WJEC (Eduqas) Biology A-level
Topic 2.6: Variation and Evolution
Questions by Topic

1. Finches that inhabit the Galapagos Islands (which include the islands of Genovesa and Champion) have become known as Darwin's Finches. They provide useful evidence to support a gene pool model of speciation.

(a) Define the term 'gene pool'. [1]

.....

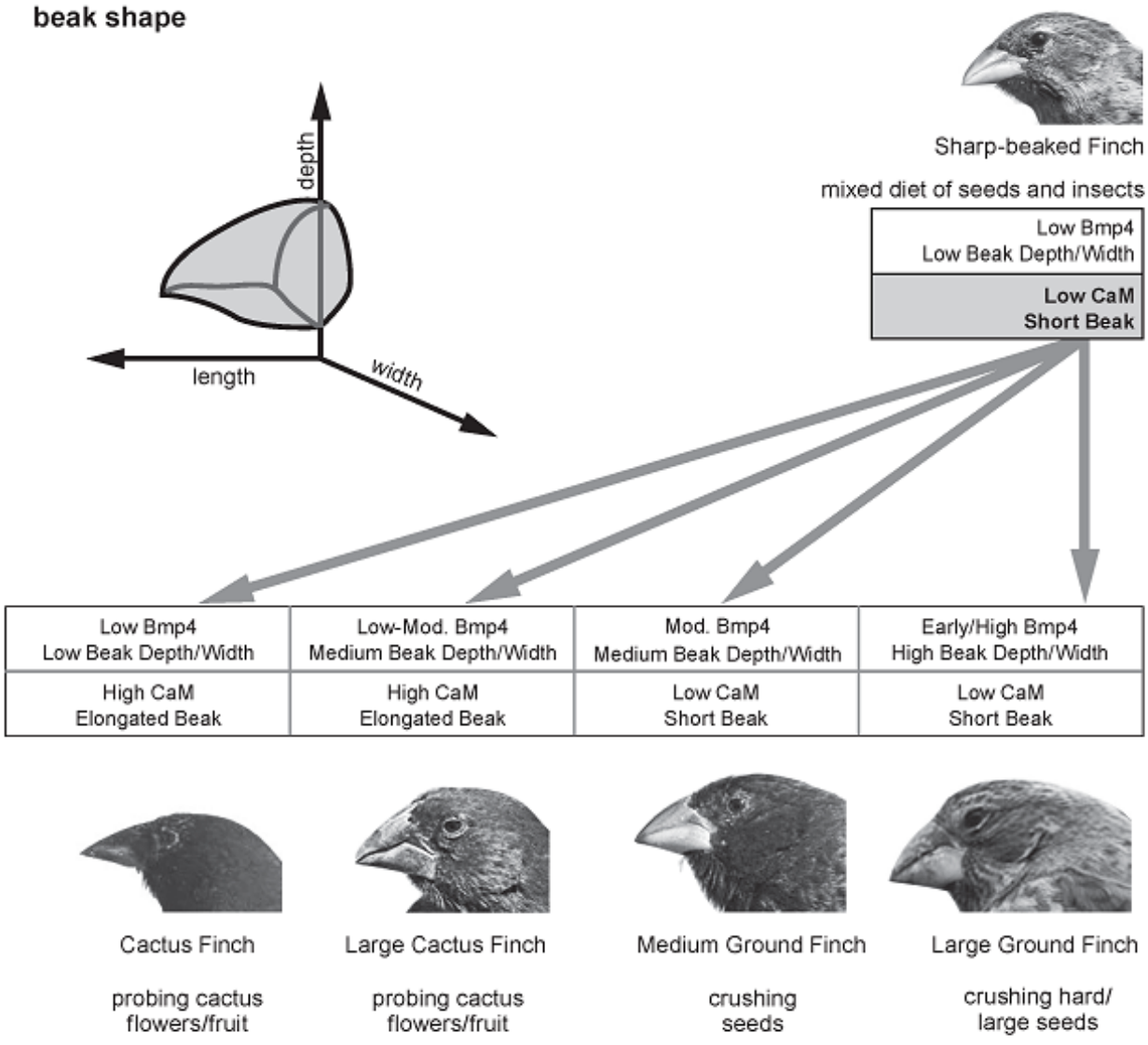
.....

