Marking Guide

Biology Unit 3

2020

Section One: Multiple-choice **30% (30 Marks)**

Question	Answer
1	d
2	d
3	d
4	a
5	b
6	c
7	b
8	b
9	c
10	b
11	c
12	d
13	b
14	a
15	d
16	b
17	a
18	b
19	a
20	b
21	d
22	c
23	b
24	c
25	b
26	d
27	b
28	a
29	c
30	b

Section Two: Short answer 50% (100 Marks)

Question 31 (20 marks)

(a) Identify the term given to mutations involving single base substitution. (1 mark)

Description	Marks
Point mutation	1
TOTAL	**1**

(b) Explain the effect of 'switching off' the lactase (LCT) gene on cellular processes. (3 marks)

Description	Marks
Gene will not be transcribed into mRNA.	1
No mRNA means that translation will not take place.	1
The protein/enzyme will not be synthesised (at ribosomes).	1
TOTAL	**3**

(c) Suggest the most appropriate genetic test which could be used to discover if a person was carrying the lactase-persistent mutation. Explain your response. (2 marks)

Description	Marks
DNA Microarray	1
Checks for genes that are 'switched on' by analysing presence of the corresponding mRNA. A person with the mutation will have mRNA.	1
TOTAL	**2**

(d) The persistence of this mutation over 10,000 years can be attributed to natural selection. Explain how natural selection has shaped the evolution of lactase-persistence in early human populations. (4 marks)

Description	Marks
Any **four** from below worth **one** mark each.	
• Individuals keeping cattle and able to drink milk products are better nourished and healthier. • During times when food is scarce, milk consumers will always have a source of nourishment. Other lactose-intolerant people may die from starvation/malnutrition. • The lactase-persistent people are more likely to have children (with other lactase-persistent individuals) and pass on the trait. • Offspring are healthier and more likely to reach adulthood and reproduce, also passing the trait on. • Allele frequency changes to favour the dominant, lactase-persistent trait in the gene pool.	1 - 4
TOTAL	**4**

(e) Lactase-persistence is an autosomal-dominant trait. Explain what is meant by

(i) autosomal dominant (2 marks)

Description	Marks
Inheritance of a single copy of the mutated gene (allele) results in expression of the trait.	1
The trait will be expressed if the organism's genotype is either homozygous or heterozygous.	1
TOTAL	**2**

(ii) autosomal recessive (2 marks)

Description	Marks
A trait that can only be expressed when both copies of a mutated gene (both alleles) are inherited.	1
The organism's genotype must be homozygous to express the trait.	1
TOTAL	**2**

(f) Alleles for the lactase-persistent trait are represented by 'L' and 'l'. Complete the Punnett squares below to show a cross between a lactose-intolerant female, and a male carrying the lactase-persistence trait. For each cross, identify the genotypic and phenotypic frequencies of the offspring.

(i) Cross 1 - heterozygous male. (2 marks)

		Male	
		L	l
Female	l	Ll	ll
	l	Ll	ll

Description	Marks
Correct completion of Punnett square.	1
Genotype frequency - 50% Ll; 50% ll. Phenotype frequency - 50% lactase-persistent; 50% lactose intolerant.	1
TOTAL	**2**

(ii) Cross 2 - homozygous male. (2 marks)

		Male	
		L	L
Female	l	Ll	Ll
	l	Ll	Ll

Description	**Marks**
Correct completion of Punnett square.	1
Genotype frequency - 100% Ll Phenotype frequency - 100% lactase-persistent.	1
TOTAL	**2**

(g) Suggest why autosomal dominance has allowed for the perpetuation of the lactase-persistent trait in humans. (2 marks)

Description	**Marks**
If an individual is homozygous, the dominant allele for the trait is always passed on to offspring.	1
If an individual is heterozygous, the dominant allele is passed on 50% of the time.	1
TOTAL	**2**

Question 32 **(20 marks)**

(a) Contrast the structure and packaging of genetic material between prokaryotic and eukaryotic cells. (8 marks)

