# 17. Selection and Evolution

## 17.3 Evolution

## Paper 4

Question Paper

**1** Variation exists in populations of a species and this may provide the opportunity for evolution to occur.

**(b) (i)** Outline the theory of evolution.

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**(ii)** The theory of evolution is supported by DNA sequence data.

Explain how DNA sequences are used to show evolutionary relationships between species.

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**2** *Spea multiplicata* is one of several species of American spadefoot toad.

**(b)** Fig. 7.3 shows the evolutionary relationships between three species of American spadefoot toad.

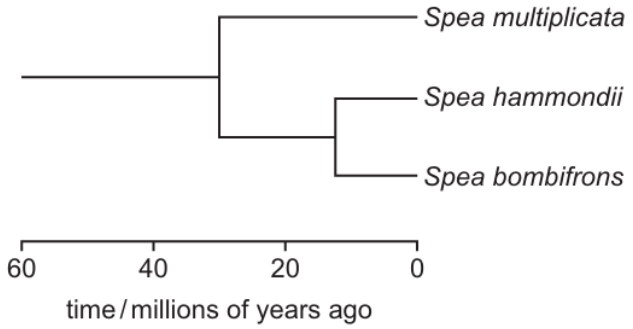



**Fig. 7.3**

Explain how analysis of DNA allowed the evolutionary relationships shown in Fig. 7.3 to be determined.

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**3** *Oryza* is a genus of grass plants that includes the rice, *Oryza sativa*, a food crop.

**(b)** *O. rufipogon* and *O. nivara* are two species of wild rice.

- *O. rufipogon* grows in places where water is always available.
- *O. nivara* grows within the same geographical range as *O. rufipogon*.
- The habitat of *O. nivara* can lack water for part of the year.
- The two species flower at different times of the year.

These two rice species may have evolved by sympatric speciation.

Explain how *O. rufipogon* and *O. nivara* may have evolved through sympatric speciation.

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**4** Green lacewings are a family of insects with more than 1300 species.

The common green lacewing, *Chrysoperla carnea*, is shown in Fig. 9.1.

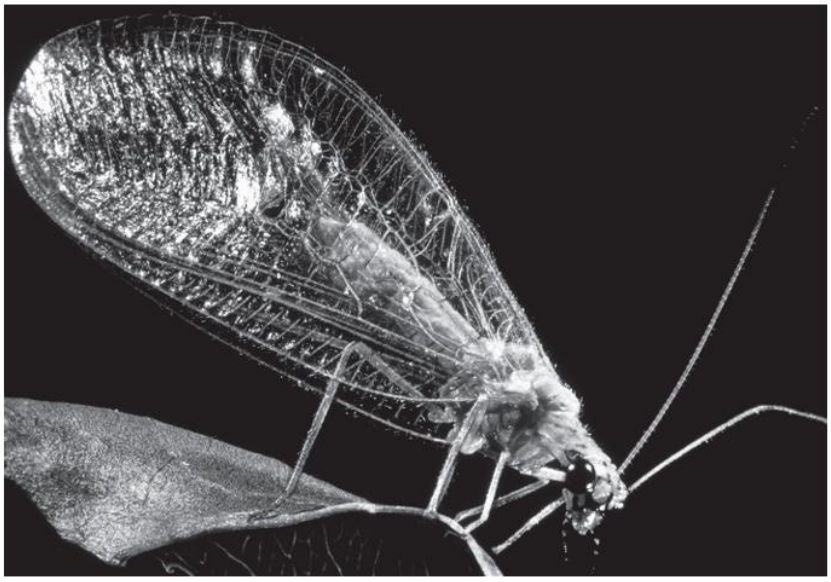


**Fig. 9.1**

**(b)** Two species of green lacewing, *C. carnea* and *C. downesi*, evolved from a common ancestor.

The two species have populations with overlapping distributions in parts of North America.

Table 9.1 shows a comparison of the characteristics of overlapping populations of the two species.

**Table 9.1**

| characteristic | *C. carnea* | *C. downesi* |
|---|---|---|
| breeding months | June to September | April to May |
| courtship song | song with a regular rhythm | song with no regular rhythm |
| colour | light green | dark green |

Suggest how speciation occurred to produce the two different species of green lacewing.

