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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.

Excellence

TOTAL 22

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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: BbFf

State the phenotype of the F1 generation: bar, feathered

(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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F_1 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

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

9 bar, feathered : 3 bar, non-feathered : 3 barless, feathered : 1 barless, non-feathered.

(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.

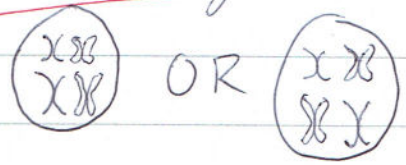
In your answer include:

- 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 is when two genes are located on the same chromosome. Therefore unless they are split up by crossing over, the two alleles for these genes are inherited together. This alters the inheritance pattern. The distance between the linked genes affects the inheritance pattern because the further apart they are, the more likely it is that crossing-over will split them up, producing recombinant chromosomes.

Usually, for genes that are located on different chromosomes, independent assortment assures the alleles are sorted independently of each other into gametes. Independent assortment is when homologous pairs of chromosomes orient themselves along the cell equator independently of the other pairs. This means that every new cell created during meiosis has a unique combination of alleles.



(but there are 23 homologous pairs so the number of possible combinations is great)

This means that, provided they are not linked, you could inherit any combination of alleles from each parent because each allele ends up in different gametes. When genes are linked, however, the alleles can end up in the same gametes, meaning they're inherited together.

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For linked genes, however, independent assortment cannot assort them independently of each other because they are attached to each other.

Therefore, there is more genetic variation in offspring when the two genes in question are unlinked, because ~~when~~ unlinked genes benefit from the random combinations of maternal and paternal chromosomes that end up in gametes due to independent assortment, whereas this is not possible for two genes that are linked because they will (unless split up due to crossing over) always end up together in the same gamete). Therefore if the mother was recessive for both traits, and you happen you inherit your mother's version of that chromosome, you would inherit both recessive alleles without a chance of inheriting your mother's allele for one trait and your father's allele for the other.

The 3:1 ratio of the linked genes shows how the ~~offspring not~~ two ~~dom~~ gene are located on the same chromosomes, and ~~the~~ for each parent the two dominant genes were on one chromosome of the homologous pair, and the two recessive genes were on the other. Therefore the offspring could not inherit a dominant allele for bar and the recessive allele for leg feathers from the same parent, therefore the phenotypes bar, no leg feathers and bardess, feathes are impossible.

	BF	bf
BF	BBFF	BbFf
bf	BbFf	bbff

= 3 ~~bar~~ : 1 phenotype ratio

This contrasts to the phenotype ratio 9:3:3:1 because when the genes are unlinked, the combination of alleles you receive is random due to independent assortment, therefore you have just a likely chance of inheriting both recessive alleles or both dominant alleles from one parent as inheriting a recessive and a dominant allele from that parent.

Because the number of possible genotypes is less with linked genes than unlinked genes, genetic variation of offspring of two genes that are linked is less varied: they are more likely to have the same genotypes as their siblings.

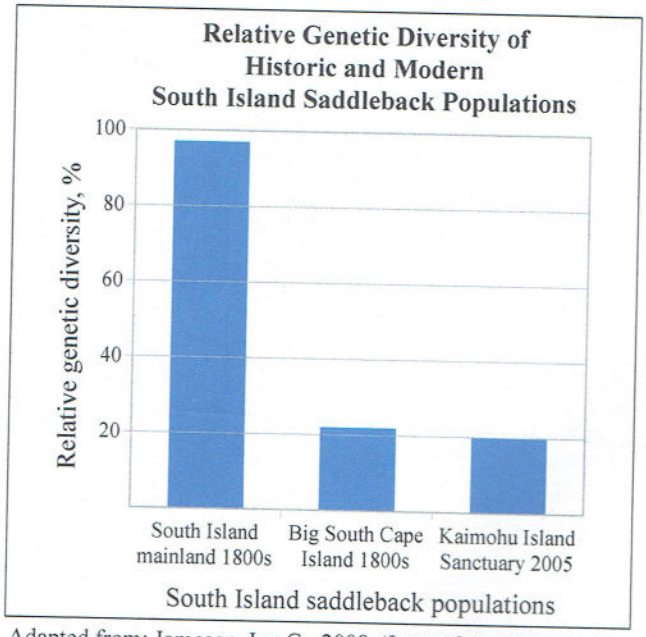
E8

QUESTION TWO: SOUTH ISLAND SADDLEBACK

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.

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

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.



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.

