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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.

Achievement

TOTAL **12**

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.

WwSs

(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

	WS	Ws	wS	ws
WS	WWSS ✓	WWSs ✓	WwSS ✓	WwSs
Ws	WWSs ✓	WWss	WwSs ✓	Wwss
wS	WwSS ✓	WwSs ✓	wwSS	wwSs
ws	WwSs ✓	Wwss	wwSs	wwss

F1 gametes

Phenotypic ratios:

9 : 3 : 3 : 1

9 orange fur and stripes : 3 orange fur and no stripes :

3 white fur and stripes : 1 white fur and no stripes

$\frac{9}{7}$

(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.

Linked genes are genes that are inherited together as they are found closely together on the same chromosome. Unlinked genes are genes that are not found close to each other but are still on the same chromosome. Crossing over is the exchange of alleles/portions of ~~chromosome~~ chromatids between chromosomes. Crossing over increases variation of a gene pool if it occurs by creating new allele combinations. This occurs, if it does occur, before independent assortment and segregation in Metaphase. Independent assortment is the random lining up of homologous pairs of ~~chromatids~~ chromosomes at the cell equator where new alleles combinations are created. Independent assortment occurs before segregation in the phase Telophase. Linked genes cannot independently assort during meiosis because they are so close to each other on the chromosome. During independent assortment, homologous Pairs of chromosomes are paired together randomly to create variation but because linked genes are inherited together on the same chromosome they cannot be seperated so they will

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

remain a linked gene and independent assortment will not occur. Genetic variation is the measure of different allele combinations within a population. Linked genes will not affect the genetic variation within the population as because the genes are linked and no independent assortment can occur with them, this does not increase but decrease the genetic variation of the population as new combination alleles will not occur. Crossing over, however, does affect the variation of a gene pool of a population as when alleles between homologous pairs of chromosomes exchange, this creates as well as increases the variation of that population. This creates new combination alleles that will be introduced into the population's gene pool if it does occur as crossing over will not always occur. Independent assortment will also affect the genetic variation within a populations as it leads to variation. As the lining up of cei chromosomes is completely random. there are over 8 million possible allele combinations that can occur. Linked genes decrease Variation compared to independent assortment and crossing over which only creates, leads or increases the genetic variation of a population. Independent assortment can only lead to variation while crossing over can create as well as increase variation.

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   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.

A mutation is a change in the sequene of DNA which can be caused by exposure and environmental factors as well as Chromosomed changes. A gene pool is the alleles frequency within a population and is the measure of those alleles within the population. A mutation will enter through a gene pool if the

the mutation or change in the DNA sequence to has occured
in the gametic or sex cells of an individual. Therefore, this mutation
will not only occur within the in the individual itself but will
be passed on and inherited by the offspring of the individual.
Thus this will cause the mutation to now enter the gene pool.
Natural & selection is the 'an individual or populations ability
to adapt and survive amongst other of it's kind, this causes the
frequency of alleles from that individual to increase thus decreasing
the genetic variation of the population's gene pool. Genetic drift is
the random change in allele frequencies of a gene pool thus changing
the gene pool of a population. The founder effect occurs when a
small number of a population has emigrated away due to factors
such as mobility, barriers and mating. It changes the gene pool
of both the founding population as well as the new population of the
individuals that have emigrated. This will have a larger affect on
the population that has left because it it is smaller and more
likely to be at higher risk of losing alleles in in the population
because of the decreased diversity. The Kakapo population
was subjected to the all these processes which has caused the
gene pool and allele frequency to completely change. The Kakapo
Was subjected to genetic drift though human activity because
humans had introduced predatory animals that almost completely
decimated the Kakapo population. Thus the population of the Kakapo
greatly decreased as well as its allele frequency. Natural selection
had also occured as the population that was left of the Kakapo
had adapted to the environment by hiding avoiding or surving
from the cats and stoats brought in. This allowed the alleles individuals
with the stronger better alleles to survive and
reproduce increasing the frequency of alleles

