

**Marking Guide**

**BIOLOGY UNIT 3**

**2023**

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

|  |  |
| --- | --- |
| **Question** | **Answers** |
| **1** | A |
| **2** | B |
| **3** | A |
| **4** | D |
| **5** | A |
| **6** | C |
| **7** | C |
| **8** | A |
| **9** | B |
| **10** | A |
| **11** | D |
| **12** | D |
| **13** | C |
| **14** | D |
| **15** | A |
| **16** | C |
| **17** | B |
| **18** | C |
| **19** | B |
| **20** | A |
| **21** | C |
| **22** | D |
| **23** | C |
| **24** | B |
| **25** | B |
| **26** | A |
| **27** | D |
| **28** | A |
| **29** | C |
| **30** | B |

**End of Section One**

**Section Two: Short answer 50% (100 Marks)**

This section has **five** questions. Answer **all** questions. Write your answers in the spaces provided.

Supplementary pages for planning/continuing your answers to questions are provided at the end of this Question/Answer booklet. If you use these pages to continue an answer, indicate at the original answer where the answer is continued, i.e. give the page number.

Suggested working time: 90 minutes.

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**Question 31 (20 marks)**

The white spot grouper fish (*Epinephelus coeruleopunctatus*) occur in the  tropical marine waters of the Indo-west-central-Pacific. Currently the white spot grouper is not endangered. However, a conservation group in Indonesia, have decided to breed the species in captivity, so they have a backup population, in case the species becomes threatened. To do this, the captive population must have a viable gene pool.

1. Describe the characteristics of a viable gene pool. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any three of: | |
| * size of population cannot be too low so unrelated organisms breed **or** high enough numbers to prevent inbreeding * high genetic diversity/variation * individuals must be able to successfully reproduce * some juveniles must survive to reproduce * able to withstand environmental adversity | 1-3 |
| **Total** | **3** |

1. State why captive populations, bred for conservation, must have a viable gene pool?

(1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| So that genetic diversity is not lost/is maximised | 1 |
| **Total** | **1** |

Establishing the captive breeding population of white spot grouper required wild caught fish to be caught. Before these fish were released into the main breeding tank, they were quarantined. Some of the fish in quarantine were found to have a white fungus growing on their scales. To effectively treat this fungus, the species of the fungus had to be determined. A sample of the fungus was sent to a scientific laboratory, where the sample was analysed by scientists. The first step in identifying specie of the fungus was to create a genetic profile from the sample. DNA was extracted from the fungal sample. To have enough DNA to create a genetic profile, the scientists needed to amplify the quantity of DNA using the Polymerase Chain Reaction (PCR).

1. Using the table below explain the main events in the three stages in a PCR cycle. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| |  |  | | --- | --- | | Stages in PCR | Description | | 1 | Denaturation of the double stranded DNA template into two single strands | | 2 | Annealing of primers to complementary bases on each original strand (ready for DNA synthesis) | | 3 | Extension of the new DNA strands from the primers with nucleotides via Taq polymerase. | | 1-3 |
| **Total** | **3** |

The scientist took the DNA and cut it with restriction enzymes at specific base sequences. To create the genetic profile the used a flatbed gel and electrophoresis.

1. Explain the process and principles of gel electrophoresis. (4 marks)

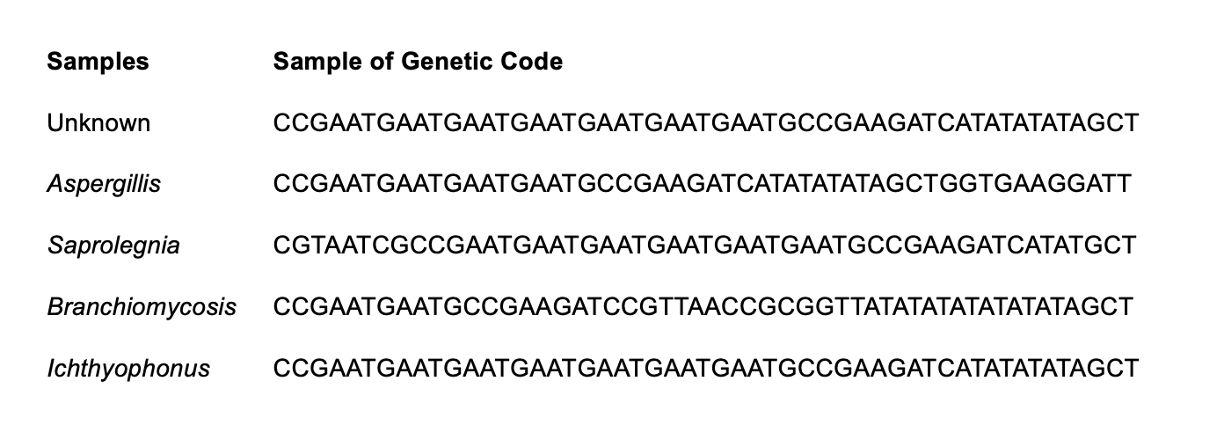
|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any four of: | |
| * DNA loaded into well /gel to separate fragments based on size * Current run through gel moving the DNA moves from the negative to positive end of the gel * Smaller fragments move further down the gel (closer to the positive terminal) * fragments arranged by size (genetic profile) | 1-4 |
| **Total** | **4** |

The scientists had genetic profiles for many different marine fungi species. They used the genetic profile of the fungus and comparative genomics to determine the species of fungus.

