# Assessment Schedule – 2024

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

## Assessment Criteria

| Achievement | Achievement with Merit | Achievement with Excellence |
|---|---|---|
| *Demonstrate* ***understanding*** involves:<br>• 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:<br>• providing reasons how or why genetic variation and change occurs. | *Demonstrate* ***comprehensive understanding*** involves:<br>• 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) BbLl</td><td>• Identifies F1 genotype as BbLl.</td><td rowspan="3"></td><td rowspan="3"></td></tr>
<tr><td>(b)
<table>
<tr><th></th><th>BL</th><th>Bl</th><th>bL</th><th>bl</th></tr>
<tr><td>BL</td><td>BBLL</td><td>BBLl</td><td>BbLL</td><td>BbLl</td></tr>
<tr><td>Bl</td><td>BBLl</td><td>BBll</td><td>BbLl</td><td>Bbll</td></tr>
<tr><td>bL</td><td>BbLL</td><td>BbLl</td><td>bbLL</td><td>bbLl</td></tr>
<tr><td>bl</td><td>BbLl</td><td>Bbll</td><td>bbLl</td><td>bbll</td></tr>
</table></td><td>• Punnett square completed with correct gametes for F2.</td></tr>
<tr><td>(c) 9:3:3:1<br>Black long: Black short: Brown long: brown short</td><td>• Phenotype ratio (with appearance correct).</td></tr>
<tr><td>(d)<br>Complete dominance is where the dominant allele completely masks the effect of the recessive allele in heterozygous conditions.<br>Co-dominance is where both alleles of the same gene are expressed to an equal degree within an organism. As a result, traits associated with each allele are displayed simultaneously, i.e. both traits show in the phenotype.<br>A sex-linked gene is located on one of the chromosomes that is responsible for the sex of the individual. Like humans, XX = female and XY = male.<br>Females have two X chromosomes, so have two alleles of this gene. FF results in orange fur; ff results in fur without any orange (black, brown, etc.); and Ff results in a tortoiseshell cat, i.e. some parts of the fur are orange, and other parts are non-orange – an example of co-dominance.<br>Male cats can typically be orange (F) or non-orange (f) due to having only <u>one</u> X chromosome; therefore, they can only inherit one dominant or one recessive allele. Having only the one allele for the gene for fur colour, they cannot display tortoise shell phenotype (arising from a co-dominance pattern).</td><td>Describes:<br>• complete dominance<br>• co-dominance<br>• sex-linked gene<br>• genotype of male or female cat for corresponding phenotype<br>• that females have a homologous pair of sex-chromosomes while males do not (XX and XY).</td><td>Explains:<br>• why female cats can have tortoiseshell-colour fur<br>• why male cats can’t have tortoiseshell-colour fur, only orange or non-orange<br>• the difference between dominant and recessive sex-linked genes<br>• why male cats are more likely to inherit a sex-linked disease.</td><td>Discusses:<br>• the co-dominant and complete dominance inheritance patterns for fur colour in male and female cats<br>• dominant and recessive sex-linked genes, with reference to why males inherit recessive diseases more frequently than females.</td></tr>
</table>

| Expected Coverage | Achievement | Achievement with Merit | Achievement with Excellence |
|---|---|---|---|
| Sex-linked inheritance of a disease occurs when the gene for the disease is present on a sex chromosome.<br>If the diseased / abnormal allele is dominant, an abnormal allele from one parent causes the disease, even though the matching allele from the other parent is normal. The abnormal allele dominates.<br>However, in recessive sex-linked inheritance, both matching alleles must be abnormal to cause disease. If only one allele in the pair is abnormal, the disease does not occur. Someone who has one abnormal allele (but no symptoms) is called a carrier. Carriers can pass abnormal alleles to their offspring.<br>Males carry one X chromosome therefore they will only ever inherit one allele that will be present in the phenotype (i.e. they cannot be carriers); thus, the presence of a recessive allele will always result in a diseased individual as males do not have the chance of acquiring a heterozygous genotype. This increases their susceptibility to recessive sex-linked diseases.<br>Unlike males, females with two X chromosomes can be heterozygous to mask the effect of a recessive, sex-linked, diseased allele, reducing their susceptibility to be diseased and can be carriers only. | | | |

| Not Achieved | | Achievement | | Achievement with Merit | | Achievement with Excellence | |
|---|---|---|---|---|---|---|---|
| **N1** | **N2** | **A3** | **A4** | **M5** | **M6** | **E7** | **E8** |
| **Describes** ONE evidence point at Achievement. | **Describes** TWO evidence points at Achievement. | **Describes** THREE evidence points at Achievement. | **Describes** FOUR evidence points at Achievement. | **Explains** TWO evidence points at Merit. | **Explains** THREE evidence points at Merit. | **Discusses** ONE evidence point at Excellence. | **Discusses** TWO evidence points at Excellence. |

