

4 The wolf, *Canis lupus*, lives in North America. Wolves may have a grey or a black coat colour. The colour of an individual wolf depends on the DNA it inherits at the *CPD103* gene locus.

- Wolves inherit two copies of *CPD103*, one from each parent.
- Wolves that inherit one copy of the black form of the *CPD103* gene have a black coat.

(a) State the term used to describe:

- an organism that has two copies of each gene
- a form of a gene
- a form of a gene that gives a phenotypic effect in a heterozygote.

[3]

In addition to producing black coat colour, the protein coded for by the *CPD103* gene also defends against infectious lung disease.

Canine distemper virus (CDV) causes serious lung disease in wolves. Wolves that have been previously infected by CDV have antibodies against CDV (anti-CDV antibodies) in their blood.

(b) CDV can be passed from domestic dogs to wolves.

- Domestic dogs are more numerous in the southern part of the area occupied by wolves.
- Domestic dogs are less numerous in the northern part of the area occupied by wolves.
- The relative frequency of black wolves compared to grey wolves increases from the north to the south of the area they occupy.

Explain how natural selection causes this trend in the distribution of black wolves.

[4]

(c) Several different populations of wolves were compared.

Fig. 4.1 shows the relationship between the percentage of wolves in a population that have anti-CDV antibodies in their blood and the percentage of wolves in that population that are black. The line of best fit was calculated after comparing the different populations of wolves.

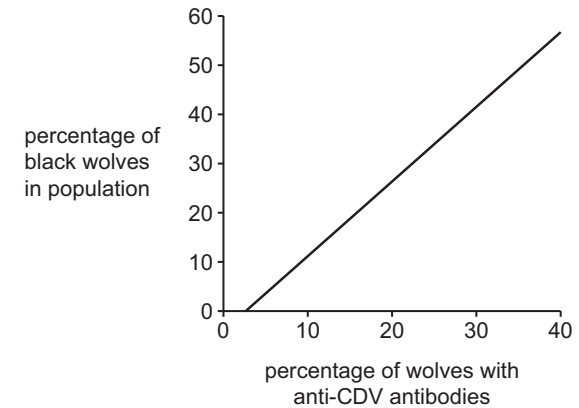


Fig. 4.1

With reference to Fig. 4.1, state the relationship between the percentage of wolves with anti-CDV antibodies and wolf coat colour, **and** suggest reasons for this relationship.

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[4]

[Total: 11]

2 *Exserohilum turcicum* is a fungal pathogen. The growth of the mycelium of the fungus damages the leaves of maize plants, *Zea mays*. Leaf damage reduces crop yield.

- (a) (i) Complete Table 2.1 to show **one** structural difference and **one** functional difference between *E. turcicum* and *Z. mays*.

Table 2.1

	<i>E. turcicum</i>	<i>Z. mays</i>
structural difference		
functional difference		

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- (ii) Describe the principles by which organisms such as *E. turcicum* and *Z. mays* are classified in the taxonomic hierarchy.

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- (b) Two inbred varieties of maize, SKV50 and CML153, were crossed. The resulting F1 hybrids were self-crossed to produce F2 offspring. The F2 plants were grown, and the percentage area of leaf damage caused by *E. turcicum* was measured.

Fig. 2.1 shows the results for the F2 generation. The arrows show the mean percentage area of leaf damage for the two parent varieties.

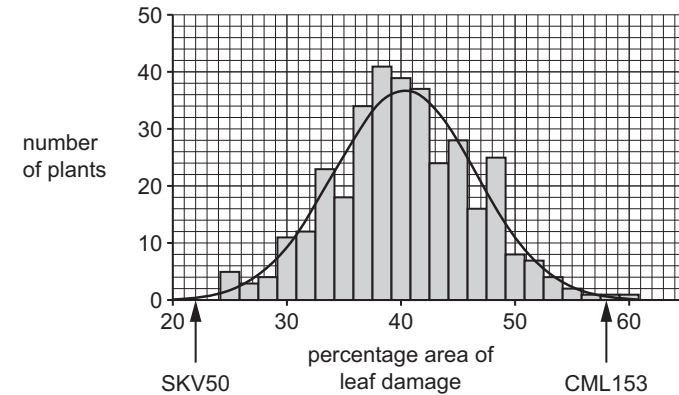


Fig. 2.1

- (i) Explain how Fig. 2.1 can be used to determine which parent maize variety shows the greatest resistance to infection by *E. turcicum*.

