

Unit 7: Natural Selection

Topic	Learning Objective(s)
7.1 Introduction to Natural Selection	EVO-1.C Describe the causes of natural selection.
	EVO-1.D Explain how natural selection affects populations.
7.2 Natural Selection	EVO-1.E Describe the importance of phenotypic variation in a population.
7.3 Artificial Selection	EVO-1.F Explain how humans can affect diversity within a population.
	EVO-1.G Explain the relationship between changes in the environment and evolutionary changes in the population.
7.4 Population Genetics	EVO-1.H Explain how random occurrences affect the genetic makeup of a population.
	EVO-1.I Describe the role of random processes in the evolution of specific populations.
	EVO-1.J Describe the change in the genetic makeup of a population over time.
7.5 Hardy-Weinberg Equilibrium	EVO-1.K Describe the conditions under which allele and genotype frequencies will change in populations.
	EVO-1.L Explain the impacts on the population if any of the conditions of Hardy-Weinberg are not met.
7.6 Evidence of Evolution	EVO-1.M Describe the types of data that provide evidence for evolution.
	EVO-1.N Explain how morphological, biochemical, and geological data provide evidence that organisms have changed over time.
	EVO-2.B Describe the fundamental molecular and cellular features shared across all domains of life, which provide evidence of common ancestry.
7.7 Common Ancestry	EVO-2.C Describe structural and functional evidence on cellular and molecular levels that provides evidence for the common ancestry of all eukaryotes.
7.8 Continuing Evolution	EVO-3.A Explain how evolution is an ongoing process in all living organisms.
7.9 Phylogeny	EVO-3.B Describe the types of evidence that can be used to infer an evolutionary relationship.
	EVO-3.C Explain how a phylogenetic tree and/or cladogram can be used to infer evolutionary relatedness.
7.10 Speciation	EVO-3.D Describe the conditions under which new species may arise.
	EVO-3.E Describe the rate of evolution and speciation under different ecological conditions.
	EVO-3.F Explain the processes and mechanisms that drive speciation.
7.11 Extinction	EVO-3.G Describe factors that lead to the extinction of a population.
	EVO-3.H Explain how the risk of extinction is affected by changes in the environment.
	EVO-3.I Explain species diversity in an ecosystem as a function of speciation and extinction rates.
	EVO-3.J Explain how extinction can make new environments available for adaptive radiation.
7.12 Variations in Populations	SYI-3.D Explain how the genetic diversity of a species or population affects its ability to withstand environmental pressures.
7.13 Origin of Life on Earth	SYI-3.E Describe the scientific evidence that provides support for models of the origin of life on Earth.

Free Response Practice

2022 #4

Existing isolated brook trout populations in Newfoundland, Canada, were once part of a larger population that was fragmented at the end of the most recent glaciation period about 10,000 to 12,000 years ago. Researchers investigated 14 naturally separated stream populations of brook trout. They found that the populations are all genetically distinct and show differences in morphology.

- (a) **Describe** the prezygotic barrier that results in these genetically distinct populations.
- (b) Brook trout with longer fins are able to swim faster than brook trout with shorter fins. In one of the Newfoundland streams, the main prey of the brook trout evolved to move faster. For brook trout living in this stream, **explain** the difference in fitness between longer-finned individuals and shorter-finned individuals.
- (c) If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, **predict** the likely impact on both populations.
- (d) Researchers claim that there are more genetic differences between any two current brook trout populations than there are between any single current population and the ancestral brook trout population from which all the trout are descended. Provide reasoning to **justify** their claim.

2021 #4

In 1981 a single immature male *Geospiza conirostris* finch flew more than 100 kilometers from the Galapagos island of Espanola to the Galapagos island of Daphne Major, where no *G. conirostris* finches were living. The immigrant finch bred with a female *G. fortis*, a species of finch common on Daphne Major. The F1 finches and later generations interbred only within their lineage. By 2012 scientists counted 23 individuals, including eight breeding pairs, within this hybrid lineage on Daphne Major. The hybrid lineage became known as Big Bird.

Bird with different beak shapes and sizes eat different types of food. The dimensions of the Big Bird beaks relative to the beaks of the major competitor finch species on Daphne Major are shown in Figure 1.

