Assessment schedule: practice paper 2026

AS 92022 Demonstrate understanding of genetic variation in relation to an identified characteristic · Vertex Academy practice paper, not an NZQA paper

QUESTION ONE

Part	Evidence	Achievement (u)	Merit (r)	Excellence (t)
(a)	gene dominant shows with one copy; recessive needs two parents Ff × Ff FF, Ff, Ff, ff	Describes a gene and an allele. Describes dominant and recessive. Correct Punnett square with a 1 in 4 chance of CF.		
(b)	parents Ff meiosis random fertilisation no F allele	Describes the parents as carriers (Ff). Describes gametes carrying one allele each.	Explains that each carrier parent passes on f in half their gametes, so random fertilisation of two f gametes gives an ff child, with no dominant allele, who has CF.	
(c)	each child independent carriers look normal DNA sequencing pedigree informed decisions; early treatment	States the chance is still 1 in 4. Describes DNA testing identifying carriers. Describes a pedigree as a family tree that tracks the characteristic.	Explains why the chance stays 1 in 4 (each fertilisation is independent), OR explains how gene tracking identifies relatives who could be carriers.	Discusses the independent 1 in 4 chance for each child AND how DNA sequencing and pedigrees identify carriers among relatives, and why this helps the family.

QUESTION TWO

Part	Evidence	Achievement (u)	Merit (r)	Excellence (t)
(a)	mutation meiosis random fertilisation	Describes all three sources: mutation, meiosis and fertilisation.		

(b)	half alleles from each parent meiosis random fertilisation	Describes a chick getting half its alleles from each parent. Describes gametes being different from each other.	Explains both: half from each parent makes the chick different from its parents, AND meiosis plus random fertilisation make siblings different from each other.	
(c)	variation bottleneck low variation genome sequencing pair less-related birds, use rare alleles (Richard Henry line)	Describes genetic variation as different alleles. Describes kākāpō as having few alleles because of their small population. Describes sequencing showing each bird's alleles.	Explains why low variation puts the kākāpō at risk (for example, no individuals resistant to a disease), OR explains how sequencing is used to choose pairs that increase variation.	Discusses why variation matters for survival (adapting to threats such as disease; inbreeding) AND how genome sequencing guides pairings, including birds with different alleles, to increase variation.

QUESTION THREE

Part	Evidence	Achievement (u)	Merit (r)	Excellence (t)
(a)	copies = 500 × 2 = 1000 R = 2 × 30 + 140 = 200 frequency of R = 200 ÷ 1000 = 0.20	Describes a population. Describes allele frequency. Calculates the frequency of R as 0.20.		

(b)	survivors = 206 R = 2 × 28 + 112 = 168 frequency of R = 168 ÷ 412 = 0.41 virus kills rr rabbits	Calculates the new frequency as 0.41. Describes rr rabbits dying from the virus.	Frequency 0.41 AND explains the increase: the virus is a selection pressure that removes rr rabbits, so R makes up a larger share of the alleles in the survivors.	
(c)	R from mutation virus survivors with R reproduce repeated outbreaks no virus	Describes rabbits with R surviving better. Describes survivors passing on their alleles. Describes R becoming more common over generations.	Explains natural selection step by step (variation, selection pressure, survival and reproduction, inheritance), linked to the frequency of R rising.	Discusses natural selection over many generations (including that R came from mutation before the virus) AND what would happen without the virus (no advantage; the frequency may stay the same or fall if R has a cost).

Judgement for each question

N0	N1	N2	A3	A4	M5	M6	E7	E8
No response, or nothing relevant.	One Achievement point, partly described.	Two Achievement points.	Three Achievement points.	Four Achievement points.	One Merit point.	Two Merit points.	One Excellence point, with a minor error or omission.	One Excellence point, complete.

Grade score out of 24 (each question's grade: N0 = 0 to E8 = 8): Not Achieved 0 to 7, Achieved 8 to 12, Merit 13 to 18, Excellence 19 to 24 (the 2025 exam's cut scores).