



# AP Bio

# FRQ Fridays

2018 #1  
Phylogenetic Tree, Mutations,  
& Natural Selection

# FRQ Friday #22

2018 #1

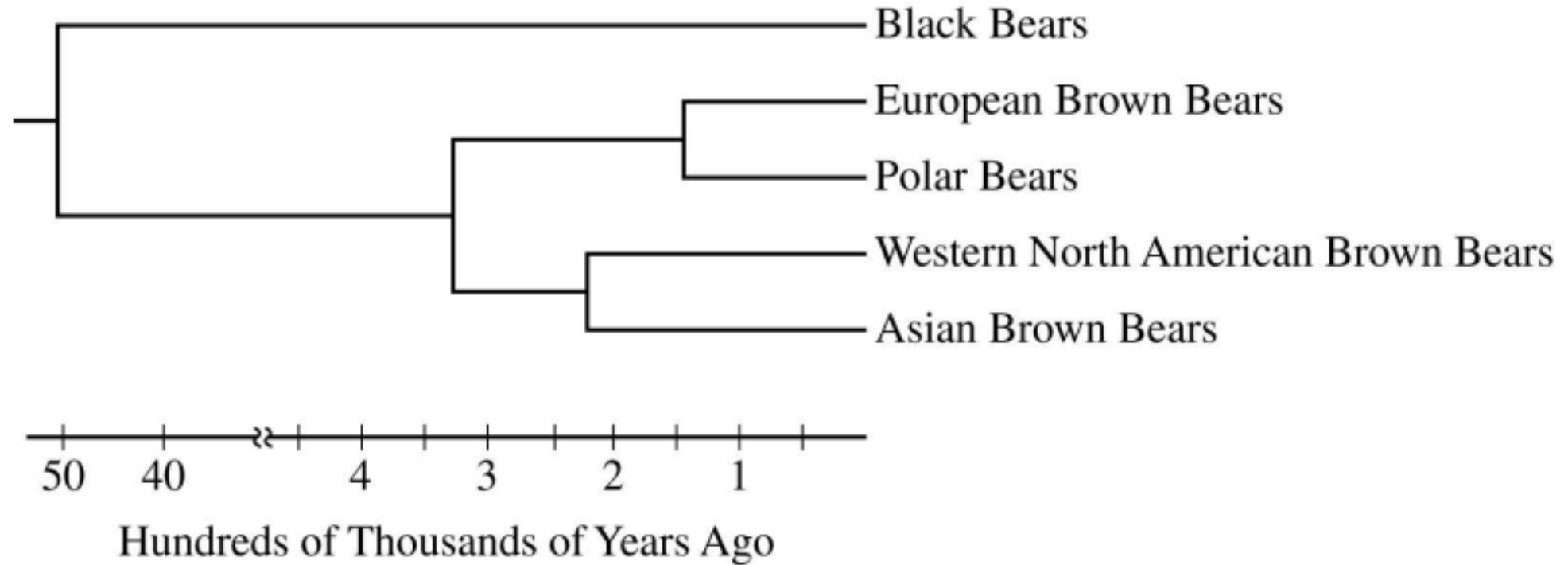


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons



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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