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**5** A large number of alpine plant species grow in the mountains of New Zealand's South Island. Alpine plants are defined as plants that live above the treeline, which is the height above which trees cannot grow. The current treeline for most of South Island is 1200 m.

**(a)** The alpine areas nearest to South Island are 1500–2000 km away across the sea. Many of South Island's alpine species live nowhere else in the world.

Explain how a large number of alpine plant species developed on South Island.

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**(b)** Fig. 5.1 shows two aspects of the history of South Island over the last 3.9 million years.

- The dashed line shows how the mean height of mountains in the Clyde region of South Island increased over time. The mountains in this range have a mean height of 2400 m at the present time.
- The solid line models the height of the treeline over time based on geological climate data. The treeline was higher when the climate was warmer, and the treeline was lower when the climate was colder, during ice ages.

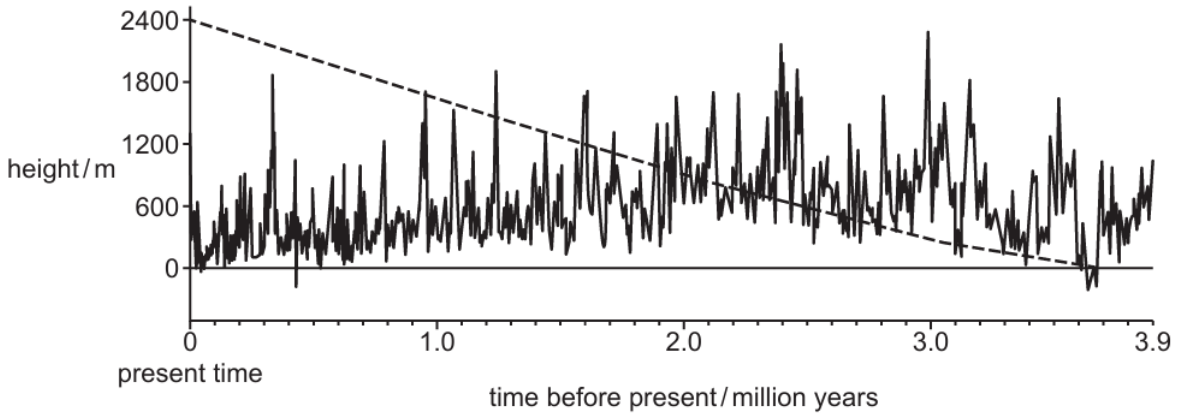



**Fig. 5.1**

**(i)** With reference to Fig. 5.1, identify with reasons the time period when South Island's alpine plant species developed.

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**(ii)** Suggest how DNA sequence data could be used to confirm the time period you identified in **(i)**.

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**6** Two subspecies of reindeer, *Rangifer tarandus*, live in North America. Members of the different subspecies belong to the same species but have some morphological differences and are found in different geographical locations.

Fig. 5.1 shows a reindeer.



**Fig. 5.1**

Table 5.1 compares the features of the two North American reindeer subspecies.

**Table 5.1**

| **feature** | **woodland subspecies, *R. tarandus caribou*** | **barren ground subspecies, *R. tarandus groenlandicus*** |
|---|---|---|
| habitat | southern woodland (warmer) | northern tundra (colder) |
| type of food | tree leaves, grass | lichens, moss |
| summer and winter feeding grounds overlap | yes | no |
| carry out long migrations | no | yes |
| body size | large | small |
| colour of fur | dark | light |

**(a)** During the last ice age an ice sheet separated southern and northern populations of *R. tarandus* in North America.

Explain how this ice sheet affected the evolution of *R. tarandus* to result in the two different subspecies.

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**7** Bison are a type of large wild cattle. Ancestors of modern bison appeared in Asia 2.5 million years ago. This ancestral bison species increased its range into Europe and North America.

While the ancestral species is now extinct, its descendants include *Bison bonasus*, the European bison, and *Bison bison*, the American bison.

Fig. 5.1 shows an American bison.



**Fig. 5.1**

**(a)** After the end of the last ice age, populations of the ancestral bison were separated by sea and by forests that were not suitable as habitats. The separation resulted in the evolution of the European bison and the American bison.