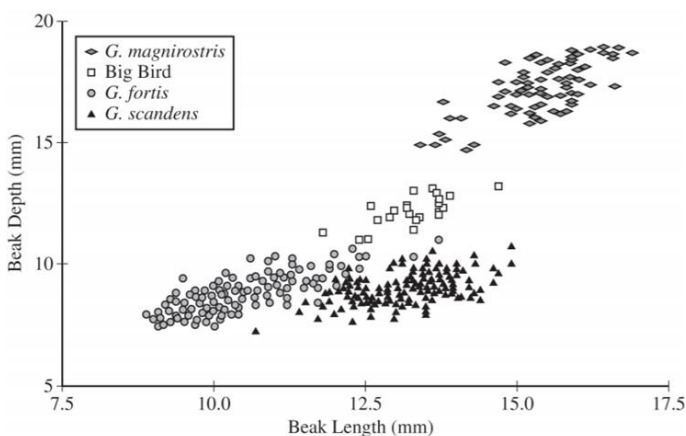


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

- (a) The Big Bird lineage became reproductively isolated from *G. fortis*. **Describe** one prezygotic mechanism that likely contributed to the reproductive isolation of the Big Bird lineage from *G. fortis*.

(b) Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.

(c) A virus infects and kills all *G. magnirostris* on Daphne Major but does not affect the other finch species. Assuming food type and availability stay the same, **predict** the most likely change in the beak phenotype of the Big Bird population after six more generations.

(d) Provide reasoning to **justify** your prediction in part (c).

2019 #5

TABLE 1. DIVERGENCE (IN PERCENT) OF MITOCHONDRIAL DNA SEQUENCES AMONG FIVE PRIMATE SPECIES

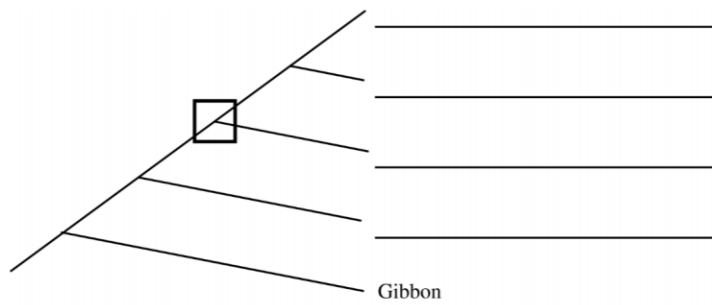
	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

A researcher studying the evolutionary relationship among five primate species obtained data from a sequence of mitochondrial DNA (mtDNA) from a representative individual of each species. The researcher then calculated the percent divergence in the sequences between each pair of primate species (Table 1).

(a) Based on fossil data, the researcher estimates that humans and their most closely related species in the data set diverged approximately seven million years ago. Using these data, **calculate** the rate of mtDNA percent divergence per million years between humans and their most closely related species in the data set. Round your answer to two decimal places.

(b) Using the data in the table, **construct** a cladogram on the template provided. **Provide reasoning** for the placement of gibbons as the outgroup on the cladogram.

(c) On the cladogram, **draw** a circle around all of the species that are descended from the species indicated by the node within the square.



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).

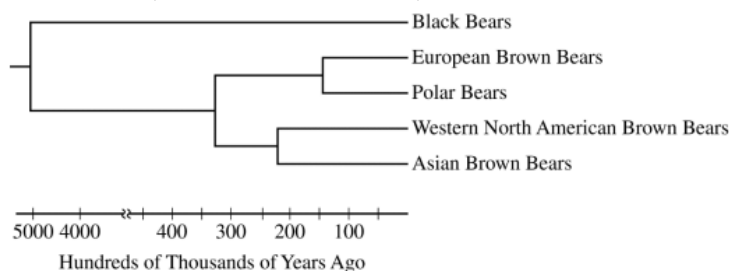


Figure 1. Phylogenetic tree representing the evolutionary relatedness among bear populations based on mitochondrial DNA sequence comparisons

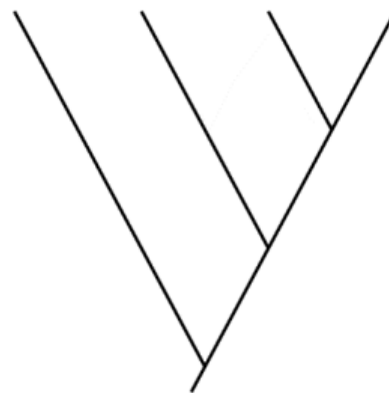
A researcher studying adaptations in bears sequenced the nuclear gene encoding a lysosomal trafficking protein (LYST) in polar bears, brown bears, and panda bears. There are seven inferred amino acid substitutions that are found only in polar bears. Mutations that cause similar substitutions in the human 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 cladogram.

(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 the fur color, **predict** the percent of white offspring produced by a mating between a polar bear and a brown bear.