.....

(b) There is a strong correlation between the size of finches' beaks and the size of the seeds the beak is able to crack. Recent research has shown that two proteins are involved in controlling beak size:

Bone promoting molecule 4 (Bmp4) and calmodulin (CaM)

The diagrams below show links between the two molecules, beak shape and food source.



(i) Describe the link between beak shape and food source. [1]

.....

.....

.....

(ii) Describe the link between CaM and beak shape. [1]

.....

.....

.....

(c) One theory for the evolution of the different species of Darwin's Finches is that a small population of Sharp-beaked Finch *(Geospiza difficilis)* was blown onto one of the islands from mainland South America. Over many generations they became adapted to feed on the different food sources available.

(i) Give **one** reason why, in the early generations of the island colony, the frequencies of the alleles responsible for producing Bmp4 and CaM might have differed from their frequency in the mainland population. [1]

.....

.....

.....

(ii) Explain how, in subsequent generations, the frequency of the allele responsible for producing CaM would have increased on an island where the main food source was cactus flowers. [4]

.....

.....

.....

.....

.....

.....

.....

.....

.....

.....

.....

(d) The Large Cactus Finch *(Geospiza conirostris)* from the island Genovesa has a beak that closely resembles that of the Cactus Finch *(Geospiza scandens)* from the island Champion.

(i) State why these two finches are considered to be separate species. [1]

.....

.....

(ii) Explain why they evolved into separate species. [2]

.....

.....

.....

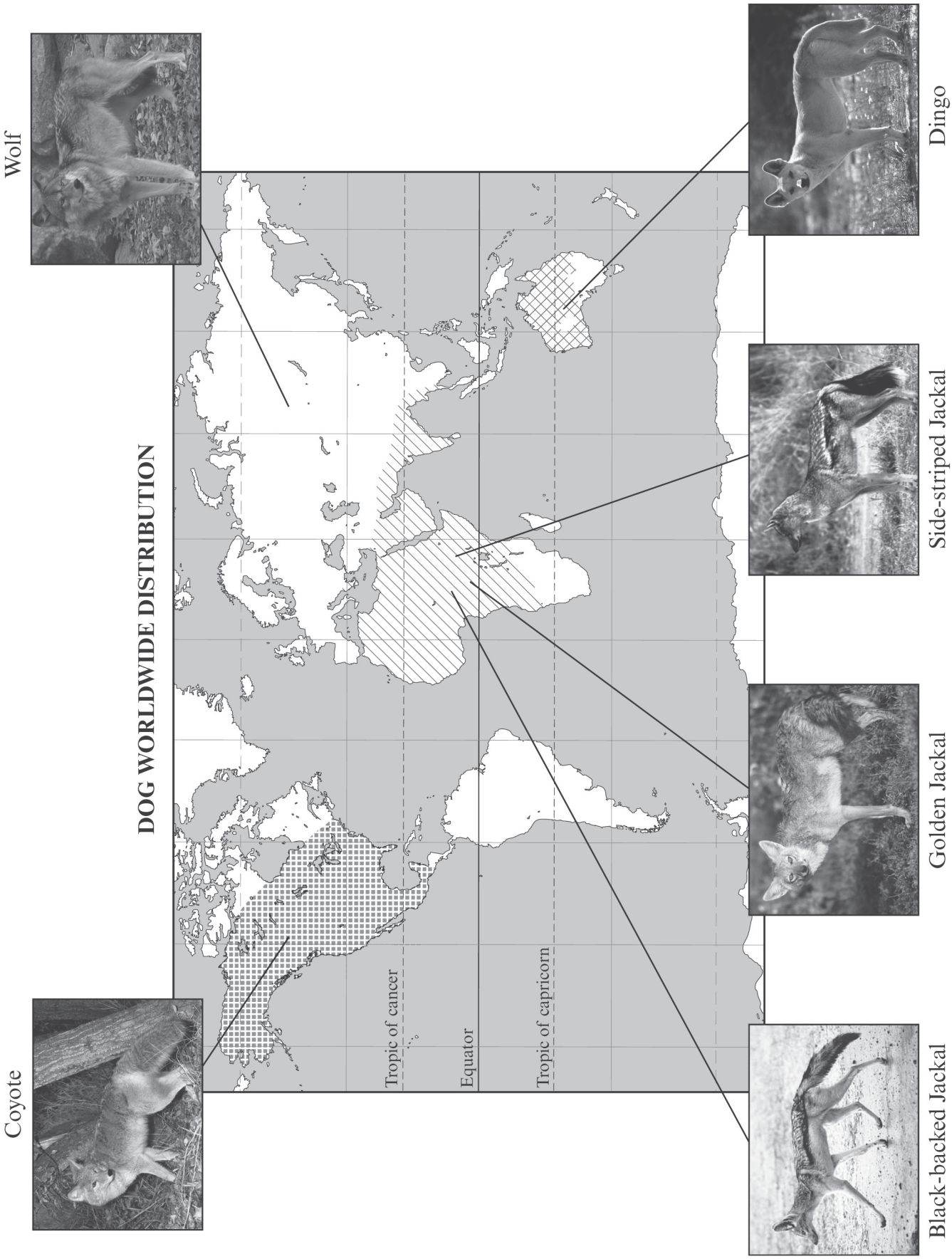
.....

