

Trial Examination 2011

VCE Biology Unit 4

Written Examination

Question and Answer Booklet

Reading time: 15 minutes Writing time: 1 hour 30 minutes

Student's Name: _____

Teacher's Name: _____

Structure of Booklet

	Section	Number of questions	Number of questions to be answered	Number of marks	
Ī	А	25	25	25	
	В	7	7	50	
				Total 75	

Students are permitted to bring into the examination room: pens, pencils, highlighters, erasers, sharpeners and rulers. Students are NOT permitted to bring into the examination room: blank sheets of paper and/or white out liquid/tape. No calculator is allowed in this examination.

Materials supplied

Question and answer booklet of 21 pages. Answer sheet for multiple-choice questions.

Instructions

Write your **name** and **teacher's name** on this booklet and in the space provided on the answer sheet for multiple-choice questions. All written responses should be in English.

At the end of the examination

Place the answer sheet for multiple-choice questions inside the front cover of this booklet.

Students are NOT permitted to bring mobile phones and/or any other electronic communication devices into the examination room.

Students are advised that this is a trial examination only and cannot in any way guarantee the content or the format of the 2011 VCE Biology Unit 4 Written Examination.

Neap Trial Exams are licensed to be photocopied or placed on the school intranet and used only within the confines of the school purchasing them, for the purpose of examining that school's students only. They may not be otherwise reproduced or distributed. The copyright of Neap Trial Exams remains with Neap. No Neap Trial Exam or any part thereof is to be issued or passed on by any person to any party inclusive of other schools, non-practising teachers, coaching colleges, tutors, parents, students, publishing agencies or websites without the express written consent of Neap. Every effort has been made to trace the ownership of copyright material. Information that will enable Neap to rectify an error or omission will be welcome.

SECTION A: MULTIPLE-CHOICE QUESTIONS

Instructions for Section A

Answer **all** questions in pencil on the answer sheet provided for multiple-choice questions.

Choose the response that is **correct** for the question.

A correct answer scores 1, an incorrect answer scores 0.

Marks will not be deducted for incorrect answers.

No marks will be given if more than one answer is completed for any question.

Question 1

Different alleles of a specific gene

- A. are located on the same chromatid.
- **B.** are identical in nucleotide sequence.
- C. may produce proteins with different degrees of functionality.
- **D.** are found at different places on sister chromatids.

Question 2



The four types of sperm cells illustrated above were produced by the process of

- A. crossing over.
- **B.** mitosis.
- C. random fertilisation.
- **D.** independent assortment.

Question 3

The spindle fibres that move chromosomes apart during cell division are made of protein.

The information needed to construct spindle fibre protein is passed from one generation of cells to the next as

- A. ribosomes.
- **B.** transfer RNA.
- C. DNA.
- **D.** messenger RNA.

Question 4

DNA replication is described as semi-conservative because

- A. half of the DNA is replicated in each cell cycle.
- **B.** each new DNA molecule contains half of the original molecule.
- C. half of the DNA molecule is destroyed during replication.
- **D.** DNA replication occurs on the right side of the cell in about half of all cell divisions.

Marfan syndrome is a rare autosomal dominant genetically inherited disease of the connective tissue. A man who has Marfan syndrome starts a family with a woman who does not have the disorder. Their first child does not have the disease.

The chance that their second child would also be unaffected would be

- **A.** 0%
- **B.** 25%
- **C.** 50%
- **D.** 100%

Question 6

You perform the following dihybrid genetic cross: $AAbb \times aaBB$

where: $\mathbf{A} = \text{big}$ $\mathbf{a} = \text{small}$ $\mathbf{B} = \text{dark}$ $\mathbf{b} = \text{light}$

In the F1 generation all of the progeny are big and dark. You now self cross the F1 progeny and score 100 of the resulting F2 progeny.

The number of the F2 progeny that would be expected to be big and light is

A. $\frac{3}{16}$ **B.** $\frac{1}{16}$ **C.** $\frac{1}{4}$

D.
$$\frac{9}{16}$$

Question 7

In 2002, "CC" was the first cat to be cloned.

Mammals are generally cloned by combining

- A. two unfertilised egg cells.
- **B.** an egg cell with a sperm cell.
- **C.** a diploid body cell with an enucleated egg.
- **D.** two sperm cells.

