

## 9.1 – EVOLUTION

- A4.1.1** Evolution as change in the heritable characteristics of a population
- A4.1.2** Evidence for evolution from base sequences in DNA or RNA and amino acid sequences
- A4.1.3** Evidence for evolution from selective breeding of domesticated animals and crop plants
- A4.1.4** Evidence for evolution from homologous structures
- A4.1.5** Convergent evolution as the origin of analogous structures
- A4.1.6** Speciation by splitting of pre-existing species
- A4.1.7** Role of reproductive isolation and differential selection in speciation

### EVOLUTIONARY THEORY

*Define evolution*

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*Outline how Darwinian evolution differs from Lamarckism*

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### SELECTIVE BREEDING

*Describe how selective breeding provides evidence for evolution, including animal and crop examples*

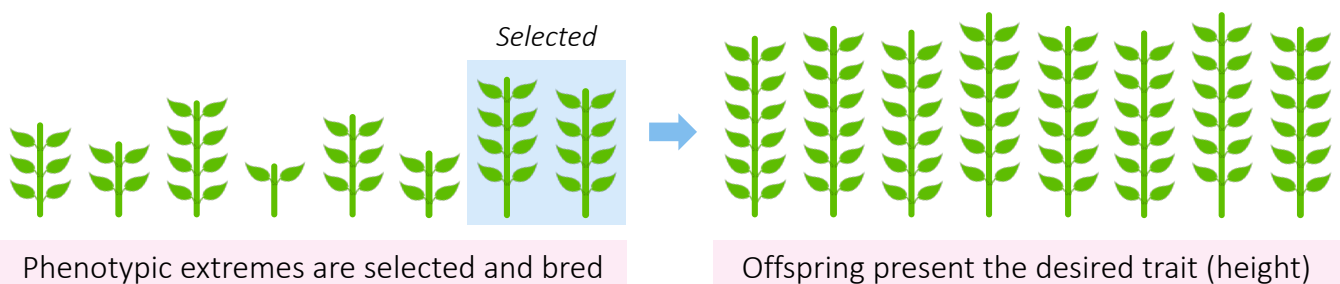
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## STRUCTURAL EVIDENCE

*Distinguish between homologous and analogous structures*

|                    | HOMOLOGOUS STRUCTURES | ANALOGOUS STRUCTURES |
|--------------------|-----------------------|----------------------|
| Definition         |                       |                      |
| Type of Evolution  |                       |                      |
| Ancestry           |                       |                      |
| Selection Pressure |                       |                      |
| Example            |                       |                      |

*Outline how the pentadactyl limb provides evidence for evolution*

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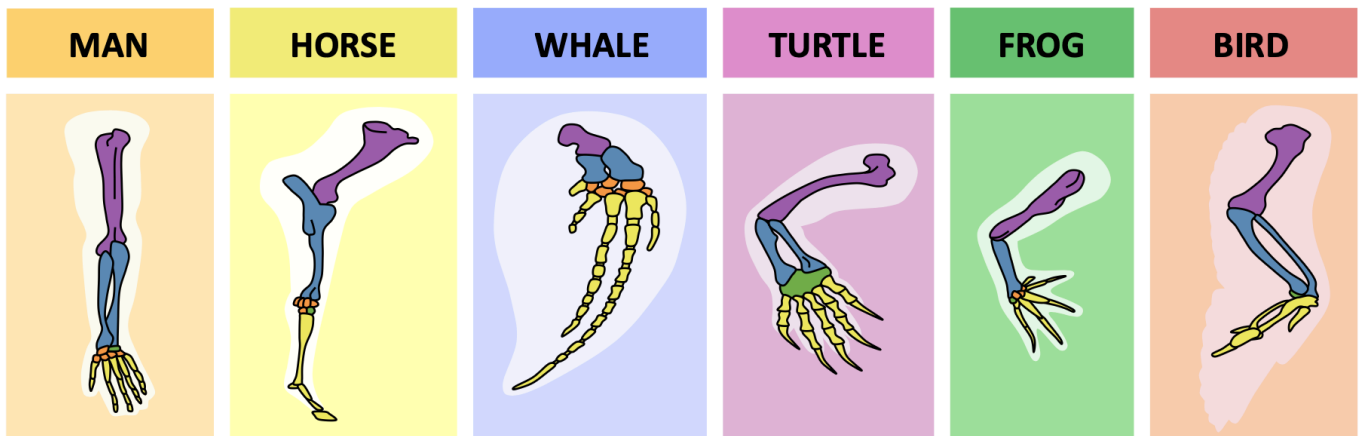
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## MOLECULAR EVIDENCE