.....

11

2.

The map shows the world distribution of different members of the canine (dog) family and the grid following shows if mating between different members of the canine family results in fertile offspring.



	dog	wolf	dingo	coyote	golden jackal	black-backed jackal	side-striped jackal
dog	✓	✓	✓	✓	✓	×	×
wolf	✓	✓	✓	✓	✓	×	×
dingo	✓	✓	✓	✓	✓	×	×
coyote	✓	✓	✓	✓	✓	×	×
golden jackal	✓	✓	✓	✓	✓	×	×
black-backed jackal	×	×	×	×	×	✓	×
side-striped jackal	×	×	×	×	×	×	✓

Key:
Fertile offspring = ✓
Infertile offspring = ×

(a) Using the data, state which members of the canine family are the same species as the dog. Give a reason for your answer. [2]

.....

.....

.....

.....

.....

.....

(b) Suggest **two** *other* pieces of evidence which would confirm that they were members of the same species. [2]

.....

.....

.....

.....

.....

(c) (i) Use the map to suggest which species are likely to have been produced by sympatric speciation. [1]

.....

(ii) Suggest a possible isolating mechanism. [1]

.....

.....

.....

(d) The chromosome number of the dog is 2n 78 and the European Red Fox is 2n 38. Rare cases of mating between dogs and foxes have been recorded (resulting in an animal called a dox) but the offspring are all sterile. Give reasons for this sterility. [4]

.....

.....

.....

.....

.....

.....

.....

.....

(Total 10 marks)

3. A species of mouse *Peromyscus polionotus* found in Florida, USA, has a number of different coat colours. Coat colour in mice is controlled by several genes. Dark fur is produced when the hair producing cells secrete a pigment called eumelanin. A high level of eumelanin is produced when a transmembrane protein called MC1R is stimulated by a hormone.

(a) The diagram below shows part of the amino acid sequence of MC1R, part of the sequence of nucleotides in the gene for MC1R and how it might change to produce light fur:

