Assessment Schedule – 2025

Biology: Demonstrate understanding of genetic variation and change (91157)

Assessment Criteria

Achievement	Achievement with Merit	Achievement with Excellence
Demonstrate ***understanding*** involves: • defining, using annotated diagrams or models to describe, and describing characteristics of, or providing an account of, genetic variation and change.	*Demonstrate* ***in-depth understanding*** involves: • providing reasons how or why genetic variation and change occurs.	*Demonstrate* ***comprehensive understanding*** involves: • linking biological ideas about genetic variation and change; discussion of ideas may involve justifying, relating, evaluating, comparing, and contrasting, or analysing.

Cut Scores

Not Achieved	Achievement	Achievement with Merit	Achievement with Excellence
0–6	7–12	13–18	19–24

Evidence

Question One

<table>
<tr><th>Expected Coverage</th><th>Achievement</th><th>Achievement with Merit</th><th>Achievement with Excellence</th></tr>
<tr><td>(a) Genotype of gametes: GB and gb
Genotype of F1: GgBb</td><td>Identifies gametes OR F1 genotype correctly.</td><td rowspan="3"></td><td rowspan="3"></td></tr>
<tr><td>(b)
<table>
<tr><th></th><th>GB</th><th>Gb</th><th>gB</th><th>gb</th></tr>
<tr><td>GB</td><td>GGBB</td><td>GGBb</td><td>GgBB</td><td>GgBb</td></tr>
<tr><td>Gb</td><td>GGBb</td><td>GGbb</td><td>GgBb</td><td>Ggbb</td></tr>
<tr><td>gB</td><td>GgBB</td><td>GgBb</td><td>ggBB</td><td>ggBb</td></tr>
<tr><td>gb</td><td>GgBb</td><td>Ggbb</td><td>ggBb</td><td>ggbb</td></tr>
</table></td><td>Punnett square completed with correct gametes for F2.</td></tr>
<tr><td>(c) 9:3:3:1
Orange striped : orange blotched : white striped : white blotched</td><td>Phenotype ratio (with correct appearance).</td></tr>
<tr><td>(d)
Linked genes: These are genes located close together on the same chromosome.
Unlinked genes: These are genes located on different chromosomes OR far apart on the same chromosome.
Crossing over: This is the exchange of alleles / segments of chromosomes / segments of DNA between homologous chromosomes / non-sister chromatids.
Segregation: This is the process by which alleles for the same gene/homologous chromosomes are separated into different gametes.

Crossing over can reshuffle / create new allele combinations of genes, while segregation ensures that each gamete only carries one allele per gene, creating gametes that are unique to each other and the parent.
Linked and unlinked genes can be on the same chromosome depending on their proximity / Loci. Linked genes that are close</td><td>Describes:
linked genes
unlinked genes
crossing over (can accept annotated diagram)
segregation</td><td>Explains:
crossing over / segregation
how the process of crossing over influences the inheritance patterns of both linked and unlinked genes on the same chromosome
how the process of segregation influences the inheritance patterns of both linked and unlinked genes
why the species of snake have different ratios.</td><td>Provides detailed discussion of:
the inheritance patterns of linked and unlinked genes with reference to the snake ratios in the source material
the processes of crossing over and segregation, confidently linked to the observed ratios in each species.</td></tr>
</table>

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
together are not separated during crossing over and hence inherited together, while genes that are not close together can be unlinked during crossing over and hence not inherited together. Segregation doesn't affect / separates linked genes and they will be inherited together / end up in the same gamete. Segregation leads to / creates new combinations of alleles for unlinked genes. The genes for body colour and scale pattern for the corn snake are unlinked and not inherited together, while the genes for body pattern and scale texture for the garter snake are linked and inherited together thus giving the observed ratios for each. **The garter snake:** The observed phenotypic ratio of 7 striped smooth : 1 striped rough : 1 unstriped smooth : 7 unstriped rough in the garter snake (*Thamnophis sirtalis*) suggests that the genes for stripe pattern and scale texture are linked. The genes for stripe pattern (Ee) and scale texture (Rr) are likely located close together on the same chromosome, thus inherited together. **The corn snake:** The observed phenotypic ratio of 9 orange striped : 3 orange blotched : 3 white striped : 1 white blotched in the corn snake shows that the genes for body colour and scale pattern are unlinked. The genes for body colour and stripe pattern are likely located on separate chromosomes or far apart on the same chromosome to be separated via crossing over. <u>Crossing over:</u> Since the genes are linked, crossing over between them is less frequent for the garter snake. However, when it does occur, it can produce recombinant phenotypes (striped rough and unstriped smooth) but at a lower frequency. Thus, giving a ratio of 7:1:1:7. <u>Segregation:</u> During meiosis, the linked genes stay together, leading to the higher frequency of parental phenotypes (striped smooth and unstriped rough) for the garter snake. The majority of offspring are parental types (striped smooth and unstriped rough) due to the linkage of the genes.			