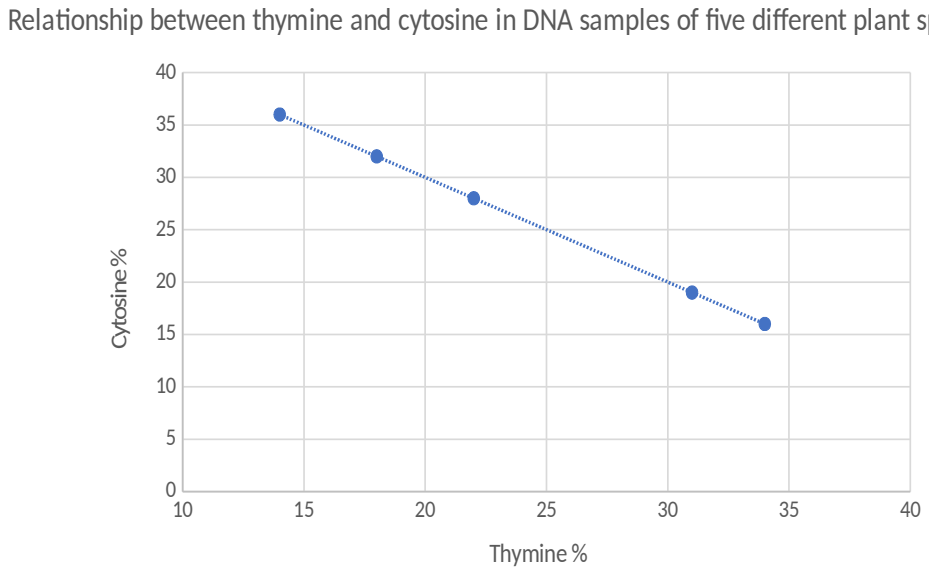
Description	Marks
One mark per correct point as per table below.	1 - 8
TOTAL	**8**

Prokaryotic cells	Eukaryotic cells
Single-stranded DNA.	Double-stranded DNA in a double helix structure.
No nucleus present to contain DNA - free floating in cytosol.	Membrane-bound nucleus containing DNA.
Whole genome is found on one length of single-stranded DNA.	DNA is condensed into multiple chromosomes so more information can be carried.
May contain plasmids - small circular double-stranded DNA that can replicate independently.	No plasmids are present - all codes are found within chromosomes.

**other appropriate responses are acceptable.*

(b) Graph the relationship between the percentage (%) composition of thymine and cytosine in the plant species from Table 1. Include a line of best fit on your graph. (5 marks)

Description	Marks
Title	1
Correct axes scale.	1
Labelled axes (are interchangeable).	1
Correctly plotted points.	1
Line of best fit.	1
TOTAL	**5**



(c) Identify the relationship between thymine and cytosine as shown in your graph. (1 mark)

Description	Marks
As the percentage of cytosine (C) decreases, the percentage of thymine (T) increases.	1
TOTAL	**1**

(d) Explain the reason for this relationship in the percentage composition of thymine and cytosine. (3 marks)

Description	Marks
The base-pairing rule shows that the amount (%) of T = A and the amount (%) of C = G.	1
The total amount of the bases combined (A + T + C + G) must equal 100%.	1
Therefore, if T increases then A increases at the exact rate and C and G will decrease at the exact rate.	1
TOTAL	**3**

Based on the data, it was concluded that the five plants were unlikely to be in the same genus.

(e) Is this conclusion valid? Explain your reasoning. (3 marks)

Description	Marks
Yes	1
Significant variation in base-pair percentages between species.	1
Suggests a large amount of variation in the gene sequence so therefore not closely related.	1
TOTAL	**3**

Question 33 **(20 marks)**

Many biotechnology procedures require large amounts of DNA to obtain accurate and useful data. Often, DNA samples collected from crime scenes, fossils or degraded tissues are small and fragmented. Polymerase Chain Reaction (PCR) is a technique specifically developed to synthesise large amounts of DNA in a short period of time. PCR involves three main processes that simulate normal cellular DNA replication.

(a) Complete the table below by comparing the structure and/or function of the molecules involved in DNA replication with the equivalent PCR molecule or process.

(6 marks)

Description	Marks
One mark per correct point as per table below.	1 - 6
TOTAL	**6**

Molecule /enzyme	DNA replication	PCR equivalent
Helicase	Helicase unzips the DNA strand by breaking the hydrogen bonds holding base pairs together.	PCR solution is heated to 95^{o}C, denaturing the hydrogen bonds between base pairs, completely splitting double-helix.
Primer	A short sequence of RNA synthesised by primase. Attaches to DNA (at complementary sequence) creating a 3' position to attach new nucleotides.	Short fragments of single-stranded DNA that bind to either end of the target sequence in 3' to 5' direction, allowing for addition of new nucleotides.
DNA Polymerase	Attaches new nucleotides to the leading strand of DNA in a 3' to 5' direction.	*Taq* polymerase is used in PCR. Adds new nucleotides to both strands in 3' to 5' direction.