Original

Amino acid sequence: Ile – Thr – Lys – Asn – Arg – Asn – Leu – His – Ser

Nucleotide sequence (allele R): ATCACCAAAAACCGCAACCTGCACTCG

Changed to produce light fur

Amino acid sequence: Ile – Thr – Lys – Asn – Cys – Asn – Leu – His – Ser

Nucleotide sequence (allele C): ATCACCAAAAACTGCAACCTGCACTCG

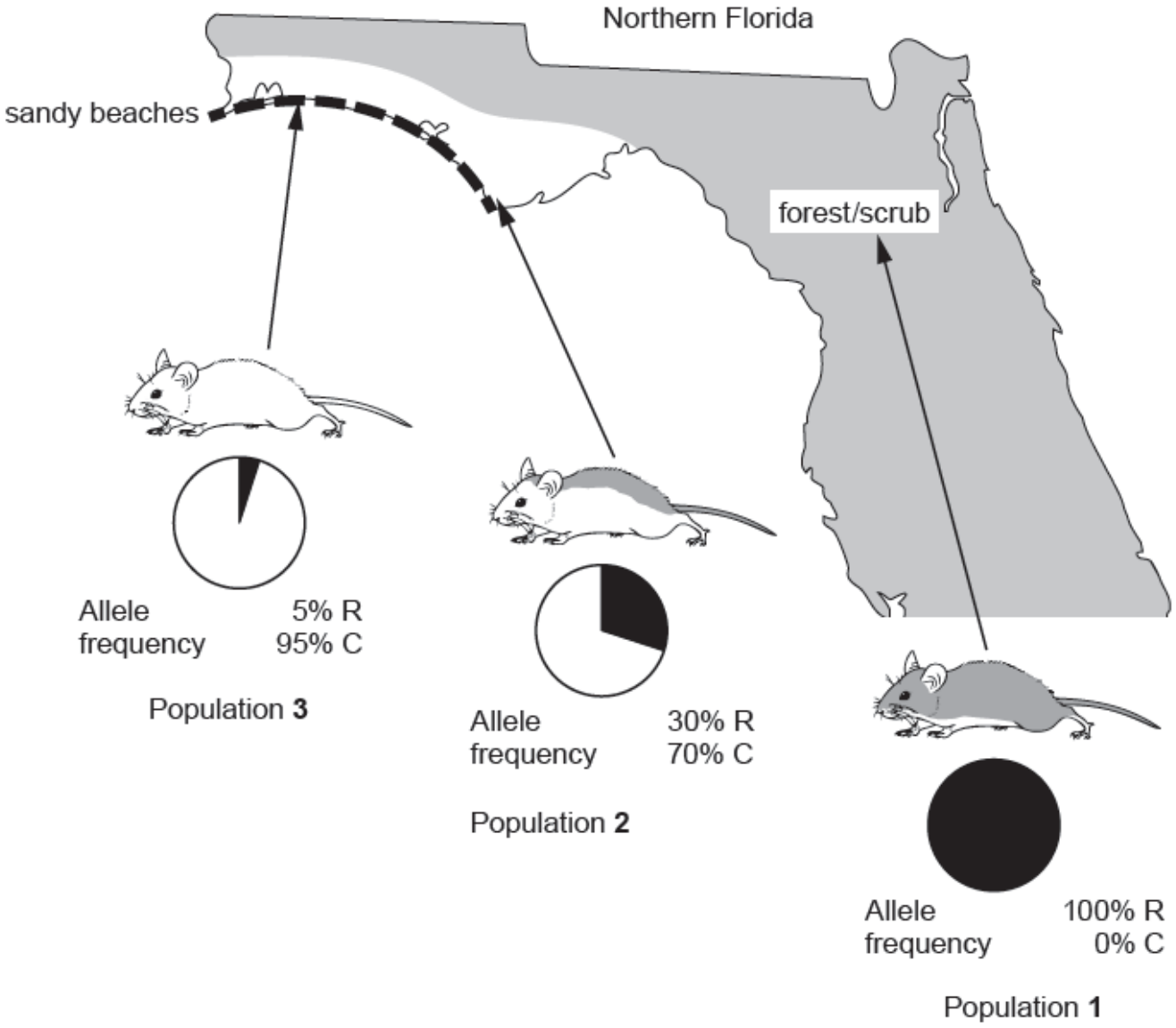
(i) Describe the change in the gene and the subsequent change in the MC1R molecule.

[2]

(ii) Using the information provided, explain how this change results in mice with light fur.

[2]

(b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



(i) Use the diagram to suggest how fur colour is related to environmental conditions.

[2]

(ii) Under what circumstance could the difference between the allele frequencies in populations **2** and **3** be explained by **genetic drift**, despite both living on beaches?

[1]

(iii) Explain how **Natural Selection** could have caused the relative allele frequency shown in population **3**.

[4]

(iv) Under what circumstances would the mouse population become a separate species?

[1]

4. The Grand Banks is an area of sea off the coast of Newfoundland in Canada. It was once one of the most productive fishing grounds in the world for Atlantic cod.

