

A3.1 Diversity of organisms

Unity and diversity—Organisms

Standard level and higher level: 3 hours

Additional higher level: 2 hours

Guiding questions

- What is a species?
- What patterns are seen in the diversity of genomes within and between species?

SL and HL

A3.1.1—Variation between organisms as a defining feature of life

Students should understand that no two individuals are identical in all their traits. The patterns of variation are complex and are the basis for naming and classifying organisms.

- **Variation** is the differences in traits between living organisms
- **Genetic** and **environmental factors** interact together to determine variation, so no two individuals are identical in all their traits (even monozygotic twins)
 - This results in complex patterns of variation/diversity that are used by scientists for naming and classifying organisms based on similarities and differences in certain traits
 - The specific traits used to classify organisms have changed with time; paradigm shifts within the field of biology have led to different systems of classification
 - These traits can be morphological, physiological, molecular (i.e. DNA), behavioral, or ecological

A3.1.2—Species as groups of organisms with shared traits

This is the original morphological concept of the species as used by Linnaeus.

- The **morphological species concept** classifies organisms based on shared physical traits
 - Under this concept, species are groups of organisms that have more structural similarities than to members of other groups
- **Benefits:** It is useful when classifying extinct, fossilized, or asexual species
- **Limitations:**
 - There is an element of subjectivity in determining the extent to which certain morphological features of a group of organisms are sufficiently distinct to warrant their classification as a separate species
 - Intraspecies variation due to sex (e.g. sexual dimorphism) & age can complicate classification

A3.1.3—Binomial system for naming organisms

Students should know that the first part of the name identifies the genus, with the second part of the name distinguishing the species. Species in the same genus have similar traits. The genus name is given an initial capital letter but the species name is lowercase.

- The **binomial system** for naming organisms identifies species using a **two-part** scientific name
 - The first name identifies the **genus** & begins with a capital letter
 - Species in the same genus have similar morphological or phylogenetic traits
 - The second name identifies the **species name** & is written in lowercase
- Species names must be shown in italics when typed or underlined when handwritten

A3.1.4—Biological species concept

According to the biological species concept, a species is a group of organisms that can breed and produce fertile offspring. Include possible challenges associated with this definition of a species and that competing species definitions exist.

- The **Biological Species Concept (BSC)** defines species as a group of actually or potentially interbreeding populations that can breed and produce fertile offspring
- **Benefits:** useful when classifying sexually reproducing organisms
- **Limitations:** makes it challenging to classify extinct, fossilized, or asexual organisms
- Many other different definitions of species exist; one or several definitions can be used at once depending on the nature of the organism & the research goals

A3.1.5—Difficulties distinguishing between populations and species due to divergence of non-interbreeding populations during speciation

Students should understand that speciation is the splitting of one species into two or more. It usually happens gradually rather than by a single act, with populations becoming more and more different in their traits. It can therefore be an arbitrary decision whether two populations are regarded as the same or different species.

- Reproductively isolated (non-interbreeding) populations accumulate differences in their traits with time, which can prompt scientists to reclassify the populations into different species
- Since evolutionary divergence is a continuous process, the decision whether two populations are regarded as the same or different species can be arbitrary & dependent on the species concept used
 - Modern taxonomists often integrate information about an organism's genome, morphology, phylogeny & other traits to classify species

A3.1.6—Diversity in chromosome numbers of plant and animal species

Students should know in general that diversity exists. As an example, students should know that humans have 46 chromosomes and chimpanzees have 48. Students are not required to know other specific chromosome numbers but should appreciate that diploid cells have an even number of chromosomes.

- A **chromosome** is a DNA molecule associated with proteins
- Different species usually but not always have different chromosome numbers
- **Diploid** cells have two sets of chromosomes (thus an even number), one inherited from each parent
 - For example, humans have 46 chromosomes and chimpanzees have 48 (both diploid)
- **Haploid** cells only have one set of chromosomes (thus an odd number)

A3.1.7—Karyotyping and karyograms

Application of skills: Students should be able to classify chromosomes by banding patterns, length and centromere position. Students should evaluate the evidence for the hypothesis that chromosome 2 in humans arose from the fusion of chromosomes 12 and 13 with a shared primate ancestor.