**N0** = No response; no relevant evidence.

## Question Two

| Expected Coverage | Achievement | Achievement with Merit | Achievement with Excellence |
|---|---|---|---|
| **Population bottleneck** is an event that drastically reduces the size of a population. The bottleneck may be caused by various events, such as an environmental disaster, the hunting of a species to the point of extinction, or habitat destruction that results in the deaths of organisms. Usually, the gene pool is reduced significantly, too.<br>This can lead to the loss / fixation of alleles, therefore reducing genetic variation.<br>**Founder effect** is the loss of genetic variation that occurs when a new population is established by a very small number of individuals from a larger population in a new area, i.e. they are reproductively isolated. This can lead to the loss / fixation of alleles therefore reducing genetic variation.<br>**Genetic drift** is the change in the frequency of an existing gene variant (allele) in a population due to random chance. Genetic drift may cause alleles to disappear completely and therefore reduce genetic variation.<br>**Gene pool** refers to the combination of all the genes (including alleles) present in a reproducing population or species.<br>**Genetic diversity** refers to the range of different inherited traits within a species / population. In a species / population with high genetic diversity, there would be many individuals with a wide variety of different traits.<br>The takahē population was reduced to almost the point of extinction, which led to an extreme loss of alleles and the fixation of others. This resulted in an unrepresentative gene pool from the original population with severely lowered genetic variation amongst the existing birds.<br>The founder effect is significant, as many of the existing birds were taken to island sanctuaries with even smaller populations. Here the breeding pairs may have been only a few individuals so the genetic diversity would be reduced even further.<br>Because genetic drift is a chance event impacting individuals, it is unrelated to natural selection in the environment. This means that 'good' genes are just as likely to be removed as 'bad' ones. In a tiny population, the loss of just one or two individuals can have a huge impact of the amount of genetic diversity, where this would be far less significant in a larger population. | Describes:<br>• population bottleneck<br>• founder effect<br>• genetic drift<br>• gene pool<br>• genetic diversity<br>• a problem arising from reduced genetic diversity (reduced phenotype / inability to adapt to changing environment)<br>• a method of improvement for the future. | Explains:<br>• how genetic diversity is impacted by population bottleneck<br>• how genetic diversity is impacted by founder effect<br>• how genetic diversity is impacted by genetic drift<br>• why the island populations, although protected from predators, are suffering the consequences of reduced / less-variable gene pools and inbreeding<br>• a possible (realistic) way to improve the situation in the future. | Discusses:<br>• the impacts of at least TWO of the three processes (bottleneck, founders, genetic drift) on genetic diversity, making reference to the information provided about the takahe population<br>• the problems arising due to reduced genetic diversity, and a possible way that conservationists could halt the decline and improve genetic diversity in the future. |

| Expected Coverage | Achievement | Achievement with Merit | Achievement with Excellence |
|---|---|---|---|
| The loss of genetic diversity can lead to a reduced ability to adapt to changing environments or the influx of a new disease, as the individuals in the small populations would have very similar genotypes and phenotypes as each other. This lowers the chances of long-term survival or population growth.<br>A reduction in fitness and fertility in inbred individuals that are closely related (inbreeding) relative to outbred individuals or populations can also directly affect population growth rates, as they are ultimately increasing extinction risk.<br>A possible way to increase the genetic variation is to ensure that individuals from isolated populations are brought together to breed / crossbreed, thereby facilitating gene flow and an increase population numbers due to sexual reproduction. Human-assisted translocation can substitute for natural migration. This can aid the maintenance of genetic variation in the mainland population, as it increases the effective population size by connecting sub-populations and creating as diverse a gene pool as possible.<br>Genetic analysis can be used to not only identify lower levels of genetic variation, but to also identify takahe with rare / favourable alleles, i.e. identify individuals to be included in the breeding programme to increase the frequency of these alleles in the gene pool, thereby increasing genetic diversity and lowering the chances of species extinction. | | | |

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## Question Three

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<tr><th>Expected Coverage</th><th>Achievement</th><th>Achievement with Merit</th><th>Achievement with Excellence</th></tr>
<tr><td>(a) A lethal allele is a version of a gene that, in some conditions, may prevent development (i.e. it is never born / or germinates) or cause the death of an organism.</td><td>• Describes a lethal allele.</td><td></td><td></td></tr>
<tr><td>(b)<br><table><tr><td></td><td>g</td><td>g</td></tr><tr><td>G</td><td>Gg</td><td>Gg</td></tr><tr><td>g</td><td>gg</td><td>gg</td></tr></table>Genotype ratio 1:1 Gg:gg<br>Phenotype ratio 1:1 golden:green</td><td>• Punnett square is correctly completed.<br>• Both ratios are correct.</td><td></td><td></td></tr>
<tr><td>(c)<br>The most common interaction between alleles is a dominant / recessive relationship. An allele of a gene is said to be dominant when it effectively overrules the other (recessive) allele, so heterozygous individuals will have the phenotype of the dominant allele. The recessive phenotype will show only when there are two recessive alleles / no dominant allele.<br>When two heterozygotes (aurea) are crossed, the expected phenotype ratio is 3 aurea:1 green; however, the observed ratio is 2 aurea:1 green. This shows that lethal alleles reduce the survivability of aurea if the genotype is homozygous dominant, i.e fewer than expected golden snapdragon survived.<br>The snapdragon must be recessive for lethality even though the allele itself is dominant because the heterozygous individuals do not die. It is only when there are two of the aurea alleles present that the individual plants die. If it were a dominant allele that caused the problem, then the heterozygous individuals would also die.<br>A dominant lethal allele can exist in an adult if the lethality is delayed beyond birth / germination and, in particular, if the individuals survive past reproductive age and do reproduce. In this case, the allele, although dominant and lethal, can be passed on to the next generation. If this didn’t happen, dominant lethal alleles would not exist at all as they would be eliminated from the gene pool because they couldn’t be passed on.</td><td>Describes:<br>• BOTH dominant and recessive alleles<br>• that heterozygous individuals do not die<br>• that the lethality must come later in life.</td><td>Explains:<br>• how lethal alleles affect the expected ratios of individual phenotypes due to the affected individuals not surviving<br>• how the test cross shows that the lethal allele must be recessive even though the colour is dominant<br>• how a dominant lethal allele can exist in an adult<br>• how a dominant lethal allele can be passed on, as it is expressed after reproduction has occurred.</td><td>Discusses:<br>• the inheritance of leaf colour for snapdragon, using punnet squares / ratio to support the discussion<br>• dominant and recessive lethal alleles, comparing the rarity of dominant alleles to recessive alleles and their existence in adult organisms.</td></tr>
</table>

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