The PCR technique does not involve Okazaki fragments or DNA ligase.

(b) Explain why these molecules are **not** required in PCR. (2 marks)

Description	Marks
The DNA strands are completely separated as the hydrogen bonds holding them together are denatured by high temperatures.	1
Both strands can therefore be copied in a 3' to 5' direction as there is no replication fork.	1
TOTAL	**2**

Taq Polymerase is an enzyme found in the heat tolerant bacteria *Thermus aquaticus* and is most active at around 70^{o}C. *Taq* Polymerase is a vital component of PCR.

(c) Suggest **two** characteristics of *Taq* Polymerase that explain its importance to the PCR technique. (2 marks)

Description	Marks
Will not denature when exposed to high temperatures required in PCR.	1
Functions most effectively at high temperatures (70^{o}C) so replication is efficient and quick.	1
TOTAL	**2**

The illegal wildlife trade industry earns around $20 billion US annually. Many animal products such as horns, teeth, hair and skin are illegally harvested and processed for use in traditional Eastern medicines. Prosecution of persons involved in trafficking requires accurate identification of the species used in these products. Geneticists can extract mitochondrial DNA (mtDNA) from these products and once processed, it can be compared to data from a 'gene bank'.

(d) Explain **two** reasons for using mtDNA instead of nuclear DNA in this particular type of genetic analyses. (2 marks)

Description	Marks
Less susceptible to mutations and recombination so there is variation between different species but not within species.	1
Many mitochondria in each cell so more mtDNA can be extracted.	1
TOTAL	**2**

Fragments of cytochrome *b* were recovered from two separate samples of ivory powder confiscated from a wildlife trafficker. The fragments were 402 base pairs long and originated from the same region on the gene; between base pairs 11476 and 11878. These fragments were amplified using PCR and then treated with three different restriction endonucleases prior to electrophoretic analysis; *Alu* I, *Hae* III and *Hinf* I.

(e) Explain how the use of these restriction enzymes can produce the species-specific genetic 'fingerprints' from the gene fragments. (4 marks)

Description	Marks
Restriction enzymes have specific base-pair sequences on the DNA to which they are complementary, called restriction sites.	1
Restriction sites are found at different positions on the DNA of different species.	1
When restriction enzymes cut the DNA, different length fragments are produced for each species.	1
When run through electrophoresis, the different sized fragments will show up in different positions in the gel, creating a 'fingerprint'.	1
TOTAL	**4**

(f) Using the gel 'fingerprints' above, predict which species the samples most closely resemble. Justify your response. (2 marks)

Description	Marks
Sample 1 - Black rhinoceros; all three fragments are same size.	1
Sample 2 - May contain African elephant as it has two matching fragments, but another species could be in the DNA sample.	1
TOTAL	**2**

(g) Variation in base sequences between different species is the result of genetic mutation. However, scientists have discovered that mutation of the third base in a codon sequence seldom leads to amino acid exchange. Explain why this is the case.

(2 marks)

Description	Marks
A change in the amino acid is most often caused by a mutation in the first or second nucleotide (base) of the codon.	1
Most amino acids are encoded by several different codons which differ only in the third base and cause no change in the protein.	1
TOTAL	**2**

Question 34 **(20 marks)**

Palaeontologists study fossils to obtain information about the history of life on Earth.

(a) Identify the type of information that scientists can observe directly from fossils. (3 marks)

Description	Marks
Three points for **one** mark each. These may include, but are not restricted to;	
• Body morphology • Diet of the organism (if animal). • Conditions in which the organism lived or died. • Climate • Mode of locomotion of animal. • Ancestry	1 - 3
TOTAL	**3**

(b) Define the term 'transitional fossil'. Use an example to explain how transitional fossils are important to our understanding of evolutionary change. (4 marks)

Description	Marks
A transitional fossil is a term used to describe a fossil that shows a transitional form of two different species.	1
The transitional fossil will show a combination of traits from the species that preceded it and the species that followed it.	1
Transitional fossils are the preserved evidence of transitional forms of organisms - the 'missing links' which provide support to the theory of descent with modification.	1
At least **one** example for **one** mark. Examples must include the two species from which it is combined. These may include but are not restricted to;	
• **Tiktaalik** - fish and four-legged land animals. • **Archaeopteryx** - dinosaur and bird. • **Pakicetus** - whale and terrestrial mammal.	1
TOTAL	**4**