Explain how this separation resulted in the evolution of the two bison species.

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**(c)** The European bison has a nuclear genome that is very similar to that of the American bison. The European bison has a mitochondrial genome that is more similar to that of wild cattle of the genus *Bos* than to the American bison.

Discuss what this implies about the evolutionary history of the European bison.

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**8** Twenty million years ago, an ocean covered the area where the country of Panama is now located. There was a gap between the continents of North America and South America through which the waters of the Atlantic and Pacific Oceans flowed freely.

The porkfish, *Anisotremus sp*, lived in this area between North America and South America.

Fig. 8.1 shows a porkfish.



**Fig. 8.1**

About 3 million years ago, volcanic activity and sedimentation formed a narrow strip of land, Panama, joining North America and South America.

Fig. 8.2 shows the area 20 million years ago and now.

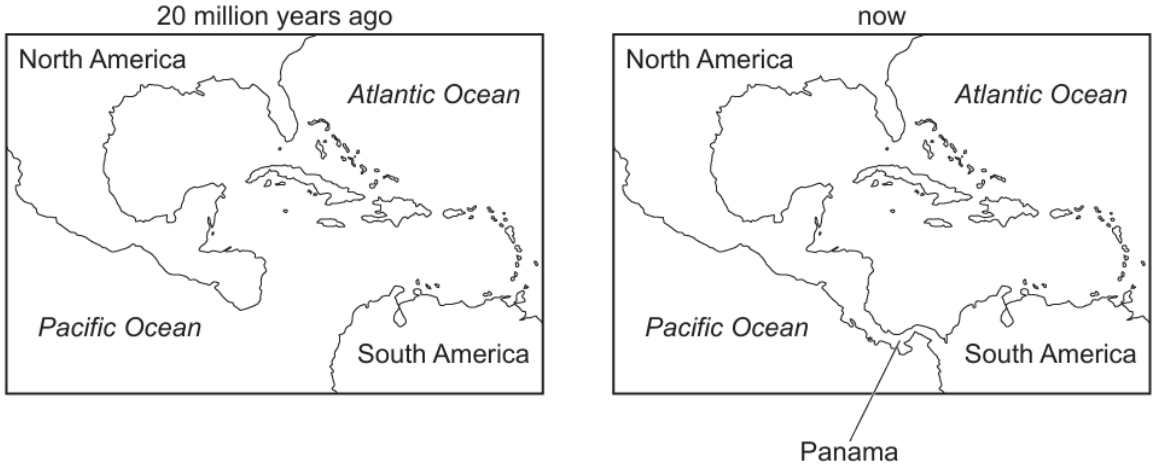



**Fig. 8.2**

Twenty million years ago, porkfish in the Atlantic and Pacific Oceans were able to breed successfully and produce fertile offspring.

Explain why Atlantic porkfish and Pacific porkfish are now **not** able to breed successfully to produce fertile offspring.

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**9** A subspecies is a genetically distinct population within a species that has some phenotypic differences from the rest of the species, but is not yet reproductively isolated.

Nine subspecies of the tiger, *Panthera tigris*, have been identified. Six of these subspecies are found on mainland Asia. Three of the subspecies originate from the Sunda Islands. These islands include Bali, Java and the large island of Sumatra.

Fig. 3.1 shows these three islands.

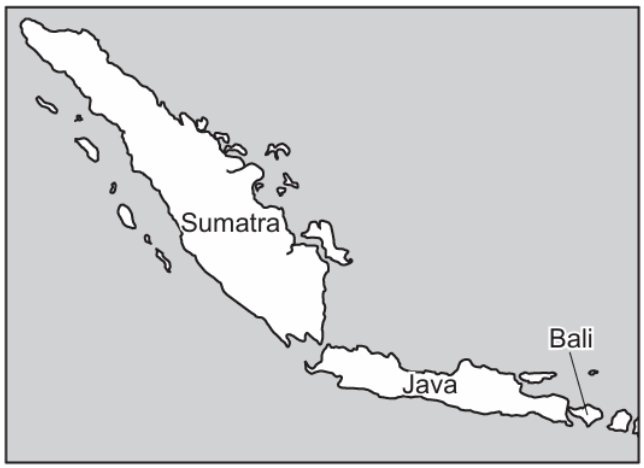



**Fig. 3.1**

- The Bali tiger, *Panthera tigris balica* (*P. t. balica*), became extinct in the 20th Century. The Bali tiger was found only on the island of Bali.
- The Javan tiger, *P. t. sondaica*, became extinct in the 20th Century. The Javan tiger was found only on the island of Java.
- The Sumatran tiger, *P. t. sumatrae*, lives only on Sumatra and is the closest living relative of Bali and Javan tigers.