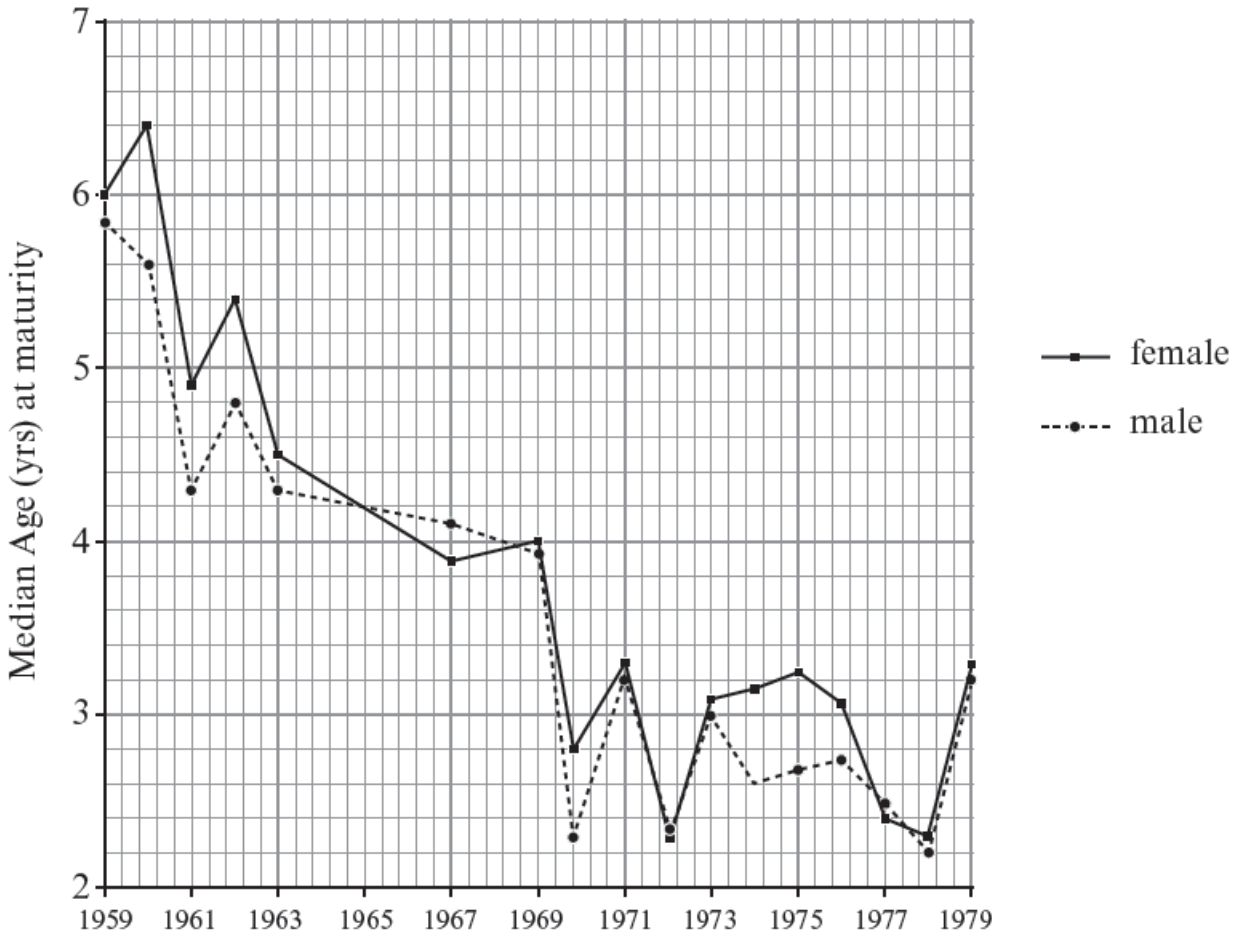
The cod was fished heavily for about 50 years.

About 60% of the total cod population of reproductive age was harvested annually.

Cod fishing in the Grand Banks was closed in 1992 but by then the population was less than 1% of what it had been.

Cod grow evenly throughout their life.

The cod that remained when fishing was finally closed were much smaller and grew more slowly than the cod that lived in the Grand Banks several decades previously.



Graph to show the median age of cod at sexual maturity in the same location during the time of heaviest fishing.

