Assessment Schedule – 2022

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

Evidence Statement

<table>
<tr><th>Q</th><th>Expected Coverage</th><th>Achievement</th><th>Merit</th><th>Excellence</th></tr>
<tr><td>ONE
(a)</td><td>WwSs</td><td>• F1 Genotype identified correctly.</td><td></td><td></td></tr>
<tr><td>(b)</td><td>
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<tr><td></td><td>WS</td><td>Ws</td><td>wS</td><td>ws</td></tr>
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</table>
Phenotypic ratios:
9 orange striped
3 orange no stripes
3 white striped
1 white no stripes
</td><td>• Punnett square completed with correct gametes and F2.
• Phenotypic ratio matched to correct phenotypes. .</td><td></td><td></td></tr>
</table>

(c)	Linked genes / alleles are found on the same chromosome (therefore are more likely to be inherited together). Unlinked genes are found on different chromosomes / Genes that are found further apart on one chromosome and are more likely to be separated during crossing over. Genetic variation are the differences in alleles / genetic information within population / gene pool. Linked genes would produce allele combinations in gametes that show fewer recombinants between each other. Hence, the offspring phenotypes will be similar to the P / parental generation. On the other hand, unlinked genes create more recombinant / unique gametes. Hence, the offspring phenotypes will show more phenotypic variation. Therefore, linked genes decrease variation within a population / gene pool while unlinked genes increase variation. The process of independent assortment is where the **homologous** pairs line up in a random / different order manner along the cell centre / equator. Independent assortment occurs during first division / metaphase 1 of meiosis. Therefore, only one chromosome from each homologous pair is placed in the gametes. Therefore, genetic variation is achieved / increased when the chromosome pairs are separated, because each new cell has a different combination of chromosomes / allele from each. Independent assortment is a process that does not separate (independently assort) linked genes. Linked genes occur on the same chromosome and are inherited together, therefore cannot be separated during independent assortment. Genes found close to each other on the same chromosome are less likely to be separated via crossing over and therefore, will also stay together during independent assortment. This means linked genes are likely to stay together and be inherited together. Since there is less genetic variation in the gametes for linked genes, they produce less genetic variation in a population than unlinked genes. Unlinked genes can independently assort, therefore produce more genetic variation in a population. Crossing over is the exchange of alleles / segments of chromosomes between homologous pairs of chromosomes / accept annotated diagram. This occurs during meiosis / metaphase 1 / meiosis 1 / before IA / after IA. Crossing over reshuffles existing alleles into new combinations, which increases genetic variation. Genes that are closer together on the same chromosome are more likely to be linked than genes found further apart, because they will stay together during crossing over.	• Describes linked genes. • Describes unlinked genes. • Describe genetic variation. • Describes independent assortment. • Identifies when independent assortment / crossing over occurs during meiosis. • Describes crossing over.	• Explains that independent assortment results in only one chromosome from each homologous pair going into each gamete; therefore, each gamete has a different combination of chromosomes. • Explains how independent assortment affects unlinked genes. • Explains how independent assortment affects linked genes. • Explains how crossing over affects linked genes that are far apart / in close proximity. • Explains how crossing over affects unlinked genes. • Explanation of how independent assortment OR crossing over affects genetic variation.	• Thorough discussion compares and contrasts how independent assortment of linked and unlinked genes affects genetic variation**.** • Thorough discussion compares and contrasts how crossing over of linked and unlinked genes affects genetic variation. • Thorough discussion compares and contrasts how linked and unlinked genes affects genetic variation**.**

	Crossing over can separate linked genes / separate genes found on the same chromosome and causes them to become unlinked. Genes found far away from each other on the same chromosome are likely to be separated via crossing over due to the large distance.			

NØ	N1	N2	A3	A4	M5	M6	E7	E8
No response; no relevant evidence.	Describes any ONE statement from Achievement.	Describes any TWO statements from Achievement.	Describes any THREE statements from Achievement.	Describes any FOUR statements from Achievement.	Explains any TWO statements from Merit.	Explains any THREE statements from Merit.	Discusses ONE criterion for Excellence.	Discusses any TWO criteria for Excellence.

