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Draw a cross through the box (☒) if you have NOT written in this booklet

Mana Tohu Mātauranga o Aotearoa
New Zealand Qualifications Authority

Level 2 Biology 2025

91157 Demonstrate understanding of genetic variation and change

Credits: Four

Achievement	Achievement with Merit	Achievement with Excellence
Demonstrate understanding of genetic variation and change.	Demonstrate in-depth understanding of genetic variation and change.	Demonstrate comprehensive understanding of genetic variation and change.

Check that the National Student Number (NSN) on your admission slip is the same as the number at the top of this page.

You should attempt ALL the questions in this booklet.

If you need more room for any answer, use the extra space provided at the back of this booklet.

Check that this booklet has pages 2–16 in the correct order and that none of these pages is blank.

Do not write in the margins (⁄⁄⁄⁄). This area will be cut off when the booklet is marked.

YOU MUST HAND THIS BOOKLET TO THE SUPERVISOR AT THE END OF THE EXAMINATION.

Excellence

TOTAL 21

Orange G Striped B
White g blotched b

QUESTION ONE: Snake genetics

Corn snakes (*Pantherophis guttatus*) are considered helpful to humans and are found in different parts of the eastern United States. This species lives in a wide variety of habitats including wooded areas, rocky hillsides, barns, and abandoned buildings.

They have a complete dominance inheritance pattern for body colour and scale pattern. The orange body-colour allele (G) is dominant to the white body-colour allele (g).The allele for striped scale pattern (B) is dominant to the allele for blotched scale pattern (b). The genes for body colour and scale pattern are not genetically linked.

Corn snake. Anerythristic Hurricane Motley corn snake.

(a) Conservationists crossed a corn snake homozygous for the orange body-colour allele and the striped pattern allele, with a corn snake homozygous for white body colour and blotched scale pattern.

State the genotype of the gametes produced by each parent:

Parent 1: GGBB Parent 2: ggbb

State the genotype of the F1 generation:

GgBb

(b) Use the Punnett square below to show the gametes of the F1 generation, and all of the possible genotypes of the F2 generation.

F1 gametes (top); F1 gametes (side)

	GB	Gb	gB	gb
GB	GGBB	GGBb	GgBB	GgBb
Gb	GGBb	GGbb	GgBb	Ggbb
gB	GgBB	GgBb	ggBB	ggBb
gb	GgBb	Ggbb	ggBb	ggbb

E striped R smooth
e unstriped r rough

(c) Describe the predicted phenotype (F2) ratio produced by the cross.

9 orange striped : 3 orange blotched : 3 white striped : 1 white blotched

(d) The garter snake (*Thamnophis sirtalis*) is another species of snake and has often been bred in captivity. When snakes are crossed that are heterozygous for a striped pattern and rough scale texture, striped (E) is dominant over unstriped (e), and smooth texture (R) is dominant over rough texture (r).

With this cross, the observed ratio is frequently found to be:

7 striped smooth : 1 striped rough :
1 unstriped smooth : 7 unstriped rough

Common garter snake.

ER linked er linked.

Discuss how genes located on the same chromosome can show both linked and unlinked characteristics, using the information provided for BOTH species of snake.

In your answer, include discussion of:

- how the processes of crossing over and segregation can influence the inheritance patterns of both linked and unlinked genes
- the effect of gene location on the observed phenotype ratios
- why the dihybrid heterozygous crosses for these identified traits are so different in these two species of snake.

Linked genes are genes found close together on the same chromosome and ~~unlinked~~ unlinked genes are found on either different chromosomes or far apart on the same chromosome. Crossing over is the process where homologous chromosomes exchange sections of alleles/genetic information between each other on non-sister chromatids. This creates new allele combinations and recombinant gametes. Crossing over can very likely move unlinked genes onto the same chromosome, or separate them to different chromosomes. It is unlikely that linked genes will be separated during crossing over as they are close together, and likely to be inherited together, (but its possible) ~~independent~~

Chiasma

☆☆

~~assortment is the process where homologous chromosomes randomly line up along the cell equator and sort independently to each other. These homologous pairs then separate into different gametes. Unlinked genes can be indepently~~ [dent] ~~sorted because they can be on different chromosomes, meaning one could be on the maternal homologue, and one on the paternal homologue. Linked genes could be~~ ~~independently sorted~~ [segregated] ~~if they are separated during crossing over, but this is much less likely. Linked genes that aren't separated, and unlinked genes on the same chromosome that weren't separated cannot be~~ ~~independently sorted~~ [segregated], and these traits will be inherited ~~together. The genes for body~~ colour (G, g) and scale pattern (B, b) are unlinked, so if these genes are found on the same chromosome, they are far apart and a chiasma can likely form between them during crossing over, and they could be ~~independently sorted~~ [segregated]. This is why the F1 gametes for the corn snake can produce a variety of different genotypes and a 9:3:3:1 ratio. However the garter snake cross produced a 7:1:7:1 ratio, with the majority of genotypes being homozygous for both traits. This suggests that the dominant alleles: E and R are linked, and the recessive alleles: e and r are also linked. This means these alleles are found close together on the same chromosome and were mostly unaffected by crossing over and ~~independent assortment~~ [segregation.] (unseparated). ☆

