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Level 2 Biology, 2018

91157 Demonstrate understanding of genetic variation and change

9.30 a.m. Friday 23 November 2018
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.

TOTAL

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QUESTION ONE: MEIOSIS

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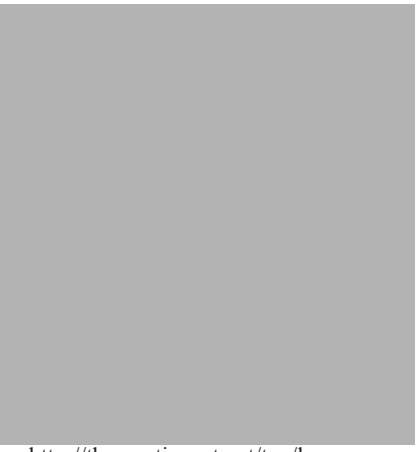
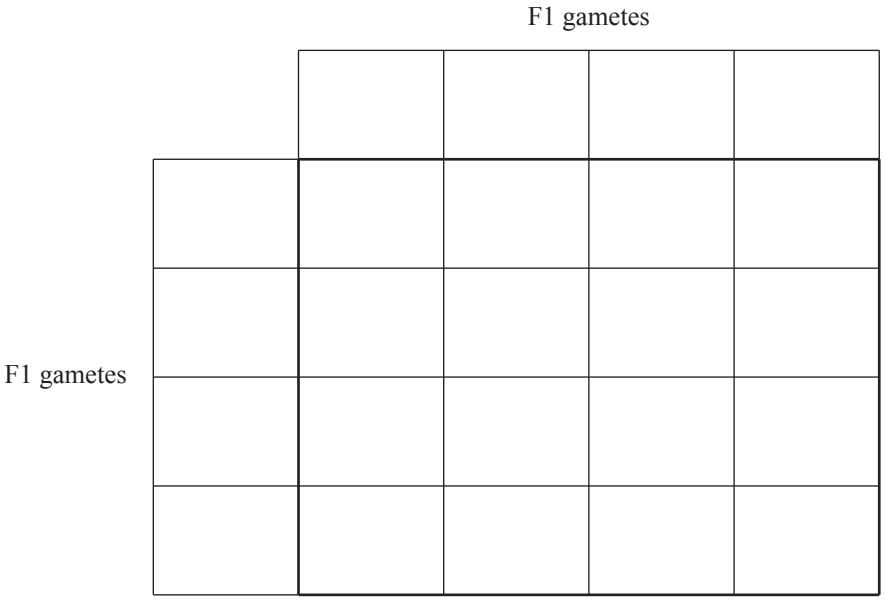
Cats display complete dominance in both their hair length and colouration. The allele for agouti (A) is dominant to the allele for non-agouti (a). The allele for short hair (H) is dominant to the allele for long hair (h). The hair shaft of the agouti phenotype has alternating bands of black and yellow colouration, also known as tabby. The hair shaft of the non-agouti phenotype is solid colouration. The genes for hair length and colouration are not linked.

Agouti (tabby) phenotype	**Non-agouti phenotype**
	
www.langfordvets.co.uk/diagnostic-laboratories/diagnostic-laboratories/general-info-breeders/list-genetic-tests/agouti-coat	http://thecreativecat.net/tag/long-haired-black-cat/

A cat that was homozygous for both agouti and short hair was crossed with a non-agouti that had long hair.

(a) State the genotype of the F1 generation this cross produces.

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



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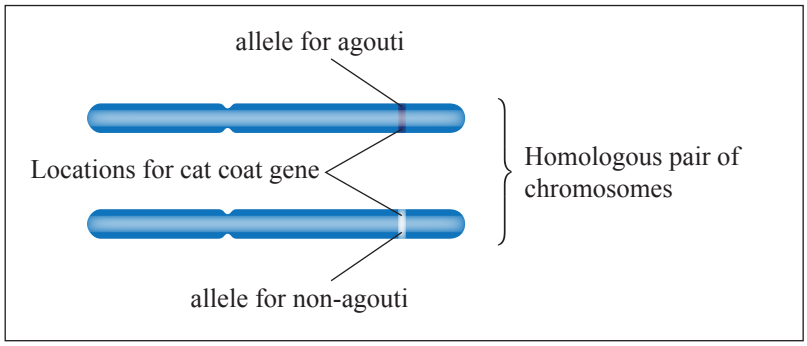
(c) Describe the predicted phenotype ratios produced by this cross.

(d) Homologous chromosomes are involved in the processes of meiosis, but they are not found in the daughter cells resulting from meiosis.

Diagram showing homologous chromosomes



Adapted from: Campbell N.A. & Reece J. B., 2005. *Biology 7th ed.* (San Francisco: Pearson/Benjamin Cummings, 2008), p. 255.

