

4 points

Question 4: Conceptual Analysis

Twenty million years ago the Caribbean Sea and Pacific Ocean were connected, and water flowed freely between the two bodies of water. Many of the same marine species were found in both areas. Over millions of years, the land referred to as the Isthmus of Panama formed, eventually closing off the connection between the Caribbean Sea and Pacific Ocean and creating two separate bodies of water. The ecology of these two marine habitats was dramatically altered by this land formation. The warmer Caribbean water could no longer flow west, so the Pacific water cooled and became more nutrient-rich, while the Caribbean water became warmer.

- A Describe** the genetic evidence that evolution is occurring in a population. **1 point**
- Examples of acceptable responses may include the following:
- There are changes in allele/gene frequencies.
 - There are heritable changes in phenotypes.
- B Explain** how the isolation of marine species by the formation of a land barrier can lead to divergent evolution of those species. **1 point**
- Examples of acceptable responses may include the following:
- Selective pressures could result in different allele/gene frequencies.
 - (The land barrier) results in reproductive isolation/lack of gene flow/allopatric speciation.
 - Different environmental conditions/pressures select for different alleles/genotypes/phenotypes.
- C** The formation of the Isthmus of Panama connected two continents, North America and South America. Many North American land animal species migrated to South America after the formation of the isthmus and occupied similar niches as South American species. **Predict** the effect the formation of the isthmus had on resource availability for South American species. **1 point**
- (Resource availability) would have decreased.
- D Justify** your prediction in part C. **1 point**
- More species would now be competing for the same resources, (resulting in fewer resources for each individual).

Question 5: Analyze Model or Visual Representation of a Biological Concept or Process

4 points

Researchers study mechanisms that enable or prevent speciation.

New genes can evolve from noncoding regions of DNA. It is not until certain regulatory elements are present in the DNA that a noncoding region becomes a new, functional gene that encodes a protein. These regulatory elements include a promoter, a 5' untranslated region (UTR) followed by a start codon, and a 3' UTR following a stop codon (Figure 1).

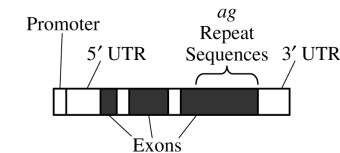


Figure 1. Basic structure of a functional *ag* gene

Researchers studied the evolution of the family of antifreeze-glycoprotein (AG) encoding genes in Gadidae, a family of marine fish known as cods. When present in the fish, these glycoproteins reduce the freezing temperature of the fish. The researchers compared genomic sequences in nine cod species and one non-cod fish species, *B. brosmie*. They recorded the presence or absence of the elements of functional *ag* genes as well as *ag*-like sequences that are similar to a functional gene but have undergone mutation and do not contain all the elements required to enable protein production (Figure 2).

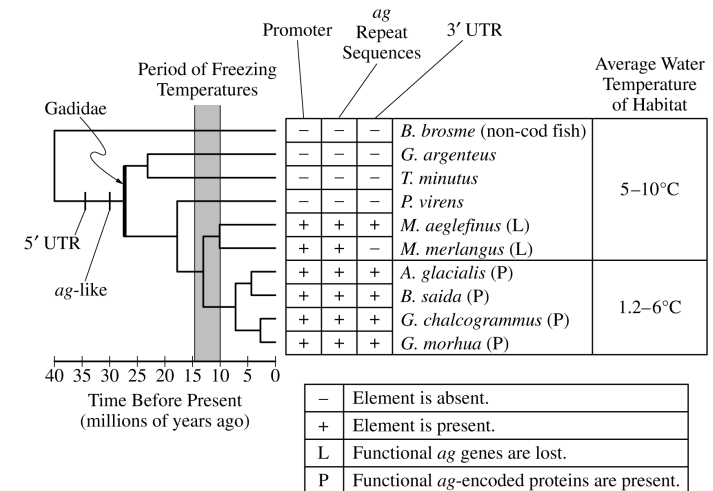
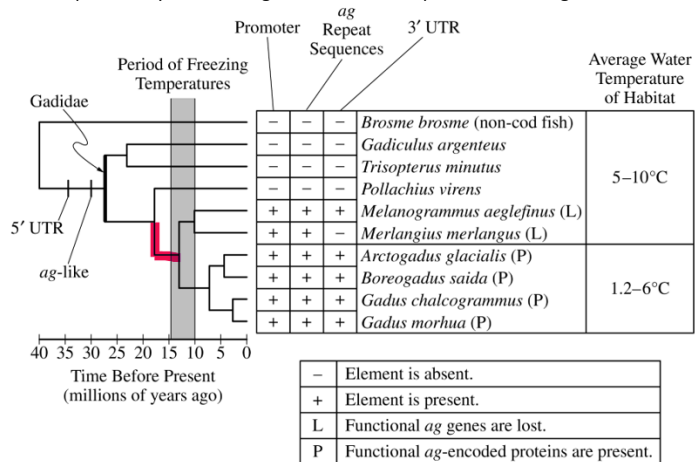