1. Define the term the comparative genomics. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| the genome of two organisms are compared to each other | 1 |
| **Total** | **1** |

Below is one section of DNA code from the genetic profiles of the fungi.



X

1. Name the feature labelled X in the table. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * short tandem repeat | 1 |
| **Total** | **1** |

1. Identify the fungus that was found on the fish. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| *Ichthyophonus*   * correct name with correct nomenclature – capital i and underlined/italics | 1 |
| **Total** | **1** |

Sequential hermaphroditism is when the sex of an organism changes from one sex to the other sex during the organisms lifetime. Sequential hermaphroditism occurs in the white spot grouper fish (*Epinephelus coeruleopunctatus*). Fish sampling was carried out in the waters of Indonesia. The following results were obtained.

|  |  |  |
| --- | --- | --- |
| The Sex and Length of White Spot Grouper | | |
|  | |  |
| Length (mm) | Sex |  |
| 10 - 184 | unable to be determined |  |
| 185 - 290 | female |  |
| 291 - 310 | males and females |  |
| 311 - 500 | males |  |

1. In what direction is the hermaphrodism? (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| female to male | 1 |
| **Total** | **1** |

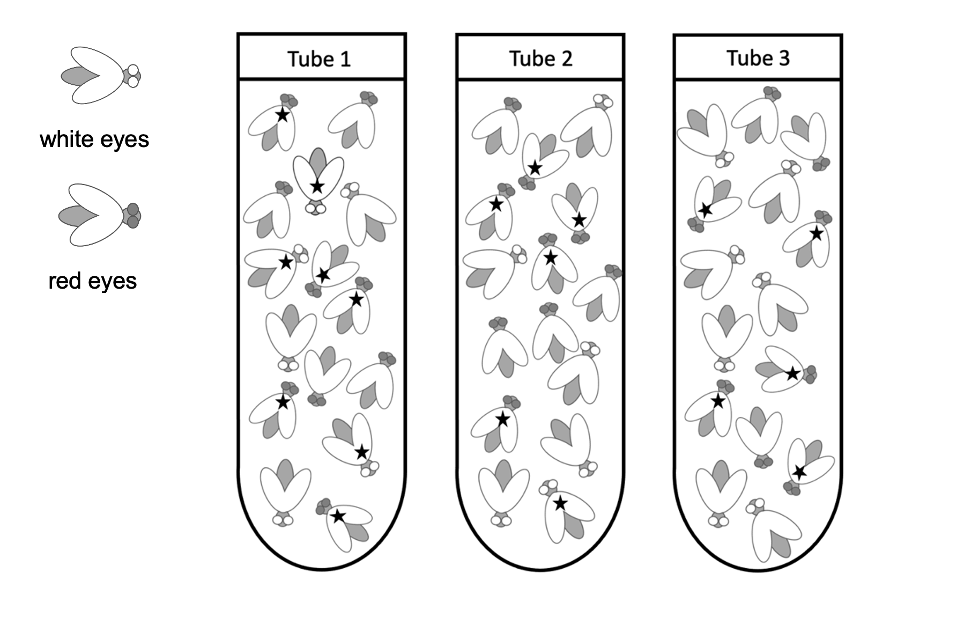
The conservation group must choose100 male and 100 female white spot groupers to start the captive breeding population.

1. What lengths of fish should be chosen for the captive population? Justify your choices. (5 marks)

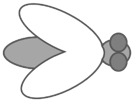
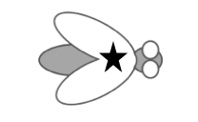
|  |  |
| --- | --- |
| **Description** | **Marks** |
| * At the lower end of the range 185 – 290 mm * To ensure there are females in the population for breeding * Before they change to males | 1-3 |
| * 311 – 500 mm * To ensure there are males in the population for breeding | 1-2 |
| **Total** | **5** |

**Question 32 (21 marks)**

The eye colour gene for fruit flies (*Drosophila melanogaster*), is located on the X chromosome. For this question assume males are XY and females are XX. Fruit flies can have white or red eyes. White (W) is recessive to red (W+). A class of biology students wanted to study the inheritance of eye colour in fruit flies. They ordered fruit flies and received the tubes shown below.



female



male

The following information came with the fruit flies.