(a) (i) Use the information provided opposite and your own knowledge of natural selection to describe and explain how the phenotype of the cod has changed since 1960.

[5]

(ii) The cod fisheries have been closed for nearly 20 years but there has been little change in the phenotype and no population recovery. Suggest why there has been little change in the phenotype and no population recovery.

[3]

5. Wheat grain size is determined by the plants' genetics (i.e. variety), and the length of the grain filling period (time between fertilisation and harvesting). Plant breeders cross varieties of wheat in order to increase grain size. The photograph below shows the results of one such cross.

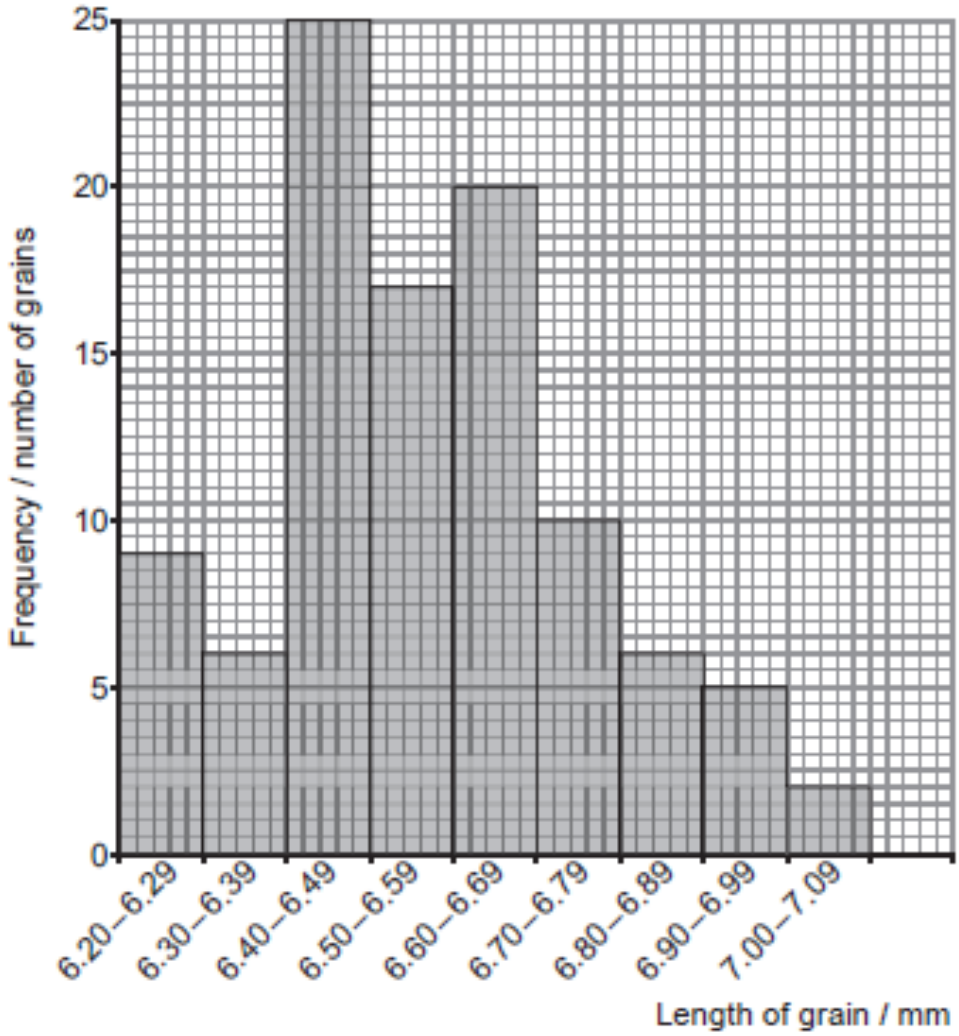
(a) Distinguish between **continuous** and **discontinuous** variation. You should give an example, which is visible in the photograph, for each one. [3]

……

……

……

The graph below shows the distribution of grain length in a sample of the hybrid wheat variety. The grains were measured to the nearest 0.01 mm.



(b) (i) What is the total number of grains in the sample? [1]

.....

