

# Past-paper walk-through

Speciation ■ 7.10

eXercise

## Questions in this set

- 2026 Q5
- 2025 Q4
- 2024 Q5
- 2022 Q4
- 2021 Q4

## 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 5

2026 ■ Q5

Anole lizards throughout the Caribbean islands and Central and South America have pads of varying sizes on the bottom surfaces of their toes. The sizes of the toe pads are genetically determined and not the result of phenotypic plasticity. During storms with high winds, anoles cling to trees with the help of their toe pads. In recent years, an increase in both the number and intensity of storms has occurred across the range of anole habitats.

In 2017, two very intense storms occurred in the Caribbean islands within a month. In 2019, scientists investigated the relationship between the intense storms and the average toe pad size of the offspring of lizards that survived the storms. The scientists determined the average toe pad size of the surviving offspring and grouped their measurements into three categories: small, medium, and large toe pads. The scientists

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then compared the 2019 toe pad measurements with measurements recorded prior to 2017. Their data are represented in the figure.

### **A Map Representing Toe Pad Size Distributions Prior to 2017 and in 2019**

[Two side-by-side maps of the Caribbean islands and northern South America, labeled “Prior to 2017” and “2019”. Symbols mark average toe pad size at various island/mainland locations: circle = Small, triangle = Medium, diamond = Large.

Prior to 2017 map: Caribbean islands region shows small circles and medium triangles (two small circles near the northern islands, two medium triangles near the central islands, one medium triangle further east/south near a smaller island). Mainland South America shows small circles at several locations (one near the northern coast, one further inland, two further south).

2019 map: Caribbean islands region shows the same island locations now marked with medium triangles (hatched, labeled “1”) near the northern islands, and large diamonds

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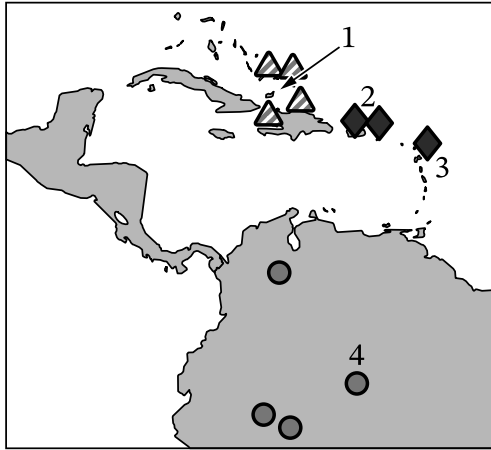
(solid black, labeled “2”) near the central islands, and a large diamond (labeled “3”) near the smaller southeastern island. Mainland South America shows darker-shaded circles at the same locations as before (one near the northern coast marked with a dark circle, region labeled “4” near an inland dark circle, two further south with dark circles). Legend: “Average Toe Pad Size” - open diamond = Large, open triangle = Medium, open circle = Small. “Storm Intensity” - a vertical gradient bar from black (Greatest) through hatched/gray shades down to gray (Least) and white (No storms), corresponding to the shading/fill of each map symbol.]

- (a) **Describe** the role that changes in abiotic factors have in natural selection.
- (b) Based on the figure, **explain** the relationship between storm intensity and average toe pad size.
- (c) **Identify** the region on the 2019 map, by indicating the number, that experienced the least storm intensity.

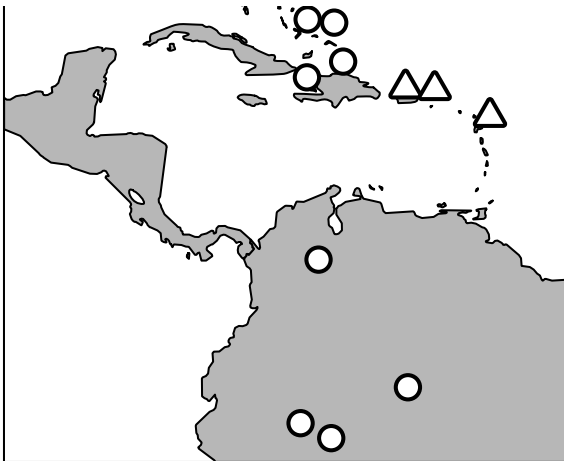
## Question 5

**(d)** Based on the information provided, **explain** how continued differences in storm intensity can apply different selective pressures on anole populations living on the Caribbean islands, eventually leading to speciation.

