2

91157

911570

SUPERVISOR'S USE ONLY

Tick this box if you have NOT written in this booklet ☐

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.

Excellence

TOTAL **23**

2

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
F1 gametes	wS	WwSS	wwSS	WwSs	wwSs
	Ws	WWSs	WwSs	WWss	Wwss
	ws	WwSs	wwSs	Wwss	wwss

Phenotypic ratios: 9 orange & striped : 3 white & striped : 3 orange & no stripes : 1 white & no stripes

(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 which are close together on the same chromosome and are likely to be inherited together. Unlinked genes are genes either far apart on the same chromosome, or on separate chromosomes, that are not likely to be inherited together. Independent assortment occurs during meiosis, when homologous pairs of chromosomes, maternal and paternal, line up randomly at the cell equator. Crossing over is when alleles are and genetic material is exchanged between chromosomes at the cell equator. Linked genes do not independently assort during the process of meiosis because they are close together on the same chromosome and so will stay together. Linked genes reduce genes Genetic variation is differences and between genetic material/make-up of individuals within a population. Linked genes reduce genetic variation in a population because

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

4

they firstly do not independently assort during meiosis. Independent assortment generally increases genetic variation within a population because the gametes produced will have different combinations of both maternal and paternal chromosomes. It is random where the homologous pairs line up at the cell-equator, as they ft assort independently of ~~chromo~~ other homologous pairs ~~However~~ ~~independent assortment~~ This usually randomises fertilisation even more resulting in increased genetic variation within the population. However linked genes are so close together that they do not independently assort themselves, resulting in fewer different combinations of alleles and reducing genetic variation within a population. Unlinked genes however, are far apart from each other or on different chromosomes, so will independently assort during meiosis. As a result, there will be more combinations of alleles in the gametes produced, and genetic variation is increased. Crossing over increases genetic variation because genetic material is swapped between homologous pairs, resulting in new and unique combinations of alleles in the gametes. Linked genes can be separated during crossing over which would increase genetic variation. However, if the linked genes are close together on the same chromosome then it is possible for them to be crossed over to other chromosomes together. This would further decrease genetic variation because. linked genes result in fewer possible combinations of alleles in the gametes. Unlinked genes however are usually separated during crossing over, because they are far apart from each other. As a result, more combinations of alleles would result, and the genetic variation of the population would increase. This shows that linked genes generally decrease genetic

variation because they are likely to be inherited together, and this results in fewer combinations of alleles within the gametes produced in meiosis. However, the process of crossing over can separate these linked genes which means they would then be unlikely to be inherited together, increasing the genetic variation of the population.

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 permanent change in the base sequence of DNA. A mutation enters the gene pool when it occurs in the gametes (sex cells) of an individual. This means that the mutation is then inheritable and able to be passed down to the next generation. As the mutation is inherited by more and more

kakapo, it becomes inherent within the population's gene pool. The kakapo population are likely to have been subjected to natural selection because it was found that a harmful mutation was lost removed from their population. Natural selection is when the environmental conditions select individuals with favourable alleles. These individuals are able to survive the environmental conditions reproduce, and pass on their favourable alleles to the next generation. Other individuals without these favourable alleles are likely to die before reproduction, and their non-favourable alleles will not be passed on to the next generation. This can result in the non-favourable alleles being lost from the population forever and the favourable alleles becoming "fixed" in the gene pool. This is likely to have happened to the kakapo population. The harmful mutation that they previously possessed likely killed off individuals before they had the chance to reproduce and pass on the harmful mutation to the next generation. This would have resulted in the mutation being removed from the gene pool forever. Genetic drift is the change of allele frequency within a population due to chance or random events. Genetic drift would have happened to the mainland kakapo because their whole population was wiped out. The random event was predation by cats and stoats which reduce caused the mainland population to become extinct. Stewart Island kakapo however may have also been subjected to genetic drift because their population was also reduced to 50 individuals, which is a random event.

The kakapo are likely to have been subjected to the founder effect. The founder effect is when a small group of individuals from

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

a population, leave their population to establish a new population that reproductively separate from the original population. This new population has ~~original~~ likely has a much smaller selection of alleles compared to the original population. It is likely that the kakapo were subjected to the founder effect because there was an original population of kakapo on the mainland, which means it is probable the newly established kakapo population was on Stewart Island. However because it was that the stewart island kakapo had been isolated for 10,000 years, ~~the~~ this founder effect would have happened a long time ago. Harmful mutations may accumulate more in small populations compared to large populations because small populations have more chance of inbreeding. Inbreeding results in more alleles becoming "fixed" within the gene pool, and decreasing the genetic diversity of the population as a whole. Harmful mutations are more likely to accumulate as related individuals with the mutation may produce offspring together who also have the mutation, causing it to continue to be passed down to the next generation. Larger populations however have a larger number of individuals and greater genetic diversity, meaning there is more chance of random mating. As a result ~~that~~ the harmful mutation would be less apparent due to the numerous other alleles able to be inherited. The Stewart Island population could have fewer harmful mutations as a result of natural selection, and mutations being permanently removed from the gene pool. It could also be because of genetic drift, and individuals with the harmful mutation were wiped out by a random event before they could reproduce. A final reason the stewart Island population has fewer harmful ~~population~~ mutations could be because