Although there ~~was~~ is still a small [predicted] percentage of heterozygous genotypes produced from this cross, meaning there's a small chance of the linked genes being separated.

This is why both dihybrid heterozygous crosses showed different traits despite being the same test. The inherited traits for the snakes is dependent on whether the genes are found on the same chromosome, and if they're linked or unlinked.

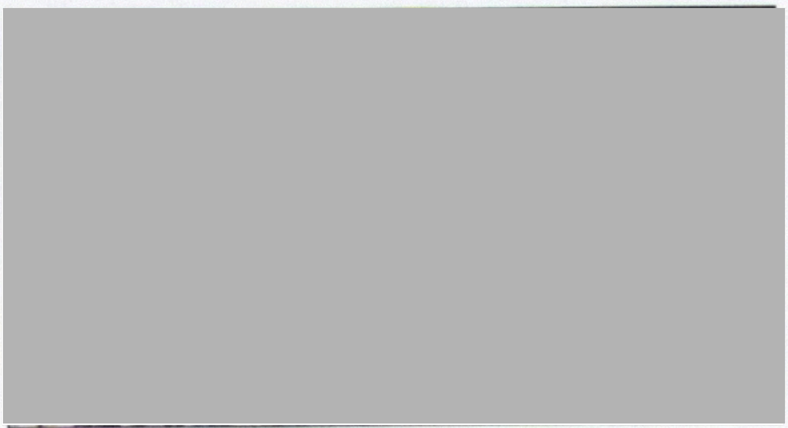
* This is why the most common phenotypes for the garter snake were striped, smooth and unstriped, rough, because these traits are linked ~~to~~ together.

** Segregation can affect unlinked genes if they are on different chromosomes, and can therefore be separated during this process. Segregation is the process where allele pairs are separated into different gametes so that each gamete only gets one allele for a gene. Linked genes mostly can't be segregated because the alleles are close together and on the same chromosome, so they will stay together UNLESS they have been separated during ~~meiosis~~ crossing over, and are now on different chromosomes. Unlinked genes may also be unaffected by segregation if they are unseparated during crossing over and found on the same chromosome.

(ignore independent assortment definition, and count stuff thats crossed out but ~~been~~ IA replaced with segregation)

QUESTION TWO: The New Zealand giraffe weevil / pepeke nguturoa

The New Zealand giraffe weevil / pepeke nguturoa (*Lasiorhynchus barbicornis*) is an insect endemic to New Zealand. The most notable phenotypic variation in this species is observed in males, particularly in the length of their snout, known as a rostrum, and overall larger body size. These phenotypes are influenced by genetic and environmental factors and are subject to strong sexual selection (mate selection) where females are choosing the males based on their phenotypes.



New Zealand giraffe weevil.

The table below shows the common distribution of these phenotypes:

	North Island	**South Island**	**Smaller offshore islands** (limited food and habitat resources, smaller populations)
Long-rostrum males	Dense native forests (e.g. Waipoua Forest, Tongariro National Park).	Dense native forests (e.g. Fiordland National Park, Westland Tai Poutini National Park).	Phenotype distribution is far more random and shows less relationship to the dominant type of vegetation.
Short-rostrum males	More open or smaller patches of native forests.	Drier or more open habitats (e.g. Canterbury Plains).	

Discuss what factors may cause allele frequencies in a gene pool to change, using the information provided above.

In your answer, include discussion of:

- how the gene pool of the New Zealand giraffe weevil could be affected by their migration between habitats AND by genetic drift
- how sexual selection (mate selection) and natural selection may have influenced these two distinct phenotypes of long-rostrum and short-rostrum males.