|  |  |  |  |
| --- | --- | --- | --- |
| **Biological Supplies** | | | |
| Date: | 1 January 2023 | | |
| **Customer Information** | | | |
| School: | Western Australian College of Biology | | |
| Email: | wacb@education.com | | |
| Phone: | --------------------- | | |
| **Species:** | *Drosophila melanogaster* | | |
| **Tube** | **Number** | **Sex** | **Details** |
| **1** | 8 | Female | 4 homozygous red eyes, 1 heterozygous red, 3 white eyes |
| 7 | Male | 4 red eyes, 3 white eyes |
| **2** | 6 | Female | 1 white eyes, 2 homozygous red eyes,  3 heterozygous red eyes |
| 9 | Male | 4 red eyes, 5 white eyes |
| **3** | 5 | Female | 5 homozygous red eyes |
| 10 | Male | 7 white eyes, 3 red eyes |

* 1. Define the term allele frequency. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| How many times an allele at a particular gene/locus appears in a population | 1 |
| **Total** | **1** |

* 1. Use the table below to determine the number of W and W+ alleles in the fruit fly population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Tube** | **Sex** | **Number Of Individuals** | **Phenotype** | **Genotype** | **Number of Alleles** | |
| **W+** | **W** |
| **1** | Female | 1 | red eyes | W+W | 1 | 1 |
| 4 | red eyes | W+W+ | 8 | 0 |
| 3 | 3 white eyes | WW | 0 | 6 |
| Male | 4 | red eyes | W+ | 4 | 0 |
| 3 | white eyes | W | 0 | 3 |
| **2** | Female | 1 | white eyes | WW | 0 | 2 |
| 2 | red eyes | W+W+ | 4 | 0 |
| 3 | red eyes | W+W | 3 | 3 |
| Male | 4 | red eyes | W+ | 4 | 0 |
| 5 | white eyes | W | 0 | 5 |
| **3** | Female | 5 | red eyes | W+W+ | 10 | 0 |
| Male | 3 | red eyes | W+ | 3 | 0 |
| 7 | white eyes | W | 0 | 7 |
| **Totals** | | 45 |  |  | 37 | 27 |

(2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| How marks are awarded for the question   * Number of W alleles in population/gene pool for trait = 27 * Number of W+ alleles in population /gene pool for trait =37 | 1-2 |
| **Total** | **2** |

(c) Determine the allele frequencies, for the W and W+ alleles, for the population of fruit flies. Show your working and then write your final answer in the table below. (3 marks)

|  |  |
| --- | --- |
| Allele | Allele Frequency |
| W | 0.42 |
| W+ | 0.58 |

|  |  |
| --- | --- |
| **Description** | **Marks** |
| How marks are awarded for the question   * Total number of alleles in population /gene pool for trait = 64 * Allele frequency of W = 0.42 * Allele frequency of W+ = 0.58 | 1-3 |
| **Total** | **3** |

The tubes were left in a storage cupboard over the weekend. When the students returned to school, they found that all the fruit flies in tubes 2 and 3 had died.

(d) Determine the allele frequencies for the population of fruit flies that remain. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| 23 alleles remain | 1 |
| Allele frequency of W = 0.43  = 0.43) | 1 |
| Allele frequency of W+ = 0.57  = 0.57) | 1 |
| **Total** | **3** |

**For reference only**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Tube** | **Sex** | **Number Of Individuals** | **Phenotype** | **Genotype** | **Number of Alleles** | |
| **W+** | **W** |
| **1** | Female | 1 | red eyes | W+W | 1 | 1 |
| 4 | red eyes | W+W+ | 8 | 0 |
| 3 | 3 white eyes | WW | 0 | 6` |
| Male | 4 | red eyes | W+ | 4 | 0 |
| 3 | white eyes | W | 0 | 3 |
| **Totals** | | 15 |  |  | 13 | 10 |

The students’ thought, that this loss of individuals, modelled the evolutionary mechanism of genetic drift.

(e) State the type of genetic drift this event models. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Bottleneck effect | 1 |
| **Total** | **1** |

(f) Describe how genetic drift would affect a natural population of fruit flies. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any three of: | |
| * changes allele frequencies * changes are random or occur by chance * (causes) loss of diversity/alleles from a population * (causes) differences between populations | 1-3 |
| **Total** | **3** |

Many populations of fruit flies are located within flying distance from each other, this allows gene flow to occur between the populations.

(g) Explain how gene flow can change the allele frequencies in the gene pools of the fruit fly populations. (4 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any four of: | |
| * allele frequencies of fruit fly populations may be different from each other * (fruit flies migrating to new populations) must breed with the new population/ add their genes to the gene pool (of the destination population) * (this will) alter the allele frequency of the (destination) population * fruit flies (migrating) may have different alleles to the fruit flies in the destination population * thus they may introduce new alleles to the (destination) population * (due to gene flow) the allele frequencies of the fruit fly populations become more similar | 1-4 |
| **Total** | **4** |

Microevolutionary changes can be the result of mutation, genetic drift, gene flow and selection.

(h) State the two main types of selection. (1 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * natural and artificial | 1 |
| **Total** | **1** |

(i) Explain the concept of selection. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Selection   * organisms with particular genotypes * preferentially survive * and reproduce to pass on the particular genotype | 1-3 |
| **Total** | **3** |

**Question 33 (19 marks)**

Green sea turtles (Chelonia mydas) are found around the world in warm subtropical and tropical ocean waters. They come ashore to nest. In southern Queensland, nesting occurs between late November and January. Most females return to the same beach every nesting season. Scientists are concerned that global warming will affect the survival of the green sea turtles. One aspect that is being investigated is the effect of rising temperatures on population structure.