In an experiment with fruit flies (*Drosophila melanogaster*), individuals homozygous for dumpy wings and brown eyes were crossed with a pure breeding wild type (dominant) with normal wings and red eyes. A test cross was carried out where the flies of the resulting F1 generation were backcrossed with individuals of the double recessive parental type. The phenotypic appearance of the next (F2) generation of individuals was as follows:

- 451 normal wings, red eyes
- 449 dumpy wings, brown eyes
- 48 normal wings, brown eyes
- 52 dumpy wings, red eyes

The most reasonable conclusion to draw from these results is that

- A. the genes coding for wing type and eye colour phenotypes are located on different pairs of homologous chromosomes.
- **B.** flies with normal wings and brown eyes show a recombinant phenotype, arising from crossing-over and independent assortment during gamete formation.
- **C.** the genes coding for wing type and eye colour are located on the same pair of autosomes so all the F2 phenotypes arise from crossing over between the loci of these genes.
- **D.** the genes coding for wing type and eye colour are linked and crossing-over occurs between their loci in the formation of 10% of gametes.

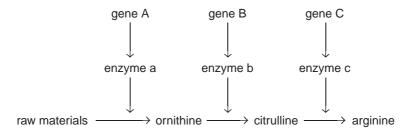
Question 9

The DNA sequence information present in a sequence of copy DNA (cDNA) that has been produced from a strand of mRNA extracted from the cytosol includes

- A. introns and exons.
- **B.** exons only.
- C. introns and promoter region.
- **D.** exons and promoter region.

Question 10

The bread mould, *Neurospora crassa*, normally produces its own amino acids from raw materials through a system of enzymes.



If a mutation occurred in gene B, the bread mould would still produce arginine if supplied with

- A. enzyme c.
- **B.** raw materials.
- C. ornithine
- **D.** citrulline.

The defective protein causing sickle cell anaemia is caused by the substitution of one nucleotide in the gene *HBB* on chromosome number 11, resulting in the change of the amino acid glutamic acid to valine.

This is an example of a

- **A.** point mutation.
- **B.** nonsense mutation.
- C. silent mutation.
- **D.** frameshift mutation.

Question 12

The figure below represents a length of DNA and its cutting sites for the restriction enzymes *Taq* I, *Hin* dIII, *Eco* RI and *Bam* HI.

Bam HI	Eco RI	Taq I	Taq I	Hin dlll Hin dlll	Bam HI	Taq I
<i>←</i>			37862 kB			\longrightarrow

The shortest single piece of DNA would be produced by incubating this DNA in a tube containing

- **A.** *Taq* I.
- **B.** *Hin* dIII.
- **C.** *Eco* RI.
- **D.** *Bam* HI.

Question 13

The liger is a hybrid cross between a male lion (*Panthera leo*) and a tigress (*Panthera tigris*). Ligers exist only in captivity because the habitats of the parental species do not overlap in the wild. Notably, ligers typically grow as large as both parents put together. Lions and tigers have different chromosome numbers.

Ligers are sterile because

- **A.** they do not survive to reproductive age.
- **B.** mitosis does not operate correctly in their sex organs.
- C. their chromosomes will not segregate independently into gametes.
- **D.** their chromosomes will not form homologous pairs correctly during meiosis I.

Question 14

Investigating the gene pools of populations can provide insight into all of the following, except

- **A.** the frequency of a genetic disease in a population.
- **B.** how long a disease is likely to persist.
- **C.** how rapidly an infectious disease can become established and spread in a population.
- **D.** what disease-associated genes are being selected against in a population.

Question 15

A possible hypothesis to explain why the different sexes of a ringed pheasant (a bird) look different could state that

- A. male pheasants with less colourful plumage are ignored by the females during mating season.
- **B.** the drab colouration of the female pheasant allows it to be camouflaged in its natural habitat.
- C. male pheasants are attracted to the most drab-coloured female pheasants.
- **D.** if female pheasants were more brightly coloured, then they will be easily caught and killed by predators.

In an infinitely large population, allele frequencies should not change over time. However, the frequencies of alleles in any real, small population (where the environment is stable) will be expected to change.

This statistical expectation is called

- A. natural selection.
- **B.** mutation.
- C. adaptation.
- **D.** genetic drift.