- A **karyotype** describes chromosome characteristics of a species (number, shape, size, centromere position, banding pattern)
- A **karyogram** is a visual photograph or diagram showing the karyotype (with chromosomes arranged in an appropriate order, e.g. by size)
- **Karyotyping** is a laboratory test that is used to examine the karyotype of species
 - A cell sample is taken from the organism's body & cultured in the lab
 - Cell division is halted during metaphase using a chemical because chromosomes are condensed & visible under a light microscope
 - The cells are treated with a hypotonic solution that causes them to burst in order to spread the chromosomes apart to make them easier to sort
 - A stain is applied that binds to DNA to reveal distinct banding patterns for different chromosomes
 - Images of the chromosomes are taken, which are then digitally sorted to form a karyogram that is ordered by homologous pairs (i.e. from longest to shortest)
- Humans have 46 chromosomes but all other great apes have 48 chromosomes; there is evidence to suggest that chromosome 2 in humans arose from the fusion of chromosomes 12 & 13 in a shared primate ancestor:
 - **Telomere sequences**, which are normally found on the edges of chromosomes, exist near the center of human chromosome 2 (consistent with end-to-end fusion)
 - **Banding patterns** of human chromosome 2 match the combined banding pattern of chimpanzee chromosomes 12 & 13
 - Remnants of a second **vestigial (inactive) centromere** exist (since the fusion of 2 chromosomes would initially produce 2 centromeres)

NOS: Students should be able to distinguish between testable hypotheses such as the origin of chromosome 2 and non-testable statements.

- A **testable statement** makes claims that can be evaluated by experiments
 - For example, the origin of human chromosome 2 is a hypothesis that can be tested using evidence from DNA sequencing & karyotyping
- A **non-testable statement** makes claims that cannot be evaluated by experiments
 - For example, subjective topics like “cats make better pets than dogs” are not testable
 - While non-testable, such statements can still be valid (e.g. opinions are non-testable but valid)

A3.1.8—Unity and diversity of genomes within species

Students should understand that the genome is all the genetic information of an organism. Organisms in the same species share most of their genome but variations such as single-nucleotide polymorphisms give some diversity.

- The **genome** is all the genetic information of an organism, which includes:
 - Coding & non-coding regions
 - Non-nuclear genetic material (e.g. mitochondrial DNA, chloroplast DNA, plasmids)
- Organisms in the same species share most of their genome, but variations like **single-nucleotide polymorphisms (SNPs)** create some genetic diversity to enable evolution

A3.1.9—Diversity of eukaryote genomes

Genomes vary in overall size, which is determined by the total amount of DNA. Genomes also vary in base sequence. Variation between species is much larger than variation within a species.

- **Genomes size** (total amount of DNA) varies between species
- **Base sequence** (order of nucleotides in DNA) variation exists within and between species
- Variation between species is much larger than variation within a species

A3.1.10—Comparison of genome sizes

Application of skills: Students should extract information about genome size for different taxonomic groups from a database to compare genome size to organism complexity.

- Genome size is **NOT** an indicator of how complex an organism is (some small eukaryotes have larger genomes than bigger eukaryotes)

A3.1.11—Current and potential future uses of whole genome sequencing

Include the increasing speed and decreasing costs. For current uses, include research into evolutionary relationships and for potential future uses, include personalized medicine.

- **Whole genome sequencing (WGS)** is a laboratory process that determines the complete DNA sequence of an organism's genome
- WGS technology was initially expensive and slow but competition between different biotech companies caused increasing WGS speed & decreasing costs
- WGS is currently used to research phylogenetic relationships and for potential future uses, including **personalized medicine** (an approach to healthcare that tailors treatment to the patient's genetic profile)

Additional higher level

A3.1.12—Difficulties applying the biological species concept to asexually reproducing species and to bacteria that have horizontal gene transfer

The biological species concept does not work well with groups of organisms that do not breed sexually or where genes can be transferred from one species to another.

- The biological species concept is difficult to apply to:
 - Asexually reproducing species because such organisms do not interbreed
 - Bacteria that carry out horizontal gene transfer because genes can be transferred from one species to another (thus making it difficult to identify common ancestors & classify species)

A3.1.13—Chromosome number as a shared trait within a species

Cross-breeding between closely related species is unlikely to produce fertile offspring if parent chromosome numbers are different.