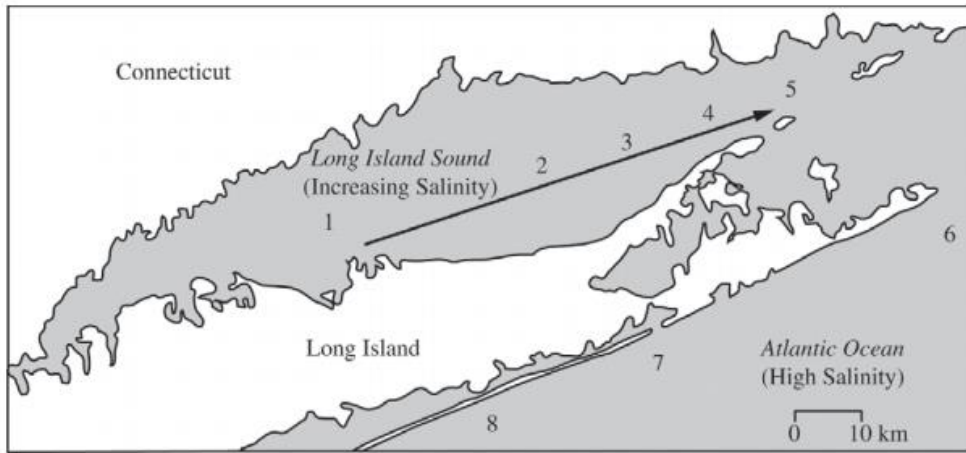


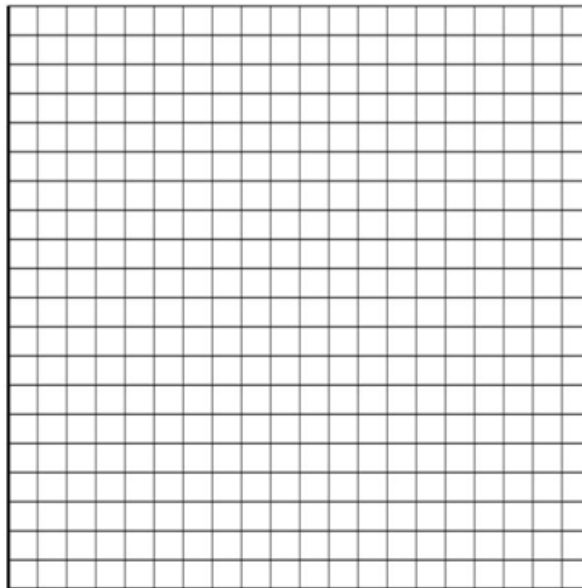
Figure 1. Sampling sites of marine mussels at various locations (1–8) in Long Island Sound and the Atlantic Ocean

TABLE 1. PERCENT OF INDIVIDUALS POSSESSING *lap*⁹⁴ ALLELE

	Long Island Sound					Atlantic Ocean		
Site	1	2	3	4	5	6	7	8
<i>lap</i> ⁹⁴ frequency (%)	13	16	25	37	55	59	59	59
Salinity	Low	→			High	High		

Leucine aminopeptidase (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1).

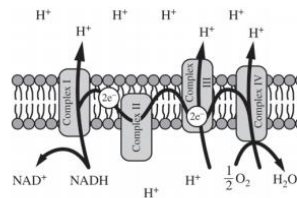
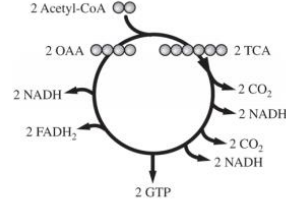
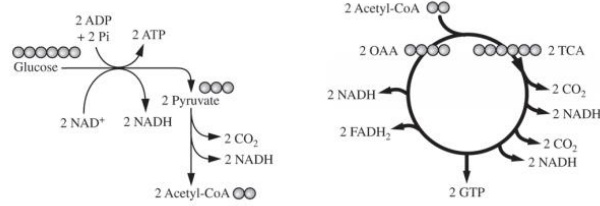
(a) On the axes provided, **construct** an appropriately labeled bar graph to illustrate the observed frequencies of the *lap*⁹⁴ allele in the study population.



(b) Based on the data, **describe** the most likely effect of salinity on the frequency of the *lap*⁹⁴ allele in the marine mussel population in Long Island Sound. **Predict** the likely *lap*⁹⁴ allele frequency at a sampling site between site 1 and site 2 in Long Island Sound.