Question 17

Occasionally, seeds of the same species of trees living in different small wooded areas are blown from one grove of trees to another. The seeds may germinate, become established in the new grove, and eventually pollinate trees of the same species in that population.

This is an example of

- A. allopatric speciation.
- **B.** gene flow.
- **C.** genetic bottle neck.
- **D.** the founder effect.

Question 18

In order for two populations of a sexually reproducing species to evolve into two different species,

- A. there must be geographic isolation.
- **B.** there must be gene flow between the two populations.
- **C.** the two populations must form fertile hybrids.
- **D.** individuals from the two populations must be unable to reproduce with each other.

Question 19

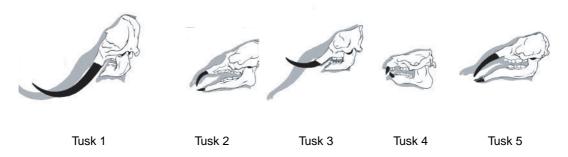
The carbon-14 content in bone is about one ${}^{12}C$ atom to every 10 billion ${}^{14}C$ atoms. The half-life of ${}^{14}C$ is about 5500 years.

Using radioisotopic dating techniques, a fossilised bone was found to have $0.125 {}^{14}C$ atoms to every 10 billion ${}^{12}C$ atoms.

The most accurate estimate of the absolute age of the bone would be

- **A.** 5500 years.
- **B.** 55 000 years.
- **C.** 16 500 years.
- **D.** 11 000 years.

The woolly mammoth (genus *Mammuthus*) became extinct about 5000 years ago. The evolution of the tusk in the woolly mammoth (Tusk 1) can be tracked over the past 40 million years by investigating the tusk length and the relative age of the mammoth and its ancestors.



If all of the tusks illustrated (in black in the diagrams above) were found in a series of stratigraphical layers of sedimentary rock, then the order of uncovering the layers from the surface downwards would most likely be

- **A.** 1, 3, 5, 2, 4 **B.** 1, 2, 3, 4, 5
- **C.** 1, 3, 4, 5, 2
- **D.** 4, 2, 5, 3, 1

Question 21

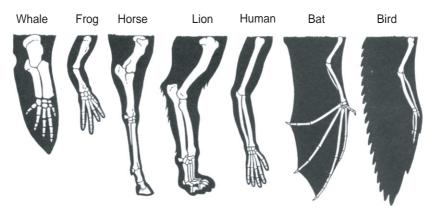
A recently found hominin called *Australopithecus sebida* was dated to be between 1.78 and 1.95 million years old.

In terms of the current evidence of human origins, this would place it

- A. between *Homo erectus* and *Homo habilis*.
- **B.** between Australopithecus africanis and Australopithicus afarensis.
- C. between Australopithecus afarensis and Homo habilis.
- **D.** between *Homo neanderthalensis* and *Homo erectus*.

Question 22

The diagram below shows the forelimb bone arrangement of seven different vertebrates.



The seven different bone arrangements show evidence of

- **A.** structural analogy.
- **B.** divergent evolution.
- **C.** convergent evolution.
- **D.** selective breeding.

Some bioethicists suggest that gene technologies should be limited to only those that do not involve the transferring of DNA from one genome into another.

According to these bioethicists, acceptable genetic technologies would include

- **A.** genetically modified food.
- **B.** production of human insulin.
- C. stem cell production of skin cells.
- **D.** gene therapy using a viral vector.

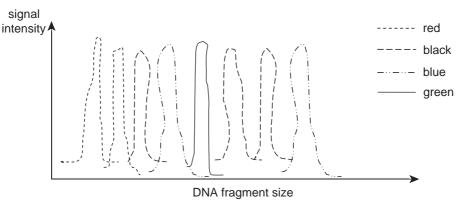
The following information relates to Questions 24 and 25.

The mapping of the human genome was a massive project initiated during the biotechnology revolution in the late 1980s. As technology became more refined, the speed at which this project progressed increased exponentially.

Researchers combined the DNA template they were interested in sequencing with DNA polymerase, a single-stranded DNA primer, free deoxynucleotide bases (dATP, dCTP, dGTP, and dTTP), and a sparse mixture of dideoxynucleotide bases (ddATP (green), ddCTP (blue), ddGTP (black), and ddTTP (red)) that were each fluorescently labelled with a different colour as indicated. These dideoxynucleotide bases would terminate new DNA strand synthesis once incorporated into the end of a growing DNA strand.