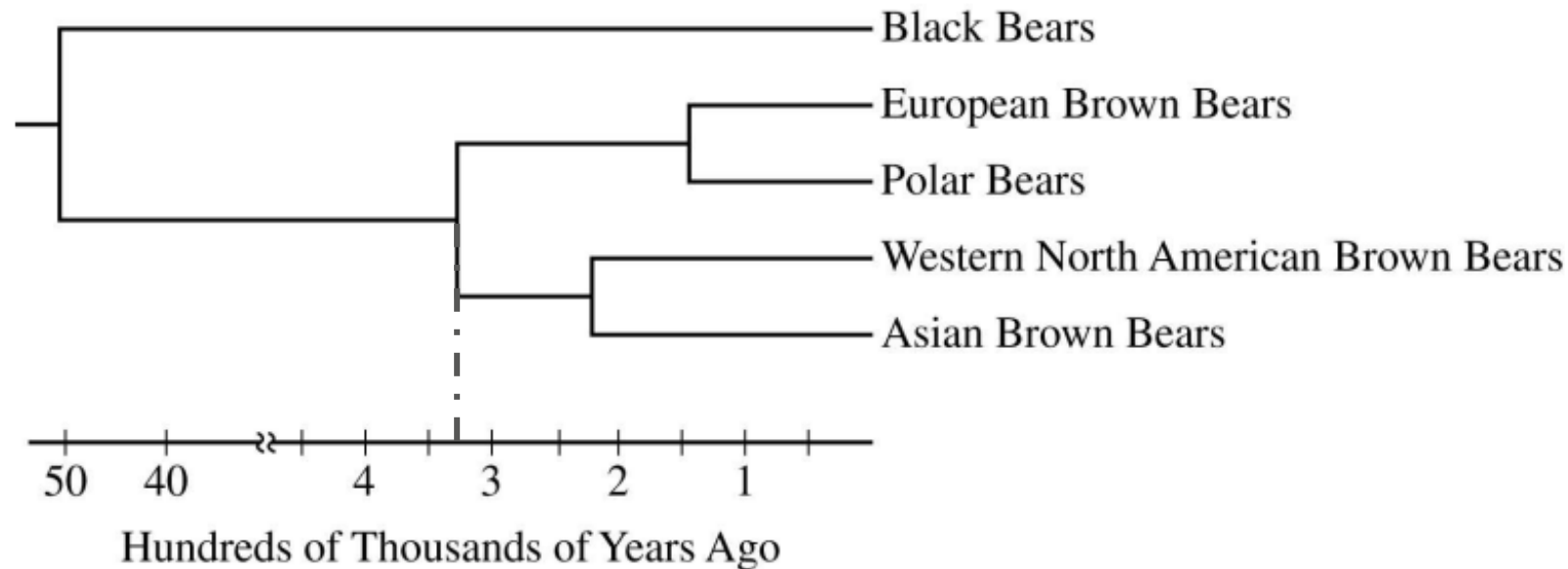
	Panda	Black	Brown	Polar
Panda	–			
Black	33	–		
Brown	34	1	–	
Polar	40	7	8	–



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- (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.



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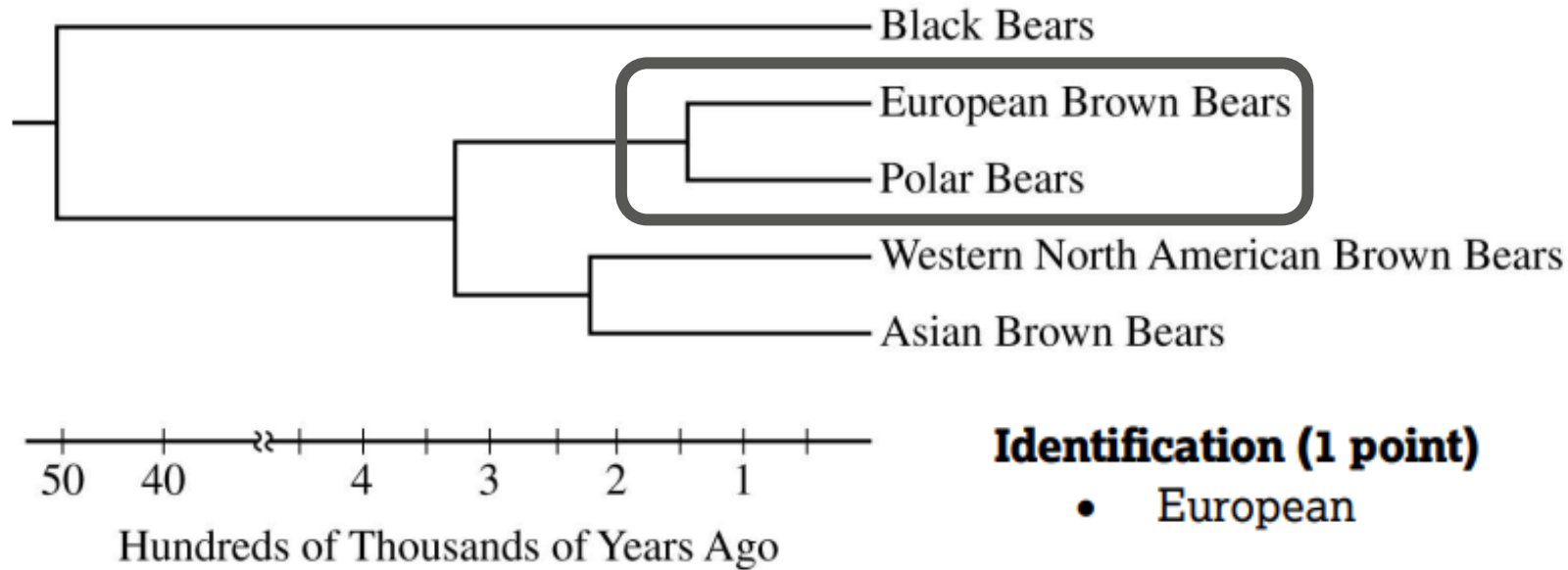