*Explain how molecular sequences can be used to provide evidence for evolution*

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## SPECIATION

*Distinguish between gradual evolutionary change and speciation*

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*Describe the process of speciation in terms of reproductive isolation and genetic divergence*

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*Outline the divergence of bonobos and chimpanzees as a specific example of speciation*

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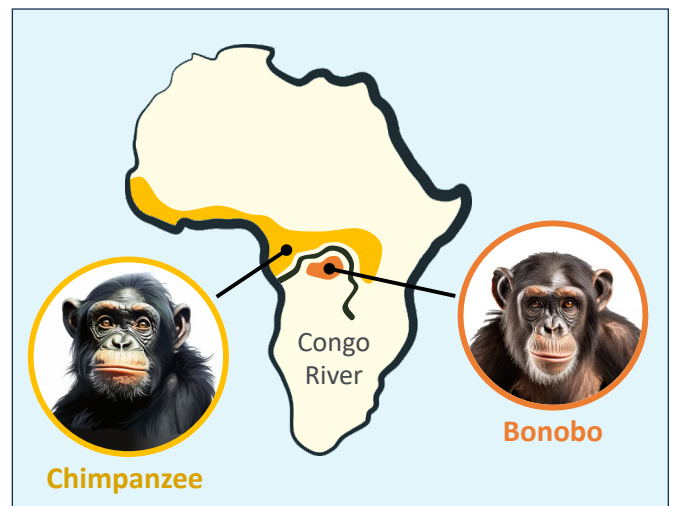
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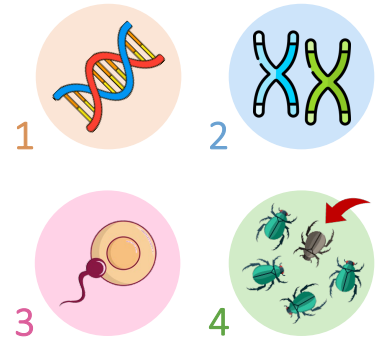
## 9.2 – NATURAL SELECTION

- D4.1.1 Natural selection as the mechanism driving evolutionary change
- D4.1.2 Roles of mutation and sexual reproduction in generating the variation for natural selection
- D4.1.3 Offspring overproduction and competition for resources as factors promoting natural selection
- D4.1.4 Abiotic factors as selection pressures
- D4.1.5 Differences between individuals in adaptation, survival and reproduction as the basis for natural selection
- D4.1.6 Requirement that traits are heritable for evolutionary change to occur
- D4.1.7 Sexual selection as a selection pressure in animal species
- D4.1.8 Modelling of sexual and natural selection based on experimental control of selection pressures

### GENETIC VARIATION

List four potential sources of genetic variation within a population

1. \_\_\_\_\_
2. \_\_\_\_\_
3. \_\_\_\_\_
4. \_\_\_\_\_



### NATURAL SELECTION

Describe the process of natural selection

**Include:** Variation, competition, selection pressure, adaptation, allele frequency

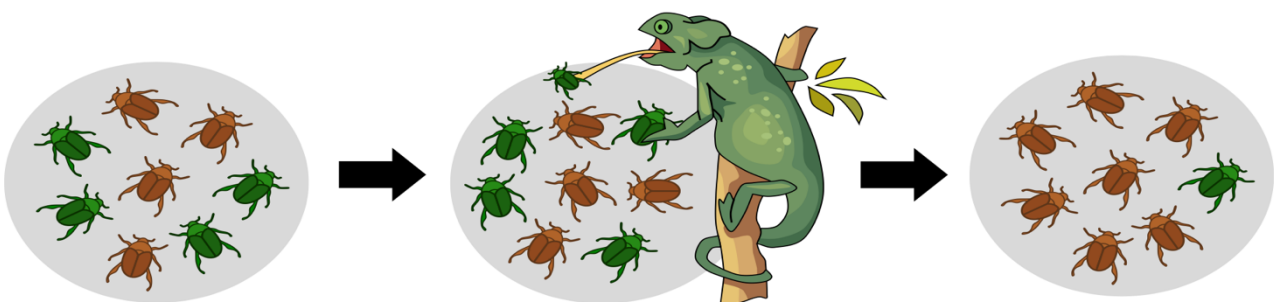
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## ENVIRONMENTAL SELECTION