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
Recombinant types: The recombinant types (striped rough and unstriped smooth) appear less frequently due to the lower likelihood of crossing over between the linked genes. However, for the corn snake the 9:3:3:1 shows that the genes are unlinked either due to being on different chromosomes or far apart on the same chromosome that the frequency of crossing over unlinking them is higher.			

N1	N2	A3	A4	M5	M6	E7	E8
ONE evidence point at Achievement.	TWO evidence points at Achievement.	THREE evidence points at Achievement.	FOUR evidence points at Achievement.	TWO evidence points at Merit.	THREE evidence points at Merit.	ONE evidence point at Excellence.	TWO evidence points at Excellence.

N0 = No response; no relevant evidence.

Question Two

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
Allele frequencies: This refers to how common an allele (a variant of a gene) is in a population. **Gene pool:** The gene pool is the total collection of alleles in a population. **Migration:** The movement of individuals / alleles from one population to another population / gene pool. (Immigration is the movement of individuals into the gene pool; emigration is the movement of individuals out of a gene pool.) Allele frequency in a population is affected by migration by adding / subtracting alleles through immigration / emigration of individuals. Immigration increases allele frequency while emigration decreases allele frequency. For the New Zealand giraffe weevil, if long-rostrum males migrate from dense forests to more open areas, they could increase the frequency of the long-rostrum allele in the new population. <u>Genetic drift:</u> This is the random/chance change in allele frequencies. Allele frequency decreases as alleles are lost or certain allele frequency increasing fixing the allele within the gene pool. Migration / genetic drift would have a more significant effect on small populations such as the smaller offshore islands resulting in **a more random phenotype distribution**. **Population bottleneck:** A sudden / rapid / drastic reduction in population numbers. **Founder effect:** When a small group of individuals from an existing population moves to another area. <u>Sexual selection (mate selection):</u> This occurs when certain traits increase an individual's chances of mating and passing on their genes, thus increasing the frequency of the allele in the population. In New Zealand giraffe weevils, long-rostrum males may be more successful in mating in dense forests because their rostrum length could be advantageous in male–male competition or female choice. This would increase the frequency of the long-rostrum allele in these environments.	Describes: • allele frequency • gene pool • migration • genetic drift • natural selection • identify any ONE selection pressure *(predation, humidity, food supply, sun exposure)*. • population bottleneck • founder effect.	Explains: • migration • genetic drift *(must have idea of allele frequency increasing (fixed) OR decreasing(lost))* (*Accept founder or bottleneck effect explained as an example of genetic drift*) • effect of migration / genetic drift on small islands • natural selection / sexual selection *(must have idea of allele frequency increasing (fixed) OR decreasing(lost))* • why long-rostrum males might be more successful in a dense forest environment • why short-rostrum males might be more successful in a drier or open environment.	Provides detailed discussion of: • how migration and genetic drift changed allele frequencies in the New Zealand giraffe weevil gene pool • the selection pressures that drive natural selection, in reference to the New Zealand giraffe weevil, and how it led to the different phenotypes seen in New Zealand.

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
Natural selection: This is the process where individuals with advantageous traits are more likely to survive and reproduce, thus increasing the frequency of the allele in the population In open or fragmented forests, short-rostrum males might have a survival advantage, perhaps due to better mobility / reduced predation / humidity-sun exposure. This would increase the frequency of the short-rostrum allele in these environments. In dense native forests, long-rostrum males are more common greater opportunities to hide from predators, greater chances of foraging for food among the foliage with longer-rostrum / higher levels of humidity prevents dehydration and covered areas protect from direct sun exposure, thus increasing chances of survival and reproduction leading to the increase in their allele frequency.			