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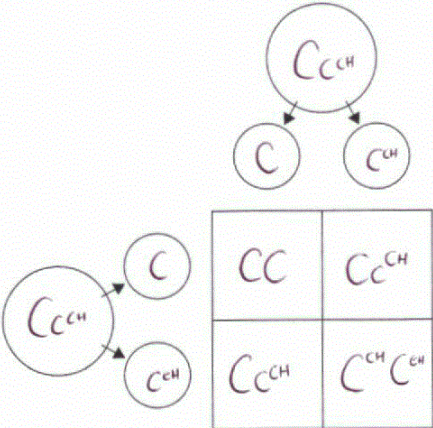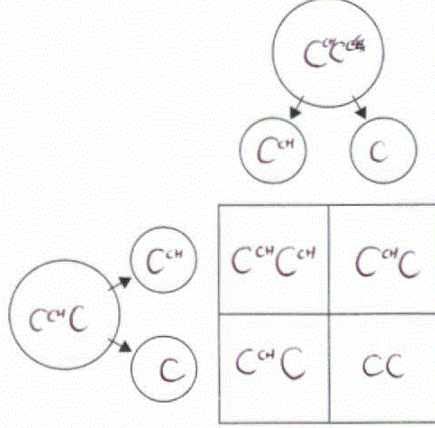
Coat colour	Wild type: black	Chinchilla: grey	Albino: white
Phenotype			
Allele symbol	C	c^{ch}	c
Order of dominance	Complete dominance over all the others	Chinchilla shows incomplete dominance over albino	Recessive to wildtype and chinchilla

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.

11

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: Cc^{ch}	Describe the genotype of the parents: $C^{ch}C$
Describe the phenotype of the parents: Black	Describe the phenotype of the parents: grey
Complete the Punnett square below, and describe the expected genotype and phenotype ratios. Parents: Cc^{ch} → gametes C , c^{ch} Cc^{ch} → gametes C , c^{ch} 		C	c^{ch}
---	---	---
C	CC	Cc^{ch}
c^{ch}	Cc^{ch}	$c^{ch}c^{ch}$		Complete the Punnett square below, and describe the expected genotype and phenotype ratios. Parents: $C^{ch}C$ → gametes C^{ch} , C $C^{ch}C$ → gametes C^{ch} , C |	C^{ch}	C
---	---	---
C^{ch}	$C^{ch}C^{ch}$	$C^{ch}C$
C	$C^{ch}C$	CC	
Expected genotype ratio: $1CC : 2Cc^{ch} : 1c^{ch}c^{ch}$	Expected genotype ratio: $1C^{ch}C^{ch} : 2C^{ch}C : 1CC$
Expected phenotype ratio: 3 black : 1 chinchilla	Expected phenotype ratio: ~~3 grey 1 albino 2 grey albino~~ 1 grey : 2 grey & white : 1 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.

Co-dominance is when there are two dominant alleles of a gene. A heterozygous individual will therefore express both traits in the phenotype. Genotype ratios are the same for the rabbit crosses because both parents of both crosses were heterozygous which produces a 1:2:1 genotypic ratio each time. However the phenotypic ratios are different. This is because the black rabbit is completely dominant over the grey chinchilla. This means that the heterozygous individuals from the first cross will express the dominant trait of the black rabbit, giving a phenotype of 3:1. In the second cross however the phenotype ratio was 1:2:1. This is because the chinchilla shows incomplete dominance over the albino rabbit. Incomplete dominance is when neither trait is dominant over the other so a heterozygous individual will express an intermediate phenotype between the two traits. This is why the heterozygous individuals of the second cross are are a mix of grey and white; an intermediate phenotype between the two. Multiple alleles is when there are more than two alleles for a particular trait. This can result in a variety of allele combinations and significantly increases the genetic variation of a species. Complete dominance could be an advantage to a species survival due to natural selection because if the unfavourable allele was the dominant one dominant allele, then heterozygous individuals would not die

out because the dominant allele would not mask the recessive allele as with recessive inheritance, and they would not express the same phenotype as the unfavourable allele, increasing their chance of survival. Alternatively, because a heterozygous individual expresses both dominant traits, it may still be susceptible to the environmental changes and die. Incomplete dominance could be an advantage to natural selection because of similar reasons to co-dominance, as the However the intermediate phenotype of the heterozygous individual could be the unfavourable allele which could result in both traits being wiped out and the possible extinction of that particular species. Multiple alleles could be an advantage to a species-link to natural selection because more alleles means it is more likely the population will survive as there is increased genetic diversity. However, a disadvantage could be that the species heterozygous phenotype could be selected against which could mean that the co-dominant genotypes' offspring will be unfavourable, possibly resulting in the extinction of the species

QUESTION
NUMBER

2a) of a population bottleneck, where a large amount of individuals were wiped out. As a result, when the kakapo's population began to rebuild, several alleles, including harmful mutations, were permanently removed from the gene pool.

QUESTION
NUMBER

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

QUESTION
NUMBER

91157

QUESTION
NUMBER

Standard	91157	Display ID	NSN 138192944	Total score	23
Q	Grade score	Annotation			
1	E8	Candidate has gained an E8 because both the processes of independent assortment and crossing over have been thoroughly explained and discussed within the context of linked and unlinked genes.			
2	E8	Candidate has been able to thoroughly discuss two mechanisms (genetic drift and founders' effect) that have affected the kakapo with comprehensive contextual references from the question. The idea of natural selection fell short of a discussion as candidate failed to show understanding of Natural selection acting on phenotype rather than genotype. Candidate has also discussed the reasons for accumulation of harmful mutations in small populations by comparing small and large populations and how allele frequencies are affected.			
3	E7	This is an E7 because candidate was able to produce a discussion using context to compare the differences between the genotype and phenotype ratios. However, candidate has failed to successfully use the idea of Natural selecting acting on phenotypes and linking this to advantages and or disadvantages of more phenotypes leading to higher chances of survival of a species.			