- (c) **Describe** the most likely effect of LAP⁹⁴ activity on the osmolarity of the cytosol. **Describe** the function of LAP⁹⁴ in maintaining water balance in mussels living in the Atlantic Ocean.
- (d) Marine mussel larvae are evenly dispersed throughout the study area by water movement. As larvae mature, they attach to the rocks in the water. **Explain** the differences in *lap*⁹⁴ allele frequency among adult mussel populations at the sample sites despite the dispersal of larvae throughout the entire study area. **Predict** the likely effect of distribution of mussels in Long Island Sound if the *lap*⁹⁴ allele was found in all the mussels in the population. **Justify** your prediction.

2015 #2



Cellular respiration includes the metabolic pathways of glycolysis, the Krebs cycle, and the electron transport chain, as represented in the figures. In cellular respiration, carbohydrates and other metabolites are oxidized, and the resulting energy-transfer reactions support the synthesis of ATP.

- (a) Using the information above, **describe** ONE contribution of each of the following in ATP synthesis.
- Catabolism of glucose in glycolysis and pyruvate oxidation
 - Oxidation of intermediates in the Krebs cycle
 - Formation of a proton gradient by the electron transport chain
- (b) Use each of the following observations to **justify** the claim that glycolysis first occurred in a common ancestor of all living organisms.
- Nearly all existing organisms perform glycolysis.
 - Glycolysis occurs under anaerobic conditions.
 - Glycolysis occurs only in the cytosol.
- (c) A researcher estimates that, in a certain organism, the complete metabolism of glucose produces 30 molecules of ATP for each molecule of glucose. The energy released from the total oxidation of glucose under standard conditions is 686 kcal/mol. The energy released from the hydrolysis of ATP to ADP and inorganic phosphate under standard conditions is 7.3 kcal/mol. **Calculate** the amount of energy available from the hydrolysis of 30 moles of ATP. **Calculate** the efficiency of total ATP production from 1 mole of glucose in the organism. **Describe** what happens to the excess energy that is released from the metabolism of glucose.
- (d) The enzymes of the Krebs cycle function in the cytosol of bacteria, but among eukaryotes the enzymes function mostly in the mitochondria. **Pose** a scientific question that connects the subcellular location of the enzymes in the Krebs cycle to the evolution of eukaryotes.

2015 #3

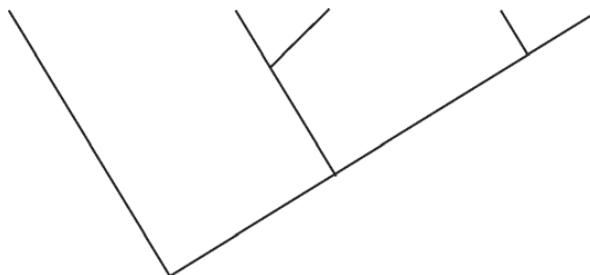
The amino acid sequence of cytochrome c was determined for five different species of vertebrates. The table below shows the number of differences in the sequences between each pair of species.

THE NUMBER OF AMINO ACID DIFFERENCES IN CYTOCHROME c AMONG FIVE SPECIES

	<i>E. ferus</i>	<i>D. polylepis</i>	<i>G. gallus</i>	<i>A. forsteri</i>	<i>E. africanus</i>
<i>E. ferus</i>	0	21	11	13	1
<i>D. polylepis</i>		0	18	17	20
<i>G. gallus</i>			0	3	10
<i>A. forsteri</i>				0	12
<i>E. africanus</i>					0

(a) Using the data in the table, **create** a phylogenetic tree on the template provided to reflect the evolutionary relationships of the organisms. **Provide reasoning** for the placement on the tree of the species that is least related to the others.

(b) **Identify** whether morphological data or amino acid sequence data are more likely to accurately represent the true evolutionary relationships among the species, and **provide reasoning** for your answer.



2014 #2

Mammalian milk contains antibodies that are produced by the mother's immune system and passed to offspring during feeding. Mammalian milk also contains a sugar (lactose) and may contain proteins (protein A, protein B, and casein), as indicated in the table.