*Differentiate between abiotic factors and biotic factors*

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*Identify specific examples of environmental selection pressures*

### Density-Dependent

- P \_\_\_\_\_
- A \_\_\_\_\_
- N \_\_\_\_\_
- D \_\_\_\_\_
- A \_\_\_\_\_

### Density-Independent

- P \_\_\_\_\_
- A \_\_\_\_\_
- W \_\_\_\_\_



## SEXUAL SELECTION

*Explain how sexual selection differs from natural selection, using birds of paradise as a specific example*

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*Outline the results of John Endler's experiments on sexual and natural selection (using guppies)*

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## 9.3 – CLASSIFICATION

- A3.1.1** Variation between organisms as a defining feature of life
- A3.1.2** Species as groups of organisms with shared traits
- A3.1.3** Binomial system for naming organisms
- A3.1.4** Biological species concept
- A3.1.5** Difficulties distinguishing populations and species due to divergence of non-interbreeding populations during speciation
- A3.1.6** Diversity in chromosome numbers of plants and animal species
- A3.1.7** Karyotyping and karyograms
- A3.1.8** Unity and diversity of genomes within species
- A3.1.9** Diversity of eukaryotic genomes
- A3.1.10** Comparison of genome sizes
- A3.1.11** Current and potential future uses of whole genome sequencing

### SPECIES

*Distinguish between the morphological and biological concepts of species*

Morphological: \_\_\_\_\_

Biological: \_\_\_\_\_

*Identify the limitations associated with the use of each concept in the classification of a species*

**Morphological:**

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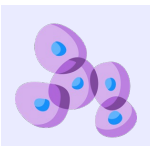
**Biological:**

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**DOMAIN**



**KINGDOM**



**PHYLUM**



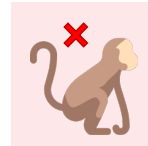
**CLASS**



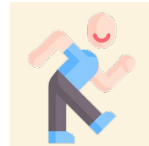
**ORDER**



**FAMILY**



**GENUS**



**SPECIES**



**Note:** Species is the final grouping in the traditional hierarchy of taxa (smallest and most specific group)

## BINOMIAL NOMENCLATURE

*Outline the binomial system of nomenclature*

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*Gorilla gorilla*

## CHROMOSOMES

*Identify the distinguishing features of a linear chromosome*

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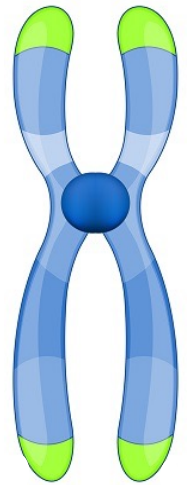
*Explain why chromosome number is a characteristic feature of a species*

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## KARYOGRAMS

*Outline information that can be discerned from a karyogram*

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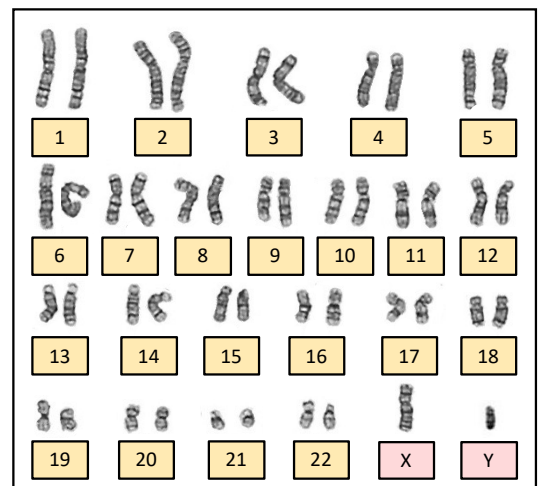
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*Describe the process of karyotyping*