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## Question 4

2025 ■ Q4

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.
- (b)** Explain how the isolation of marine species by the formation of a land barrier can lead to divergent evolution of those species.

## Question 4

**(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.

**(d)** Justify your prediction in part C.

## Solution 4

(a)

### Mark scheme

- Genetic evidence of evolution occurring in a population includes changes in allele/gene frequencies over time, and/or heritable changes in phenotypes across generations.

## Solution 4

(b)

### Mark scheme

- A land barrier isolating marine species results in reproductive isolation / lack of gene flow between the separated populations (allopatric speciation); different environmental conditions/pressures on each side then select for different alleles/genotypes/phenotypes, so selective pressures produce different allele frequencies, driving divergent evolution.

## Solution 4

(c)

### Mark scheme

- Resource availability for South American species would have decreased, since migrating North American land animals now occupy niches similar to those of South American species and compete for the same resources.

## Solution 4

(d)

### Mark scheme

- More species (native South American plus the migrated North American species) would now be competing for the same set of resources, resulting in fewer resources available to each individual — justifying the prediction that resource availability decreased.

## Question 5

2024 ■ Q5

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).

## Question 5

[Figure 1. Basic structure of a functional *ag* gene. A linear diagram of a gene, drawn left to right as a rectangle divided into segments: a white “Promoter” segment, then a “5’ UTR” segment, then a region labeled “*ag* Repeat Sequences” bracketed over several dark “Exons” segments alternating with white intron/gap segments, and finally a white “3’ UTR” segment at the right end.]

## Question 5

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. brosme*. 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).

## Question 5

[Figure 2. Phylogenetic tree showing the evolution of *ag* genes. Left side: a phylogenetic tree with x-axis “Time Before Present (millions of years ago)” running from 40 down to 0 in increments of 5. The tree root is labeled “Gadidae” and branches split over time; a vertical gray shaded band marks the “Period of Freezing Temperatures” roughly between 15 and 10 million years ago. Branch labels along the tree indicate “5’ UTR” arising at one internal node and “*ag*-like” sequences arising at another (later) internal node, with the tree then splitting into the ten terminal branches (species) listed at right. Right side: a table with columns “Promoter”, “*ag* Repeat Sequences”, “3’ UTR” (each showing “+” for present or “–” for absent, aligned to each species’ branch tip), followed by the species name and, where relevant, a code letter “(L)” or “(P)”; then a column “Average Water Temperature of Habitat”. The rows, top to bottom, are:

## Question 5

| Promoter | ag  | Repeat Sequences | 3' UTR | Species                    | Average Water Temp of Habitat |
|----------|-----|------------------|--------|----------------------------|-------------------------------|
| ---      | --- | ---              | ---    | ---                        | ---                           |
| -        | -   | -                | -      | *B. brosme* (non-cod fish) | 5-10°C                        |
| -        | -   | -                | -      | *G. argenteus*             | 5-10°C                        |
| -        | -   | -                | -      | *T. minutus*               | 5-10°C                        |
| -        | -   | -                | -      | *P. virens*                | 5-10°C                        |
| +        | +   | +                | +      | *M. aeglefinus* (L)        | 5-10°C                        |
| +        | +   | +                | -      | *M. merlangus* (L)         | 5-10°C                        |
| +        | +   | +                | +      | *A. glacialis* (P)         | 1.2-6°C                       |
| +        | +   | +                | +      | *B. saida* (P)             | 1.2-6°C                       |
| +        | +   | +                | +      | *G. chalcogrammus* (P)     | 1.2-6°C                       |
| +        | +   | +                | +      | *G. morhua* (P)            | 1.2-6°C                       |

## Question 5

A legend below the table reads: “—” Element is absent. “+” Element is present. “L” Functional *ag* genes are lost. “P” Functional *ag*-encoded proteins are present.]