To speed up the sequencing process, a laser can be used to scan the DNA fragments and generate a sequence trace showing the colour and signal intensity of each DNA fragment produced by this process.

A typical sequence trace is shown below.



Question 24

The main method used to separate the DNA fragments according to size would be

- **A.** polymerase chain reaction.
- **B.** gel electrophoresis.
- **C.** genetic transformation.
- **D.** DNA cloning.

Question 25

The original template DNA sequence would be

- A. TTGCAAGC
- **B.** TTGCAGGC
- **C.** AACGUUCG
- **D.** AACGTCCG

SECTION B: SHORT-ANSWER QUESTIONS

Instructions for Section B

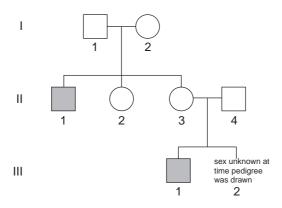
Answer this section in pen.

Answer **all** questions in the spaces provided.

Question 1

Menkes' disease (MNK) in humans is characterised by sparse and wiry hair, growth failure, and deterioration of the nervous system. Onset of Menkes' syndrome typically begins during infancy.

A family in which this X-linked disorder was present underwent Restriction Fragment Length Polymorphism (RFLP) analysis using gel electrophoresis. The family pedigree is shown below.



The RFLP analysis resulted in the following distribution of bands in the gel.

The probe used in the RFLP analysis detected a 2.3 kb fragment and a 5.2 kb fragment in this family.

a. What is meant by the term 'probe'? Explain.

1 mark

b. i. Explain why Person II-2 showed only one band on the gel.

ii. Draw in the bands (on the gel above) you would expect to see for Person II-3.

2 + 1 = 3 marks

c. Is this disorder dominant or recessive? Use evidence from the pedigree to explain your answer.

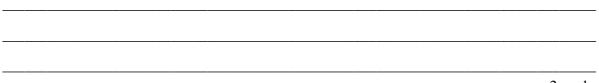
2 marks

d. What is the probability that Person III-2 will be a girl with Menkes' disease?

1 mark Total 7 marks

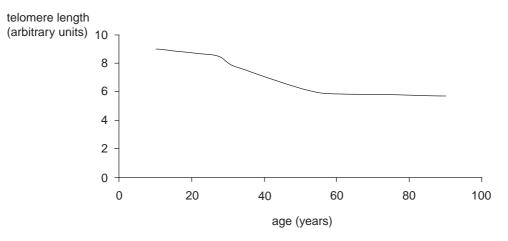
Telomeres are sections of DNA at the end of each chromosome that serve as a protective 'cap' to the genetic material. They help keep the ends of the chromosomes from becoming attached to each other or rearranging during cell division. If cells divided without telomeres, they could lose the necessary information at the end of each chromosome. In this way, telomeres prevent chromosomal 'fraying'.

a. Describe the general structure of a single eukaryotic chromosome at the beginning of a cell division.



2 marks

A telomere test can determine the length of a patient's telomeres in relation to the patient's age. A telomere score that is above the average line is desirable. The graph below illustrates how telomere length is an indicator of how rapidly one ages relative to a normal population. Therapies directed at slowing the loss of telomere length may slow aging and age-related diseases.



b. i. Predict the age of a person with a telomere length of 8 arbitrary units.

1 mark

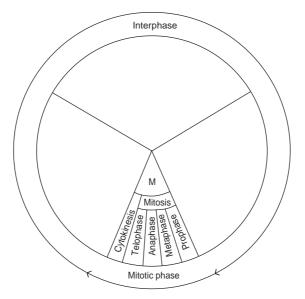
ii. Discuss the implications of a 30 year old female having a telomere length of 6 arbitrary units.

1 mark

Telomerase is an enzyme that maintains telomere length. It was found by a group of geneticists that the amount of telomerase activity is important in determining telomere length in aging cells and tissues.

In the absence of telomerase activity, telomeres progressively shorten which eventually limits the growth of cells. This is called a G1 cell cycle block.

c. i. Show on the cell cycle diagram below where a G1 cell cycle block would occur.