Scientists have been using artificial nests, at specific temperatures, to hatch green sea turtle eggs. The results of the investigation are shown below.

|  |  |  |  |
| --- | --- | --- | --- |
| Temperature of Nest (ºC) | No of Eggs | No of Male Hatchlings | Percentage Female Hatchlings (%) |
| 27.6 | 500 | 500 | 0 |
| 28.2 | 550 | 456 | 17 |
| 28.4 | 489 | 399 | 17 |
| 28.7 | 753 | 489 | 35 |
| 29.4 | 544 | 294 | 46 |
| 30.0 | 598 | 299 | 50 |
| 30.6 | 532 | 0 | 100 |

* 1. Propose an hypothesis for the investigation. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * relates independent and dependent variables * is testable | 1-2 |
| **Total** | **2** |

* 1. Calculate the percentage of female hatchlings per nest and add these calculations to the results table . (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Answers in table above   * At least three correct answers * At least six correct answers | 1-2 |
| **Total** | **2** |

* 1. State an assumption that you have made when calculating the percentage of female hatchlings for each nest temperature. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any **one** of: | |
| * all eggs in each nest hatched * sex of hatchlings could be determined * eggs that were not male were female | 1 |
| **Total** | **1** |

* 1. Construct a graph showing the percentage of female hatchlings for each nest temperature. (6 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Title - must include both variables | 1 |
| Line graph | 1 |
| Correct axes | 1 |
| Correct scale | 1 |
| Labelling - accurate labelling on both axes, including units | 1 |
| Plotting - data points accurate and accurately joined | 1 |
| **Total** | **6** |

Chart, line chart

Description automatically generated



* 1. Would increasing the number of eggs, in each nest, at each temperature, improve the reliability or validity of the results? Give two reasons for your answer. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * reliability | 1 |
| Any **two** of: | |
| * increased amount of data/evidence to support the conclusion * increases chances of representative sampling * reduces the influence of outliers | 1-2 |
| **Total** | **3** |

(f)     What could the results of the investigation suggest about sex determination in green

sea turtles?                                                           (5 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| ·     temperature affects sex of the hatchlings | 1 |
| ·     sex could be due to genotype and nest temperature  ·     resulting in sex reversal | 1-2 |
| ·     as sex could be due to temperature only  ·     so therefore there would be no sex chromosomes present | 1-2 |
| **OR** | |
| * Less than 30°C there is more chance of hatchling being male * 27.6°C there are no female hatchlings only males   *(or any other data supporting this statement)* | 1-2 |
| * Greater than 30°C more chance of hatchling being female * 30.6°C there are no male hatchlings only females * *(or any other data supporting this statement)* | 1-2 |
| * Sex determination is temperature dependent | 1 |
| **Total** | **5** |

**Question 34 (19 marks)**

During interphase of the cell cycle of eukaryotic cells, DNA replication takes place. This process is said to be semi-conservative.

1. In the space below, draw and label a diagram of the cell cycle. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Example |  |
| * diagram present * labels present * phases in correct order | 1-3 |
| **Total** | **3** |

1. Explain why some cells never enter the S phase of the cell cycle. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * some cells may enter G0 phase/cell “resting” phase * cells that have DNA damage do not get replicated. * apoptosis may occur * mutation that prevents DNA synthesis/replication | 1-2 |
| **Total** | **2** |

1. Explain what is meant by semi conservative DNA replication. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * every new DNA double helix molecule produced consists of one strand of the parent DNA and one strand of newly synthesised DNA. | 1 |
| **Total** | **1** |

During DNA replication, one strand is synthesized continuously, and the other strand is synthesised discontinuously.

(d)        Explain how both continuous and discontinuous replication of DNA occurs.     (4 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| ·         DNA polymerase only reads the template strand/works in the 5’ to 3’ direction **or**nucleotides are added at the 3’ end of the strand that is being synthesised  ·         DNA strands are antiparallel (therefore synthesis occurs in opposite directions  ·         therefore, DNA polymerase can work towards the replication fork for the leading strand creating a continuous strand  ·         but has to work backwards, away from the replication fork for the lagging strand which is discontinuous as short sequences of DNA are created (Okazaki fragments) | 1-4 |
| **Total** | **4** |

Part of the cell cycle is interphase. Interphase is when protein synthesis occurs. The processes of DNA replication and protein synthesis both require enzymes. Ligases are a group of enzymes required in both processes.

(e) State one similarity and one difference in the role of ligases in DNA replication and protein synthesis. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Difference   * joins RNA nucleotides in protein synthesis and joins DNA nucleotides in DNA replication   OR   * joins amino acids in protein synthesis and joins DNA nucleotides in DNA replication | 1 |
| Any **one** of: | |
| Similarity   * form chemical bonds/phosphodiester bonds between nucleotides * joins monomers into polymers | 1 |
| **Total** | **2** |

Similarities between biological molecules across different organisms can be evidence of evolution. DNA is one such molecule. All organisms have the same basic DNA.