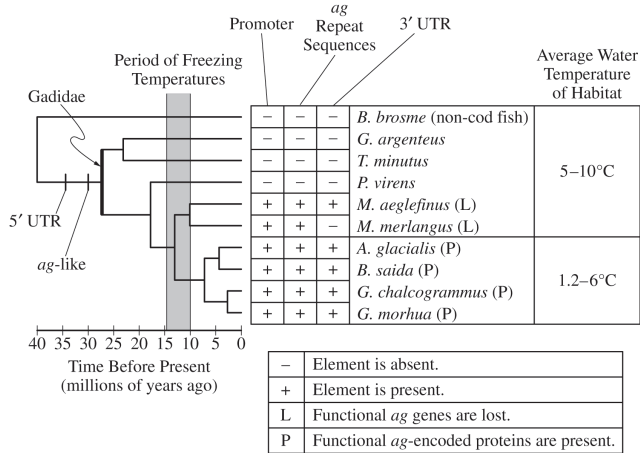
**(a) Describe** a post-zygotic mechanism that prevents gene flow and thus enables speciation.

**(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.

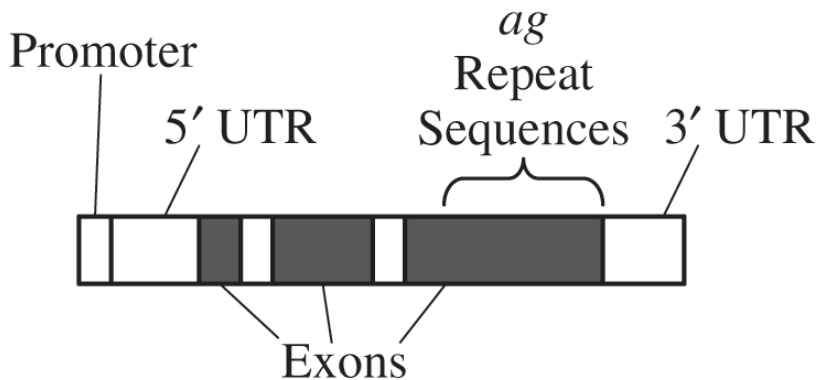
**(c)** Using the template in the space provided for your response, place an “X” on the phylogenetic tree to **represent** the origin of the functional *ag* gene.

**(d)** Based on Figure 2, **explain** how genetic differences among the species in the Gadidae family determine the habitats in which they can survive.

# Question 5



## Question 5



## Solution 5

(a)

### Mark scheme

- A post-zygotic mechanism that prevents gene flow: the offspring do not survive long enough to reproduce, or cannot successfully reproduce (e.g., hybrid inviability or hybrid sterility), so genes cannot flow between the diverging populations even though fertilization/zygote formation occurred.

## Solution 5

(b)

### Mark scheme

- Over time, the addition/gain of the promoter, ag repeat sequences, and 3' UTR (the regulatory/functional elements) led to the emergence of new, functional ag genes/gene products (antifreeze glycoproteins) from the previously nonfunctional ag-like sequence; these antifreeze proteins lower the freezing point of body fluids, allowing cods to survive and reproduce through the period of freezing temperatures 10–15 million years ago.

## Solution 5

(c)

### Mark scheme

- An X placed anywhere along the highlighted L-shaped branch segment in the figure — i.e., on the branch of the phylogenetic tree between the ag-like ancestral lineage and the node/lineage where all three elements (promoter, ag repeat sequences, 3' UTR) first become jointly present (the lineage leading to the (L)- and (P)-labeled species). On this typed practice system, credit the leaf if the student's stated location correctly identifies this branch/interval as the origin point of the functional ag gene.

## Solution 5

(d)

### Mark scheme

- Species with the functional ag gene/antifreeze glycoprotein (all three elements "+") are able to live in colder water/lower temperatures (species labeled (P), habitat 1.2–6°C), while species lacking the functional gene are restricted to warmer water (habitat 5–10°C); species that lost the functional gene (labeled (L)) also live in the warmer range.

## Question 4

2022 ■ Q4

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.

## Question 4

**(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.

## Solution 4

(a)

### Mark scheme

- The prezygotic barrier is geographic isolation, which prevents gene flow between the separated brook trout stream populations.