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*List evidence suggesting human chromosome 2 arose from chromosome 12 and 13 in a primate ancestor*

1. \_\_\_\_\_
2. \_\_\_\_\_
3. \_\_\_\_\_

## GENOMES

*Define genome*

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*Outline how single nucleotide polymorphisms create diversity within the genomes of a species*

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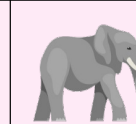




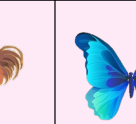


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*Using data, evaluate the hypothesis that genome size and organism complexity are positively correlated*

|                | <br>HUMAN | <br>LUNGFISH | <br>ELEPHANT | <br>GUINEA PIG | <br>EAGLE | <br>BEAR | <br>CHICKEN | <br>BUTTERFLY |
|----------------|--|---|---|---|--|--|--|--|
| DIPLOID NUMBER | 46   | 54  | 56  | 64  | 66   | 74   | 78   | 448  |
| GENOME SIZE    | 3.2 Gb   | 43 Gb   | 3.3 Gb  | 3.4 Gb  | 1.2 Gb   | 2.5 Gb   | 1.2 Gb   | 0.5 Gb   |

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## WHOLE GENOME SEQUENCING

*State two current uses and two potential future applications of whole genome sequencing*

**Current Uses:**

1. \_\_\_\_\_
2. \_\_\_\_\_

**Future Applications:**

1. \_\_\_\_\_
2. \_\_\_\_\_

## 9.4 – EXTINCTION

- A4.2.1** Biodiversity as the variety of life in all its forms, levels and combinations
- A4.2.2** Comparisons between current number of species on Earth and past levels of biodiversity
- A4.2.3** Causes of anthropogenic species extinction
- A4.2.4** Causes of ecosystem loss
- A4.2.5** Evidence for a biodiversity crisis
- A4.2.6** Causes of the current biodiversity crisis
- A4.2.7** Need for several approaches to conservation of biodiversity
- A4.2.8** Selection of evolutionarily distinct and globally endangered species for conservation prioritisation in the EDGE of Existence programme

### BIODIVERSITY

*Differentiate between the different types of biodiversity*

|                     |  |
|---------------------|--|
| Genetic Diversity   |  |
| Species Diversity   |  |
| Ecosystem Diversity |  |

*Compare the number of current species on Earth and past levels of biodiversity*

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*Define extinction*

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*Define mass extinction and outline the underlying cause of the current sixth mass extinction*

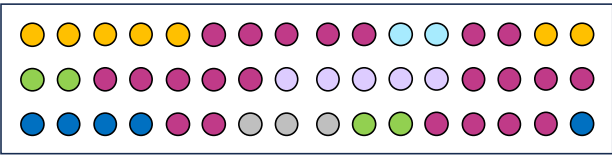
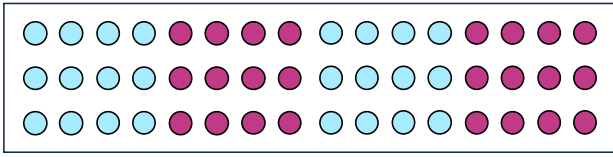
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## ASSESSING BIODIVERSITY

*Differentiate between species richness and species evenness*

| SPECIES RICHNESS   | SPECIES EVENNESS  |
|--|---|
|  <p style="text-align: center; margin-top: 10px;"><b>High richness (low evenness)</b></p> |  <p style="text-align: center; margin-top: 10px;"><b>High evenness (low richness)</b></p> |

**Note:** Ecosystem stability requires high richness and evenness to resist environmental change

*Use the Simpson's reciprocal index to compare the biodiversity of two different regions*

|                         |  |
|-------------------------|--|
| <p><b>Equation:</b></p> | <div style="background-color: #e8f5e9; padding: 5px; margin-bottom: 10px;"> <b>Site 1:</b> A = 7 ; B = 5 ; C = 2 ; D = 3         </div> <div style="background-color: #e1bee7; padding: 5px;"> <b>Site 2:</b> A = 3 ; D = 9 ; E = 4 ; F = 1         </div> |
|-------------------------|--|

| Species      | n | n (n – 1) |
|--------------|---|-----------|
| A            | 7 |           |
| B            | 5 |           |
| C            | 2 |           |
| D            | 3 |           |
| <b>Total</b> |   |           |

| Species      | n | n (n – 1) |
|--------------|---|-----------|
| A            | 3 |           |
| D            | 9 |           |
| E            | 4 |           |
| F            | 1 |           |
| <b>Total</b> |   |           |