20 000 years ago land bridges temporarily connected the Sunda Islands.

A recent study carried out a genetic analysis of the nine subspecies of tiger. Specific sections of mitochondrial DNA (mtDNA) that are useful in studies of evolution were amplified using PCR and compared to assess their evolutionary history.

- The source of DNA for the extinct subspecies came from museum specimens.
- mtDNA was extracted and polymerase chain reaction (PCR) carried out using primers based on specific sections of tiger mtDNA.
- The mtDNA sections for the three island subspecies were genetically distinct from the other six mainland subspecies.
- The mtDNA sections for the three island subspecies were all found to be very similar.

**(a)** Suggest **and** explain how the three subspecies of tiger on the Sunda Islands formed.

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**(c)** Describe **and** explain **one** characteristic of mtDNA that makes it more useful than using nuclear DNA to provide evidence of evolution.

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**10** California salamanders are terrestrial amphibians.

An original population of California salamanders occupied an area of forest in northern California. Approximately 10 million years ago, two separate populations, **A** and **B**, started to migrate from the original population.

- Population **A** travelled along the coast of California, to the west of the Great Central Valley.
- Population **B** travelled east of the Great Central Valley.

The two populations now live close to each other in southern California.

Fig. 8.1 outlines the migratory routes of populations **A** and **B**.

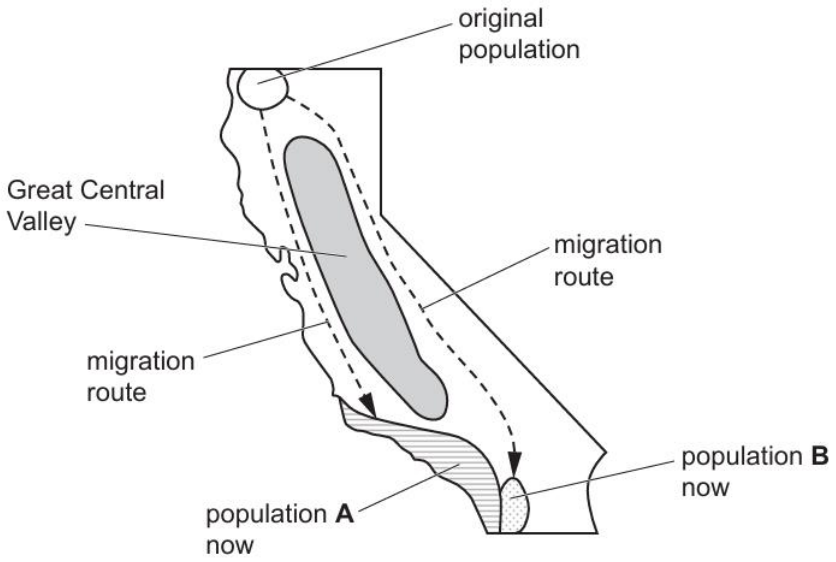



**Fig. 8.1**

Salamanders from population **A** rarely interbreed with salamanders of population **B**. If they do interbreed, the offspring are infertile.

Suggest **and** explain the sequence of events that have resulted in these two populations becoming reproductively isolated from each other.

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**11** Cats are members of the Felidae family. Two genera of Felidae are *Leopardus* and *Panthera*.

**(a)** The genus *Leopardus* consists of species of wild cats that are small and spotted. In 2013, biologists investigated the evolution of *Leopardus tigrinus* in South America.

Fig. 3.1 shows the locations in South America of two populations of. *L. tigrinus*, population **A** and population **B**.