## Solution 4

**(b)**

### Mark scheme

- Longer-finned individuals swim faster and are therefore more likely to capture the (now faster-evolved) prey and survive to reproduce, giving them higher fitness than shorter-finned individuals, which are less able to catch the faster prey and thus have lower fitness (fewer offspring).

## Solution 4

(c)

### Mark scheme

- If the two populations remain isolated for many generations, they will likely become separate species; alternatively, the two populations will continue diverging behaviorally, morphologically, and/or genetically (increasing reproductive isolation over time, i.e. potential speciation).

## Solution 4

(d)

### Mark scheme

- Justification: each isolated population accumulates its own mutations and experiences its own genetic drift (distinguishing it from the ancestral population), and the mutations each population accumulates are likely to differ as a result of different selective pressures; so, allele production via random mutation plus genetic drift and selection by local environmental conditions produces a collection of alleles unique to each population - making any two current populations differ more from each other than either does from the shared ancestral population.

## Question 4

2021 ■ Q4

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: Scatter plot, “Beak Depth (mm)” (y-axis, 5 to 20) vs. “Beak Length (mm)” (x-axis, 7.5 to 17.5), with four symbol categories: diamonds = *G. magnirostris*

## Question 4

(clustered in upper right, beak length  $\sim 14.5$ -17, beak depth  $\sim 15$ -19); open squares = Big Bird (clustered in the middle, beak length  $\sim 12.5$ -14, beak depth  $\sim 11$ -13.5); grey circles = *G. fortis* (clustered lower left, beak length  $\sim 8.5$ -12.5, beak depth  $\sim 7.5$ -10.5); filled triangles = *G. scandens* (clustered lower middle, beak length  $\sim 10.5$ -14.5, beak depth  $\sim 7.5$ -11). Caption: "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*.

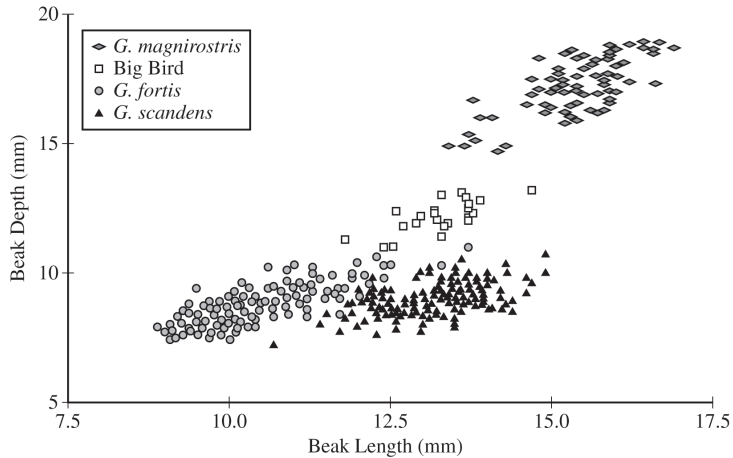
**(b)** Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.

## Question 4

(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).

## Question 4



## Solution 4

(a)

### Mark scheme

- One prezygotic mechanism likely contributing to reproductive isolation (accept any): differences in beak shape/size, song, behavior, mechanical/chemical compatibility, timing of mating, or location on the island, or primary food source, between the Big Bird lineage and *G. fortis*; or any other description of a mechanism that prevents males and females from different populations from encountering or recognizing each other as potential mates.

## Solution 4

(b)

### Mark scheme

- The Big Bird population has survived and reproduced because its beak size/shape differs from the beaks of the competitor finch species on the island (per Figure 1); thus the Big Bird lineage likely does not compete directly with the other finch species for food, but instead eats food that the other finches do not consume (reduced interspecific competition/resource partitioning).

## Solution 4

(c)

### Mark scheme

- Predicted change in Big Bird beak phenotype after six generations without *G. magnirostris* (accept any one): 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.

## Solution 4

(d)

### Mark scheme

- Justification (accept, matching the option chosen in part c): for Options 1, 2, and 3 — there will be directional selection for larger beaks because larger seeds (previously exploited by *G. magnirostris*) are now more accessible/available, favoring big-beaked Big Bird individuals; for Option 4 — there is little genetic diversity in the Big Bird population because all birds are descended from a single founding pair, and the population is only six generations from the founder, so selection has little variation to act on.