MILK COMPONENTS IN DIFFERENT MAMMALS

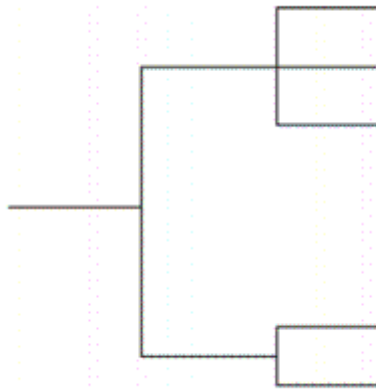
Character	Cat	Cow	Horse	Human	Pig
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	?	+	+	?	+
Casein	?	+	+	?	+
? indicates the absence of the character + indicates the presence of the character					

(a) Using the data in the table, **construct** a cladogram on the template provided to indicate the most likely evolutionary relationships among the different mammals. **Indicate** on the cladogram where each of the characters most likely arose in the evolutionary process, and **justify** the placement of the characters on the cladogram.

Note: part b & c are out of scope

(b) **Describe** FOUR steps in the activation of the mother's specific immune response following exposure to a bacterial pathogen. **Predict** how the mother's immune response would differ upon a second exposure to the same bacterial pathogen a year later.

(c) **Predict** the most likely consequence for a nursing infant who is exposed to an intestinal bacterial pathogen (e.g. *Salmonella*) to which the mother was exposed three months earlier. **Justify** your prediction.



2014 #8

A research team has genetically engineered a strain of fruit flies to eliminate errors during DNA replication. The team claims that this will eliminate genetic variation in the engineered flies. A second research team claims that eliminating errors during DNA replication will not entirely eliminate genetic variation in the engineered flies.

- (a) **Provide** ONE piece of evidence that would indicate new genetic variation has occurred in the engineered flies.
- (b) **Describe** ONE mechanism that could lead to genetic variation in the engineered strain of flies.
- (c) **Describe** how genetic variation in a population contributes to the process of evolution in the population.

2013 #3

Fossils of lobe-finned fishes, which are ancestors of amphibians, are found in rocks that are at least 380 million years old. Fossils of the oldest amphibian-like vertebrate animals with true legs and lungs are found in rocks that are approximately 363 million years old.

Three samples of rocks are available that might contain fossils of a transitional species between lobe-finned fishes and amphibians: one rock sample that is 350 million years old, one that is 370 million years old, and one that is 390 million years old.

- (a) **Select** the most appropriate sample of rocks in which to search for a transitional species between lobe-finned fishes and amphibians. **Justify** your selection.
- (b) **Describe** TWO pieces of evidence provided by fossils of a transitional species that would support a hypothesis that amphibians evolved from lobe-finned fishes.

Free Response Scoring Guidelines

2022 #4		
Part	Scoring Guidelines	Topic
(a)	<p>Describe the prezygotic barrier that results in these genetically distinct populations.</p> <ul style="list-style-type: none"> Geographic isolation prevents gene flow between the populations. 	7.10
(b)	<p>Brook trout with longer fins are able to swim faster than brook trout with shorter fins. In one of the Newfoundland streams, the main prey of the brook trout evolved to move faster. For brook trout living in this stream, explain why there is a difference in fitness between longer-finned individuals and shorter-finned individuals.</p> <ul style="list-style-type: none"> Individuals with longer fins are more likely to capture prey and reproduce. 	7.2
(c)	<p>If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, predict the likely impact on both populations.</p> <p>Accept one of the following:</p> <ul style="list-style-type: none"> The two populations will become separate species. The two populations will continue diverging (behaviorally/morphologically/genetically). 	7.10
(d)	<p>Researchers claim that there are more genetic differences between any two current brook trout populations than there are between any single current population and the ancestral brook trout population from which all the trout are descended. Provide reasoning to justify their claim.</p> <p>Accept one of the following:</p> <ul style="list-style-type: none"> Each single population has <u>accumulated mutations/experienced genetic drift</u> (distinguishing it from the ancestral population). The mutations each population accumulated are likely to differ (as a result of different selective pressures). Allele production (as a result of random mutation) and <u>genetic drift/selection by local environmental conditions</u> has resulted in a collection of alleles unique to each population. 	7.10

2021 #4		
Part	Scoring Guidelines	Topic
(a)	<p>The Big Bird lineage became reproductively isolated from <i>G. fortis</i>. Describe one prezygotic mechanism that likely contributed to the reproductive isolation of the Big Bird lineage from <i>G. fortis</i>.</p> <p>Accept one of the following:</p> <ul style="list-style-type: none"> Beak shape/size or song or behavior or mechanical/chemical differences or time of mating or location on the island or primary food source differs between the Big Bird lineage and <i>G. fortis</i>. Description of another mechanism that prevents males and females from different populations from encountering each other/recognizing each other as potential mates. 	7.10
(b)	<p>Based on the data in Figure 1, explain why the Big Bird population has been able to survive and reproduce on Daphne Major.</p> <ul style="list-style-type: none"> The birds have a beak size/shape that differs from the beaks of the competitor finches on the island. Thus, they probably do not compete with the other finch species for food but instead, eat food that the other finches do not consume. 	7.1