(c) Explain the purpose of an index fossil in palaeontology. (2 marks)

Description	Marks
Fossil remains of an organism that lived in a particular (narrow) geological time frame and is widely distributed.	1
Characteristic of particular geological formations so are used to determine the age of related formations.	1
TOTAL	**2**

Like many birds, the Splendid Fairy-wren (*Malurus splendens*) is represented by different male and female forms. The adult male has brilliant blue plumage while the non-breeding male, female and juvenile is grey-brown with a muted blue tail.

(d) State the name given to this phenomenon. (1 mark)

Description	Marks
Sexual dimorphism	1
TOTAL	**1**

During mating season, the male Splendid Fairy-wren has been observed presenting females with pink and purple flower petals and flaring their cheek feathers. New research has found that breeding males will sing their courtship songs following the call of the predatory Grey Butcherbird (*Cracticus torquatus*).

(e) Define 'sexual selection'. (2 marks)

Description	Marks
Inherited characteristics/traits in an organism,	1
that improve its chance of attracting a mate/breeding success.	1
TOTAL	**2**

(f) Explain why the appearance and behaviour of the Splendid Fairy-wren is considered an example of sexual selection. (2 marks)

Description	Marks
Bright plumage and behaviour only occur in breeding season.	1
Attracting a mate is the only reason for courtship behaviour and plumage.	1
TOTAL	**2**

(g) Sexual selection is not considered an example of adaptive or natural selection. Explain why this is the case. (4 marks)

Description	Marks
Sexual selection is determined by mating success due to favourable inherited characteristics.	1
Adaptive/natural selection is influenced by environmental pressures.	1
Environmental pressures do not influence the frequency of phenotypes associated with successful courtship.	1
Mate selection by female counterparts will determine the allelic frequency of sexual characteristics.	1
TOTAL	**4**

(h) Identify **two** other evolutionary processes that are **not** influenced by natural selection. (2 marks)

Description	Marks
Genetic drift	1
Founder effect	1
TOTAL	**2**

Question 35 **(20 marks)**

(a) Identify **two** structures, common to each developing embryo, used in comparative embryology. (2 marks)

Description	Marks
Any **two** from below worth **one** mark each.	
• Pharyngeal slits • Tail • Dorsal notochord • Limb buds	1 - 2
TOTAL	**2**

(b) Explain how comparative embryology provides evidence to suggest ancestral relatedness of these vertebrate species. (3 marks)

Description	Marks
The embryonic form of organisms with a common ancestor share homologous structures.	1
These structures are not present (in the same form) in the adult organism.	1
Similar embryonic structures and pattern of development suggests a common ancestor with similar embryonic development.	1
TOTAL	**3**

(c) Define the terms;

(i) Homologous structure (2 marks)

Description	Marks
Similar physical structures in different organisms, often with a different function.	1
Organisms with homologous structures share a recent common ancestor and evolved though divergent evolution.	1
TOTAL	**2**

(ii) Analogous structure (2 marks)

Description	Marks
Similar structures in unrelated organisms that have the same function.	1
Organisms with analogous structures have no recent common ancestor and developed as a result of convergent evolution.	1
TOTAL	**2**

(d) Using the information provided in the previous image and phylogenetic tree, explain how it is possible for birds and bats to possess both homologous and analogous structures adapted for flight. (4 marks)

Description	Marks
Before wings evolved for flight, birds and bats shared a common ancestor.	1
This ancestor had a similar arm structure to both birds and bats - homologous structures.	1
This ancestral species diverged into separate lineages containing ancestors of birds and bats.	1
The ability to fly emerged separately in these lineages as different wing structures evolved - analogous structures.	1
TOTAL	**4**

(e) Identify and briefly outline the technique widely used to measure the genetic relatedness between different species. (4 marks)

Description	Marks
Molecular/DNA hybridisation	1
Strands of DNA from related species are mixed together and heated, separating strands and exposing bases.	1
DNA strands from different species (are cooled and) recombine/hybridise by base-pair matching at genetically identical regions.	1
Level of hybridisation between different species' DNA reveals how genetically similar/related they are to each other.	1
TOTAL	**4**

Molecular clocks are an essential tool for evolutionary biologists. Scientists can use DNA, amino acids and proteins from different species to estimate evolutionary divergence times.

