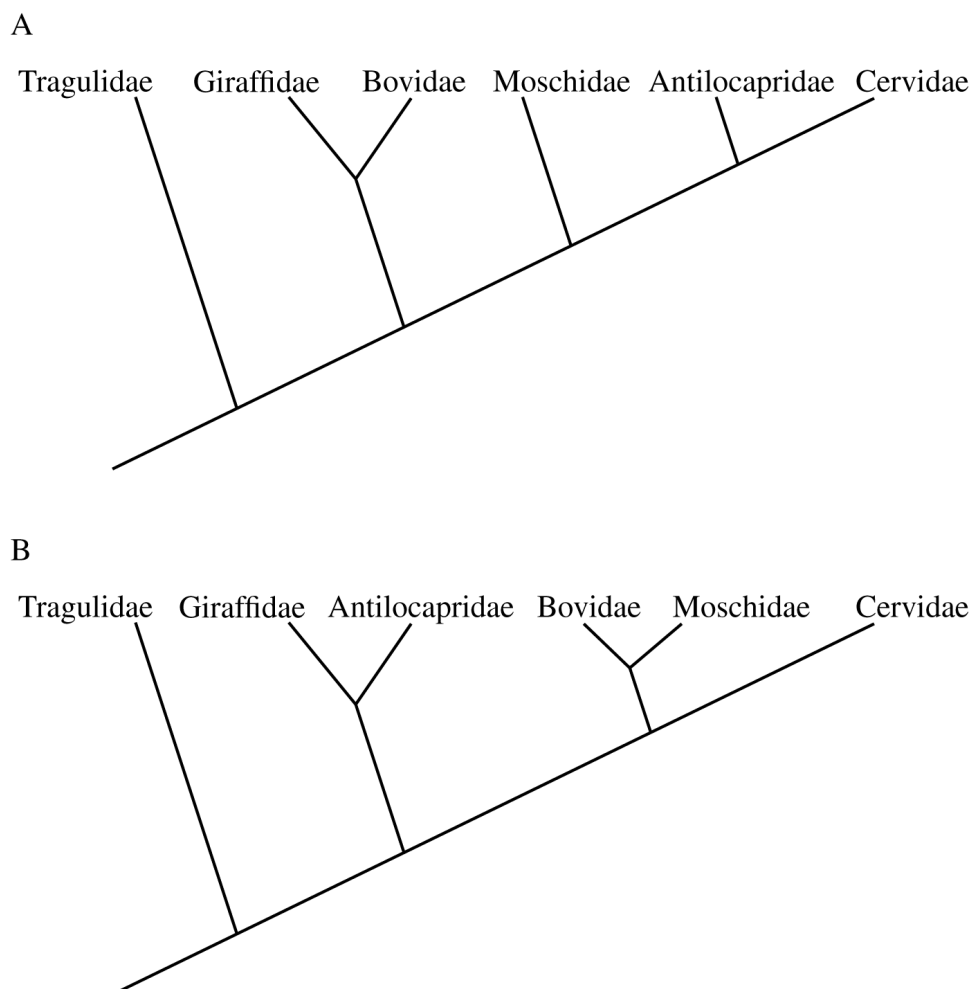


Figure 1. Cladogram of six ruminant families based on (A) morphological data and (B) molecular data

TABLE 1. MORPHOLOGICAL CHARACTERISTICS FOUND IN EACH RUMINANT FAMILY

Characteristic Number	Morphological Characteristic	Tragulidae	Giraffidae	Bovidae	Moschidae	Antilocapridae	Cervidae
1	Extra tooth material			X		X	
2	Third stomach		X	X	X	X	X
3	Double opening for tear ducts					X	X

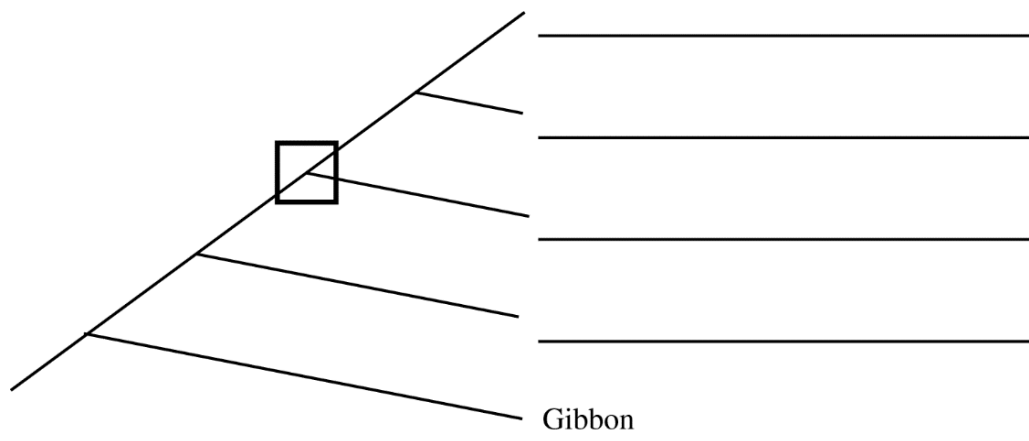
- (a) **Describe** how a scientist would use a comparison of the DNA sequences of different organisms to suggest the most likely evolutionary relationship among the organisms.
- (b) Based on Figure 1, **explain** why Bovidae is likely to be more closely related to Moschidae than it is to Giraffidae.
- (c) Using the template in the space provided for your response, **represent** the point(s) at which characteristic 1, listed in Table 1, evolved by marking “X” on the line(s) of the cladogram in the correct location(s).
- (d) Based on Figure 1A, **explain** why a characteristic found only in the Cervidae and Bovidae families is more likely evidence of convergent evolution than it is of common ancestry.
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Write your responses to this question only on the designated pages in the separate Free Response booklet.