(f) Explain how organisms having the same basic DNA, suggests that there is a common origin for all life on earth. (3 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * As DNA/genes code for organism | 1 |
| Any **one** of: | |
| * all organisms have DNA with the same basic structure * DNA codes for the same (20) amino acids across all organisms | 1 |
| * DNA is passed onto offspring (over generations and time) therefore all organisms have a common origin (as they have the same basic DNA structure) | 1 |
| **Total** | **3** |

(g) Explain how comparing DNA between species is evidence for the theory of evolution. (4 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any **four** of: | |
| * DNA is used in protein synthesis/DNA has the same process for gene expression * the DNA codes for the same (20) amino acids across organisms * comparing DNA sequences/proteins for the same gene in different species * the more similar the DNA sequence /amino acid sequence in a protein * the more closely related the organism/species are * the more recent the common ancestor | 1-4 |
| **Total** | **4** |

**Question 35 (21 marks)**

A new herbicide resistant crop, ‘GTC’, was genetically engineered to be glyphosate tolerant. ‘GTC’ plants are transgenic plants with recombinant DNA.

1. Define the term ‘recombinant DNA’. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * DNA from two species that are combined and placed/in an organism | 1 |
| **Total** | **1** |

1. Explain a possible adverse effect, that the farmer may encounter, when growing a ‘GTC’ crop. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * These plants could pollinate to other parts of the farm/non GM crops/ other plants * herbicide resistant weeds/plants cannot be killed using glyphosate | 1-2 |
| **Total** | **2** |

1. Explain possible adverse effects on non-target species when ‘GTC’ crop is grown. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any **two** of: | |
| * Leading to evolution of glyphosate herbicide resistant weeds/ non-target species * Potential for the glyphosate herbicide resistance gene to spread to other species. * Create a superweeds that are resistant to glyphosate herbicides | 1-2 |
| **Total** | **2** |

Having had success using the ‘GTC’ crop, the same farmer decided to plant another transgenic crop. The farm had recently had an invasion of grasshoppers, so the farmer planted a crop of ‘GRO’, that was genetically engineered to be pesticide resistant. Once the crop was planted, the field was sprayed with pesticide, to kill the grasshoppers. As the crop grew, the field was sprayed with pesticide every 4 weeks. Initially, the farmer noticed a significant decrease in the number of grasshoppers, in and around the crop. However, over time, the grasshopper population increased. The farmer continued to spray the ‘GRO’ crops with pesticide but found that the grasshopper population still continued to increase.

1. Suggest a reason for the increase in grasshoppers, after there had been a significant decrease in the grasshopper population. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| the grasshoppers had developed /evolved pesticide resistance | 1 |
| **Total** | **1** |

1. Name the evolutionary mechanism that allowed the grasshopper population to survive and increase, after being sprayed with pesticide. (1 mark)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Natural selection  **Note**: Adaptation is not considered an evolutionary mechanism | 1 |
| **Total** | **1** |

1. Explain how the grasshopper population was able to survive and increase, after being sprayed with pesticide. (6 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Variation   * Genetic variation with the grasshopper population   **or**   * mutation for pesticide resistance in the grasshopper population | 1 |
| Struggle   * competition for survival * with the selection pressure being the pesticide | 1-2 |
| Selection   * grasshoppers without the pesticide resistant gene die off * grasshoppers with the pesticide resistant gene survive and reproduce * and the pesticide resistant gene is passed on to offspring | 1-3 |
| **Total** | **6** |

Prior to the development of biotechnology that has allowed transgenic crops to be created, crops were artificially selected to have characteristics such as increased protein and increased yield.

1. Explain the impact ‘artificial selection’ has on the genetics of the crops. (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| * Crop is monogenic/decreased genetic diversity of the crop * Gradual change in allele frequencies of the crops overtime | 1-2 |
| **Total** | **2** |

1. State two similarities between ‘artificial selection’ and the genetic engineering of transgenic organisms . (2 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any **two** of: | |
| * both alter the genetic composition of individuals * both reduce genetic variation * both require human intervention | 1-2 |
| **Total** | **2** |

1. Describe four differences between ‘artificial selection’ and the genetic engineering of transgenic organisms . (4 marks)

|  |  |  |
| --- | --- | --- |
| **Description** | | **Marks** |
| Artificial Selection | Genetic Engineering for Transgenic Organisms |  |
| Any **four** of: (*must have both for 1 mark*) | | |
| slower process | quicker/fast process | 1-4 |
| specialist equipment required | specialist equipment required |
| changes genes/alleles frequency in target organisms | changes genes/alleles frequency in target organisms and from the donor organism/species |
| natural process/environmentally friendly | artificial/unnatural/environmentally threatening process |
| affects most of the genome | affects one gene |
| No foreign/donor DNA inserted into DNA | Foreign/donor DNA inserted into DNA |
| **Total** | | **4** |