However, molecular clock dating does not provide an absolute timeframe. As such, molecular clocks are calibrated against the fossil record to narrow estimates of divergence.

(f) Suggest why calibrating the molecular clock against the fossil record can help scientists provide a more precise timeframe for species divergence. (1 mark)

Description	Marks
Fossils can be dated quite accurately using radioisotopes.	1
TOTAL	**1**

(g) Explain why there is a lack of precision when measuring divergence patterns of evolution. (2 marks)

Description	Marks
Speciation can occur over millions of years.	1
A precise time cannot be given to a gradual process.	1
TOTAL	**2**

End of Section Two

Section Three: Extended answer 20% (40 marks)

Part A

Question 36 (20 marks)

(a) Explain how complementary base-pairing allows replication, transcription and translation to occur. (10 marks)

Description	Marks
In DNA replication each strand is copied in the semi-conservative model, resulting in two identical strands.	1
Nucleotides that comprise DNA will only pair in a specific way - adenine with thymine and cytosine with guanine.	1
A and T are held together by two hydrogen bonds while C and G are held by three hydrogen bonds.	1
In transcription the base-paring rule is used to synthesise a single-stranded molecule of messenger RNA (mRNA) of a particular gene sequence, from the DNA strand.	1
Thymine is replaced with uracil in mRNA, so adenine bonds/pairs to uracil.	1
Base-pair rule in transcription ensures that the code in DNA is copied exactly and transferred to the ribosome for translation.	1
Translation uses the code carried in mRNA to synthesise polypeptides from amino acids.	1
Each sequence of three bases in mRNA, called a codon, codes for an amino acid.	1
Transfer RNA (tRNA) have anticodons that are matched sequentially to the mRNA (through base-pairing) as it moves through the ribosome.	1
Each tRNA carries the correct amino acid to its corresponding mRNA codon until the polypeptide is complete and represents the original code in the DNA.	1
TOTAL	**10**

Fraternal twins, Jake and Leo, are so dissimilar in appearance and personality that they are rarely considered as brothers.

(b) Explain how meiosis can generate such variation in genetic traits inherited by the twins.
(10 marks)

Description	Marks
The events that occur during meiosis greatly increase the genetic variability of the gametes produced and therefore any resulting offspring. These events include genetic mutation, crossing over and independent assortment.	1
Mutations • Genetic mutations that occur during meiosis are passed on to offspring through affected gametes. • Mutations change the code in gene sequences which can affect how a protein is synthesised. • Any measurable change in the protein/s for a genetic trait will affect how it is expressed in an individual.	1 - 3
Crossing over (and recombination) • During prophase of meiosis I, genetic information can be mutually exchanged between the non-sister chromatids of homologous chromosomes. • A chiasmata forms where the non-sister chromatids come into contact, and segments of DNA (with genes it contains) are exchanged. • The result of this recombination of alleles is the creation of four (4) genetically unique chromosomes, different to any other produced.	1 - 3
Independent assortment (of alleles) • During the first cell division (meiosis I), all the homologous chromosomes (with sister chromatids) line up separately at the equator. • This allows each pair to move independently of one another into the two (intermediate) daughter cells. • These daughter cells now contain a recombined version of every chromosome, allowing for huge variation in the genetic makeup of resulting gametes.	1 - 3
TOTAL	**10**

Question 37 **(20 marks)**

(a) Discuss gene mutations and the affect they can have on cellular function.

(10 marks)

Description	Marks
A gene mutation is any change in the DNA sequence of a gene where a base/nucleotide is altered.	1
There are three (3) different types of gene mutation; • Substitution - one nucleotide is swapped for another, also called a point mutation. • Insertion - addition of a nucleotide in the sequence causing a 'frameshift' mutation. • Deletion - omission of one or more nucleotides from the sequence, causing a 'frameshift' mutation.	1 - 3
Gene mutations can result in a change in the structure of the protein for which they code, which can change, inhibit or have no effect on its function, depending on the type of mutation.	1
Potential effects of these gene mutations are manifested as;	
Silent mutations - nucleotide change has no effect on the amino acid code or protein synthesised.	1
Missense mutations - a change in the amino acid sequence alters the polypeptide made (primary structure). This can affect the final 3D shape of the protein and the active site of an enzyme so it cannot perform its function.	1 - 2
Nonsense mutations - the gene is cut short because the altered nucleotide caused a 'STOP' codon to be incorporated into the DNA sequence. mRNA carries an altered/shortened code. Translation is incomplete and a polypeptide is not produced.	1 - 2
TOTAL	**10**

(b) Explain the use of bacterial plasmids in the creation of transgenic plants to improve agricultural productivity. Use specific examples to support your response.

