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91157



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SUPERVISOR'S USE ONLY

Level 2 Biology, 2017

91157 Demonstrate understanding of genetic variation and change

2.00 p.m. Wednesday 22 November 2017
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 space for any answer, use the page(s) provided at the back of this booklet and clearly number the question.

Check that this booklet has pages 2–11 in the correct order and that none of these pages is blank.

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

Merit

TOTAL

16

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QUESTION ONE: PIGEON GENETICS

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Pigeon wing pattern and leg feathering both show complete dominance. The bar wing allele (**B**) is dominant to the barless allele (**b**). The allele for leg feathers (**F**) is dominant to the allele for not feathered (**f**). These two genes are not linked.



Bar (B)

Barless (b)

<http://learn.genetics.utah.edu/content/pigeons/pattern/>



Feathered (F)

Not Feathered (f)

<http://unews.utah.edu/pigeon-foot-feather-genes-identified/>

- (a) A breeder crossed a pigeon homozygous for the bar allele and the leg feathers allele with a pigeon that had a barless wing pattern and no feathers on its legs.

State the genotype of the F1 generation: Bb Ff

State the phenotype of the F1 generation: Bar wing pattern with feathered legs

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

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F₁ gametes

	BF	BF	BF	BF
bF	BbFf	BbFf	BbFf	BbFf
bF	BbFf	BbFf	BbFf	BbFf
bF	BbFf	BbFf	BbFf	BbFf
bF	BbFf	BbFf	BbFf	BbFf

F₁ gametes

- (c) Describe the predicted phenotype ratios produced by this cross.

9 bar ~~wing~~ wing pattern and feathered feet,
 3 barless and feathered feet
 3 bar wing pattern and not feathered
 1 barless and not feathered
9 : 3 : 3 : 1.

F₁ gametes : BbFf

F₁ gametes

	BF	Bf	bF	bf
BF	BBFF	BBFf	BbFF	BbFf
Bf	BBFf	BBff	BbFf	Bbff
bF	BbFF	BbFf	bbFF	bbFf
bf	BbFf	Bbff	bbFf	bbff

- (d) If the wing pattern and leg feather genes were linked, the phenotype ratios would be 3:1 with:
- 12 bar wings and leg feathers
 - 4 barless wings and no leg feathers.

Discuss why the phenotype ratio from the F2 cross in part (c), is different to the 3:1 ratio of the linked genes.

You should refer to your Punnett square in part (b), and the given phenotype ratios, in your discussion.

Note: Crossing over is NOT required in your answer.

In your answer include:

- a description of linked genes ✓
- a discussion that contrasts how independent assortment affects the inheritance of linked genes AND unlinked genes ✓
- a discussion of how linked AND unlinked genes affect the genetic variation of offspring ✓

You may use diagrams to clarify your discussion.

Linked genes are ~~alleles~~ alleles that are close together on a chromosome. Due to their close proximity they often don't separate during independent assortment. This results in them commonly being inherited together. If bar wings and leg feathers were linked then they would be inherited together resulting in 12 offspring of this phenotype ~~being~~ expressing the phenotype bar wing and leg feathers. This 3:1 ratio is higher than the expected of non-linked phenotype ratio of the F2 ~~cross~~ cross. The expected ratio was for only 9 offspring of this phenotype.

Independent assortment is when genes randomly assort ~~between~~ between chromosomes during Meiosis. This results in variation between offspring. Unlinked genes independently assort and aren't inherited together. This means that traits

coded for in offspring are completely random. In comparison linked genes are inherited together and don't separate during ~~independent~~ independent assortment.

Genetic variation is affected by linked ~~genes~~ genes, it reduces allele combinations in a given population.

Due to linked genes being inherited together, ~~variation~~ variation is reduced in the pigeon population.

Less barless wings and no leg feathers are expressed in the population. Unlinked genes

~~in the population~~ means more variation due to independent assortment being successful during meiosis.

With less genetic variation a population is more at risk of disease and not being suited to environmental change. ~~example~~

~~example~~

Reduction in variation of offspring occurs with linked genes as the ~~most~~ ~~common~~ 2 genes don't separate resulting in most offspring having the same alleles.

ms

QUESTION TWO: SOUTH ISLAND SADDLEBACK

ASSESSOR'S
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The South Island saddleback's gene pool has been affected by both the founder effect and the bottleneck effect at different points in history. The South Island saddleback was originally widespread over the mainland and also had established populations on some of the offshore islands, such as Big South Cape Island, because they were within flying distance from the mainland. The graph below compares the genetic diversity of historic saddleback populations on the offshore island of Big South Cape Island and the South Island mainland in the 1800s with the current population (in 2005) on Kaimohu Island.

After Māori and European settlers arrived, the South Island saddleback eventually became extinct, with the exception of the population on Big South Cape Island. In 1964 all South Island saddlebacks were removed from Big South Cape Island and taken to pest-free island sanctuaries such as Kaimohu Island. Safe from rats and other predators, the South Island saddleback population on Kaimohu Island is increasing, and is being used to establish other populations around the South Island.

Discuss how the founder and bottleneck effects have influenced the current South Island saddleback gene pool on Kaimohu Island.

Refer to the information above, and the graph, to support your discussion.

