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92022

Mana Tohu Mātauranga o Aotearoa
New Zealand Qualifications Authority

Level 1 Chemistry and Biology 2024

92022 Demonstrate understanding of genetic variation in relation to an identified characteristic

Credits: Five

ASSESSMENT TASK

Achievement	Achievement with Merit	Achievement with Excellence
Demonstrate understanding of genetic variation in relation to an identified characteristic.	Explain genetic variation in relation to an identified characteristic.	Evaluate genetic variation in relation to an identified characteristic.

Refer to this document to respond to the task for Chemistry and Biology 92022.

Check that this document includes page 2.

Do not use chatbots, generative AI, or other tools that can automatically generate content.

DO NOT TAKE THESE ASSESSMENT MATERIALS OUT OF THE ASSESSMENT ROOM.

INSTRUCTIONS

Produce one report with your answers to both parts (a) and (b).

Your report can be written or oral. Recommended length: 800 words or 3–4 minutes of audio and/or video.

TASK

(a) **Familiar context**

Write an account of the **genetic variation** in a population you have studied.

In your report, you should include discussion of:

- the sources of the genetic variation for an individual **and** for a population
- the relationship between DNA, alleles, genes, chromosomes, and the variation of a specific phenotype
- how meiosis and sexual reproduction contribute to variation of that phenotype in subsequent generations
- why some individuals in a population are more closely related than others, and why genetic variation is significant in a population.

Allele for HIV resistance

The human immunodeficiency virus (HIV) is a virus that infects the white blood cells of the human immune system. The virus is able to specifically bind to a receptor (a protein) on the surface of the cell membrane of white blood cells. This receptor protein is expressed by the CCR5 allele.

Once the virus attaches to the surface of the cell membrane, it is able to 'hijack' the cell, use the resources from the cell to produce multiple copies of itself, and eventually destroy the cell. The virus will then repeat the cycle again by infecting another cell.

Individuals who have a normal CCR5 gene are susceptible to HIV infection.

Scientists have used several gene tracking methodologies on different individuals who have a mutant CCR5 allele.

Individuals who are **homozygous** for the mutant CCR5 allele are completely resistant to HIV, while individuals who are **heterozygous** are still susceptible to HIV infection.

Scientists hope to use this information to advance their understanding of how the virus attaches to cells and provide better health outcomes for both HIV patients and the general population.

(b) Evaluate the findings and discuss how these findings can lead to better health outcomes.

In your answer, you should include a discussion of:

- what a mutation is
- what the possible genotype of individuals who are resistant and individuals who are susceptible to HIV infection is (you should use 'h' for the mutant CCR5 allele and 'H' for the normal CCR5 allele)
- use one or more Punnett squares to identify the gene relationships between resistant and susceptible individuals (you may want to cross two heterozygous parents)
- how understanding these genetic relationships could lead to the discovery of the mutant CCR5 allele
- how the discovery of the mutant CCR5 allele may help scientists to provide better health outcomes for HIV patients and the general population.