Q	Expected Coverage	Achievement	Merit	Excellence
TWO	Mutation is a **permanent** change in DNA sequence / genetic material / genome / gene. Mutation is the original / ultimate source of variation because it introduces totally new alleles to a population, and this enters a population when present as a gametic mutation Therefore, mutations increase genetic variation in a species OR There is variation of *phenotypes* and *genotypes* in a species because of mutations. Natural selection is the process where individuals with favourable / beneficial phenotypes survive and reproduce. These individuals pass the favourable alleles for these phenotypes onto the next generation, increasing the allele frequency. This would lead to increased frequencies of favourable alleles / decreased frequencies of unfavourable alleles in the Kakapo population of Stewart Island. Genetic drift: **chance / random** change in the allele frequencies within a population. These can result in alleles being lost / removed / 0% frequency or fixed / 100% allele frequency. Random events such as random non-reproduction / indiscriminate predation / random death can increase / decrease allele frequencies in the Kakapo population of Stewart Island. Founder effect is when a small group of individuals from an existing (main) population moves to another area / establishes a new population AND are reproductively isolated from the original population / OR are subjected to different selection pressures / OR the gene pool of the new population of Kakapo were non-representative of the original population's gene pool. (Students must have 2 out of 3 mechanisms discussed in relation to Kakapo population Harmful mutations (usually) decrease survival, and therefore are more likely not to be passed onto offspring / eliminated from a population. Harmful mutations are removed from a population because they decrease an individual's survival / ability of reproduce and pass on. Small populations mostly likely have more accumulation of harmful mutations because there are fewer individuals (less alleles) in the population, and most likely allele frequency not representative of the original population / increased likelihood of inbreeding. Small populations are also more likely to lead to fixed alleles / death has a larger proportional effect, decreases genetic diversity / variation While large populations would have more individuals which acts as a buffer against random deaths / non-mating and also reduces the chances of inbreeding.	• Describes mutation. • Describes natural selection. • Describes genetic drift. • Describes founder effect. • Describes a harmful mutation. • States that rate of inbreeding higher in small population / lower in large population. • States that harmful mutation in Stewart Island population is selected. against / unfavourable / non-beneficial.	• Explains how a mutation enters a gene pool. • Explains how mutations affect genetic variations. • Explains natural selection. • Explains genetic drift. • Explains founder effect. • Explains why small populations more likely to have harmful mutations. • Explains one reason why Stewart Island population has fewer harmful mutations.	• Comprehensively discusses how two of either founder effect, genetic drift and natural selection may have affected the kākāpō. • Compares and contrasts the accumulation of harmful mutations between small and large populations. • Discussion of TWO possible reasons why the Stewart Island population has fewer harmful mutations.

	Stewart Island kakapo may have fewer harmful mutations because of: • natural selection leading to the removal of harmful mutations from the gene pool • low mutation rate in the population, and high inbreeding • Individuals with harmful mutations may have been randomly removed via genetic drift. • individuals in the founding population had lower proportion of harmful mutation compared to mainland population. Therefore, the harmful mutations are not represented in the Stewart Is population.			

NØ	N1	N2	A3	A4	M5	M6	E7	E8
No response; no relevant evidence.	Describes any ONE statement from Achievement.	Describes any TWO statements from Achievement.	Describes any THREE statements from Achievement.	Describes FOUR statements from Achievement.	Explains any TWO statements from Merit.	Explains THREE statements from Merit.	Discusses ONE criterion for Excellence.	Discusses TWO criteria for Excellence.