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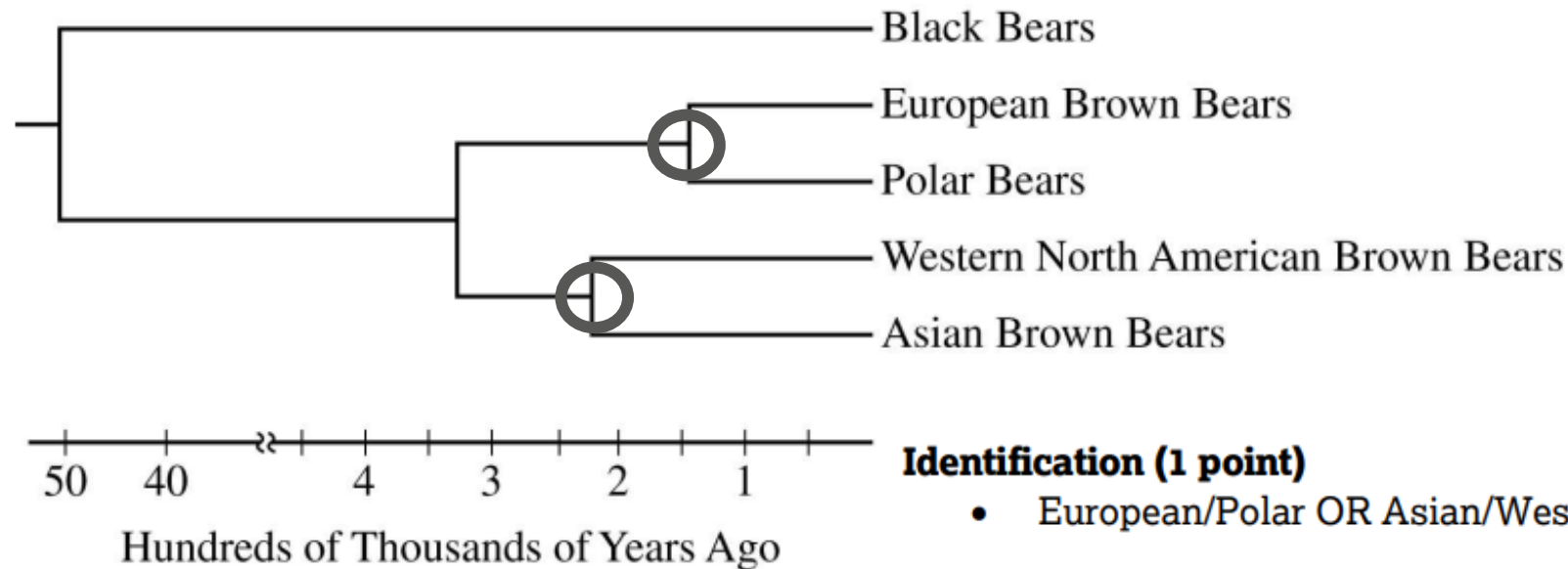