N1	N2	A3	A4	M5	M6	E7	E8
ONE evidence point at Achievement.	TWO evidence points at Achievement.	THREE evidence points at Achievement.	FOUR evidence points at Achievement.	TWO evidence points at Merit.	THREE evidence points at Merit.	ONE evidence point at Excellence.	TWO evidence points at Excellence.

N0 = No response; no relevant evidence.

Question Three

<table>
<tr><th>Expected Coverage</th><th>Achievement</th><th>Achievement with Merit</th><th>Achievement with Excellence</th></tr>
<tr>
<td>
Multiple alleles: More than two / three or more alleles for one gene / same locus.
Possible genotypes for the mother would be either AA or AO

Possible genotypes of Child 1:
<table>
<tr><th></th><th>A</th><th>A</th></tr>
<tr><td>A</td><td>AA</td><td>AA</td></tr>
<tr><td>B</td><td>AB</td><td>AB</td></tr>
</table>
<table>
<tr><th></th><th>A</th><th>O</th></tr>
<tr><td>A</td><td>AA</td><td>AO</td></tr>
<tr><td>B</td><td>AB</td><td>BO</td></tr>
</table>

Child 1 has two possible genotypes because his mother’s genotype is not known. A is dominant over O, so it will be expressed in a heterozygous child. The child could inherit A from his father and A from his mother or A from his father and O from his mother, so there is a 50% chance of either genotype.
<u>Complete dominance</u>: This occurs when one allele masks the effect of another allele / when the allele is always expressed when present in a heterozygote
For example, blood type A and B, with genotype AA or AO, OR genotype BB or BO.
<u>Co-dominance:</u> This occurs when both alleles in a heterozygous are expressed in the phenotype. In human blood types, alleles I^A and I^B show co-dominance. If a person inherits both I^A and I^B, they will have type AB blood, where both A and B are expressed.

The offspring of child 1 with an OO female
<table>
<tr><th></th><th>A</th><th>A</th></tr>
<tr><td>O</td><td>AO</td><td>AO</td></tr>
<tr><td>O</td><td>AO</td><td>AO</td></tr>
</table>
<table>
<tr><th></th><th>A</th><th>O</th></tr>
<tr><td>O</td><td>AO</td><td>OO</td></tr>
<tr><td>O</td><td>AO</td><td>OO</td></tr>
</table>
Genotypes: AO, OO Phenotype: Type A and Type O
</td>
<td>
Describes:
• multiple alleles
• the possible genotypes of the mother
• the possible genotypes of Child 1
OR
monohybrid Punnett square showing possible genotypes of Child 1
• complete dominance
• co-dominance.
• possible phenotypes OR genotypes of the offspring of Child 1 with an OO female.
OR
provides a Punnett square.
</td>
<td>
Explains:
• why Child 1 has TWO possible genotypes (must mention alleles of gametes from BOTH parents)
• complete dominance with a blood-type allele example
• co-dominance with a blood-type allele example
• why Child 1 has two possible genotypes based on the genotype of the offspring produced with a blood type O partner (must mention alleles of gametes from BOTH parents).
</td>
<td>
Provides detailed discussion:
• linking the idea of co-dominance and complete dominance to discuss two possible genotypes for Child 1, based on the parents’ genotypes and phenotypes
• of the possibility to determine the genotype of Child 1, based on the blood types of his children, if his partner was a blood type O female, and why such a determination cannot be guaranteed to be correct (must use parental gametes and offspring genotypes with ratios / percentages).
</td>
</tr>
</table>

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
Determining the genotype of Child 1 by testing his children's blood types tested: Child 1's offspring can only receive an O allele from their mother as her genotype must be homozygous recessive to have blood type O expressed and with an A blood type Child 1 can either contribute an A or an O allele. • Option 1: None of his children will have blood group O because he is homozygous AA; therefore, all the children from an AA x OO cross will be heterozygous AO. • Option 2: If he is heterozygous AO, then children he has with a homozygous OO woman will be 50:50 AO:OO. However, as the genotype of each child is random, it is possible that no OO children would be born. Although statistically the likelihood is 50:50, it may not occur that way, so the determination of him being AO cannot be guaranteed.			

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