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that had been naturally selected. Furthermore this caused the
founder effect to occur on the Kakapo population as due to
many factors including mobility, barriers, predators and the need
for a better mate, one of the surviving kakapo emigrated from
the mainland to Stewart Island. Harmful mutations are
mutations that will decrease an individuals ability to
survive and adapt. In smaller populations, because the gene
pool is incredibly smaller than larger populations and there
is a lower allele frequency and decreased genetic diversity,
smaller populations are more affected. This is because the lack
of genetic diversity will cause more individuals to inherit the
harmful mutation whereas larger populations have a
higher genetic diversity because there are more individuals.
This means that when an individual becomes affected by that
mutation because there are a more diverse amount of alleles,
only those individuals will be affected and the total population
will not suffer much loss from that mutation compared to small
populations. However the population of Kakapo on stewart Island
has less harmful mutations ~~because it~~. One reason this could be
is that natural selection has occured and the alleles of this individual
allow the harmful mutation to filter out over time. Another reason
for this is because of migration, ~~specifically~~. As the singular kakapo
~~entered the~~ immigrated into the population of other birds, the alleles
of the other population has ~~created an~~ filtered out the mutations
over time as the populations inbred with each other. Finally this
could be because the gene pool of the Kakapo increased as well
as the genetic diversity due to the offspring of the surviving kakapo
inbreeding with various other species introducing new genes

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.

2:2

hetro black + chin

$C \, c^{ch}$ + $c^{ch} c^{ch}$
   or   or
$C c$ $c^{ch} c$

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: 1 cc : 1 $c^{ch}c^{ch}$	Describe the genotype of the parents: 1 $c^{ch}c$: 1 cc
Describe the phenotype of the parents: 1 black : 1 grey	Describe the phenotype of the parents: 1 grey : 1 white
Complete the Punnett square below, and describe the expected genotype and phenotype ratios.	Complete the Punnett square below, and describe the expected genotype and phenotype ratios.

For the first cross:

C · c^{ch}

	C	c^{ch}
c^{ch}	Cc	$C^{ch}c$
c	Cc^{ch}	$c^{ch}c$

For the second cross:

c^{ch} · C → c^{ch} , c

	c^{ch}	C
	$c^{ch}c$	CC
	$c^{ch}C$	Cc

Expected genotype ratio: 1 Cc : 2 Cc^{ch} : 2 $c^{ch}c$	Expected genotype ratio: 2 $c^{ch}C$: 2 cc
Expected phenotype ratio: 4 black rabbits 2 black : 2 chinchilla	Expected phenotype ratio: 2 grey : 2 white
Pattern of inheritance:	Pattern of inheritance:

(b) Using the table completed in part (a) discuss why the genotype ratios are the same for both crosses, but the phenotype ratios are different.

In your answers include:

• a description of complete dominance

• an explanation of why the genotype ratios are the same for the above crosses, but the phenotype ratios are different

• an explanation of incomplete dominance and multiple alleles

• a discussion of why complete dominance, incomplete dominance, and multiple alleles could be an advantage AND a disadvantage to a species-link to natural selection.

Complete dominance is when the alleles of this specific gene has dominance over all the other alleles meaning they cannot be masked or overpowered itself. This can be seen in the alleles of the wildtype as it has complete dominance over all other fur genes.

Incomplete dominance occurs when both alleles are fully expressed in the phenotype of an organism. Both alleles cannot be shown so there is an intermediate phenotype that is reached in incomplete dominance.

Multiple alleles is when there is more then one or two alleles that can be produced from reproduction, it includes the new alleles created from co-dominance or incomplete dominance.

Complete dominance can be an advantage as they ~~can both~~ are more frequent in the gene pool, ~~because it is~~ this allows the organism to better hide among the numbers of individuals with ~~similar~~ the same phenotype when being hunted.

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QUESTION
NUMBER

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15

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QUESTION
NUMBER

QUESTION
NUMBER

Standard	91157	Display ID		NSN 139633773	Total score	12
Q	Grade score	Annotation				
1	M5	This is an M5 because candidate was able to explain how independent assortment affects linked genes. The candidate was also able to show their understanding of how the process of Meiosis affects genetic variation through crossing over and independent assortment.				
2	M5	This is an M5 as candidate has been able to correctly define both founders' effect and genetic drift and has explained how these processes affect the frequency of alleles within a population. There is some context utilised when explaining genetic drift within the Kakapo population. The definition and subsequent explanation given by candidate for natural selection is incorrect due to their failure to identify the idea that natural selection acts on phenotype rather than alleles.				
3	N2	Candidate has given correct definitions for complete and incomplete dominance, to gain an N2. Candidate has been unable to gain any points from either of the punnet squares.				