(c)	<p>A virus infects and kills all <i>G. magnirostris</i> on Daphne Major but does not affect the other finch species. Assuming food type and availability stay the same, predict the most likely change in the beak phenotype of the Big Bird population after six more generations.</p> <p>Accept one of the following predictions:</p> <ul style="list-style-type: none"> • Option 1: The (mean) beak size will increase (in the population). • Option 2: The (average) beak (in the population) will be longer and deeper. • Option 3: The frequency of large beaks will increase (in the population). • Option 4: The (mean) beak size will stay the same (in the population). 	7.1 7.1.1
(d)	<p>Provide reasoning to justify your prediction in part (c).</p> <p>Accept one of the following:</p> <ul style="list-style-type: none"> • Justification for options 1, 2, and 3: There will be directional selection for larger beaks because larger seeds are more accessible. • Justification for option 4: There is little genetic diversity because all birds are descended from a single pair, and the birds are only six generations from the founder. 	7.1

2019 #5		
Part	Scoring Guidelines	Topic
(a)	<p>Calculation (1 point)</p> <ul style="list-style-type: none"> • 1.25 OR 1.26 	7.6
(b)	<p>Construction (1 point)</p> <ul style="list-style-type: none"> • From top to bottom: Human/Chimpanzee (interchangeable), Gorilla, Orangutan <p>Reasoning (1 point)</p> <ul style="list-style-type: none"> • Gibbon mtDNA is the least similar (to all of the other species)/most different (from all of the other species). • Gibbon mtDNA is the most divergent (from all of the other species). 	7.9
(c)	<p>Circle (1 point)</p> <ul style="list-style-type: none"> • Circle species 1, 2, and 3, as numbered from the top. 	7.9

2018 #1		
Part	Scoring Guidelines	Topic
(a)	<p>Estimate (1 point)</p> <ul style="list-style-type: none"> • First two digits of the answer must be between 30 and 35. <p>Identification (1 point)</p> <ul style="list-style-type: none"> • European <p>Identification (1 point)</p> <ul style="list-style-type: none"> • European/Polar OR Asian/Western (North American) 	7.9
(b)	<p>Construction (1 point)</p> <ul style="list-style-type: none"> • Correctly illustrated evolutionary relationship among the four species <p>Circling (1 point)</p> <ul style="list-style-type: none"> • Correctly circled out-group based on orientation of cladogram 	7.9
(c)	<p>Reasoning (1 point)</p> <ul style="list-style-type: none"> • Genes show more variability (in nucleotide sequence) than proteins do (in amino acid sequences). • mtDNA genome contains multiple genes vs. one <i>lyst</i> gene. • The phenotype associated with the <i>lyst</i> gene is under strong selection. 	6.7

(d)	<p>Prediction (1 point)</p> <ul style="list-style-type: none"> • Mouse fur and/or eyes will not have pigment/will have reduced pigment. • Mouse (fur) will be white/lighter. <p>Justification (1 point)</p> <ul style="list-style-type: none"> • Polar bear <i>lyst</i> gene/LYST protein is associated with a lack of pigment/white hair. • Mutated human <i>lyst</i> gene/ LYST protein is associated with a lack of pigment in hair and eyes. 	6.7
(e)	<p>Description (1 point)</p> <ul style="list-style-type: none"> • Natural selection for the white fur phenotype <p>Prediction (1 point)</p> <ul style="list-style-type: none"> • 0% 	5.3 7.1

2016 #1				
Part	Scoring Guidelines			Topic
(a)	<p>Construct graph (3 points)</p> <ul style="list-style-type: none"> • Correctly plotted bar graph that accurately represents the trend • Correct axis labeling • Correct scale and units 			7.12
(b)	Description (1 point)		Prediction (1 point)	7.12
	<ul style="list-style-type: none"> • As salinity increases <i>lap⁹⁴</i> frequency increases • As salinity decreases <i>lap⁹⁴</i> frequency decreases 		Between 13 and 16 percent (or a selected value between 13 and 16 percent)	
(c)	Describe effect of LAP⁹⁴ activity (1 point)		Describe function of LAP⁹⁴ in maintaining water balance (1 point)	2.8
	<ul style="list-style-type: none"> • LAP⁹⁴ increases osmolarity/solute concentration of the cytosol • LAP⁹⁴ decreases water potential of the cytosol 		Prevents water loss to the environment	
(d)	Explanation (1 point)	Prediction (1 point)	Justification (1 point)	7.12
	<ul style="list-style-type: none"> • Mussels with <i>lap⁹⁴</i> allele are more likely to survive in high salinity/less likely to survive in low salinity. • Mussels without <i>lap⁹⁴</i> allele are less likely to survive in high salinity/more likely to survive in low salinity. 	<ul style="list-style-type: none"> • Mussel population will increase in high salinity. • Mussel population will decline in low salinity. 	<ul style="list-style-type: none"> • Mussels in high salinity with <i>lap⁹⁴</i> allele will osmoregulate. • Mussels in low salinity with <i>lap⁹⁴</i> allele will not osmoregulate. 	

