Assessment Schedule – 2024

Chemistry and Biology: Demonstrate understanding of genetic variation in relation to an identified characteristic (92022)

Assessment Criteria

Achievement	Achievement with Merit	Achievement with Excellence
Demonstrating understanding of genetic variation in relation to an identified characteristic involves: • describing the source and the nature of genetic variation using an identified characteristic • describing a purpose for identifying genetic relationships through the use of a gene tracking methodology.	*Explaining genetic variation in relation to an identified characteristic* involves: • explaining how and why the genetic variation occurs using an identified characteristic • explaining how the purpose for identifying genetic relationships through the use of a gene tracking methodology is met.	*Evaluating genetic variation in relation to an identified characteristic* involves: • evaluating findings when genetic variation has been identified and tracked for the purpose of identifying genetic relationships.

Sufficiency Statement

N1	N2	A3	A4	M5	M6	E7	E8
Attempts to describe genetic variation in either part (a) or part (b).	Attempts to describe genetic variation in part (a) and part (b).	Describes genetic variation in part (a) and part (b), and the purpose of genetic tracking. May be uneven in description across both parts.	Describes genetic variation in part (a) and part (b), and the purpose of genetic tracking.	Explains how and why genetic variation occurs in part (a) and part (b), and the purpose of genetic tracking May be uneven in explanation across both parts.	Explains how and why genetic variation occurs in part (a) and part (b), and the purpose of genetic tracking.	Evaluates the purpose of the tracking of genetic variation in both part (a) and part (b), and the implications of this tracking in relation to an identified characteristic. May be uneven in evaluation across both parts.	Evaluates the purpose of the tracking of genetic variation in both part (a) and part (b), and the implications of this tracking in relation to an identified characteristic.

N0 = No response; no relevant evidence.

Cut Scores

Not Achieved	Achievement	Achievement with Merit	Achievement with Excellence
0–2	3–4	5–6	7–8

Sample Evidence

What follows is not a complete list of all acceptable responses, nor is it an indication of the exact wording required. Assessment judgments are based on the level of understanding shown.

Part	Evidence	Achievement	Achievement with Merit	Achievement with Excellence
(a) Shows an understanding of the genetic variation in a population that has been studied in class.	• Description of mutation and the random meeting of gametes. • Sources of genetic variation for an individual and population: mutation, sexual reproduction, random fertilisation, meiosis, migration, mutagens, etc. • DNA: double helix structure made up of three sub-units (sugar, phosphate, base). • Chromosome: thread-like structure found in nucleus, containing the genetic / hereditary information; long strand of DNA containing many genes. • Alleles: different forms of the same gene; different sequence of bases. • Genes: specific section of the DNA that codes for a protein / trait. • Phenotype: physical expression of the genotype / allele. • Genotype: allele combination of a specific gene. • Genetics maintain continuity (combination of alleles from both parents being passed on to offspring) and allow for change. • The inherited sequence of DNA is the basis of an organism's phenotype. Heritable mutations allow evolution or genetic change over time. • More different genomes are less related than genomes that are more similar to each other. This can be shown in pedigree charts and phylogenetic trees. • Crossing over is when homologous chromosomes exchange genetic information so that every chromosome has a unique combination of alleles. • Independent assortment randomly shuffles homologous chromosomes, ensuring different combinations of alleles in gametes. • Offspring are genetically unique from both parents, as one set of chromosomes is inherited from each parent. Offspring will inherit two copies of each gene, which does not always express both copies. • More genetic variation within a species can help that species to have a better chance of survival, because if the environment changes, there is a chance some individuals may have beneficial alleles that help them to survive that change, and pass on those alleles.	Demonstrates understanding of genetic variation in a population by identifying a characteristic and describing how that characteristic is expressed differently in different individuals based on the genetic code.	Explains genetic variation in a population by using an identified characteristic and explaining how that characteristic is expressed differently in different individuals based on the genetic code, sexual reproduction, meiosis and genetic relatedness / inheritance.	Evaluates genetic variation in a population by using an identified characteristic and explaining how that characteristic is expressed differently in different individuals and whether this genetic variation is important in a population.