Allele frequencies are the frequency/occurance of an allele within a gene pool of a population. The gene pool is all the alleles present within a population. When these weevils migrate between habitats, specifically emigration, they could experience the founder effect. This is when a small group of individuals emigrate from the original population and establish a new population elsewhere. This may have happened to the weevils on the offshore islands, and they became geographically isolated from the original mainland population. This smaller population would not have a representative gene pool of alleles of the original population and overall be less genetically diverse. Any small weevil population like this one would experience genetic drift as well. This is when allele frequencies change due to chance. In a small population, the death of an organism or random mating can have a major impact on allele frequencies and cause alleles to become fixed or lost completely. This is why the phenotype distribution of the island weevils is much more random, because allele frequencies are less stable and any event can randomly shift alleles. Another reason for this is because resources and food are limited. Some weevils may gain more nutrition and show larger body and long rostrum phenotypes while other weevils may miss out on sufficient nutrition and have smaller bodies and rostrums. Because of the random and unfair resource distribution on the island, the phenotypes are also randomly distributed. This is because the island shows a variety of habitats rather than only dense forest or only open patches. Sexual selection is when females choose males with the the healthiest/best genes so that offspring will carry advantageous traits and be better suited to survive environmental changes. This is a type of ~~a~~ selection pressure which drives natural selection. Natural selection is the process where favourable traits/alleles remain within a population because those with them pass them down to offspring by ~~surviving~~ surviving and finding a mate. In the North and South islands, long-rostrum males are found in dense native forest. This likely because 1. there are plentiful resources all around so males will have sufficient nutrition to grow large and long-rostrum(ed) and 2. therefore sexual selection, the allele for a long-rostrum will be passed on because ~~an~~ females will want and mate with the weevils with the longest rostrums. Through natural selection those with the long rostrum trait will find mates and pass down alleles to offspring, increasing the frequency of that allele within the gene pool. Those with ~~&~~ allele combinations that give short rostrum phenotypes won't find a mate and their alleles will be lost from the gene pool through natural selection, decreasing the frequency of that allele. This is why long rostrum males are found in dense forest. Short rostrum males may be found in drier/open/smaller areas because there are less resources available so this environmental factor ~~make~~ gives them a smaller bodied, shorter rostrum phenotype. The opposited affect of the forest environmental factor of more resources. (An environmental factor is something that influences the phenotype of an organism but not the genotype). ~~Females~~ Sexual selection will still occur and females will still choose males with

QUESTION THREE: Blood types

If a patient needs a blood transfusion during surgery, it is essential to match their blood type correctly. Receiving the wrong blood type can cause serious, potentially life-threatening reactions.

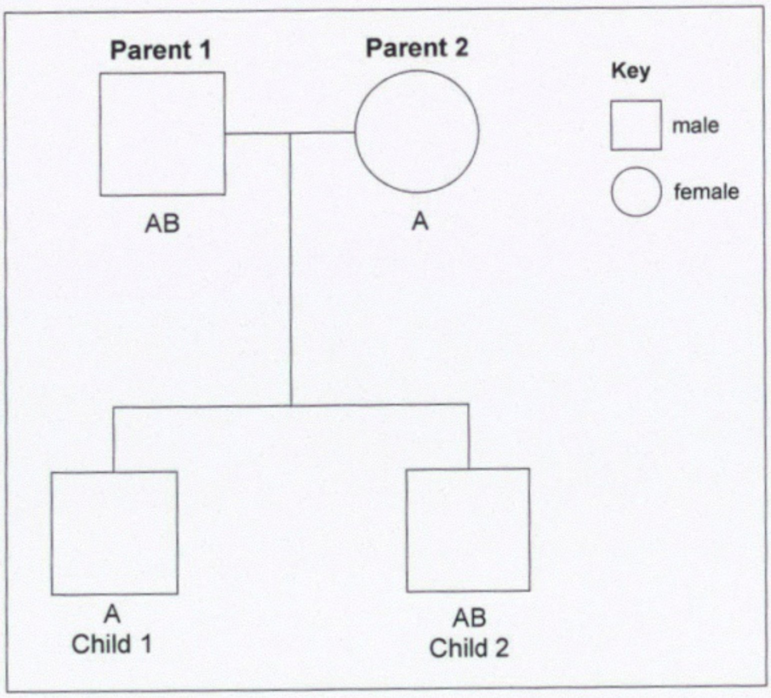
Blood type in humans is controlled by multiple alleles. The alleles I^A and I^B are dominant over i^O. I^A and I^B are examples of alleles that show co-dominance.

The pedigree chart below shows the blood types/phenotypes of two children and their parents.

Blood types

Phenotype	Genotype
A	I^AI^A, I^Ai^O
B	I^BI^B, I^Bi^O
AB	I^AI^B
O	i^Oi^O

Pedigree chart



Discuss the inheritance of these blood types, using the information provided above. You may include a Punnett square to support your answer (optional).