2015 #2				
Part	Scoring Guidelines			Topic

(a)	Process	Description (1 point each box; 3 points maximum)	3.6
	Catabolism of glucose in glycolysis and pyruvate oxidation	<ul style="list-style-type: none"> • Produces NADH for use in ETC • Produces acetyl-CoA for entry into Krebs cycle • Provides energy for (substrate level) phosphorylation of ADP 	
	Oxidation of intermediates in the Krebs cycle	<ul style="list-style-type: none"> • Produces NADH or FADH₂ for use in ETC • Releases high energy electrons for use in ETC • Provides energy to pump protons against their concentration gradient • Produces GTP for (substrate level) phosphorylation of ADP 	
	Formation of a proton gradient by the electron transport chain	<ul style="list-style-type: none"> • The flow of protons through membrane-bound ATP synthase generates ATP • Provides energy for (oxidative) phosphorylation of ADP 	
(b)	Observation	Justification (1 point each box; 3 points maximum)	3.6
	Nearly all existing organisms perform glycolysis	<ul style="list-style-type: none"> • Trait/gene/process originated early and was inherited/passed down/highly conserved • Glycolysis provided a selective advantage that was passed on to descendants 	
	Glycolysis occurs under anaerobic conditions	Origin of glycolysis pre-dates free atmospheric oxygen/photosynthesis	
	Glycolysis occurs only in the cytosol	Origin of glycolysis pre-dates cell types with membrane-bound organelles/eukaryotes/endsymbiosis	
(c)		Calculation/description (1 point each box; 3 points maximum)	3.6
	Calculate available energy in ATP	219 kcal	
	Calculate efficiency	0.31 - 0.32 or 31 - 32%	
	Describe fate of excess energy	Released as heat/increases entropy	
(d)	Question (1 point) <ul style="list-style-type: none"> • A valid scientific question related to evolution of eukaryotes (e.g., Since the Krebs cycle occurs in the "cytoplasm" of the mitochondria (matrix), does it suggest that mitochondria were once prokaryotes?) 		7.6

2015 #3		
Part	Scoring Guidelines	Topic
(a)	<p>Phylogenetic tree (1 point)</p> <p>NOTE: There can be free rotation around the nodes in the tree.</p> <pre> graph TD Root --- Node1 Node1 --- Dpolylepis[D. polylepis] Node1 --- Node2 Node2 --- Node3 Node2 --- Node4 Node3 --- Aforsteri[A. forsteri] Node3 --- Ggallus[G. gallus] Node4 --- Eafricanus[E. africanus] Node4 --- Eferus[E. ferus] </pre> <p>Reasoning (1 point)</p> <ul style="list-style-type: none"> • D. polylepis has the most differences in amino acids (or changes in DNA or proteins as they relate to amino acids). 	7.9