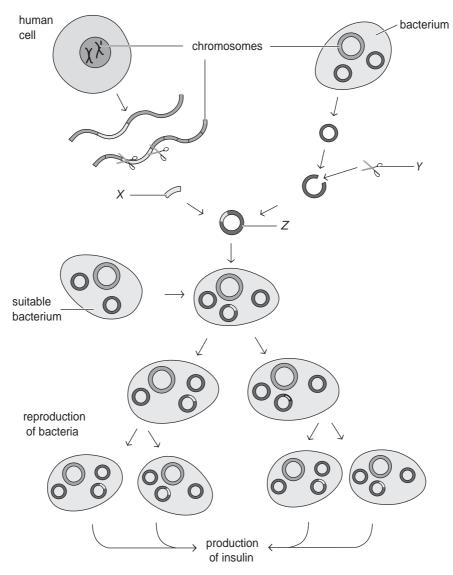
1 mark

ii. Describe the likely relationship between the cell cycle, telomere length and longevity of an individual if the telomerase activity is increased.

3 marks Total 8 marks

Biotechnology now plays an important role in the production of synthetic hormones. Recombinant DNA technology provides the technique currently used to manufacture hormones like human insulin.

The diagram below represents the process of recombinant DNA technology used to produce human insulin.



a. Name structures *X*, *Y* and *Z* in the table below and state each structure's role in the production of insulin.

Structure	Name of structure	Role in recombinant DNA process
X		
Y		
Z		

b. What risks and benefits are associated with recombinant DNA technology for a patient requiring insulin?

2 marks Total 5 marks

Cystic fibrosis (CF) is a common genetic disease. CF is caused by a mutation in a gene for a chloride channel called CFTR (cystic fibrosis transmembrane regulator).

The disorder is inherited as an autosomal recessive condition which involves a fault in some cells' membrane ion channels.

a. What advice would a genetic counsellor give to an **unaffected** individual (who has an affected sibling but unaffected parents) of their chance of being heterozygous for CF?

1 mark

The toxin secreted by the cholera bacteria cannot bind to the faulty CFTR channel and people with the mutation are less likely to die from cholera. Historically, people with CF died as children, so this protection against cholera was less significant for a homozygous person but very significant for the heterozygous person.

b. What is the selective pressure in this scenario?

1 mark

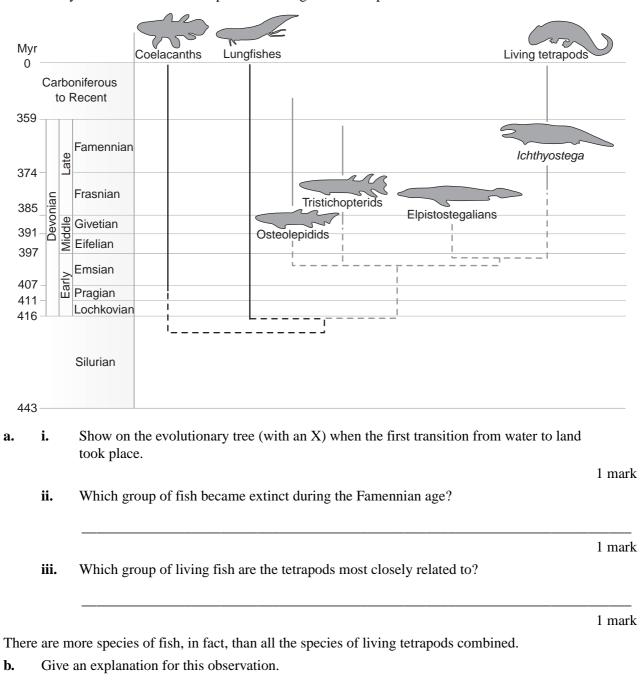
Many scientists believe that cholera epidemics have selected for those with one CFTR mutation. In other words, because the mutation gives an advantage to those who have it, they lived while other people died, so the mutated gene continued to be passed along.

- **c.** Discuss how each of the following pieces of evidence support the belief that cholera epidemics selected those with one CFTR mutation.
 - i. There are many different defects in the CFTR gene.
 - **ii.** The mutated gene has a very high frequency in the population.

iii. The very old age of the mutation (scientists estimate it is 50 000 years old).