In your answer, include discussion of:

- what is meant by the term multiple alleles
- the possible genotypes of Child 1
- the difference between dominant alleles and co-dominant alleles
- how to determine the genotype of Child 1 using the blood types of **his** children, if his partner is a blood type O female
- why the determination of Child 1's genotype may **not** be guaranteed as correct if determined using his children's blood types.

random chance in P2

Multiple alleles is when a gene has 3 or more possible alleles. Dominant alleles completely mask the effect of recessive alleles, meaning the phenotype associated with them will always be expressed when it is present. Co-dominance occurs when a gene has more them one dominant allele for the trait, and heterozygous individuals with 2 dominant alleles will show both traits in the phenotype. Since the I^A allele is dominant over the I^O allele, Child A could have 2 possible genotypes. The first would be if the child inherited an I^A allele from both parents, giving genotype I^AI^A and phenotype A-type. But Parent 2 could have a hidden I^O recessive allele as their phenotype is A, meaning I^A could mask I^O. This means Child A could also have the I^AI^O genotype if they inherit an I^A allele from P1 and possible hidden I^O allele from P2. If Child A had kids with a blood type O female, his genotype could be determined. Since I^A is dominant over I^O, if all his children show the A blood-type phenotype then this must mean that he has a I^AI^A genotype. This is because each child must inherit an I^A allele from him, and must inherit an I^O allele from mum since both parents are homozygous. The I^O would always be masked.* If some of his kids had the O blood phenotype then he must be I^AI^O (heterozygous) because for the recessive phenotype to be expressed, kids must inherit 2 copies of the recessive allele. So for them to be O type, they must inherit one I^O from dad, and one I^O from mum, hence meaning "Child 1" must have the heterozygous A blood genotype. However, these predictions are determined by punnett squares, which are, just predictions. Due to

*and his kids would all express the A blood phenotype because they must inherit an I^A allele from him if he's I^AI^A (homozygous dominant for A) the random nature of sexual reproduction with the factors of meiosis and fertilization, genotypes are always random and predictions aren't facts. If Child 1's kids all showed the A blood type phenotype, he could still be heterozygous I^AI^o, because this type of offspring can still be produced from that cross. Just because the punnett square predicts that 50% of children will be A-type and 50% O-type (from a I^oI^o + I^AI^o cross) doesn't mean that this result will be guaranteed to show in offspring.

	I^o	I^o
I^A	I^AI^o	I^AI^o
I^A	I^AI^o	[crossed out] I^AI^o

if child A has I^AI^A phenotype

&

	I^o	I^o
I^A	I^AI^o	I^AI^o
I^o	I^oI^o	I^oI^o

Extra space if required.
Write the question number(s) if applicable.

QUESTION NUMBER

2 long rostrums, but these will still be short due to environmental factors. OR the short rostrum phenotype may be the more favourable, more beneficial phenotype for drier/open/small habitats so through natural selection and/or sexual selection, the short rostrum phenotype is favoured by nature and/or females, and those with that trait will pass down those favourable alleles to offspring. This increases the frequency of the short rostrum allele in these areas.

Migration between populations can also change allele frequencies. When weevils from a forest population who have the allele(s) for a long rostrum migrate to another forest population or a drier/open/small population, they breed and ~~establish~~ increase the frequency of their (long rostrum) allele within that population's gene pool. Migration increases the frequency of an allele in one population and decreases the frequency of the allele in the other. Overall migration increases allele frequencies between populations, but makes gene pools between populations more similar, and decreases genetic variation.

Excellence

Subject: Biology

Standard: 91157

Total score: 21

<table>
<tr><th>Q</th><th>Grade score</th><th>Marker commentary</th></tr>
<tr><td>One</td><td>E8</td><td>The response explained:
the patterns of linked and unlinked genes, using the ratios provided in the question for the named examples.
the processes of crossing over and segregation, linking them to the idea of linked and unlinked genes found on the same chromosome.
The processes were linked to discuss the ratios found in both the named examples.</td></tr>
<tr><td>Two</td><td>M6</td><td>The response explained:
the process of genetic drift and its effect on a small population
the process of natural selection
The response could be improved by explaining a selection pressure for the different environments and link it to the named examples correctly.

Further explanation of the process of migration and discussion of both the processes of genetic drift and migration in relation to the random phenotype distribution would have allowed this response to reach Excellence level.</td></tr>
<tr><td>Three</td><td>E7</td><td>The response linked the inheritance pattern shown in the pedigree chart in the question to explain the genotype of child 1.

The gametes for child 1 and their partner were explained and linked to the observed ratios for both the genotype and the phenotype of the offspring.

The response used percentages to link the idea that the genotype of child 1 cannot be guaranteed using the information provided in the pedigree chart.

Further discussion of the patterns of complete and co-dominance using the genotypes of child 1’s parents linked to the possible genotypes for child 1 would have satisfied the second Excellence criteria.</td></tr>
</table>