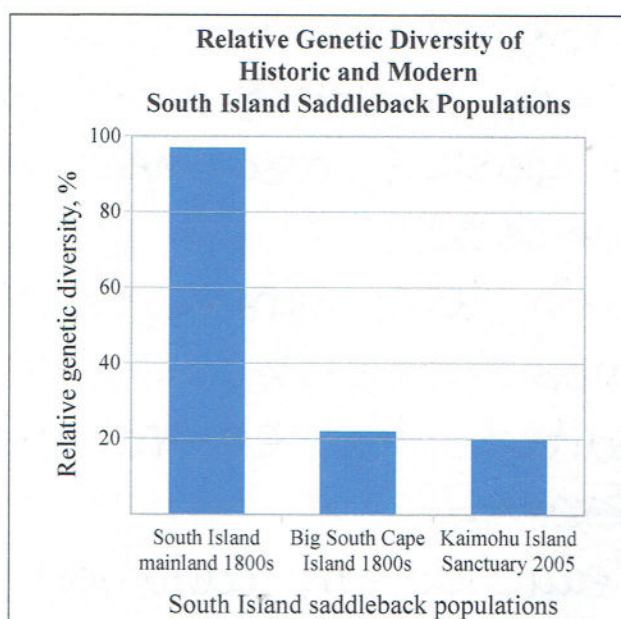
Your discussion should include:

- a description of a gene pool
- an explanation of the bottleneck effect AND the founder effect
- a discussion of why the 1800s Big South Cape Island population had low genetic diversity compared to the 1800s South Island population
- a discussion of why the Kaimohu Island population has low genetic diversity.

A gene pool is the frequency of alleles in a population. The bottle neck effect is when an extreme decrease in the population occurs due to chance, human intervention or an environment ^{change}. ~~Then~~ When Maori and European settlers arrived in NZ the saddle



<http://nzbirdsonline.org.nz/species/south-island-saddleback>



Adapted from: Jameson, Ian G., 2009, 'Loss of genetic diversity and inbreeding in New Zealand threatened bird species'. *Science for Conservation* 293, p. 20. Department of Conservation, Wellington.

backs became ~~extinct~~ ^{less common and then eventually became extinct.} - this was due to humans. This illustrates the bottleneck effect as the population dramatically reduced in size due to chance. Prior to human arrival the saddleback was widespread across mainland, once humans arrived numbers reduced. Founder effect is when ~~individuals~~ individuals from a large population migrate to a new one. This results in a reduction of genetic variation. This is demonstrated by the saddle backs having ~~around 20%~~ around 20% ~~genetic~~ genetic diversity compared to the nearly 100% genetic diversity prior to the founder effect. The South Island was the large population that some individuals moved from to Big South Cape island. This meant all the population on Big South Cape island was offspring of a few individuals who migrated from the big population to the small. This results in less genetic diversity. Kaimohu island's population is the remaining population taken from Big South Cape island. Therefore less diversity is expressed. This is another example of a bottleneck as numbers of saddlebacks reduced thus reducing genetic variation due to human intervention. The gene pool is smaller in Kaimohu as only a few individuals started the population, as there were predators that caused a bottle neck in numbers.

QUESTION THREE: NATURAL SELECTION AND MIGRATION

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Lactase is an enzyme produced by babies that allows them to digest and gain nutrition from milk. Most young children lose the ability to produce lactase after they stop drinking their mother's milk, at about three years old. Adults and older children who cannot produce lactase suffer severe stomach upsets if they drink milk. This is called lactose intolerance.

Between 7 000 and 9 000 years ago, two different mutations arose independently in north-European and African populations that allowed these populations to produce lactase into adulthood (lactose persistence – see areas A and B on the map). Both populations A and B used cattle and their milk as a food source. Over time, the mutations became established in each of these European and African populations.

The map below shows the percentage of humans in the population who can digest milk today.



<http://www.hhmi.org/biointeractive/making-fittest-got-lactase-co-evolution-genes-and-culture>

Discuss how a mutation would become established in a population's gene pool and spread to other gene pools.

Your discussion should refer to specific populations on the map, and include:

- a description of both natural selection AND migration
- an explanation of how the mutations became established in A and B populations
- a discussion of why populations B, C, and D would have different percentages of the mutation.

Natural selection is Darwin's theory about the survival of the fittest. The best suited individuals to an environment will thrive. This will means they will be able to reproduce and have offspring that carry the desired geneotype and express the

favourable phenotype. Migration is when individuals move ~~from~~ from one population to another.

Natural selection is shown in location A and B, In these area's having the gene that enables you to digest milk as an adult is favourable. Those with the ability to produce lactase would have a higher chance of survival due to being able to consume an food source. This would result in humans that could consume dairy products being able to be more healthy and fitter. Therefore they would be able to have more offspring than those that where lactose intolerant. Thus passing on the favourable lactase enzyme producing gene.

The mutation would have to be gametic and likely dominant in order to become established. It would have occurred in the sex cells in order to be passed onto offspring. In order to be expressed it ~~would likely~~ be dominant over lactose intolerant. As it is favourable it would be selected for in natural selection and eventually would become more common than the lactose intolerent. Different area's have different percentages of the mutation as lactose wasn't available in those area's so the mutation had no need to develop. Furthermore the distribution indicates that natural selection isn't favouring the lactase enzyme in adults in D region. C indicates migration of idividuals from B showing that the two populations are interbreeding and as a result the lactase enzyme in adults is commonly expressed.

Subject:	Biology	Standard:	91157	Total score:	16
Q	Grade score	Annotation			
1	M5	Learner is able to identify genotype and phenotype, complete the F2 punnett square and describe the phenotypic F2 predicted ratios. Learner has identified that linked genes are on the same chromosome and inherited together as opposed to unlinked genes that assort independently. No discussion about the the variation in gametes and offspring is made in detail with reference to			
2	E7	Learner has an E7 as they were able to correctly reference the graph and link lower genetic diversity to the biological idea of the Founder effect in the Big South Cape Island population as compared to the original South Island Population.			
3	A4	Learner was able to define Natural Selection, gametic mutation affecting the increase in numbers of the mutation in the population. They were unable to link the idea of <i>Gene flow</i> between populations or Genetic drift affecting the saddleback population.			