

Past-paper walk-through

Mendelian Genetics ■ 5.3

eXercise

Questions in this set

- 2018 Q1
- 2018 Q7
- 2017 Q3
- 2016 Q7

Reading the mark scheme

- **B1** a mark that stands on its own – the point is either made or not.
- **M1** a *method* mark: the right approach, even if the number is wrong.
- **A1** an *answer* mark, and it usually needs its M mark first.
- **C1** a working mark on the way to the answer.
- **//** separates answers the examiner accepts equally.
- **ecf** = error carried forward: a later part is marked on your own earlier answer.
- **owtte** = “or words to that effect” – the wording need not match.

Question 1

2018 ■ Q1

Question 1

[Figure 1: Phylogenetic tree (cladogram) representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons. The tree branches, from top to bottom: Black Bears, European Brown Bears, Polar Bears, Western North American Brown Bears, Asian Brown Bears. European Brown Bears and Polar Bears share a node; that node and (Western North American Brown Bears + Asian Brown Bears, which share their own node) share a deeper node; that node and Black Bears share the deepest node shown. Below the tree is a time axis labeled “Hundreds of Thousands of Years Ago” with tick marks at 50, 40, then a break (squiggle) then 4, 3, 2, 1, with the deepest node aligning near 40-50 and shallower nodes aligning at successively smaller values toward 1. Caption: “Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons.”]

Question 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).

Question 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.

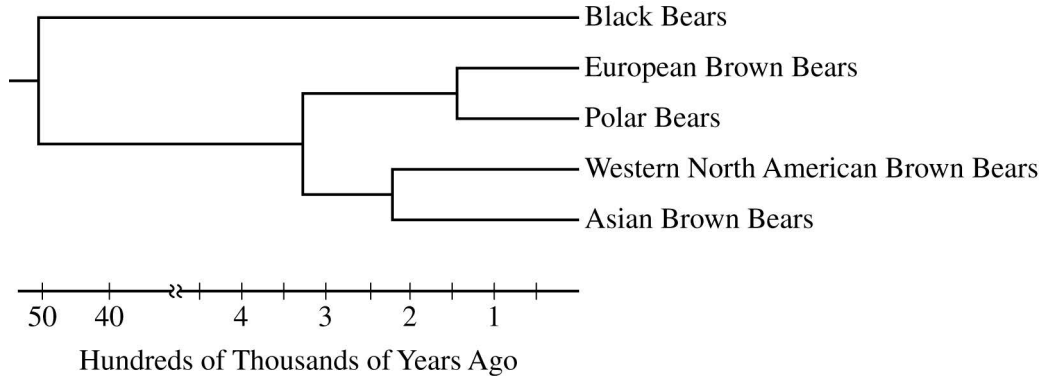
TABLE 1. AMINO ACID DIFFERENCES IN THE LYST PROTEIN AMONG BEAR SPECIES

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

Question 1

(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.

Question 1

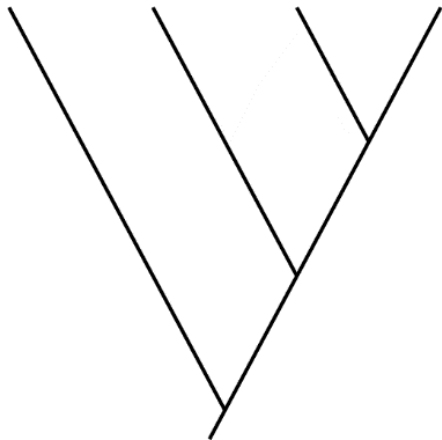


Question 1

DATA FROM THE ABOVE BEAR STUDY

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

Question 1



Question 1

2018 ■ Q1

Question 1

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