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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.

Merit

TOTAL

18

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/

WW, SS

WW, ss

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.



F₁ gen

Outs

Inside

Last

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

Ww, Ss

- (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

		W, S	W, s	w, S	ws
		W, S	W, S	W, S	W, S
		W, s	W, S	W, s	W, s
		W, S	W, S	W, S	W, S
		ws	W, S	W, S	W, S
		W, s	W, S	W, s	ws
		ws	W, S	W, S	ws

- Orange & Striped 4

- Orange & no stripes 3

- White & Striped 3

- White & no stripes 1

Phenotypic ratios:

Phenotype ratio: { 9 orange ~~no stripes~~: 3 orange ~~no stripes~~: 3 White ~~no stripes~~:
1 white ~~no stripes~~.

Genotype ratio: { 9:3:3:1)

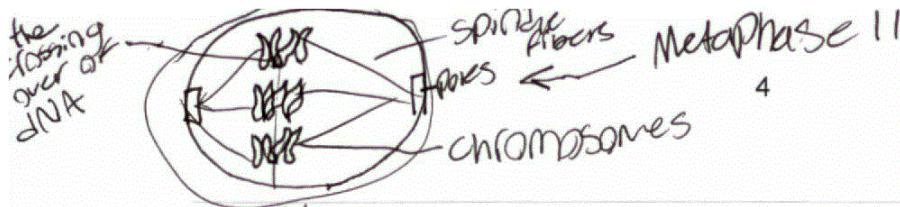
- (c) Discuss how independent assortment and crossing over affects linked genes and unlinked genes AND how they both affect genetic variation in a population.

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 found close together on the same chromosome. These genes are inherited together and aren't affected by crossing over. Unlinked genes can be found on the same chromosome but are far apart and are not inherited together. These genes ~~are~~ are separated by crossing over & independent assortment. Crossing over is a process that occurs in the second stage of Meiosis. Meiosis happens in the gamete cells. ~~Meiosis~~ Crossing over occurs at Metaphase II where the chromosomes are lined up in the middle of the cell. This is when they cross over each other and parts of ~~the~~ one chromosome swap the other.

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



AS they do this, the section of DNA that they took gets swapped. Before crossing over occurs, the chromosomes must independently assort themselves. This means the chromosomes line themselves up in a random way. This assures that ~~the eight chromosomes from the Parents~~ ^{each of the} will be split up. this process occurs ^{at the start of} in Miosis. Although unlinked genes independently assort themselves, linked genes do not. This is because they ~~assort~~ have to be inherited together so don't separate in independent assortment. They are also found on the same chromosome so cannot be separated by independent assortment. These linked genes reduce genetic variation in a population. This is because it limits the amount of allele combinations in a gene pool. Unlike linked genes, unlinked genes increase genetic variation in a population because it creates more allele combinations as they are inherited separately. like crossing over also increases genetic variation. This is because it swaps DNA from each of the parent chromosomes. This will ensure that the offspring won't be identical to their parents. This process only increases genetic diversity for unlinked genes as linked genes ~~are~~ are not affected by crossing over. Independent assortment also increases genetic variation. this is because ~~the~~ the chromosomes assort

unlinked genes,

However, it's not following the order from other

This means that the offspring from the parents won't all look the same. They will also be different from their parents as they will have a mix of chromosomes from each parent.

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. - *founder effect*

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. ✓ *natural selection*



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.
- *Natural Selection - not random mating*
- *founder effect*
- *genetic drift*

A mutation is a change in DNA sequence which creates new alleles. Mutations occur during in either gamete cells which can be inherited by further generations or somatic cells (body cells) which

cannot be inherited. These mutations enter a populations gene pool as they create new alleles in an individual in that gene pool. Mutations can either be neutral, harmful or unnoticeable. Natural Selection is affected when certain characteristics (such as survival genes) are favoured and passed on to fitter generations, while unfavourable characteristics are not passed on and become lost or uncommon.

For the kakapo, we see natural selection has occurred as birds found on the island had no ~~harmful~~ mutations like they had ~~had~~ when they before they introduced the predators. As birds with more survival ~~phenotypes~~ survived and breed with birds with ~~the~~ same characteristics, the birds with harmful mutations slowly died out, creating a fitter, more equipped to their environment bird.

The kakapo had also been subjected to the founder effect. ~~Because~~ the 50 birds who went on the island would have had a smaller gene pool and therefore less genetic diversity.

~~As~~ they did again as the population grew, some of the genes from the original population were lost, (like the harmful mutations.) Genetic drift happens when something affects a large portioned the gene pool, completely by chance. When the predators were introduced, a large amount of the population was killed off. Because of this, the gene pool would have had less alleles and

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

Would have become smaller, decreasing genetic variation. Harmful mutations would accumulate more in smaller populations. This is because the gene pool is smaller and a small change in the population ~~is~~ actually affects a large amount of the gene pool. (When a mutation spreads to only one other organism in a low population, the gene pool is affected more). This is not the case for the kakapo. Due to natural selection in their new environment, the birds with those harmful mutations would have slowly died off while birds who didn't inherit those mutations would have survived. Non random mating is also a reason for the disappearance of the harmful mutations. The birds may have only mates with those who didn't have the harmful mutation. This would mean that the offspring would not inherit the mutation. Due to genetic drift, the predators that killed off the mainland kakapo creates a big impact on the allele frequency of that harmful mutation in the gene pool. This could mean only 1 or 2 of the birds in Stewart island had the mutation while the rest didn't, and as non random mating and natural selection occurred, the gene was more likely not to be passed on as it was only a small amount who had it.

