

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.

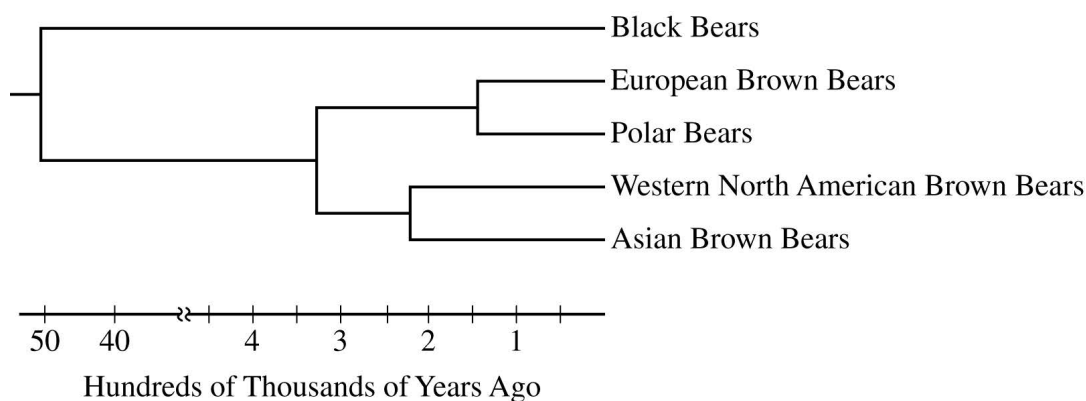


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

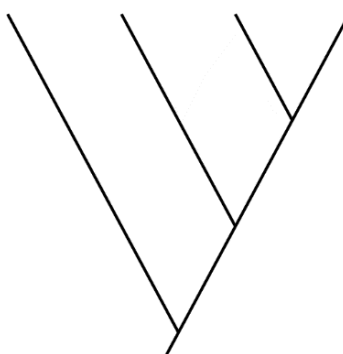
1. Polar bears are highly adapted for life in cold climates around the North Pole. Brown bears, black bears, and pandas are found in warmer environments. Researchers collected complete mitochondrial DNA sequences from several populations of bears and constructed a phylogenetic tree to represent their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



7. In the tongue sole fish (*Cynoglossus semilaevis*), sex is determined by a combination of genetics and environmental temperature. Genetically male fish have two Z chromosomes (ZZ), and genetically female fish have one Z chromosome and one W chromosome (ZW). When fish are raised at 22°C, ZZ fish develop into phenotypic males and ZW fish develop into phenotypic females. However, when fish are raised at 28°C, the Z chromosome is modified (denoted as Z*). Z*W individuals develop as phenotypic males that are fertile and can pass on the Z* chromosome to their offspring even when the offspring are raised at 22°C. A cross between a ZW female and a Z*Z male is shown in the Punnett square below.

	Z	W
Z*	Z* Z	Z* W
Z	ZZ	ZW

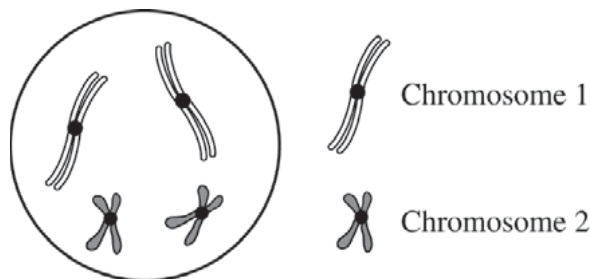
- (a) **Predict** the percent of phenotypic males among the F₁ offspring of the cross shown in the Punnett square if the offspring are raised at 22°C.
- (b) At least one Z or Z* chromosome is necessary for survival of the fish. A researcher crossed two fish and observed a 2:1 ratio of males to females among the offspring. Based on the information, **identify** the genotype of the male parent in the cross. **Describe** ONE fitness cost to the female of mating with this particular male.

3. Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydroxylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the *GA3H* gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F₁ generation are tall. When the F₁ plants are crossed with each other, 75 percent of the plants in the F₂ generation are tall and 25 percent of the plants are short.

		Second Base in Codon					
		U	C	A	G		
First Base in Codon	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA Stop UAG Stop	UGU } Cys UGC } UGA Stop UGG Trp	U C A G	Third Base in Codon
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G	
	A	AUU } AUC } Ile AUA } AUG Met or Start	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G	
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G	

Figure 1. The universal genetic code

- (a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.
- (b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.
- (c) **Describe** how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype.



7. In a certain species of plant, the diploid number of chromosomes is 4 ($2n = 4$). Flower color is controlled by a single gene in which the green allele (G) is dominant to the purple allele (g). Plant height is controlled by a different gene in which the dwarf allele (D) is dominant to the tall allele (d). Individuals of the parental (P) generation with the genotypes $GGDD$ and $ggdd$ were crossed to produce F_1 progeny.
- (a) **Construct** a diagram below to depict the four possible normal products of meiosis that would be produced by the F_1 progeny. Show the chromosomes and the allele(s) they carry. Assume the genes are located on different chromosomes and the gene for flower color is on chromosome 1.
- (b) **Predict** the possible phenotypes and their ratios in the offspring of a testcross between an F_1 individual and a $ggdd$ individual.
- (c) If the two genes were genetically linked, **describe** how the proportions of phenotypes of the resulting offspring would most likely differ from those of the testcross between an F_1 individual and a $ggdd$ individual.