(ii) The student calculated three different averages for the length of hybrid grains. The mean was 6.57 mm. The other two values were 6.45 mm and 6.52 mm. With reference to the graph, state which of these values is more likely to be the mode and give a reason for your choice. [2]

.....

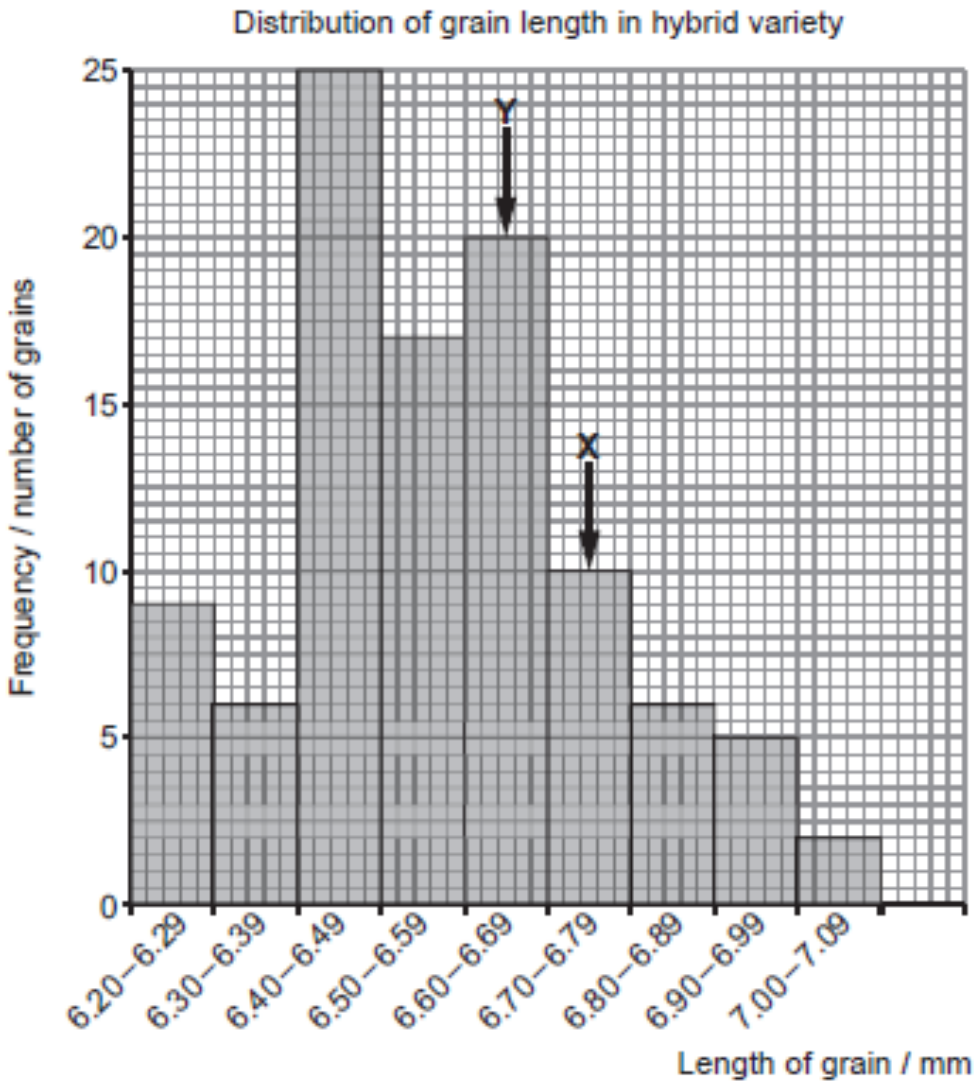
.....

.....

(iii) What evidence is there from the graph that the length of hybrid grains is not normally distributed? [1]

.....

For each parental variety the mode and median were the same. Arrow **X** shows the mode and median for parental variety A and Arrow **Y** shows the mode and median for parental variety B.



(iv) Consider the following statement:

'There is no significant difference in the length of the hybrid grains and the length of the grains of parental type B.'

Describe any evidence from the graph above to support the statement and name the terms used to describe; the type of hypothesis represented by the statement and the statistical test that could be used to test the hypothesis. [3]

Evidence .....

.....

Type of hypothesis .....

Statistical test .....