**Fig. 3.1**

- Population **A** lives in grassland and desert habitats and population **B** lives in forest habitats.
- The cats in population **A** have a lighter coat colour and a different pattern of spots from the cats in population **B**.
- Genetic analysis shows that population **A** is genetically distinct from population **B**.
- Population **B** has now been reclassified as a new species, *L. guttulus*.

**(ii)** Explain how the two species, *L. tigrinus* and *L. guttulus*, have evolved from one original population in South America.

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**12** A subspecies is a genetically distinct population of a species that has some phenotypic differences but is not yet reproductively isolated.

500 000 years ago, the European house mouse, *Mus musculus*, evolved into two subspecies, *Mus musculus domesticus* and *Mus musculus musculus*.

**(a)** Suggest **and** explain how the two subspecies *M. m. domesticus* and *M. m. musculus* could have evolved from the original *M. musculus* population.

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**(b)** Today, *M. m. domesticus* populations are separated from *M. m. musculus* populations by a large hybrid zone. The hybrid zone formed 5000–1000 years ago when populations of the two subspecies overlapped and interbreeding occurred between the two subspecies, resulting in hybrids.

Researchers investigated the populations in the hybrid zone.

It was observed that:

- hybrid mice were infected by more intestinal worms than *M. m. domesticus* and *M. m. musculus*
- *M. m. domesticus* and *M. m. musculus* individuals frequently mate together
- hybrid male mice had a very low fertility score based on testis weight and total sperm production, whereas *M. m. domesticus* and *M. m. musculus* males had a very high fertility score
- some female hybrids were sterile
- crosses between a fertile female hybrid and a male from either subspecies produced a very low number of offspring.

*M. m. domesticus* and *M. m. musculus* usually have the same diploid number ($2n = 40$). Some individuals of *M. m. domesticus* have a different diploid number ($2n = 34$).

Discuss the extent to which pre-zygotic and post-zygotic isolating mechanisms maintain *M. m. domesticus* and *M. m. musculus* as two separate subspecies within the hybrid zone.

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**13** DNA barcoding is used in species identification.

To create a DNA barcode, a specific region of DNA is sequenced so that it can be compared to an online database of reference DNA. One region of DNA that is commonly used is 648 base pairs long within a mitochondrial gene, coding for the enzyme cytochrome c oxidase I.

**(a)** The solitary sandpiper, *Tringa solitaria*, is a migratory bird.

DNA barcoding has shown that approximately 2.5 million years ago *T. solitaria* evolved into two subspecies, *Tringa solitaria solitaria* and *Tringa solitaria cinnamomea*.

A subspecies is a genetically distinct population of a species that has some phenotypic differences but is not yet reproductively isolated.

*T. s. solitaria* breed in eastern North America whereas *T. s. cinnamomea* breed in western North America.

Suggest **and** explain how the two subspecies *T. s. solitaria* and *T. s. cinnamomea* could have evolved from the original *T. solitaria* population.

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**(b)** Fig. 3.1 shows an American oystercatcher, *Haematopus palliatus*.



**Fig. 3.1**

The black oystercatcher, *Haematopus bachmani*, has all black feathers.

DNA barcoding analysis suggests that the American oystercatcher and the black oystercatcher are **not** separate species.

Suggest how DNA barcoding evidence could indicate that the American oystercatcher and black oystercatcher are **not** separate species.

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**14** The genus *Heliconius* contains more than 40 species of brightly patterned butterflies.

Researchers have investigated in the laboratory how one species, *Heliconius heurippa*, could have developed as a separate species. The phenotype of *H. heurippa* is intermediate between that of two other species, *H. cydno* and *H. melpomene*.

Laboratory breeding experiments showed that:

- matings between *H. cydno* and *H. melpomene* (parent species) produce fertile hybrid offspring
- controlled matings of the hybrids produces individuals identical in appearance to *H. heurippa* within three generations
- hybrid butterflies prefer to mate with each other, rather than with individuals of either of the parent species.

The researchers concluded that the *H. heurippa* species could contain DNA from the two parent species as a result of hybridisation.

**(a) (i)** Suggest, with reasons, **one** prediction that can be made about the chromosome numbers of *H. cydno* and *H. melpomene*.

