

91157



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2

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Level 2 Biology 2022

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 any cross-hatched area (///). This area may be cut off when the booklet is marked.

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

QUESTION ONE: MEIOSIS

In tigers, coat colour and stripe pattern are determined by two different genes that are not linked. The orange (W) coat colour is completely dominant to white (w), and the striped (S) pattern is completely dominant to no stripe (s).



www.recreoviral.com/fotografia/fotografias-llamaran-atencion-cualquier-curioso/

A tiger homozygous for orange fur and stripes is crossed with a tiger homozygous for white fur and no stripes. All the next generation tigers (F1) have the same genotype.

- (a) Identify the genotype of the F1 generation.

- (b) Two of these F1 tigers are crossed to produce the F2 generation.

Use the Punnett square to:

- show the F1 gametes and all the expected genotypes of the F2 generation of the tigers
- give the phenotypic ratios for the completed cross.

		F1 gametes			
F1 gametes					

Phenotypic ratios: _____

(c) Discuss how independent assortment and crossing over affects linked genes and unlinked genes AND how they both affect genetic variation in a population.

In your answer include:

- a description of linked genes AND unlinked genes
- an explanation of the processes of independent assortment and crossing over, including when they occur
- an explanation of why linked genes do not independently assort during the process of meiosis
- a discussion comparing and contrasting how linked genes, independent assortment, and crossing over affect genetic variation in a population.

There is more space for your answer to this question on the following pages.

QUESTION TWO: POPULATION GENETICS

Kākāpō numbered in the hundreds of thousands before humans arrived in Aotearoa. Humans introduced predators such as cats and stoats, and by 1995 there were only 51 kākāpō: 50 on Stewart Island and one on the mainland. Data shows that the surviving population on Stewart Island had been isolated for 10 000 years. During this time these birds had been inbreeding with each other.

Biologists sequenced and analysed kākāpō genomes from 35 living birds from Stewart Island and 14 samples from the extinct mainland population. Surprisingly they found that the kākāpō on Stewart Island have lost harmful mutations rather than accumulating them. Biologists found they now carry fewer harmful mutations than the extinct population on the mainland once did.



Adapted from [https://www.cell.com/cell-genomics/pdfExtended/S2666-979X\(21\)00002-1](https://www.cell.com/cell-genomics/pdfExtended/S2666-979X(21)00002-1)

Source: <https://nzbirdsonline.org.nz/species/kakapo>

- (a) Discuss the possible reasons for the removal of harmful mutations from the Stewart Island birds, even though the population is small.

In your answer include:

- a description of what a mutation is and how it enters a gene pool
- an explanation of how kākāpō might have been subjected to natural selection, genetic drift, and founder effect
- an explanation of why harmful mutations may accumulate more in small populations than in larger populations
- a discussion of THREE possible reasons why the Stewart Island population has fewer harmful mutations.

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The examination continues on the following page.**

QUESTION THREE: PATTERNS OF INHERITANCE

Rabbit coat colour is produced by a variety of different inheritance patterns. Some studies have shown that coat colour shows incomplete dominance.

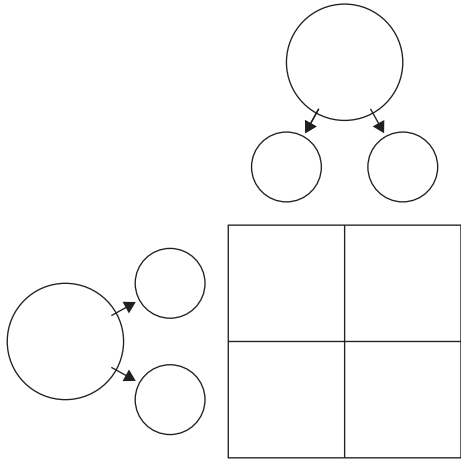
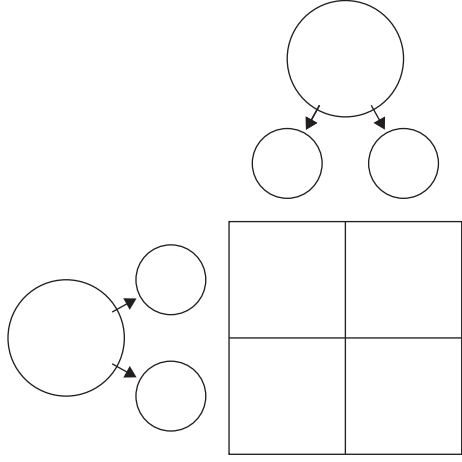
The coat-colour gene has multiple alleles which show an order of dominance. The simplified table below show the coat colour, allele symbol, and order of dominance for three phenotypes.

Coat colour	Wild type: black	Chinchilla: grey	Albino: white
Phenotype			
Allele symbol	C	c ^{ch}	c
Order of dominance	Complete dominance over all the others	Chinchilla shows incomplete dominance over albino	Recessive to wildtype and chinchilla

Adapted from: www.macmillanhighered.com/BrainHoney/Resource/6716/digital_first_content/trunk/test/hillis2e/asset/img_ch8/c08_fig09.html

(a) Complete the monohybrid Punnett squares in the table opposite.

Work through the instructions in the table opposite to complete and compare the two monohybrid crosses for rabbit fur inheritance.

A rabbit breeder crossed two rabbits that were heterozygous for black fur and chinchilla.	A rabbit breeder crossed two rabbits that were heterozygous for chinchilla and albino.
Describe the genotype of the parents:	Describe the genotype of the parents:
Describe the phenotype of the parents:	Describe the phenotype of the parents:
<p>Complete the Punnett square below, and describe the expected genotype and phenotype ratios.</p> 	<p>Complete the Punnett square below, and describe the expected genotype and phenotype ratios.</p> 
Expected genotype ratio:	Expected genotype ratio:
Expected phenotype ratio:	Expected phenotype ratio:
Pattern of inheritance:	Pattern of inheritance:

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

QUESTION
NUMBER

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