**Section Three: Extended answer 20% (40 marks)**

**Part A**

**Question 36 (20 marks)**

1. Describe chromosomal mutations, gene mutations resulting in frame shift and gene mutations that do not result in frame shift and explain their impact on gene expression.

|  |  |
| --- | --- |
| Description | Marks |
| A mutation is a spontaneous, permeant change in the DNA structure/base sequence. | 1 |
| Any **two** of: | |
| Chromosomal mutation   * mutations that change the chromosome structure * only affect gene expression if they occur in coding DNA/exons * (if affected) different proteins would be produced * due to the change in base sequence and/or codons | 1-2 |
| Any **two** of: | |
| * Duplications – part of chromosome is copied, resulting in duplicate sections * Deletions – a portion of the chromosome is removed * Inversions – a segment of a chromosome is removed and then replaced within the chromosome in reverse order * Translocations – segments of two chromosomes are exchanged Translocation | 1-2 |
| Gene mutation   * mutation that occurs within the coding sequence of a gene | 1 |
| Any **three** of: | |
| Gene mutation resulting in frame shift   * a deletion or insertion of one or more nucleotides in a gene * the rest of the sequence is unchanged, these insertions/deletions change the reading frame (and thus all of the codons that follow) * resulting in different amino acids being coded for * resulting in a different protein being expressed | 1-2 |
| Any **two** of: | |
| Gene mutation that do not result in frame shift   * substitution of one base (point mutation) * only the codon where the substitution occurred is altered * resulting in a different amino being coded for * the rest of the sequence is unchanged | 1-2 |
| **Total** | **10** |

1. Compare mitosis and meiosis. (10 marks)

|  |  |  |
| --- | --- | --- |
| **Description** | | **Marks** |
| Differences | | |
| Any **six** of: (*must have both for 1 mark*) | | |
| Mitosis | Meiosis |  |
| Produces somatic cells | Produces gametes | 1 - 6 |
| 1 diploid (2n) cell produces 2 diploid cells | 1 diploid (2n) cell produces 4 haploid (n) cells |
| Daughter cells are clones/genetically identical to parent cell | Daughter cells are not clones/genetically identical to parent cell |
| No crossing over occurs | Crossing over between homologous chromosomes occurs during metaphase I |
| 1 cellular division | 2 cellular divisions |
| Chromosomes align in single file along the cells equator during metaphase | Pairs of homologous chromosomes align along the cells equator in metaphase 1 |
| Identical sister chromatids are pulled apart in anaphase | Homologous chromosomes are pulled apart in anaphase I  or  Non-identical sister chromatids are pulled apart in anaphase II |
| Any **four** of: | | |
| Similarities | | |
| * both forms of cell division/replication/nuclear division * both require centrioles and spindles for chromosome division/splitting * both have cytokinesis where the cell membrane furrows and cleaves * both have the same stages of prophase, metaphase, anaphase, telophase and cytokinesis * both processes begin with a diploid parent cell (2n) * have interphase where DNA replication occurs | | 1-4 |
| **Total** | | **10** |

**Question 37 (20 marks)**

Convergent evolution is when two species evolve similar features for the same function, but do not have a common ancestor. Convergent evolution results in analogous structures. Wings of birds and bats are analogous structures. The wings of birds and bats perform the same function, however, they have different evolutionary origins. Divergent evolution leads to different species having homologous structures.

1. Using a named example explain why the pentadactyl limb structure is considered a homologous structure and why it is considered evidence for divergent evolution.

(10 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Homologous structures   * similar physical features/structures in different organisms that serve completely different functions and are derived from common ancestry | 1 |
| Any **two** of: | | |
| Pentadactyl limb   * found in vertebrate tetrapods/4 legged animals * the same basic limb plan/bone structure across species/taxa * includes a labelled diagram of a pentadactyl limb **or** describes pentadactyl limb structure (e.g., limb that has one bone, then 2 bones, then group of bones joining limb to five digits ) | 1-2 |
| Any **three** of: | | |
| Evidence for evolution   * explanations for evolution/cladistics are based on the simplest explanation * (the simplest explanation) the basic limb plan/bone structure of pentadactyl limbs in many species/taxa is that the structure evolved once (in evolutionary history) * therefore, suggesting common ancestry for species/taxa with pentadactyl limbs * it is unlikely that the pentadactyl limb structure evolved more than once/in several species/taxa independently (due to its complexity) | 1-3 |
| Any **two** of: | | |
| Evidence for Divergent evolution   * the basic structure is “modified”/has evolved in response to the environment (in which the species/taxa live) * resulting in different locomotive functions across species/taxa * thus, suggesting divergent evolution | 1-2 |
| Named Example   * explains how the pentadactyl limb of each named example is modified/evolved * relates modified/evolved structure to environment | 1-2 |
| *Example 1*   * *Kangaroos have well developed toes (and some reduced toes) to hop* * *to cover larger distances in a vast open environment*   *Example 2*   * *Blue whales have shorter thicker limb bones (humerus, radius, ulna) and modified digits to form a flipper that acts as robust paddle in the water* | |
| **Total** | **10** |