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- (ii) State the name of the type of variation shown by the maize F2 generation in Fig. 2.1.

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- (iii) Explain the **genetic** basis of the type of variation shown by the maize F2 generation.

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- The relative frequency of each allele of a gene in a population can change over time due to factors such as selection, genetic drift and the bottleneck effect.

- At generation 0, the number of **T** alleles and the number of **t** alleles in the population was equal, so the relative frequency of each allele was 0.5. The relative frequencies of the two alleles of the gene add up to 1.

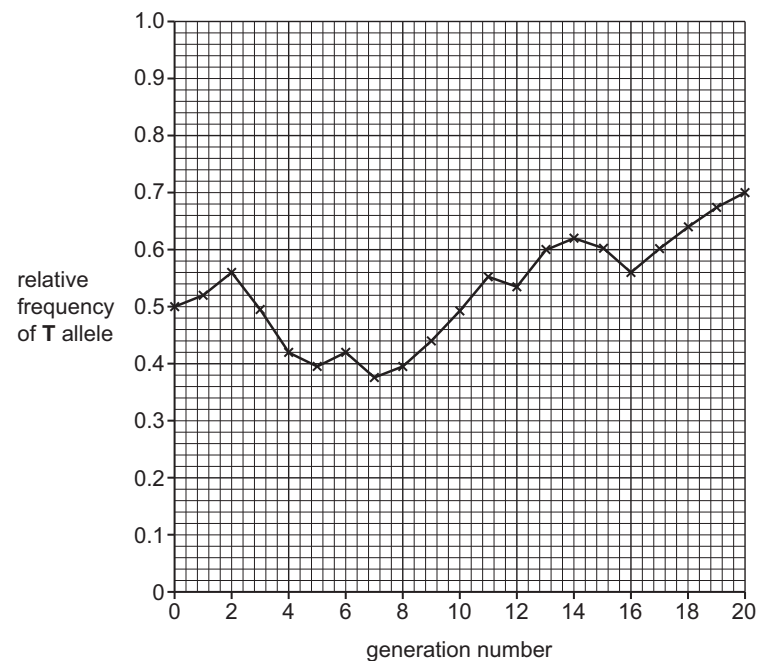


Fig. 4.1

- (i) With reference to Fig. 4.1, state the relative frequency of the **t** allele after 20 generations.

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[4]

- (b) The relative frequency of the **T** allele in a population of only 10 individuals was determined over 20 generations. The environmental conditions remained the same throughout the experiment.

Fig. 4.2 shows the results.

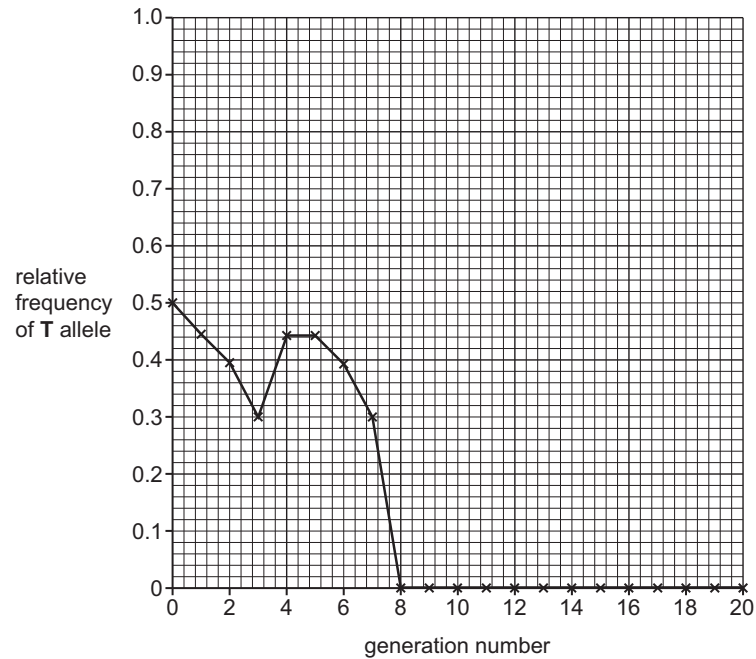


Fig. 4.2

Explain why Fig. 4.2 shows a different result from Fig. 4.1.

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- (c) State the name of the principle that can be used to calculate relative frequencies of two alleles by counting the numbers of organisms in the population showing dominant and recessive phenotypes.

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[Total: 9]