	• Sickle cell mutation causes red blood cells to form in the shape of a sickle and decreases the ability of red blood cells to carry oxygen efficiently. The disease also decreases life expectancy. • Homozygous dominant – no disease Homozygous recessive – has the disease Heterozygous – partly has the trait (half red blood cells normal, half red blood cells sickle) OR is a carrier of the recessive allele, but that means they can pass on the allele. • Phenotype is determined by the inherited alleles from both parents. If the population size is small, then the possible selection of mates is much smaller, thus this could inadvertently lead to more individuals selecting sexual partners who are nearby / closer and potentially inbreeding. This causes some individuals in a population to be more closely related. However, if there is migration (of new individuals) into the population, this will provide new mating partners with new alleles, thus potentially producing offspring with more genetic variation.			
(b) Shows an understanding of the genetic variation in a given context.	• Mutation is a permanent change in the DNA base sequence. • A slight change in the DNA sequence of the normal CCR5 gene, which produces a mutant CCR5 allele, results in a 'variation' of the protein on the cell surface membrane (phenotype). • Resistant individuals = hh. Susceptible individuals = Hh and HH. • Evidence of a Punnett square cross between an individual who is resistant and an individual who is susceptible to HIV (e.g. hh x Hh or HH). A discussion could follow regarding offspring having to inherit both 'h' alleles to be resistant to HIV. • Evidence could include a hypothetical pedigree chart where scientists track the lineage of an individual who is resistant, and investigate the genotype of the parents of that individual (both parents must at least have one h allele) as well as the (potential) offspring produced by the individual. The genetic relationship would be that the mutant CCR5 allele must have occurred in the gametic cell and therefore, must be passed on as there are several individuals who have the mutant CCR5 allele. • DNA sequencing and genetic markers: Scientists sequence the DNA of an individual who is susceptible and an individual who is resistant to HIV, then compare the base sequence for the CCR5 gene to identify the specific sequence of the mutant CCR5 allele. • The DNA sequence could also be used as the genetic marker for individuals who have the normal or mutant allele. • The discovery of the mutant CCR5 allele would allow scientists to understand how the virus is able to (specifically) infect white blood cells			

	and could allow further studies on other receptor proteins targets that have a genetic basis. Greater understanding of the genetic relationship to viral resistance could allow for tailored medical treatment options, reduced transmission rates, and predictive models for inherited resistance for future generations. • The discovery of the mutant CCR5 allele would allow scientists to understand how the virus is able to (specifically) infect white blood cells. For example, the mutant CCR5 allele could produce a different receptor (protein) on the cell membrane of white blood cells, thus preventing HIV from binding to white blood cells. • Scientists could use this to create a potential chemical / drug / medicine that blocks the receptors of individuals, therefore preventing the virus from further infection. This could be used as a preventative measure before exposure to HIV or treatment for those who have been infected with HIV. Scientists could use the information to find cheaper alternatives for HIV medication, making it more accessible for all individuals, therefore providing more equitable health outcomes.			

Appendix: Authenticity of candidate work

To assess whether a candidate's evidence is genuine, the marker uses their professional judgement, considering all the evidence provided. Where the marker believes there is a possibility the work is inauthentic, they must raise a ‘malpractice exception’, flagging the issue for further review.

Evidence might be considered inauthentic if:

- large portions of the text are identical to other candidates’ work
- the evidence does not match the assessment prompt or task
- the response shows evidence of someone else’s input other than the candidate’s (e.g., teacher feedback)
- the style or voice of the writing is inconsistent with the rest of the candidate’s work
- complex pieces of evidence are copied from other sources but are presented as the candidate’s own work, or the evidence is deemed significantly unnatural.

Properly referenced, relevant, and integrated information is acceptable. Uncertainty about the authenticity of evidence should be resolved in favour of the candidate.