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.
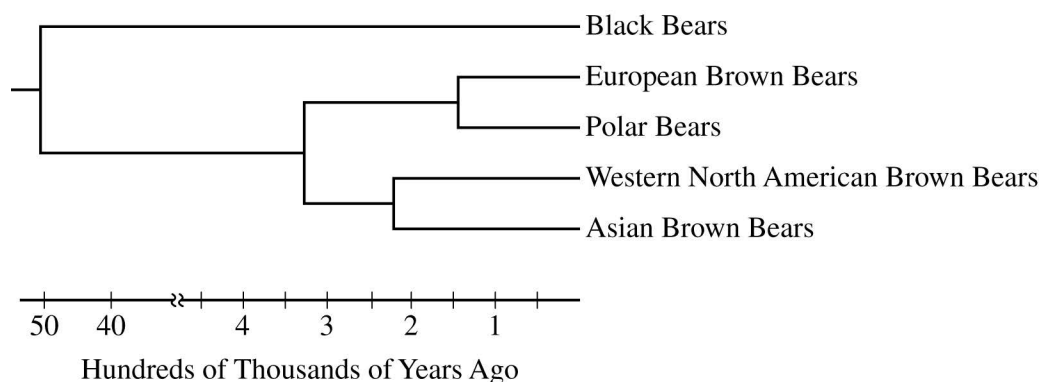

Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

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).

GO ON TO THE NEXT PAGE.

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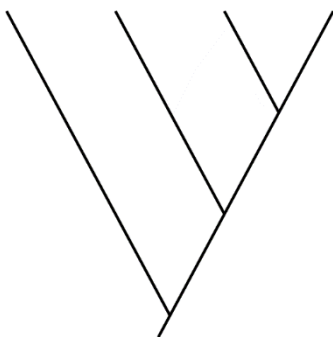- First two digits of the answer must be between 30 and 35.

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.

(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%