**Solution:**

**Solution:**

*Outline what the Simpson's reciprocal index shows concerning the state of an ecosystem*

High Index: \_\_\_\_\_

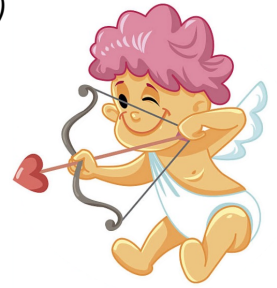
Low Index: \_\_\_\_\_

## HUMAN PRESSURES

Identify consequences of human population growth on biodiversity (HINT: O! Cupid)

- O \_\_\_\_\_
- C \_\_\_\_\_
- U \_\_\_\_\_

- P \_\_\_\_\_
- I \_\_\_\_\_
- D \_\_\_\_\_



## ECOSYSTEM LOSS

Describe two examples of ecosystem loss

**Mixed Dipterocarp Forests:**

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**Great Barrier Reef:**




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## EXTINCTION

Outline three examples of anthropogenic species extinction

| North Island Giant Moa  | Caribbean Monk Seal   | Tasmanian Tiger   |
|---|---|---|
|  |  |  |

## CONSERVATION

Define conservation and distinguish between *in situ* and *ex situ* conservation

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In situ: \_\_\_\_\_

Ex situ: \_\_\_\_\_

Describe the advantages of *in situ* conservation versus *ex situ* conservation

| <i>In situ</i> Conservation | <i>Ex situ</i> Conservation |
|-----------------------------|-----------------------------|
| <br><br><br><br><br>        | <br><br><br><br><br>        |

List three specific examples of each type of conservation

**In situ:**

1. \_\_\_\_\_

2. \_\_\_\_\_

3. \_\_\_\_\_

**Ex situ:**

1. \_\_\_\_\_

2. \_\_\_\_\_

3. \_\_\_\_\_

Outline the function of the EDGE of Existence programme

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List the two criteria used to select species for conservation prioritisation

1. \_\_\_\_\_

2. \_\_\_\_\_



## 9.5 – SPECIATION (AHL)

- A4.1.8** Differences and similarities between sympatric and allopatric speciation
- A4.1.9** Adaptive radiation as a source of biodiversity
- A4.1.10** Barriers to hybridisation and sterility of interspecific hybrids as mechanisms for preventing the mixing of alleles between species
- A4.1.11** Abrupt speciation in plants by hybridisation and polyploidy
- A4.1.12** Difficulties applying the biological species concept to asexually reproducing species and to bacteria that have horizontal gene transfer
- A4.1.13** Chromosome number as a shared trait within a species
- A4.1.14** Engagement with local plant or animal species to develop a dichotomous key
- A4.1.15** Identification of species from environmental DNA in a habitat using barcodes

### ADAPTIVE RADIATION

*Outline how adaptive radiation acts as a source of biodiversity*

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### ISOLATION BARRIERS

*Describe the different types of isolation barriers that prevent the mixing of alleles between species*

Pre-Zygotic Barriers:

|             |  |
|-------------|--|
| Geographic  |  |
| Behavioural |  |
| Temporal    |  |

Post-Zygotic Barriers:

|                    |  |
|--------------------|--|
| Hybrid Inviability |  |
| Hybrid Infertility |  |

