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# AP Biology

## Sample Student Responses and Scoring Commentary

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**2018 SCORING GUIDELINES**

**Question 1**

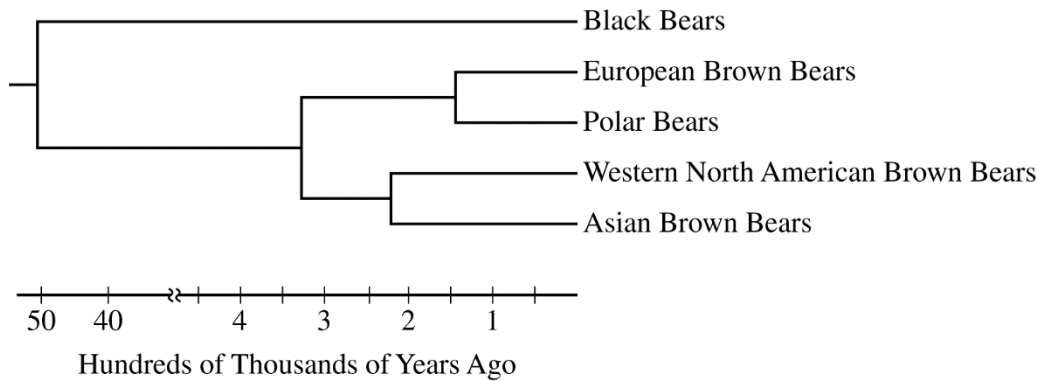


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

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	–

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**Question 1 (continued)**

- (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.

**Estimate (1 point)**

- First two digits of the answer must be between 30 and 35.

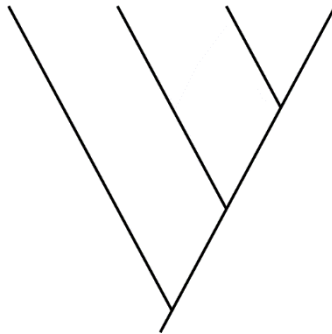
**Identification (1 point)**

- European

**Identification (1 point)**

- European/Polar OR Asian/Western (North American)

- (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.



**Construction (1 point)**

- Correctly illustrated evolutionary relationship among the four species

**Circling (1 point)**

- Correctly circled out-group based on orientation of cladogram

- (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.

**Reasoning (1 point)**

- Genes show more variability (in nucleotide sequence) than proteins do (in amino acid sequences).
- mtDNA genome contains multiple genes vs. one *lyst* gene.
- The phenotype associated with the *lyst* gene is under strong selection.

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**Question 1 (continued)**

(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.

**Prediction (1 point)**

- Mouse fur and/or eyes will not have pigment/will have reduced pigment.
- Mouse (fur) will be white/lighter.

**Justification (1 point)**

- Polar bear *lyst* gene/LYST protein is associated with a lack of pigment/white hair.
- Mutated human *lyst* gene/ LYST protein is associated with a lack of pigment in hair and eyes.

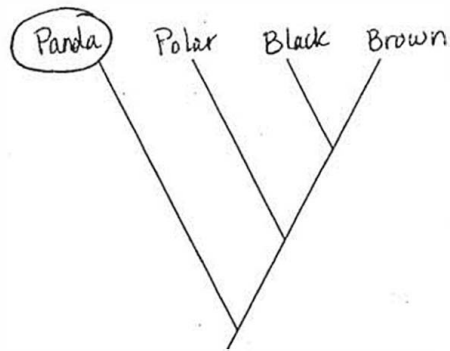
(e) **Describe** how the mutation in the *lyst* gene became common in the polar bear population. If the *lyst* gene were the only determinant of fur color, **predict** the percent of white offspring produced by a mating between a polar bear and a brown bear.

**Description (1 point)**

- Natural selection for the white fur phenotype

**Prediction (1 point)**

- 0%



a) The age is around 325,000 years old. Based off mitochondrial DNA, polar bears are closest to European brown bears. Western North American brown bears + Asian brown bears could switch position w/o changing any relationships.

c) Mitochondrial DNA has a wider array of genes, therefore amino acids, to study + compare from species to species than the LYST gene does — there are only seven amino acids. With fewer comparisons, LYST has fewer opportunities + is less accurate than mitochondrial DNA.

d) The most likely change is that the mouse will appear white due to a lack of pigment in its fur. This seems likely because ~~because~~ polar bears are normally only white; humans who have similar LYST mutations (Chediak-Higashi Syndrome) also display a lack of pigment in hair + eyes. Overall, the mutations appear to cause the

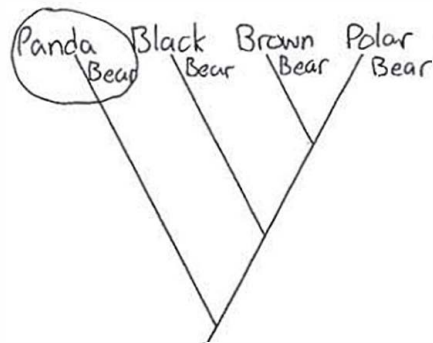
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lack of pigment.

e.) The *LYST* gene became common through the process of natural selection. After the mutation appeared, white individuals gained an advantage in their environment - hunting became easier ~~and~~ since they were blending in with the snow + ice. Because these individuals were more successful in eating, therefore surviving more, they were able to reproduce + ~~spread~~ carry on the mutation. The mutation was so advantageous it eventually became commonplace.

The percent of white offspring (assuming the offspring survived/could be conceived) ~~is~~ should be zero, since the similar mutation of *LYST* in humans is recessive. Therefore, brown bears would be dominant + pass the dominant coloring to all offspring.