TABLE 1. DIVERGENCE (IN PERCENT) OF MITOCHONDRIAL DNA SEQUENCES AMONG FIVE PRIMATE SPECIES

	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

5. A researcher studying the evolutionary relationship among five primate species obtained data from a sequence of mitochondrial DNA (mtDNA) from a representative individual of each species. The researcher then calculated the percent divergence in the sequences between each pair of primate species (Table 1).
- (a) Based on fossil data, the researcher estimates that humans and their most closely related species in the data set diverged approximately seven million years ago. Using these data, **calculate** the rate of mtDNA percent divergence per million years between humans and their most closely related species in the data set. Round your answer to two decimal places.
- (b) Using the data in the table, **construct** a cladogram on the template provided. **Provide reasoning** for the placement of gibbons as the outgroup on the cladogram.
- (c) On the cladogram, **draw** a circle around all of the species that are descended from the species indicated by the node within the square.



BIOLOGY**Section II****Total Time—1 hour and 30 minutes****Reading Period—10 minutes****Writing Period—1 hour and 20 minutes****8 Questions**

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

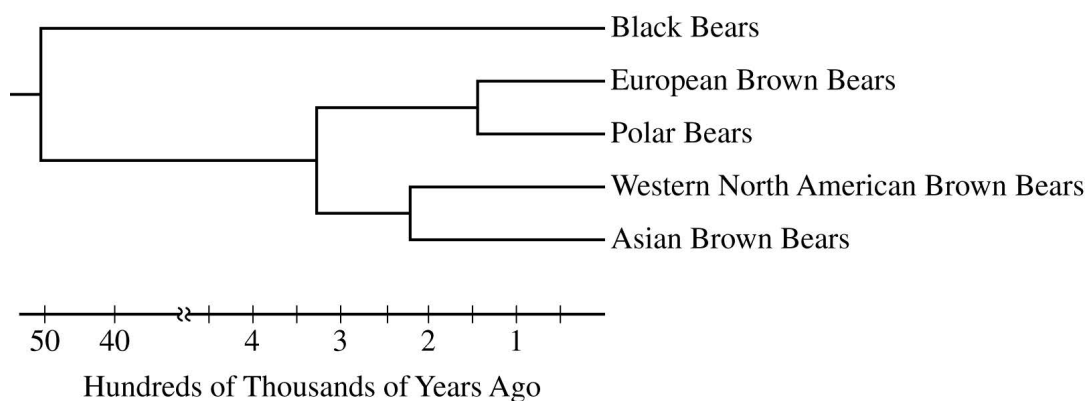


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

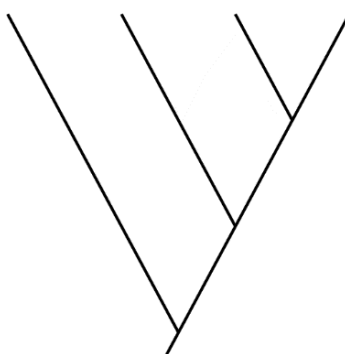
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their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

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

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

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

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

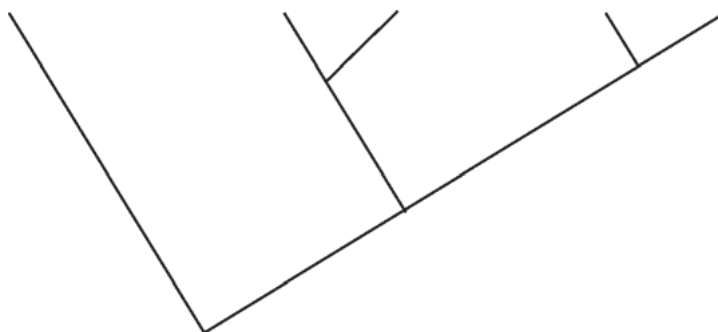


3. The amino acid sequence of cytochrome *c* was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

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

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

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



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

MILK COMPONENTS IN DIFFERENT MAMMALS

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

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