## TYPES OF SPECIATION

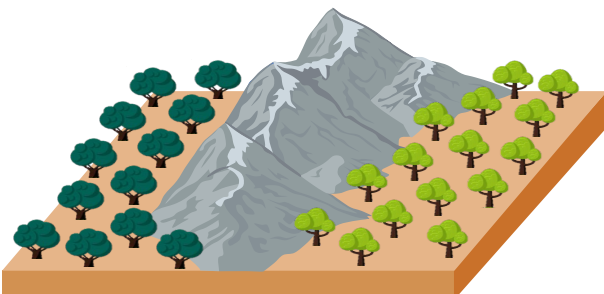
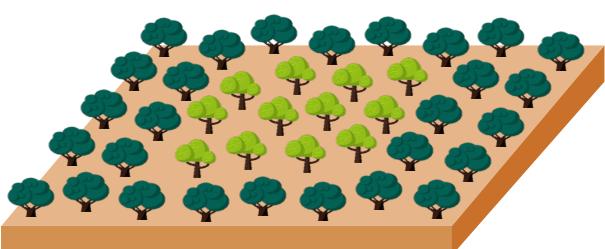
*Compare and contrast allopatric and sympatric speciation*

**Similarities:**

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**Differences:**

| Allopatric Speciation  | Sympatric Speciation  |
|--|---|
|  A 3D illustration showing a mountain range in the center. On the left side of the mountain, there is a cluster of dark green trees. On the right side, there is a cluster of light green trees. The ground is brown, and the sky is white. |  A 3D illustration showing a flat, brown ground surface. In the center, there is a cluster of light green trees. To the left and right of this cluster, there are clusters of dark green trees. The sky is white. |

## POLYPLOIDY

*Explain how polyploidy can lead to abrupt speciation (using knotweed as an example)*

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*Distinguish between allopolyploidy and autopolyploidy*

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## SPECIES IDENTIFICATION

*Explain why chromosome number is a shared trait within a sexually reproducing species*

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*Describe the difficulty in applying the biological species concept to asexually reproducing species*

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## DICHOTOMOUS KEYS

*Construct a dichotomous key using the organisms included below (native Australian wildlife)*



## DNA BARCODING

*Describe the use of environmental DNA to identify species via barcoding*

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## 9.6 – GENE POOLS (AHL)

- D4.1.9** Concept of the gene pool
- D4.1.10** Allele frequencies of geographically isolated populations
- D4.1.11** Changes in allele frequency in the gene pool as a consequence of natural selection between individuals according to differences in their heritable traits
- D4.1.12** Differences between directional, disruptive and stabilising selection
- D4.1.13** Hardy-Weinberg equation and calculations of allele or genotype frequencies
- D4.1.14** Hardy-Weinberg conditions that must be maintained for a population to be in equilibrium
- D4.1.15** Artificial selection by deliberate choice of traits

### GENE POOLS

*Define gene pool*

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*Describe evolution in the context of gene pools*

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### ALLELE FREQUENCY

*Summarise the different mechanisms by which allele frequencies may change*

**Natural Selection:**

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**Sexual Selection:**

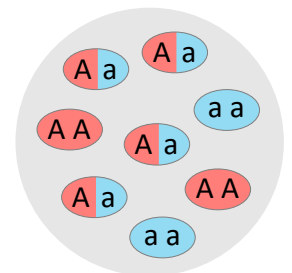
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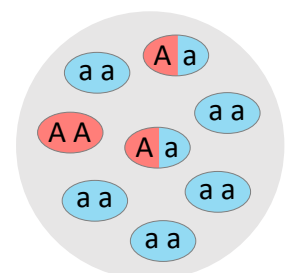
**Artificial Selection:**

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**Generation 1**  
 $A = 0.5, a = 0.5$



**Generation 10**  
 $A = 0.25, a = 0.75$

## TYPES OF SELECTION

Differentiate between directional, stabilising and disruptive selection (including specific example of each)

**Directional:** \_\_\_\_\_

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**Stabilising:** \_\_\_\_\_

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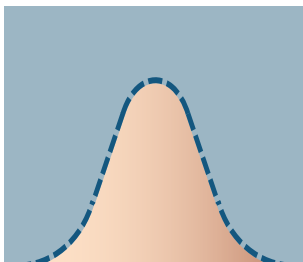
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**Disruptive:** \_\_\_\_\_