1 + 1 + 1 = 3 marks Total 5 marks

Tetrapods are one branch of the fish family tree, the members of which just happen to be adapted for life out of water. The first transition from water to land took place more than 360 million years ago. The evolutionary tree below illustrates a possible cladogram of tetropod evolution.



2 marks

c. Discuss the accuracy of the following statement.

"Over many generations fins became legs. This was because food was found on the land and fish moved out of the water to get the food. This would have initially been a difficult thing to do but over many generations, the fins got progressively longer and stronger, which meant gaining the food was more successful."

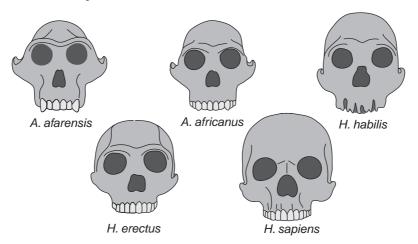
2 marks

In 2006 a spectacularly well-preserved fossil of an elpistostegid known as *Tiktaalik* was found that allowed palaeontologists to build up a good picture of an aquatic predator with distinct similarities to tetrapods – from its flexible neck, to its very limb-like fin structure.

d. What would be the selective advantage of a flexible neck and limb-like fins on land?

2 marks Total 9 marks

The skulls below show the evolutionary sequence of hominin skulls from the oldest, *Australopithecus afarensis* to the current, *Homo sapiens*.



a. The skull of *A. afarensis* is a fossil. Explain how this fossil was formed.

2 marks

b. Name and describe a technique that scientists would have used to assist them in determining the ages of these fossil skulls.

2 marks

c. Identify one physical evolutionary change that is evident from comparing the skulls in the diagram. Suggest a reason for this change.

2 marks

d. i. What is meant by cultural evolution?

1 mark

ii. Describe one cultural evolutionary change that accompanied the evolution of *Homo habilis* from the genus *Australopithecus*.

1 mark Total 8 marks

It is hypothesised that the eruption of Mount Toba in Sumatra 71 000 years ago ejected a massive amount of material into the atmosphere. Sunlight was blocked for so long that a thousand years of very cold global climate followed. This volcanic winter reduced the total population of the human species *Homo sapiens* to only a few thousand people in small populations in Africa. It is suggested that the 6.8 billion people that now populate the earth are all descendants of those small African populations that later migrated out of Africa. Modern human races may have evolved divergently from this population bottleneck.

a. What is meant by divergent evolution?

1 mark	
--------	--

b. i. Evidence for the rapid recent genetic divergence of modern humans is based on studies of mitochondrial DNA (mtDNA).

Explain two reasons why mtDNA, rather than nuclear DNA, is more useful for providing this evidence.

2 marks

ii. The (matrilineal) most recent common ancestor (MRCA) is the most recent person from whom everyone now living on Earth has inherited his or her mtDNA. Our MRCA is sometimes called "Mitochondrial Eve".

Explain what has happened to the mtDNA of the other women who lived during Eve's time.

1 mark

Fossil evidence shows that Neanderthals (*Homo neanderthalensis*) and modern humans (*Homo sapiens*) lived in the same areas of Europe and the Middle East at the same time. This led to speculation that the (now extinct) Neanderthals were ancestral to modern humans, or could have formed part of an interbreeding population with modern humans.

In 2008, scientists announced the first complete sequencing of Neanderthal mtDNA. A complete mtDNA genome of 16 565 base pairs was extracted from a 38 000 year old Neanderthal fossil from the Vindija cave in Croatia. This genome was compared, one base pair at a time, with the mitochondrial genomes of several modern humans of different ethnic origins.

The table below shows the numbers of base pair differences between the mtDNA of the modern humans and the Neanderthal mtDNA.

	Number of base-pair differences	
	Between modern humans	Between modern humans and the Neanderthal
Smallest	1	200
Largest	146	361
Average	79	269

c. Using data from the table, describe two genomic differences between the mtDNA of modern humans and the Neanderthal.

2 marks

d. Does this evidence support the hypothesis that Neanderthals were ancestral to modern humans or that both were part of an interbreeding population? Explain your answer.

2 marks Total 8 marks

END OF QUESTION AND ANSWER BOOKLET