(b)	<p>Identification (1 point)</p> <ul style="list-style-type: none"> Amino acid/molecular data <p>Reasoning (1 point)</p> <ul style="list-style-type: none"> Morphology may be similar (due to convergent evolution/analogous structures) even if there are differences in amino acid/DNA sequences. Molecular data (e.g. amino acid changes, DNA changes) directly show genetic make-up/ reveal evolution. <p>OR</p> <p>Identification (1 point)</p> <ul style="list-style-type: none"> Morphological data <p>Reasoning (1 point)</p> <ul style="list-style-type: none"> Similar molecular sequences may result in different morphologies. An example of species with similar proteins but different morphology (e.g., chimps and humans). 	7.9
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2014 #2								
Part	Scoring Guidelines	Topic						
(a)	<p>NOTE: Points are earned in one column only.</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 50%; text-align: center; vertical-align: middle;"> </td> <td style="width: 50%; text-align: center; vertical-align: middle;"> </td> </tr> <tr> <td style="text-align: center;">Justification (1 point)</td> <td style="text-align: center;">Justification (1 point)</td> </tr> <tr> <td>Lactose and Protein A arose in a common ancestor to all 5 animals. Protein B and Casein arose only in the common ancestor to the pig/cow/horse clade/branch.</td> <td>Lactose, Casein, Protein A, and Protein B arose in a common ancestor to all 5 animals. Protein B and Casein were lost in the common ancestor to the cat/human clade/branch.</td> </tr> </table>			Justification (1 point)	Justification (1 point)	Lactose and Protein A arose in a common ancestor to all 5 animals. Protein B and Casein arose only in the common ancestor to the pig/cow/horse clade/branch.	Lactose, Casein, Protein A, and Protein B arose in a common ancestor to all 5 animals. Protein B and Casein were lost in the common ancestor to the cat/human clade/branch.	7.9
Justification (1 point)	Justification (1 point)							
Lactose and Protein A arose in a common ancestor to all 5 animals. Protein B and Casein arose only in the common ancestor to the pig/cow/horse clade/branch.	Lactose, Casein, Protein A, and Protein B arose in a common ancestor to all 5 animals. Protein B and Casein were lost in the common ancestor to the cat/human clade/branch.							
(b)	<p>Description (1 point each; 4 points maximum)</p> <ul style="list-style-type: none"> Endocytosis of antigen by dendritic cell/macrophage/B-cell Degradation of antigen Antigen complexed with MHC molecule Presentation of antigen on surface of cell Recognition of antigen on surface of antigen presenting cell by (helper) T-cell Activation of signal transduction mechanism in T-cell Activation of (helper) T-cell (Helper) T-cells release chemicals that recruit/activate B-cells Antigen recognition by B-cell Activation of signal transduction mechanism in B-cell Activated B-cell or T-cell will clone itself Plasma cells/B-cells produce antibodies Antibodies recognize antigen Antibody binding to antigen is specific Memory B cells/memory helper T cells are produced <p>Prediction (1 point)</p> <ul style="list-style-type: none"> Results in more rapid immune response Presence of memory cells Greater production of antibodies Antibodies circulate longer Antibodies have a greater affinity for the antigen 	N/A						

(c)	NOTE: Points are earned in a single row only.		N/A
	Prediction (1 point)	Justification (1 point)	
	Infant will be protected/not get sick	Antibodies are passed to infant <i>in utero</i> /via breast milk/infant receives B-cells in breast milk	
	Infant will become sick/die	Insufficient antibodies were transferred to the offspring/infant exposed to high infecting dose of the pathogen	

2014 #8		
Part	Scoring Guidelines	Topic
(a)	Piece of evidence <ul style="list-style-type: none"> New phenotypes Different DNA sequence New genotypes Chromosomal differences Different mRNA sequence Protein with different amino acid sequence 	5.2 6.7 6.8
(b)	Describe mechanism <ul style="list-style-type: none"> Sexual reproduction produces offspring with new combinations of alleles/traits Meiosis produces new combinations of alleles/traits Crossing over produces new combinations of alleles/traits Independent assortment produces new combinations of alleles/traits Random fertilization produces new combinations of alleles/traits Immigration/gene flow introduces new alleles/gene sequences Viral infection inserts DNA into genome Nondisjunction causes anomaly in chromosome number Chromosomal rearrangements (e.g., large deletions, duplications, translocations, inversions, transposons, etc.) inactivate genes or result in multiple copies of genes Radiation or chemicals or mutagens induce mutations/changes in DNA 	5.2 6.7
(c)	Description <ul style="list-style-type: none"> Genetic variation is the basis of phenotypic variation that can be acted upon by natural selection Without genetic variation, there is no phenotypic variation on which natural selection can act 	7.1 7.6

2013 #3		
Part	Scoring Guidelines	Topic
(a)	<ul style="list-style-type: none"> Selection: Rocks from 370 MYA sample. Justification: Transitional fossils are found between 380 MYA (when lobe-finned fishes lived) and 363 MYA (when amphibians appeared) OR between different strata/layers in the correct order. 	7.6
(b)	Descriptions include but are not limited to the following: <ul style="list-style-type: none"> Bones OR specific skeletal structures <ul style="list-style-type: none"> legs /limbs/digits vertebrae flat skulls (interlocking) ribs flexible neck Scales Teeth Other homologous structures Has traits of both the lobe-finned fish and the amphibian Finding the transitional fossils in the same area/same environment as either the lobe-finned fish or the amphibian Molecular (DNA) evidence 	7.6