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 total number of alleles present in a population.

The Bottleneck effect is seen when, as due to a catastrophic event like a natural disaster or humans hunting and destroying habitats, a population is suddenly reduced to a small size. This means the population becomes a lot less genetically diverse, because many alleles would have been removed from the gene pool,

thus decreasing the gene and the range of alleles present in the population.
The founder effect is seen when some individuals of a population colonise a new, isolated area such as an island, and start a new population there. Again, the gene pool will be greatly reduced and the ranges of alleles present in the population will be small, therefore genetic diversity is decreased. The allele frequences of the new population are unlikely to be representative of those of the original population.

The 1800s Big South Cape Island (BSCI) population had been established by individuals from the mainland population, therefore it is an example of the founder effect. This means despite the possibility of ~~gene flow~~ migration ~~to and~~ from the larger mainland population, and therefore gene flow, (increasing genetic diversity due to the possibility of the introduction of new alleles to the island gene pool), the genetic ~~di~~ diversity on BSCI would be low because the original gene pool of the founders was limited due to its small size, therefore the range of alleles is limited.

The South Island ~~(SI)~~ (SI) 1800s population, on the other hand, was very large. This meant the gene pool was substantial, with a large range of alleles and therefore diversity. There could be a lot of gene flow across the island, and genetic drift (chance change in allele frequences) would have little effect, meaning this population was also very stable.

Kaimohu Island has a low genetic diversity because it was based off the BSCI, ~~it~~ which had not only begun with little genetic diversity due to the founder effect, but had also been stagnating from the 1800s to 1964 because the extinct SI population meant no migration was possible. (ie the BSCI population was stuck with only the alleles in its small gene pool) Genetic drift has the biggest effects on small populations, and can cause alleles to become extinct, and ~~this is another~~ (because it may have lost alleles) reason why the Kaimohu Island population would have a small ~~re~~ range of alleles and therefore not be genetically diverse. (Kaimohu Island is not an example of founder effect because all saddlebacks from BSCI were taken there). As the BSCI population was transferred to Kaimohu Islands this is why Kaimohu Island is also genetically not diverse.

E7

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 about an ~~organism's~~ individuals survival based on its adaptations: Individuals best suited to their environment will survive and reproduce, passing their alleles on to their offspring. Migration is when individuals either leave or move into populations, thus possibly ~~other~~ removing alleles (emigration) from the population or introducing new alleles to the population (immigration). ~~The~~ Migration can increase or decrease

allele frequencies.

~~The mutation~~ A mutation is a change in the base sequence of a ~~change~~ gene, or a change ~~in the~~ DNA of an organism. It can be beneficial or harmful. Both of the mutations allowing lactose persistance would be beneficial in populations A and B, therefore when this mutation occured, organisms with the new allele would have a survival advantage as they'd be better adapted to their environment as part of that environment included having milk as a food source. Therefore the individuals with the new, mutated allele would survive and reproduce, passing this favourable allele onto offspring, and hence it would become established in the population.

In populations where milk was not a food source, ~~their~~ the mutation may still have occured, but individuals with the new allele would not have had a survival advantage, therefore it would not have been passed onto offspring and thus didn't become established in the population.

Therefore eventually almost all of the individuals in population B would have this allele as it was a favourable adaptation for their environment. In areas like D, ~~There are~~ where ~~it wasn't as wasn't a fa~~ didn't give a survival advantage, it wasn't harmful so it didn't go extinct due to natural selection, but there was no need for it to be present so it didn't become established.

The same could be true of C - that it didn't give a survival advantage because they didn't ~~drink~~ have milk as a food source — but as it is so close to B, migration would cause the allele to be common in C as well.

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E7

Subject:	Biology	Standard:	91157	Total score:	22

Q	Grade score	Annotation
1	E8	Learner able to identify genotype, phenotype of F1 generation. Is able to work out the F2 Punnett square with phenotypes and further discuss comprehensively the reasons for genetic variation in offspring due to independent assortment in both linked and non-linked genes. They have further used phenotypic ratios to justify their answer.
2	E7	Learner able to identify the low genetic diversity in the Kaimohu population and the Big South Cape Island as a result of Genetic Drift and how this affects small populations. Learner has not used specific references from the graph to explain the changed genetic diversity in the island populations.
3	E7	Learner has been able to define Natural Selection, Migration and mutation and explain why the individuals in populations A and B survived. They are also able to identify and discuss that in Population D there is no selective survival advantage for the individuals as probably milk was not found as a food source.