1. Explain how phenotypes are the result of genotypes. (10 marks)

|  |  |
| --- | --- |
| Description | Marks |
| Any **one** of | |
| Genetic Code   * DNA contains the genes which code for traits * in the form of base sequences which code for proteins | 1 |
| Any **one** of | |
| Genotype   * different alleles result in different protein being expressed * the interaction of alleles results in different protein/amount of protein being expressed | 1 |
| Transcription   * The genes are transcribed from DNA into RNA in the nucleus * mRNA has the base sequence that is complementary to the DNA/mRNA carries the DNA/genetic code | 1-2 |
| Any **one** of | |
| * introns are removed from mRNA * as they are non-coding/do not code for proteins | 1 |
| Any **three** of | |
| Translation   * mRNA attaches to a ribosome/s * each tRNA molecule brings a specific amino acid to the ribosome * the amino acid is specified by its anticodon * the appropriate amino acid is moved into place * more amino acids are added resulting in a protein | 1-3 |
| Any **two** of | |
| Proteins   * proteins released from the ribosomes undergo folding to become functional proteins * many different proteins work together * resulting in specific phenotypes | 1-2 |
| **Total** | **10** |

**Part B**

**Question 38 (20 marks)**

Atrazine is one of the most widely used herbicides in Australian agriculture. It that is used both before and after the emergence of grass and weeds in crops such as sugarcane, lupins and eucalypt plantations. The broad use of this herbicide has resulted in significant pollution of Australian waterways.

Scientists have genetically engineered bacteria to break down atrazine pollution in the soil, thus preventing it reaching and polluting waterways. The gene atzA, found in the *Pseudomonas* bacteria, produces the enzyme, atrazine chlorohydrolase, that breaks down atrazine. Scientists inserted the gene atzA, found in *Pseudomonas*, into *Escherichia coli*  bacteria.

1. Explain the process, that scientists would use, to create transgenic *Escherichia coli*  containing the gene atzA. (10 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Any **ten** of: | |
| * *Pseudomonas* treated with chemical to causes lysis (plasmid released) * Plasmid collected * Restriction enzyme used to cut at recognition sites (around gene atzA) * gene atzA isolated * *Escherichia coli* treated with chemical to causes lysis (plasmid released) * Plasmid collected * Using the same restriction enzyme (that was used to cut the *Pseudomonas plasmid),* cut the *Escherichia coli*  at a recognition site to open the plasmid * Insert antibiotic resistance gene also * Insert gene atzA (from *Pseudomonas)* into *Escherichia coli*  using ligase to join the DNA * Insert antibiotic resistance gene also * Heat shock *Escherichia coli* to take up the recombinant plasmid * Culture transgenic *Escherichia coli* in the presence of antibiotics * Transgenic *Escherichia coli* replicate via binary fission * Only *Escherichia* coli containing the antibiotic resistance gene will survive * Thus, selecting for the transgenic *Escherichia coli* | 1 - 10 |
| **Total** | **10** |

1. Compare the inheritance patterns of complete dominance, co-dominance, incomplete dominance in terms of the genotypes, phenotypes, allele interactions and phenotypic and genotypic ratios (for generation P, F1 and F2). (10 marks)

|  |  |
| --- | --- |
| **Marking guide for possible comparisons** | |
| compares dominant to co-dominant | 1 mark |
| compares dominant to incomplete dominance | 1 mark |
| compares incomplete dominance to co-dominance | 1 mark |
| OR |  |
| compares incomplete dominance to co-dominance to complete dominance. | 3 marks |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Must have 1 mark from each of the 5 categories below | **Description** | | | **Marks** |
| Differences | | | Maximum of 7 marks |
| Dominance | Co-dominance | Incomplete dominance |  |
| Allele interactions | Both alleles come together, only the dominant allele is expressed | Both alleles come together and are expressed as a hybrid**.** | Both alleles come together to contribute equally to an intermediate trait | 1-3 |
| A heterozygote will not result in the formation of a new phenotype | A heterozygote will not result in the formation of a new phenotype | A heterozygote will always result in a new phenotype | 1-2 |
| Possible phenotypes | 2 possible phenotypes | 2 possible phenotypes | 3 possible phenotypes | 1-2 |
| Phenotypes in F1 | Only one parents phenotype is expressed in their offspring | both parents phenotypes are expressed together in their offspring | both parents phenotypes blend together to create a new phenotype in their offspring | 1-3 |
| Phenotypic ratio in F1 | All dominant phenotype | All co-dominant phenotype | All incomplete dominant phenotype | 1-3 |
| Phenotypic ratio in F2 | 3 :1  dominant : recessive | 1:2:1  allele 1 : codominant: allele 2 | 1:2:1  allele 1 : incomplete dominant: allele 2 | 1-2 |
| Any **three** of: | | | | |
| Similarities | | | | |
| One from each of the following  In both incomplete dominance and codominance   * neither allele is dominant nor recessive. * both alleles are expressed * only for monogenic traits * phenotypic ratio is 1:2:1, in the F2 generation. * a heterozygote will not result in the formation of a new phenotype   In both dominance and codominance   * both parents phenotypes are expressed together in their offspring * 2 possible phenotypes   In incomplete dominance, codominance and dominance   * phenotype is a result of the interaction of 2 alleles | | | | 1 - 3 |
| **Total** | | | | **10** |