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.

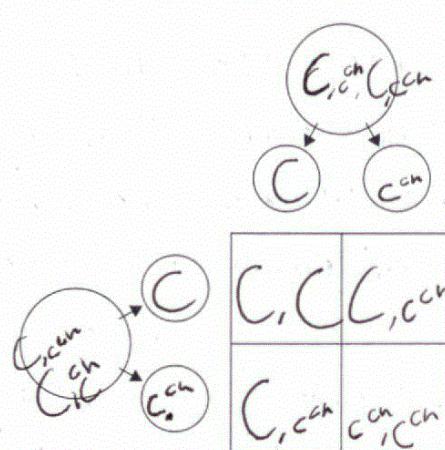
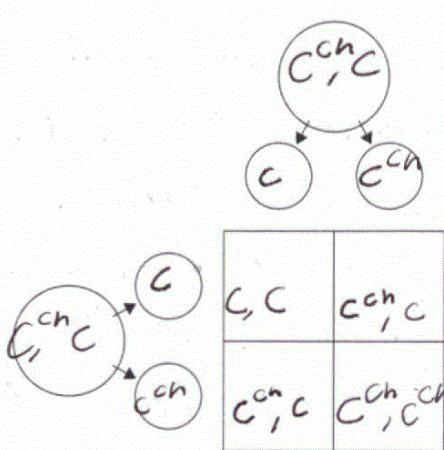
The coat-colour gene has multiple alleles which show an order of dominance. The simplified table below show the coat colour, allele symbol, and order of dominance for three phenotypes.

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: <i>Rabbit 1 - C, c^{ch} Parent 2 - C, c^{ch}</i>	Describe the genotype of the parents: <i>C^{ch}, c + C^{ch}, C</i> <i>Parent 1 Parent 2</i>
Describe the phenotype of the parents: <i>They would both be black as the allele C is completely dominant</i>	Describe the phenotype of the parents: <i>They would both be grey because gene C^{ch} is incompletely dominant over C</i>
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. 
Expected genotype ratio: <i>1C,C : 2C,c^{ch} : 1c^{ch},c^{ch}</i>	Expected genotype ratio: <i>1C,C : 2c^{ch},c : 1C^{ch},C^{ch}</i>
Expected phenotype ratio: <i>3 Black : 1 chinchilla grey.</i>	Expected phenotype ratio: <i>3 grey : 1 white : 1 grey</i>
Pattern of inheritance: <i>complete dominance.</i>	Pattern of inheritance: <i>incomplete dominance</i>

- (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 one allele completely dominates the other. This means that when the allele is shown, it will always be shown in the phenotype. Incomplete dominance is when neither allele is dominant over the other and instead they create a new mixed phenotype when both alleles are present. For the rabbit pheno type ratios in part (A), both are the same because the both rabbits that were bred were heterozygous. The phenotype for the ~~grey~~ white rabbits was different to the black and grey. Because the genotype C^{black} shows complete dominance, that phenotype was shown. For the grey ~~at~~ white rabbits, the genotype c^h shows incomplete dominance over c. So both mix of both alleles were shown. This is why the new allele phenotype light grey was created. Multiple alleles is when more than one allele codes for a characteristic. This is shown for the c^h allele c^h, as it has another allele which codes for grey fur. Complete dominance could be an advantage in natural selection if

that completely dominant allele was a favourable phenotype that helped the organism survive such as a lizard's tail being long instead of short to climb places easier. If the dominant allele was not favourable it would be a disadvantage as the organisms would be more likely to get that unfavourable gene e.g. a lizard having a short tail. Incomplete dominance could also be an advantage to natural selection as it creates a mix of phenotypes which could be helpful, if the other phenotypes were ~~also~~ not favourable for the organism's survival, it would be a disadvantage that for natural selection if the incomplete dominant phenotype was a bad mix and didn't help the survival of the organism. e.g. if a bird needed either very long or very short wings to survive, if there was a mix (medium wings) that organism may not survive. This could also be an advantage to natural selection as those unfavorable traits would die out, leaving ~~of~~ that species with the good phenotypes. Multiple alleles could be an advantage to natural selection as it increases the chance of new phenotypes which could be beneficial to the organism. ~~if these~~ if these alleles helped the organism it would be a disadvantage for natural selection as those organisms won't have the right phenotypes for survival and they can't pass them on to offspring. A downside of multiple alleles is the lethal alleles.

Writings of India - The origin will

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Standard	91157	Display ID	NSN 138087420	Total score	18
Q	Grade score	Annotation			
1	E7	This is an E7 as candidate was able to define both linked and unlinked genes correctly; explained how they affect genetic variation and some context of processes within meiosis have been used to compare between the two. Candidate however has failed to complete more comprehensive discussion of how each of independent assortment or crossing over affects linked and unlinked genes.			
2	M5	Candidate has been able to successfully define natural selection but failed to explain how this affects a population as there was a lack of understanding of how allele frequencies change within a population. Candidate has gained an M5 because the prevalence of harmful mutations in small populations was explained using the idea of proportional effect. Candidate has also explained that Stewart Island could have lower mutation rates due to random non-mating tying in holistically to the idea of genetic drift.			
3	M6	Candidate has gained an M6 for correctly completing all sections of the table in Part A. Candidate has also been able to explain why the genotype ratios are the same while the phenotype ratios are different, however candidate fell short of a discussion due to a lack of a comprehensive use of the context provided. Candidate was also able to explain the advantages of multiple alleles and how this helps with the survival of the organism but once again failed to discuss this in relation to the overall survival of a species, using the idea of Natural selection.			