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a) The most recent common ancestor of all brown bears is 325 hundred thousand years old. Based on DNA sequence comparison, Polar Bears are most closely related to European Brown Bears. Two populations that could be switched would be Polar Bears and European Brown Bears.

b) Mitochondrial DNA sequences show evolutionary differences of over time, whereas LYST comparisons do not.

d) The mouse would begin growing pigment-less hair, and its eyes, if previously colored, would lose pigment as well. This would occur because the LYST gene in a polar bear encodes for lack of pigment in hair and eyes.

e) Mutation of the LYST gene became popular in Polar Bears most likely due to natural selection. Polar Bears live in a snowy, white climate, and the lack of pigment in their fur allows them to blend in.

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ADDITIONAL PAGE FOR ANSWERING QUESTION 1

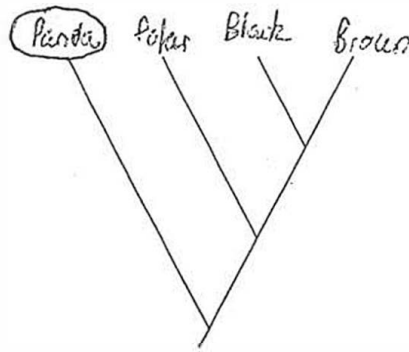
If a ~~f~~ Polar Bear and a Brown Bear were bred, there would probably be no white offspring.

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B)



- A) The most common recent ancestor of all brown bears appears to be around 325 hundreds of thousands years old. Based on the DNA sequence comparison polar bears are most closely related to European Brown Bears. The polar bear's & the European Brown Bear's positions on the cladogram can be switched without affecting the relationships.
- C) More errors can be made during the synthesizing of a protein than the replication of DNA, therefore using mitochondrial DNA is more accurate.
- D) The transgenic mouse strain are more likely to have Chondro-epiphyseal dysplasia because the new *Lyst* gene is able to cause it at higher rates.
- E) In the polar bear population white fur is advantageous because it allows the bear to use the snow as camouflage. This made the mutation more common overtime because those without it had a lower survival rate. The percent of offspring with white coloration would be 0% between this cross because the polar bear would be homozygous recessive.

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## 2018 SCORING COMMENTARY

### Question 1

#### Overview

This question is based on recent investigations into the evolutionary history of polar bears. Students were presented with a phylogenetic tree created from mitochondrial DNA (mtDNA) data for five populations of bears. Using this phylogenetic tree, students were asked to estimate the age of the most recent common ancestor of all brown bears, to identify what population of brown bears was most closely related to polar bears, and to identify two populations of bears whose positions on the phylogenetic tree could be switched without altering the proposed relationships. Students were presented with a data table indicating the number of amino acid differences in the lysosomal trafficking protein *LYST* among four species of bears. Using these data, the students were asked to construct a cladogram on a provided template and circle the outgroup position on that cladogram. Students then were asked to provide one piece of reasoning to support a claim that mtDNA sequence comparisons provide a more accurate prediction of bear phylogeny. The students were then asked to predict the most likely difference in the phenotype of a mouse that was genetically altered to contain the polar bear-specific *lyst* allele. The students were asked to justify their prediction. Finally, students were asked to describe how the *lyst* allele became common in the polar bear population and to predict what percentage of the offspring resulting from a mating between a brown bear and a polar bear would be white.

The key understandings and skills students were expected to demonstrate included the following:

- Basic concepts of evolution were used to evaluate and interpret data and to describe evolutionary relationships and processes.
- Knowledge of Mendelian and molecular genetics was used to predict the outcomes of a genetic alteration and a mating based on experimental design.

#### Sample: 1A

##### Score: 10

The response earned 1 point in part (a) for estimating that the most recent common ancestor of all brown bears existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that Western North American Brown Bear and Asian Brown Bear positions could be switched on the phylogenetic tree. The response earned 1 point in part (b) for constructing a cladogram that correctly orders the taxa, from left to right, Panda, Polar, Black, and Brown. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (c) for supporting the student's claim by reasoning that mtDNA would include more genes that code for more proteins that could be compared in contrast to one gene coding for a single *LYST* protein. The response earned 1 point in part (d) for predicting that the mouse's fur would lack pigment. The response earned 1 point in part (d) for justifying that humans having the mutant form of the *LYST* protein lack pigment in hair. The response earned 1 point in part (e) for describing that the *lyst* gene became common when white individuals had a selective advantage. The response earned 1 point in part (e) for predicting that zero percent of offspring should be white.

#### Sample: 1B

##### Score: 8

The response earned 1 point in part (a) for estimating that the most recent common ancestor existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that Polar Bear and European Brown Bear positions could be switched on the phylogenetic tree. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (d) for predicting that the mouse would be growing pigmentless hair. The

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**Question 1 (continued)**

response earned 1 point in part (d) for the justification that because the *lyst* gene in Polar Bears encodes for a lack of pigment in hair, the mouse would begin growing pigmentless hair. The response earned 1 point in part (e) for describing that the *lyst* gene became common as a result of natural selection for white Polar Bears that were able to blend into a snowy white environment. The response earned 1 point in part (e) for predicting that no offspring should be white.

**Sample: 1C**

**Score: 6**

The response earned 1 point in part (a) for estimating that the most recent common ancestor existed 325,000 years ago. The response earned 1 point in part (a) for identifying that European Brown Bears are most closely related to Polar Bears. The response earned 1 point in part (a) for identifying that the position of the Polar Bear and the position of the European Brown Bear could be switched on the phylogenetic tree. The response earned 1 point in part (b) for constructing a cladogram that correctly orders the taxa, from left to right, Panda, Polar, Black, and Brown. The response earned 1 point in part (b) for circling a correct outgroup at the leftmost terminal branch, without including the ancestral node of the cladogram. The response earned 1 point in part (e) for predicting that zero percent of offspring should be white.