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**(ii)** The researchers thought that, because the hybrid butterflies preferred to mate with each other, this could make speciation more likely to occur.

Give reasons why the researchers thought that this made speciation more likely.

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**(b)** *Heliconius* butterflies taste unpleasant to predators such as birds. The bright colours on the wings of the butterflies act as warnings so that birds avoid eating them.

Individual birds have to learn which patterns to avoid. If one *Heliconius* species is abundant, or if it has a pattern shared with another similar species, predators learn to avoid this pattern faster. Therefore this pattern provides a selective advantage.

In the wild, *Heliconius* hybrids occur in small numbers and have patterns that do not resemble the established warning pattern of either parent species. These hybrids have a selective disadvantage.

This is an example of a post-zygotic isolating mechanism.

Explain how selection against hybrids can act as a post-zygotic isolating mechanism.

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**15** **(a)** State the general theory of evolution.

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**(b)** Different types of organism have evolved different structures containing light receptors. Eyes are organs containing light receptors.

Fig. 6.1 describes the light receptors of several types of organism.

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| *Euglena* (a single-celled eukaryote) has a simple eyespot that can only detect the intensity and direction of light. |
| Turbellarian flatworms have cup-shaped eyes, each with a layer of light receptor cells. They can detect the intensity and direction of light better than *Euglena*. They also detect movement. |
| The mollusc *Nautilus* has eyes with deeper cups and narrower openings for light to enter. They can form a rough image, see shapes and detect the direction of light better than turbellarian flatworms. |
| The mollusc *Nucella* has eyes with lenses made of jelly. They can form a more detailed image than the eyes of *Nautilus* and can focus light to a small degree. |
| Mammals have eyes that are more complex than *Nucella*. They have a fixed lens (the cornea) that bends light and a lens that can change shape to focus on objects at different distances. The lenses focus light onto a deeply cup-shaped layer of light receptor cells. The eyes form a very detailed image. |

**Fig. 6.1**

Using the information in Fig. 6.1, suggest how a complex eye such as that of mammals could have evolved in successive stages.

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**(c)** Octopuses are molluscs that have eyes very similar to those of mammals.

Octopuses and mammals are not closely related.

Octopuses and mammals have lenses that can change shape to focus on objects at different distances.

Suggest reasons why octopuses and mammals have evolved similar eye structures.

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**(d)** Molecular evidence is used to investigate evolution. One study involved a marine worm, *Platynereis dumerilii*, that still has characteristics similar to its ancestors from 600 million years ago.

Researchers sequenced all the proteins in light receptor cells of *P. dumerilii* and humans. The results showed that there are many similarities between the protein sequences of *P. dumerilii* and humans, particularly in the light-detecting protein opsin.

**(i)** State what this molecular evidence indicates about the evolutionary origins of *P. dumerilii* and humans.

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**(ii)** Explain how amino acid sequences indicate how close the relationship is between two species.

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**16** Researchers investigated the extent to which the founder effect and natural selection affected evolutionary change.

Fig. 5.1 shows the brown anole lizard, *Anolis sagrei*. These lizards live on a number of Caribbean islands and feed on a variety of invertebrates and other small animals.




**Fig. 5.1**

*A. sagrei* spends a lot of time perching (resting) on, or moving along, branches of shrubs and trees. The width of the branch that *A. sagrei* perches on is known as the perch diameter, as labelled in Fig. 5.1.

There is a positive correlation between perch diameter and hind limb length of *A. sagrei*.

- Longer hind limbs allow *A. sagrei* to run faster on vegetation with a larger diameter.
- Shorter hind limbs are needed to provide stability on vegetation of a smaller diameter.

In 2004, a hurricane caused the death of all the *A. sagrei* lizards on seven islands.

In 2005, the researchers randomly collected seven male and seven female lizards from a source population on a nearby island. For each of the seven islands affected by the hurricane, a male and female lizard were mated and placed on each island. These islands formed the experimental founder islands where new populations of *A. sagrei* were successfully established from each founding pair.

Fig. 5.2 shows the difference in vegetation between the source island and the seven experimental founder islands.