(10 marks)

Description	Marks
Plasmids are small, circular DNA molecules found in prokaryotic cells, separate from chromosomal DNA, that replicate independently and more frequently.	1
Plasmids can be easily recombined/spliced with foreign DNA to induce the expression of a gene not normally found in the given organism.	1
Recombinant plasmids have been created to produce crops that are; • higher in protein. • enriched with vitamins. • nutrient rich. • herbicide resistant. • resistant to insect attack. **Two points must be mentioned for full marks.*	1
Agrobacterium tumefaciens is a soil bacterium widely used as a vector. *A. tumefaciens* contains a tumour-inducing plasmid (Ti plasmid) that it 'injects' into plant cells (in nature).	1
The Ti plasmid is isolated from *A. tumefaciens* and manipulated to remove the tumour-forming gene. The specific gene of interest is also isolated from the donor organism's DNA.	1
The foreign gene is incorporated into the Ti plasmid using appropriate restriction enzymes. The recombinant Ti plasmid is reinserted into the *Agrobacterium* cell.	1
Small plant cuttings (via tissue culture) or plant embryos are exposed to the recombinant bacteria. The Ti plasmid is readily taken up by the plant cells and then incorporated into its DNA.	1
The recipient plant cells are able to produce the protein and express the trait coded for by the inserted gene.	1
Brief explanation of **one** example in agriculture. Examples include;	
• Round-up Ready Canola - glyphosate resistant plants so farmers can spray weeds and not kill crop. • Golden Rice - production of rice grains containing increased amounts of beta-carotene. • Bt Cotton - cotton plants produce a toxin that kills a pest caterpillar, reducing need for pesticides. • GM soybean - herbicide resistance so weeds can be controlled without killing soybean plants. • *Other examples are acceptable at teacher's discretion.*	1 - 2
TOTAL	**10**

Part B

Choose **either** Question 38 **or** Question 39.

Question 38 **(20 marks)**

The rock pocket mouse (*Chaetodipus intermedius*) is a nocturnal mammal endemic to the deserts of America's southwest. Most mice are sand coloured, providing them with camouflage from predatory birds. However, populations of a dark-haired rock pocket mouse have been found living on basalt outcrops in Arizona. These dark-haired rock pocket mice possess a mutant version of the *Mc1r* gene which controls the synthesis of hair pigment.

(a) Explain how the dark-haired form of the rock pocket mouse has emerged as a successful phenotypic variation to the normal 'wild-type' sand-coloured mouse.

(10 marks)

Description	Marks
Mutation during meiosis occurred to alter the *Mc1r* gene, its protein and the final hair pigment.	1
In the 'wild-type' mouse, the dark pigment allele was likely a recessive trait, requiring two copies of the mutated allele.	1
The mutated allele would have been present in low frequencies in the 'wild-type' population.	1
Rock pocket mice born with dark hair and living on light-coloured sand would likely have been caught by predators and not survived to reproduce and pass on the altered gene.	1
In those populations living around the basalt outcrops, the expression of the dark-haired phenotype would be beneficial to their survival.	1
Dark-haired mice can seek food and shelter on the rocky outcrops whilst maintaining their camouflage from predatory birds.	1
Dark-haired mice form a population on the basalt outcrops where they survive and reproduce.	1
Offspring born from the dark-haired mice will have two copies of the mutant allele and always express the dark-haired phenotype.	1
The dark-haired rock pocket mouse is considered a variant of the 'wild-type' sand-coloured mouse, not a separate species.	1
The dark-haired and 'wild-type' mice can still mate and produce viable offspring because the mutant allele is present in the original population.	1
TOTAL	**10**

(b) Discuss the concept of gene flow and explain how disruption to gene flow can contribute to allopatric speciation.

