1. Nov/2021/Paper_41/No.3

Ecological surveys are conducted before conservation decisions are made. For example, surveys can be carried out before deciding whether to reintroduce a species to its former habitat.

(a) Outline how an ecological survey can measure the biodiversity of a terrestrial habitat.

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(b) Table 3.1 lists some mammal species that became extinct in Great Britain or were introduced into Great Britain in the last 12400 years.

The reasons for each extinction or introduction and the time of each event are shown.

Table 3.1

species	number of years before present time	event	reason
arctic fox	12400	extinction	climate change
sheep	5400	introduction	farming
house mouse	3500	introduction	accidental
lynx	1500	extinction	hunting
fallow deer	900	introduction	food
South American coypu	86	introduction	fur
South American coypu	33	extinction	conservation culling

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With reference to Table 3.1, state **and** explain the factors that have had a negative impact on biodiversity in Great Britain.

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(c) Non-governmental and government organisations are working together to reintroduce a lynx population to its former habitat in a remote part of Great Britain. Lynx are predatory big cats.

Fig. 3.1 shows a lynx.

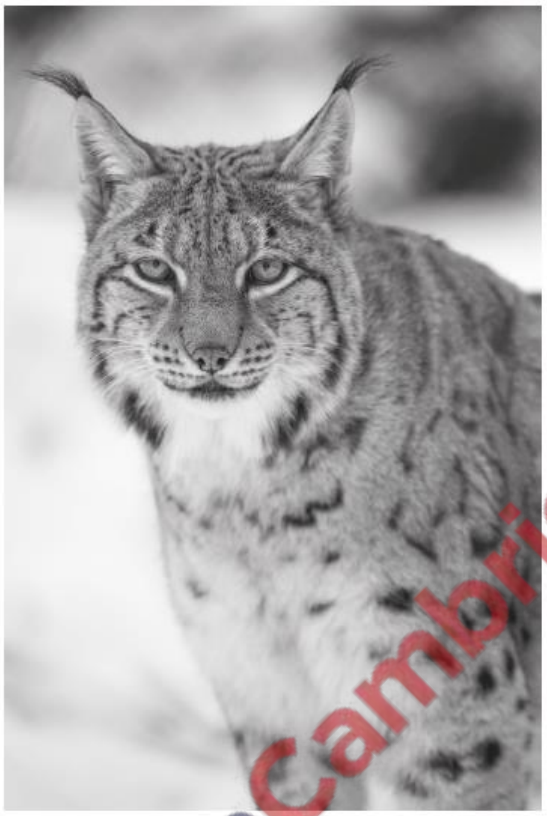

Fig. 3.1

Suggest the factors that need to be considered by organisations to successfully reintroduce and restore a breeding population of lynx in Great Britain.

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2. Nov/2021/Paper_42/No.4

(a) Genome-wide association studies find links between single nucleotide polymorphisms (SNPs) and phenotypic features such as human diseases. SNPs are points on the DNA that vary in the population because of DNA base substitutions.

A genome-wide association study investigates the effect of genetic variation on a disease. A large number of people with the disease and a large number of healthy control individuals provide DNA. Microarray chips are used to identify the genotype of each individual at many SNPs.

The Wellcome Trust Case Control Consortium (WTCCC) study was an important genome-wide association study.

- The study used a microarray chip that identified each person's genotype at 500 000 different SNPs.
- The study looked for links between SNPs and 7 different diseases.
- For each disease, 2000 people with the disease were tested.
- Their results were compared with the results of 3000 healthy control individuals.

(i) Outline how microarrays are used in the analysis of genomes.

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(ii) Explain why bioinformatics was important to the WTCCC study.

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(b) Fig. 4.1 summarises results for three diseases in the WTCCC study. The 22 human autosomes and the X chromosome (chromosome 23) are shown.

Chromosome locations with SNPs that are associated with a disease at a statistically significant level (greater than 5 arbitrary units) are shown in black.

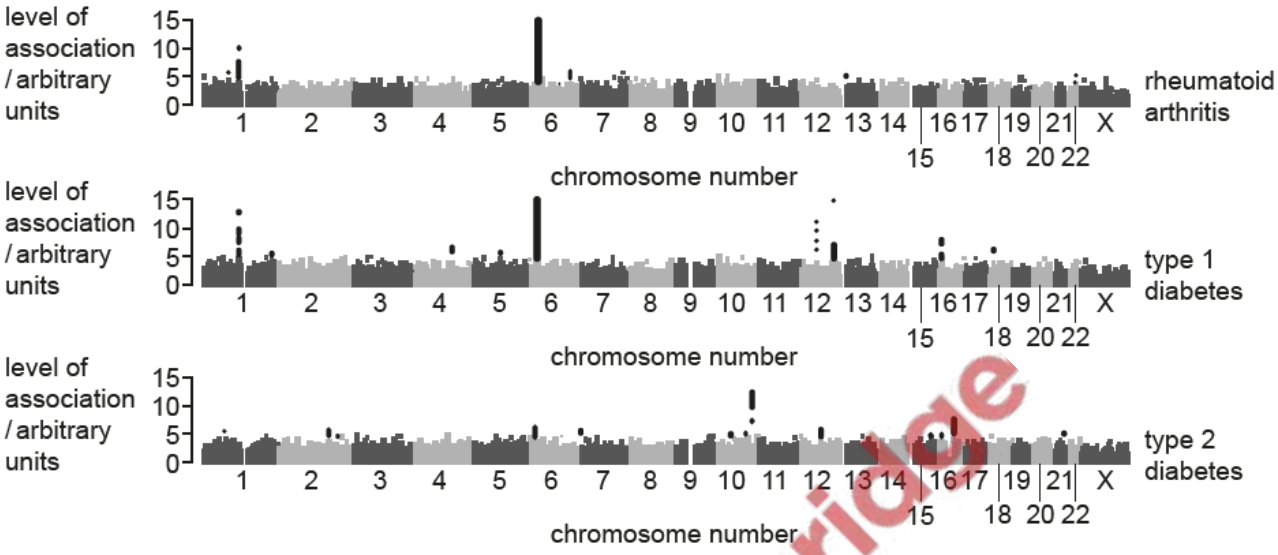

Fig. 4.1

(i) Identify the chromosomes that contain SNPs that have a high level of association with **both** rheumatoid arthritis and Type 1 diabetes.

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(ii) With reference to Fig. 4.1, compare the genetic basis of the three diseases.

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(c) Individuals can choose to have their DNA analysed on a microarray chip to predict their risk of developing different diseases.

Outline the social **and** ethical considerations of this type of DNA analysis.

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