**Fig. 5.2**

**(c)** In the investigation, one population of *A. sagrei* was established on each experimental founder island.

Outline how speciation may occur on the seven experimental founder islands.

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**17** Adult *Drosophila* fruit flies feed on yeasts on the surface of ripe fruits. Female flies lay their eggs inside the fruit and the larvae feed inside the fruit before developing into adults.

The tree *Morinda citrifolia* produces fruits called noni fruits. Noni fruits contain a toxin and are avoided by nearly all *Drosophila* species, including *Drosophila yakuba* in mainland Africa.

One population of *D. yakuba* lives on the island of Mayotte off the coast of Africa. The population of *D. yakuba* on Mayotte has specialised to feed on noni fruit. Flies of this population produce enzymes that give them resistance to the toxin in noni fruits. Adults are able to feed on yeasts on the fruit surface and their eggs and larvae can develop and grow inside the fruit.

Scientists have used bioinformatics to estimate that the unique *D. yakuba* population on Mayotte originated in the last 30 000 years.

**(b)** Explain why living on an island increases the likelihood of the noni toxin-resistant population of *D. yakuba* on Mayotte becoming a separate species to the mainland population of *D. yakuba*.

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**(c)** Suggest how scientists can use bioinformatics to estimate the length of time that the population of *D. yakuba* has been living on Mayotte.

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**18** The Hawaiian archipelago is a group of volcanic islands in the Pacific ocean.

Fig. 4.1 shows the relative locations of five of these islands.

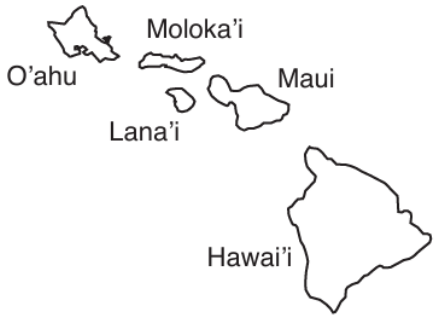



**Fig. 4.1**

Table 4.1 shows the size and age of these five islands and the total number of *Mecyclothorax* ground beetle species and their species density, on each island.

Data for the island of Maui is shown as two distinct regions, West and Haleakalã. This is because they formed at different times from two separate volcanoes.

**Table 4.1**

| **island** | **area / km$^2$** | **age of island / million years** | **total number of *Mecyclothorax* species** | **species density / number of species per km$^2$** |
|---|---|---|---|---|
| Hawai'i | 10 433 | 0.4 | 30 | 0.003 |
| Lãna'i | 364 | 1.3 | 3 | 0.008 |
| Maui (West) | 443 | 1.3 | 27 | 0.061 |
| Maui (Haleakalã) | 1440 | 1.1 | 116 | 0.081 |
| Moloka'i | 673 | 1.9 – 1.8 | 43 | 0.064 |
| O'ahu | 1545 | 3.7 – 2.6 | 20 | ..... |

Fig. 4.2 shows a ground beetle of the genus *Mecyclothorax*. All the beetle species of this genus on the Hawaiian archipelago form a monophyletic group, descended from one original colonising species that reached Maui from Australia.

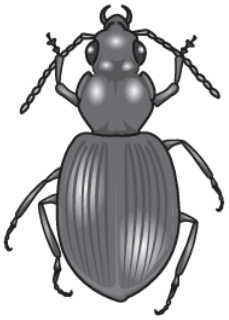


**Fig. 4.2**

**(a) (i)** Complete Table 4.1 by calculating the density of *Mecyclothorax* beetle species on the island of O'ahu. [1]

**(ii)** Use Table 4.1 to explain why the island of Hawai'i has the lowest density of *Mecyclothorax* beetle species.

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**(iii)** Use Fig. 4.1 and Table 4.1 to suggest why O'ahu has a lower number of *Mecyclothorax* beetle species than Moloka'i.

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**(b)** The rate of speciation of *Mecyclothorax* beetles on the slopes of the volcano Haleakalã, on Maui, is the highest recorded for any genus or location on earth.

The volcano last erupted 400 years ago. This produced lava flows which cut through ancient forest and vegetation, dividing it into many separate microhabitats.

Explain how the large number of *Mecyclothorax* beetle species on Haleakalã developed.

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