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**Estimate (1 point)**

- 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)

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.



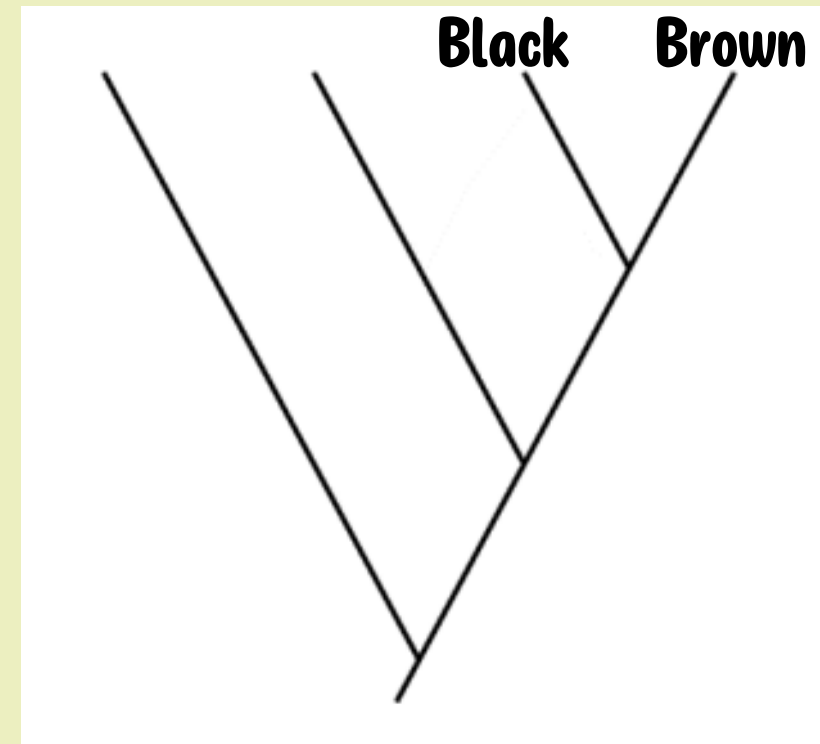
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(b) **Construct** a cladogram on the template to represent a model of the evolutionary relatedness among the bear species based on the differences in LYST protein sequences (Table 1). **Circle** the position on the cladogram that represents the out-group.