Discuss how homologous chromosomes are involved in increasing genetic variation AND why they are found in the cells at the start of meiosis, but not in the cells at the end of meiosis.

In your answer include:

- a description of homologous chromosomes
- an explanation of homologous chromosomes in the processes of crossing over, independent assortment, and segregation
- a discussion of why homologous chromosomes are found in parental cells (diploid), but not daughter cells (haploid) of meiosis.

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

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QUESTION TWO: POPULATION GENETICS

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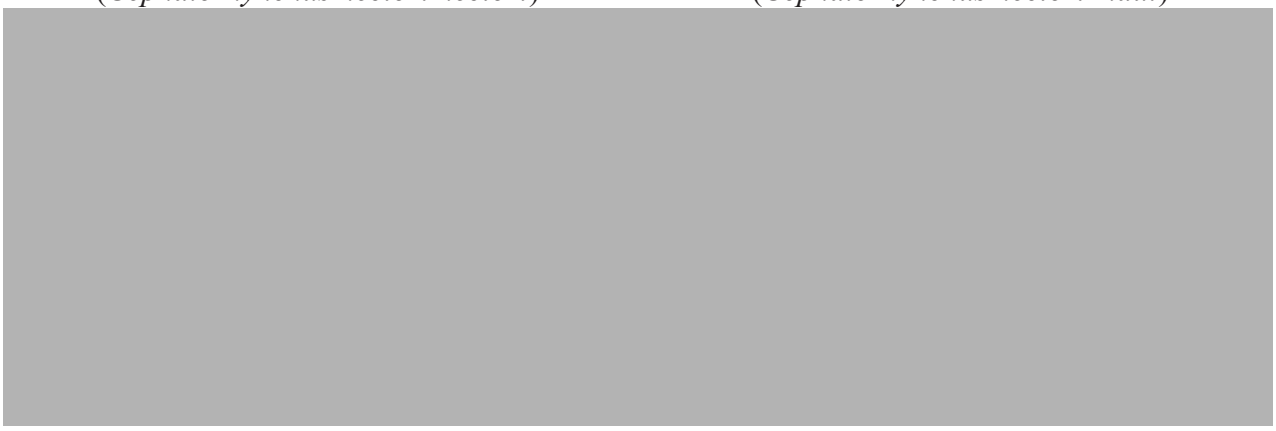
Hector's Dolphin
(*Cephalorhynchus hectori hectori*)

Māui Dolphin
(*Cephalorhynchus hectori maui*)



www.takepart.com/article/2015/05/28/world-smallest-dolphins-could-be-gone-15-years/

www.thinglink.com/scene/636989356719996928

Hector's and Māui dolphins are endemic to New Zealand (found only in New Zealand). They are considered separate subspecies; however, they are so closely related that they are able to interbreed.

Hector's dolphin population is estimated to be 7270 individuals and is classified as 'Endangered'. Māui dolphin population is estimated to be 80 individuals and is classified as 'Critically Endangered'.

Discuss the factors that affect allele frequency in the Hector's and Māui dolphin populations AND the consequences if interbreeding takes place between the two species.

In your answer include:

- a description of allele frequency
- an explanation of a genetic bottleneck AND its effects on the Māui dolphins' allele frequency
- a description of genetic drift and AND how it affects both populations
- a discussion of how interbreeding Hector's and Māui dolphins might affect allele frequency AND genetic diversity of both populations.

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

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QUESTION THREE: NATURAL SELECTION

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Blood vessel with both normal and sickle blood cells

Source: http://kidshealth.org/en/parents/sickle-cell-anemia.html

Haemoglobin is the protein in the blood that carries oxygen. Sickle cell disorder is caused by a mutation to the haemoglobin gene. The mutated allele (r) causes a normal red blood cell (R) to alter shape and become irregular and spiky-sickle shaped. Sickle cells have a tendency to clump together and work less efficiently to carry oxygen.

Sickle cell disorder is considered a recessive lethal allele and shows co-dominance inheritance.

(a) Describe the term lethal allele.

(b) Co-dominance inheritance produces three possible genotypes and phenotypes.

Describe co-dominance AND state the phenotypes for Rr and rr in the table below.

Genotype	Phenotype
RR	normal
Rr	
rr	

(c) The frequency of the sickle cell allele corresponds to the distribution of the parasite *Plasmodium falciparum*. This parasite causes the disease malaria. In severe cases malaria can cause death. The sickle cell allele (r) offers a survival advantage against malaria. Sickle cells have low potassium levels, which causes the parasite inside these cells to die. Individuals with normal phenotype (RR) are very susceptible to malaria.

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Use the information provided to **discuss** why the sickle cell allele remains in populations, even though it is a lethal allele.

In your answer include:

- an explanation of natural selection
- a discussion of how natural selection affects the phenotypes produced by the sickle cell genotypes AND provide justified reasons why the recessive lethal allele remains in the population.

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

QUESTION NUMBER

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