Figure 2. Phylogenetic tree showing the evolution of *ag* genes

- (a) Describe a post-zygotic mechanism that prevents gene flow and thus enables speciation. **1 point**
- The offspring do not survive (long enough to reproduce)/cannot (successfully) reproduce.
- (b) Based on the data in Figure 2, explain how changes to the genome enabled cods to survive and reproduce after a period of freezing temperatures between 10 and 15 million years ago. **1 point**
- (Over time) the addition of the promoter/ag repeat sequences/3' UTR/regulatory elements led to emergence of new genes/ag genes/functional gene products (that prevent freezing).
- (c) Using the template in the space provided for your response, place an "X" on the phylogenetic tree to represent the origin of the functional *ag* gene. **1 point**
- An X is placed anywhere along the colored L-shaped line in the figure.



- (d) Based on Figure 2, explain how genetic differences among the species in the Gadidae family determine the habitats in which they can survive. **1 point**
- Species with the functional *ag* gene/antifreeze glycoprotein are able to live in colder water/lower temperatures (than are species without the functional gene).

Total for question 5 **4 points****Question 4: Conceptual Analysis** **4 points**

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. **1 point**
- Geographic isolation prevents gene flow between the 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 why there is a difference in fitness between longer-finned individuals and shorter-finned individuals. **1 point**
- Individuals with longer fins are more likely to capture prey and reproduce.
- (c) If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, predict the likely impact on both populations. **1 point**
- Accept one of the following:
- The two populations will become separate species.
 - The two populations will continue diverging (behaviorally/morphologically/genetically).
- (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. **1 point**
- Accept one of the following:
- Each single population has accumulated mutations/experienced genetic drift (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 genetic drift/selection by local environmental conditions has resulted in a collection of alleles unique to each population.

Total for question 4 **4 points**

Question 4: Conceptual Analysis**4 points**

In 1981 a single immature male *Geospiza conirostris* finch flew more than 100 kilometers from the Galápagos island of Española to the Galápagos 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 F_1 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.

Birds 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.

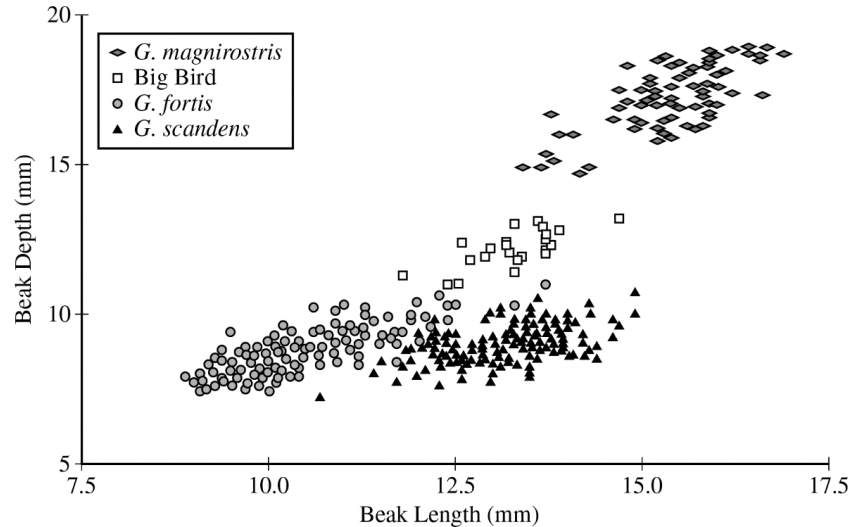


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

- (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*. **1 point**

Accept one of the following:

- 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 *G. fortis*.
- Description of another mechanism that prevents males and females from different populations from encountering each other/recognizing each other as potential mates.

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

- 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.

- (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. **1 point**

Accept one of the following predictions:

- 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).

- (d) Provide reasoning to **justify** your prediction in part (c). **1 point**

Accept one of the following:

- 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.

Total for question 4 4 points