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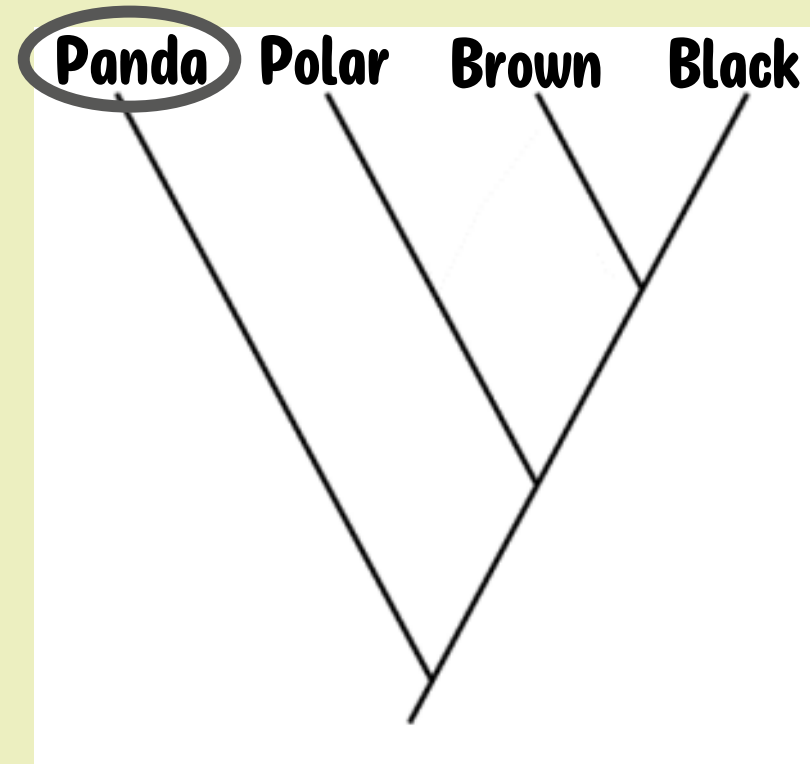
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### Construction (1 point)

- Correctly illustrated evolutionary relationship among the four species

### Circling (1 point)

- Correctly circled out-group based on orientation of cladogram



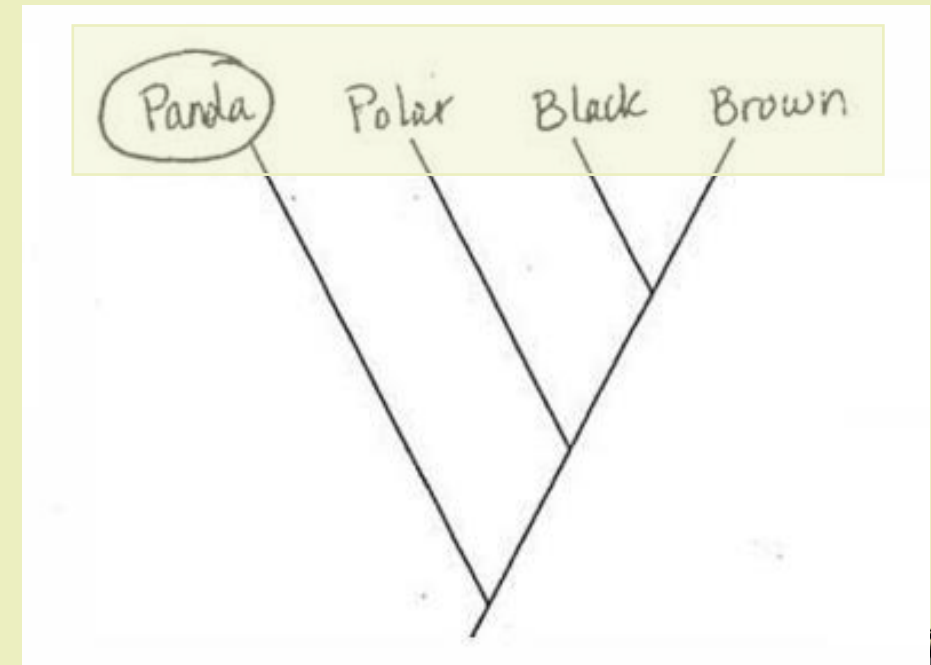
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(c) A student claims that mitochondrial DNA sequence comparisons provide a more accurate phylogeny of bear species than do LYST protein sequence comparisons. **Provide ONE piece of reasoning** to support the student's claim.

## 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.

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.



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(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.



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- Polar bear *lyst* gene/LYST protein is associated with a lack of pigment/white hair.
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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 ~~fur is white~~ 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 lack of pigment.



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- (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

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.

## Prediction (1 point)

- 0%



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## Description (1 point)

- Natural selection for the white fur phenotype

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.



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## Prediction (1 point)

- 0%

The percent of white offspring (assuming the offspring survived/could be conceived) 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.