(10 marks)

Description	Marks
Gene flow is the movement or transfer of genes (or alleles) between interbreeding populations of a particular species.	1
Gene flow is an important mechanism for transferring genetic diversity amongst populations.	1
Migration of individuals in to and out of a population can result in a change in allelic frequency of both populations.	1
Migration changes the distribution of genes and genetic diversity within the populations.	1
High rates of gene flow can reduce genetic differentiation between populations and increase heterogeneity of alleles.	1
High rates of gene flow prevent the development of genetically different populations, reducing the possibility of speciation.	1
Gene flow that is disrupted by physical and geographical barriers such as rivers, mountain ranges or human-made structures may lead to allopatric speciation.	1
Disrupted gene flow leads to genetic divergence of separated/isolated populations.	1
Isolated populations can be exposed to different selection pressures. These pressures will favour the phenotypes that are better 'suited' to survive the environment.	1
Allelic frequencies (and gene pool) of each population become significantly different over time leading to reproductive isolation. The two populations can no longer interbreed so gene flow cannot occur.	1
TOTAL	**10**

Question 39 **(20 marks)**

Underneath the rainforest of Mexico's Yucatan Peninsula lies an expansive, underground limestone cave system flooded with freshwater. The cave system opens into the rainforest through small freshwater pools, called Cenotes (*sen-oh-tays*). These Cenotes have been isolated from each other (and other aquatic ecosystems) for thousands of years. Each Cenote has its own diverse aquatic ecosystem, of which many support species endemic to individual pools.

(a) Discuss the mechanisms that may have influenced the evolution of new species in individual Cenotes, from common ancestors.

(10 marks)

Description	Marks
Geographical isolation occurs - small populations of ancestral species are separated amongst different Cenotes.	1
Genotypic variation (genetic diversity) in new populations is due to heterozygosity of alleles and/or random mutations during gamete formation.	1
Speciation may occur through **two** different processes or a combination of these processes.	
The founder effect occurs when a new population is founded with a small sample of the original gene pool's alleles. Subsequent populations will only contain this limited pool of genes. **Genetic drift** may then occur due to the founder effect. Variation in the allelic frequency in subsequent generations is by chance/random. Any mutations are more likely to become fixed and lead to speciation.	1 - 2
Natural selection • Each Cenote has slightly different environmental pressures - light availability, water temperature, water chemistry, food resources and shelter. • Individuals expressing phenotypes better suited to these pressures will more likely survive and reproduce, passing on genetic information. • The phenotypes 'selected' will become more prominent in the gene pool over time as species adapt to their specific environment. • Each Cenote's isolated population may eventually diverge from its ancestral population (divergent evolution) through accumulation of genetic differences. • Allopatric speciation will result from this divergence and continual reproductive isolation, with species evolving in response to specific environmental pressures. • Lack of gene flow between Cenotes, and therefore species'	1- 6

populations, further amplifies the effect of mutations and genetic drift.	
TOTAL	**10**

"*The extinction of species, each one a pilgrim of four billion years of evolution, is an irreversible loss. The ending of the lines of so many creatures with whom we have travelled this far is an occasion of profound sorrow and grief...But the loss of lineages and all their future young is not something to accept. It must be rigorously and intelligently resisted*."

(b) Explain why reduced genetic diversity in small populations of endangered species puts them at greater risk of extinction. Discuss how scientists use modern technology to reduce extinction rates and maintain biodiversity.

(10 marks)

Description	Marks
Increasing extinction risk - **four** points must be discussed for **one** mark each. These may include, but not restricted to;	
• Inbreeding occurs in small populations leading to homozygosity of alleles in gene pool. • Genetic drift occurs (loss of alleles by chance events) leading to bottleneck effect. • Any deleterious alleles will remain in gene pool and increase in frequency. • Inbreeding and deleterious alleles may also decrease reproductive success, further reducing population size. • Further deaths and reproductive failure will cause removal of alleles from gene pool, further reducing diversity.	1 - 4
Modern technology applications - at least **three** different technologies must be discussed for **two** marks each, for a total of **six** marks. These may include, but not restricted to;	
Computer modelling • Predicting the chance of survival of threatened species populations under specific conditions. • Enables scientists to better develop conservation strategies to maintain biodiversity and ecosystem function.	1 - 2
DNA fingerprinting/profiling • Identification of inbreeding in small populations and sub-species identification. • Degree of relationship between members of rare species prior to captive breeding to ensure compatibility and prevent inbreeding.	1 - 2
Recombinant DNA technology • Developing transgenic organisms containing foreign genes which offer resistance to the specific threat. • Threatened species can be modified to thrive in affected habitats (saline soils) or be resistant to pests, chemicals, disease that threaten their survival.	1 - 2
TOTAL	**10**

End of questions