**Question 39 (20 marks)**

Perth Zoo is involved in the conservation of the critically endangered Sumatran Orangutan. As part of the Australasian breeding program, they have successfully breed over 25 Orangutans. Part of the program is the release of some animals into the protected Bukit Tigapuluh ecosystem in Sumatra, Indonesia.

1. Explain how DNA biotechnology could be used in the monitoring of Sumatran Orangutans, the breeding program and the reintroduction of animals into Sumatra, Indonesia.

|  |  |
| --- | --- |
| **Description** | **Marks** |
| DNA profiling could be used to   * determine the genetic diversity of the gene pool of the wild orangutan population * to see the relatedness between individual orangutans in the wild * determine the genetic diversity of the gene pool of captive orangutan populations * to selectively breed individuals to maintain genetic diversity in the captive breeding program * to minimise inbreeding in the breeding program * construct accurate pedigrees to improve the effectiveness of the breeding program * to determine which animals should be released into the wild population * thus, maintaining genetic diversity (and hopefully increase) in the wild population   Could use eDNA from droppings to   * monitor the location and distribution of the orangutans * determine range boundaries of populations and understanding the barriers to gene flow * may lead to humans providing more effective strategies to conserve orangutan populations * to identify other animals (that also live in the same ecosystem) that may be a threat to the orangutans. * then allow management of predators/threats * e.g., baiting, limiting access to where humans reside * The genetic information and DNA profiles could be stored on a data base (bioinformatics) for future use. | 1-10 |
| *any other reasonable correct answer* | |
| **Total** | **10** |

Phylogenetic trees can be constructed using a variety of information. With the emergence of bioinformatics, they are now mostly constructed from the comparison of DNA or proteins. The table below, shows sequences of DNA, form five different species.

Table 1: Homologous Chromosomes Sequences Compared Across Five Species

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** | **15** | **16** | **17** | **18** | **19** | **20** |
| **A** | T | G | A | C | G | G | C | T | A | G | C | G | T | T | G | C | A | T | C | G |
| **B** | T | G | A | C | G | G | C | A | A | G | C | G | T | T | G | C | A | T | C | G |
| **C** | T | G | A | C | G | C | C | T | T | C | C | C | T | T | G | C | T | T | C | G |
| **D** | T | G | A | C | C | G | C | T | A | G | C | G | A | T | G | C | A | A | C | G |
| **E** | T | G | T | C | G | G | C | - | A | G | C | G | T | T | G | C | A | T | C | G |

1. Using the DNA sequences provided, construct a phylogenetic tree **and** explain how you constructed the tree from the information given. (10 marks)

|  |  |
| --- | --- |
| **Description** | **Marks** |
| Phylogenetic trees are diagrams used to show the relatedness between organisms. | 1 |
| Any three of: | |
| Explains how to compare base sequences   * Compare the sequences, to see how similar/different they are to each other * Choose one species as a “base line”/as a comparison/ States baseline species (e.g., species A) * Note: the answers given will vary, depending on the baseline species the student chooses. * Using the “base line” species count the number of differences between each species and the “base line” species * States/shows the number of base differences between the baseline species and all other species   Note: The table below is an example of how a table may be used in the explanation. This is not an answer for the question, as the student chooses the baseline species from species A, B, C, D, E.  e.g., Table: Number of Base Differences Compared to Species 1   |  |  | | --- | --- | | Species | Number of Base Differences | | 1 | 0 | | 2 | 1 | | 3 | 3 | | 4 | 5 | | 5 | 1 or 2 | | 1-3 |
| Any two of: | |
| Explains how to construct the tree   * Start phylogenetic tree with a backbone or root * Place baseline species on the backbone * The next species placed on the tree will have the smallest number of differences from the baseline species * The species are then in order from: the least number of differences from the baseline species to the greatest number of differences from the base line species | 1-2 |
| * Phylogenetic tree diagram present   Note: the phylogenetic tree will vary, depending on the baseline species the student chose.  e.g.  Diagram  Description automatically generated | 1 |
| Any two of: | |
| Diagram of phylogenetic tree has   * correct order of species shown * all branch tips end on the same line * tips labelled with species name | 1-2 |
| Any one of: | |
| Assumptions made when constructing the phylogenetic tree   * The more similar the DNA sequences, the more closely related the species are * There are many ways in which organisms can be related, the simplest way is most likely to be correct | 1 |
| **Total** | **10** |

**For reference only**

Comparisons of DNA Sequences for Five Species

Compared to Species One Species

**Text, table

Description automatically generated**