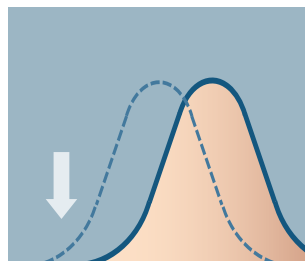
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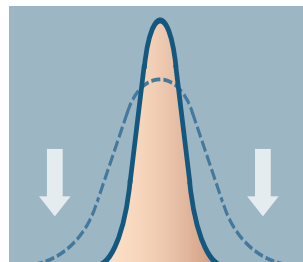
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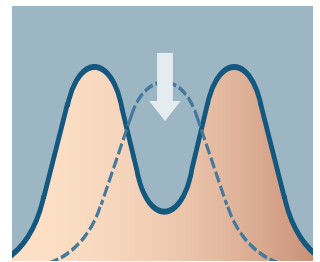
**NORMAL**



**DIRECTIONAL**



**STABILISING**



**DISRUPTIVE**

## HARDY-WEINBERG

State the Hardy-Weinberg equations

**Equation 1:**

**Equation 2:**

Determine the number of individuals with each of the genotypes:

**Let:** B = black fur (dominant)

**Let:** b = white fur (recessive)



BB: \_\_\_\_\_ Bb: \_\_\_\_\_ bb: \_\_\_\_\_

375 black

125 white

State the Hardy-Weinberg conditions required for a population to maintain genetic equilibrium

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## 9.7 – CLADISTICS (AHL)

- A3.2.1** Need for classification of organisms
- A3.2.2** Difficulties classifying organisms into the traditional hierarchy of taxa
- A3.2.3** Advantages of classification corresponding to evolutionary relationships
- A3.2.4** Clades as groups of organisms with common ancestry and shared characteristics
- A3.2.5** Gradual accumulation of sequence differences as the basis for estimates of when clades diverged from a common ancestor
- A3.2.6** Base sequences of genes or amino acid sequences of proteins as the basis for cladograms
- A3.2.7** Analysing cladograms
- A3.2.8** Using cladistics to investigate whether the classification of groups corresponds to evolutionary relationships
- A3.2.9** Classification of all organisms into three domains using evidence from rRNA base sequences

### CLASSIFICATION SCHEMES

*Explain the need for the classification of living organisms*

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### DOMAINS OF LIFE

*Identify the evidence used to initially establish the three domains of life*

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*Compare the three domains of life (by ticking the appropriate boxes)*

|                                       | Bacteria | Archaea | Eukarya |
|---------------------------------------|----------|---------|---------|
| Has a nucleus                         |          |         |         |
| Membrane-bound organelles present     |          |         |         |
| Has a cell wall made of peptidoglycan |          |         |         |
| DNA packaged by histone proteins      |          |         |         |
| Found in extreme environments         |          |         |         |

## HIERARCHY OF TAXA

Outline the limitations associated with classifying according to a hierarchy of taxa

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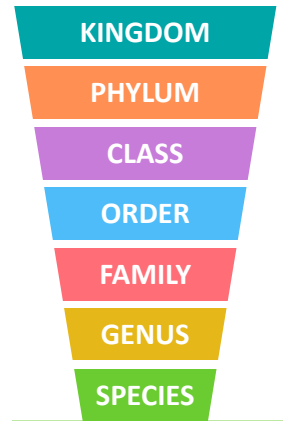
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## MOLECULAR PHYLOGENY

Explain how biochemical evidence can be used to show evolutionary relationship

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Describe the use of a 'molecular clock' to estimate the timing of evolutionary divergence

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Identify two examples of taxonomic reclassification based on molecular evidence

1. \_\_\_\_\_
2. \_\_\_\_\_

## CLADISTICS

Define clade

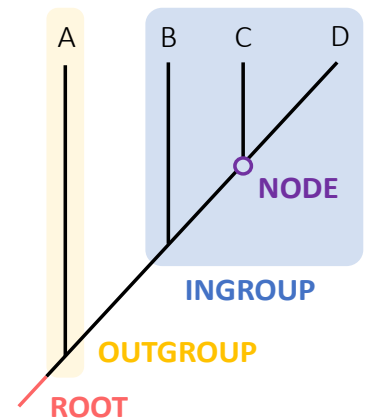
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Explain the function of the outgroup in a cladogram