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<tr>
<td>THREE
(a)</td>
<td>
A rabbit breeder crossed two rabbits that were heterozygous for black fur and chinchilla:
Genotype of parents: Cc^{ch}
Phenotype of parents: Black
Punnett Square:
<table>
<tr><td></td><td>C</td><td>c^{ch}</td></tr>
<tr><td>C</td><td>CC</td><td>Cc^{ch}</td></tr>
<tr><td>c^{ch}</td><td>Cc^{ch}</td><td>c^{ch} c^{ch}</td></tr>
</table>
Genotype ratio: 1CC:2 Cc^{ch} :1 c^{ch} c^{ch}
Phenotype ratio: 3 Black: 1 Chinchilla
Pattern of inheritance: complete dominance
A rabbit breeder crossed two rabbits heterozygous for chinchilla and albino:
Genotype of patents: c^{ch}c
Phenotype of parents: grey / light gey
Punnett Square:
<table>
<tr><td></td><td>c^{ch}</td><td>c</td></tr>
<tr><td>c^{ch}</td><td>c^{ch} c^{ch}</td><td>c^{ch}c</td></tr>
<tr><td>c</td><td>c^{ch}c</td><td>cc</td></tr>
</table>
Genotype ratio: 1 c^{ch} c^{ch}: 2 c^{ch}c: 1cc
Phenotype ratio: 1: Chinchilla : 2 grey / light grey: 1 white / albino
Pattern of inheritance: incomplete dominance
</td>
<td>
• Correct genotype and phenotypes of parents.
• Correct Punnett square either of the two crosses.
• Correct Punnett square AND genotype / phenotype ratio for (c) 2.
• Describes the pattern of inheritance for both crosses.
</td>
<td>
• Both Punnett squares correct with correct genotype and phenotype ratio.
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(b)	Complete dominance is when a phenotype is always expressed / masks the effect of recessive even if only one copy of the allele is present in the genotype. Incomplete is a form of dominance where the alleles of a gene pair in a heterozygote are expressed in an intermediate / blended / mixed form. This results in offspring, forming a new in-between phenotype / three different phenotype / extra phenotype. Multiple alleles are alleles of which there are **more than two** / **three or more** alternatives available at one locus / for one gene. This results in multiple phenotypes. The genotype ratios for the crosses are both 1:2:1 because each Punnett square is crossing individuals that are heterozygous. However, the phenotypes' ratios are different because the alleles are expressed differently. One shows recessive inheritance (3:1) / complete dominance inheritance and the other incomplete dominance (1:2:1). In incomplete dominance, heterozygous genotype is different to both of the homozygous genotypes. In incomplete dominance you see the dominant and recessive allele interact to form an intermediate phenotype (e.g. grey fur / pale / light / intermediate). So, it depends on what alleles are present as to what phenotype is expressed in the incomplete dominance heterozygous phenotype. Thus, the phenotype appearance results from the combination / interaction of the alleles, not the presence of a dominant allele, as with recessive inheritance / complete dominance. The advantages of incomplete dominance inheritance are that it increases phenotype variation in a species / three phenotype are produced / . A disadvantage of complete dominance is that it masks / hides the recessive allele in a heterozygous individual / only two phenotypes are produced. The advantages of multiple alleles within a species means more phenotypes are expressed, and therefore more different phenotypes can respond to natural selection pressures and increases the chances of survival of species (especially if environmental conditions change).	• Describes complete dominance. • Describes incomplete dominance. • Describes multiple alleles. • States that variation increases chances of survival of a species.	• Explains why genotype are the same, but phenotype ratios are different. • Explains incomplete dominance and multiple alleles. • Explains an advantage / disadvantage of multiple alleles. • Explains an advantage / disadvantage of complete dominance. • Explains an advantage / disadvantage of incomplete dominance.	• Discusses using context why the genotype ratios are the same, but phenotypes ratios are different. • Discusses ONE advantage and ONE disadvantage of any of the TWO patterns of inheritance: multiple alleles / complete dominance / incomplete dominance. (context not required).

NØ	N1	N2	A3	A4	M5	M6	E7	E8
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Cut Scores

Not Achieved	Achievement	Achievement with Merit	Achievement with Excellence
0 – 7	8– 12	13 – 18	19 – 24