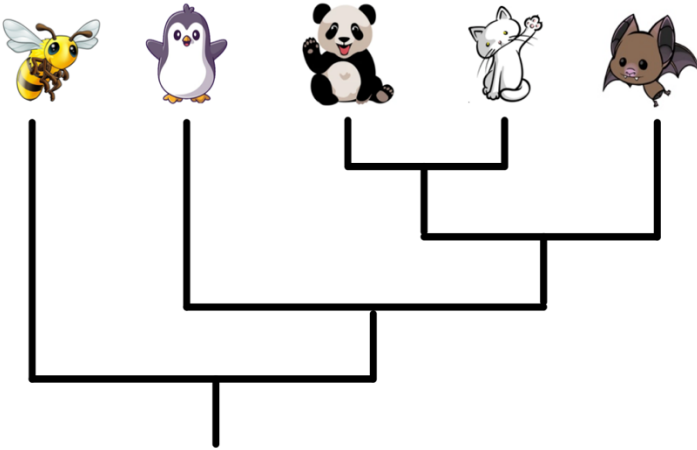
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## CLADOGRAMS

Describe the evolutionary relationships that can be determined from the following cladogram




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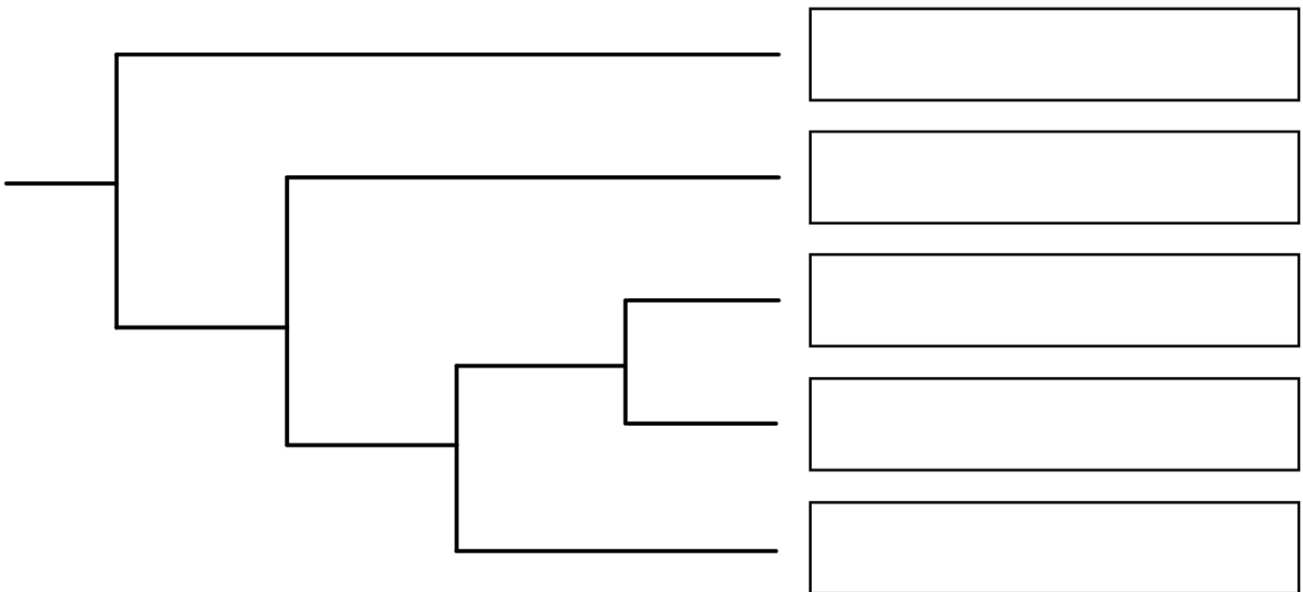
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Use the protein sequence alignment to construct an appropriate cladogram via parsimony analysis

| human   | F | S | V | H | P | L | V | R | R | L | D | A | F | Q | % Homology |
|---------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|------------|
| mouse   | F | S | V | H | P | L | V | R | R | L | N | A | P | Q | 86         |
| pig     | F | S | I | A | P | L | V | R | R | L | D | A | P | Q | 79         |
| dog     | F | S | V | H | P | L | V | R | R | L | D | A | L | Q | 93         |
| chicken | F | T | I | Q | P | L | V | R | R | L | N | A | P | Q | 57         |
| frog    | F | A | I | P | P | M | V | H | R | L | D | S | R | Q | 50         |



Suggest why molecular evidence is preferred when assigning organisms to clades

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