- All individuals within a species have the same chromosome number
- A **hybrid** organism is the result of **crossbreeding** (mating of individuals from different species)
- If two closely related species crossbreed, they are unlikely to produce fertile offspring if parent chromosome numbers are different
 - This is because some chromosomes would not exist within a homologous pair due to mismatched chromosome number, which disrupts segregation during meiosis & leads to inviable gametes
 - Other reasons for hybrid sterility exist, like physiological incompatibility

A3.1.14—Engagement with local plant or animal species to develop a dichotomous key

Application of skills: Students should engage with local plant or animal species to develop a dichotomous key.

- A **dichotomous key** is a tool used to identify organisms based on morphological traits
- To develop a dichotomous key:
 - Choose a group of organisms & record their observable traits
 - Identify a characteristic that divides all organisms within the group into 2 groups
 - Continue subdividing each group until every organism can be uniquely identified using the key
 - Write 2 opposing or mutually exclusive sentences for each observable trait so that an organism can only match one of them (e.g. "(1) trait present (2) trait absent")

A3.1.15—Identification of species from environmental DNA in a habitat using barcodes

Using barcodes and environmental DNA allows the biodiversity of habitats to be investigated rapidly.

- **DNA barcoding** is a method of identifying species using a **DNA barcode**; a short section of DNA from a specific gene
 - DNA barcodes are conserved enough to be easily located and amplified across many species, but variable enough to identify different species
 - Since it is difficult to find a DNA barcode with these characteristics for all organisms, different DNA barcodes are used for different groups of organisms
- **Environmental DNA** is genetic material collected from an environmental sample like water, soil, & air
 - The genetic material can be amplified by PCR & sequenced, then researchers can use DNA barcodes to quickly identify the species within the sample
 - This allows biodiversity of habitats to be investigated rapidly, with little habitat disturbance, and enables identification of rare species at low abundance in the area of study

Linking questions

- What might cause a species to persist or go extinct?
- How do species exemplify both continuous and discontinuous patterns of variation?

Review questions

SL and HL

- Distinguish between DNA sequencing and whole genome sequencing. [1]
- Define whole genome sequencing. [1]
- Distinguish variation in genome size from variation in base sequence. [1]
- Explain the challenges associated with classifying two diverging populations as different species. [3]
- Describe how the binomial system is used to name organisms. [3]
- Outline the current and potential future uses for whole genome sequencing. [4]
- Discuss evidence for the human chromosome 2 fusion hypothesis. [4]
- Describe how a karyogram is produced. [5]
- Discuss how genomes demonstrate both unity and diversity within and between species. [8]

Additional Higher Level

- Define environmental DNA. [1]
- Discuss the limitations of the biological species concept. [2]
- Explain why crossbreeding often results in sterile offspring. [3]
- Describe how a dichotomous key would be developed for a sample of 6 organisms. [4]
- Explain how DNA barcoding can be used in biodiversity studies. [5]

References

Aldhebiani AY. Species concept and speciation. Saudi J Biol Sci. 2018;25(3):437-440. doi:10.1016/j.sjbs.2017.04.013

Ann Clark, Mary, et al. *Biology 2e*. E-book, OpenStax, 2018, <https://openstax.org/books/biology-2e/pages/1-introduction>. OpenStax.

Campos PB, Sartore RC, Abdalla SN, Rehen SK. Chromosomal spread preparation of human embryonic stem cells for karyotyping. J Vis Exp. 2009;(31):1512. Published 2009 Sep 4. doi:10.3791/1512

Gordon Betts, J., et al. *Anatomy and Physiology 2e*. E-book, OpenStax, 2022, <https://openstax.org/books/anatomy-and-physiology-2e/pages/1-introduction>. OpenStax.

Kress WJ, Erickson DL. DNA barcodes: genes, genomics, and bioinformatics. Proc Natl Acad Sci U S A. 2008;105(8):2761-2762. doi:10.1073/pnas.0800476105

van Belkum A, Struelens M, de Visser A, Verbrugh H, Tibayrenc M. Role of genomic typing in taxonomy, evolutionary genetics, and microbial epidemiology. Clin Microbiol Rev. 2001;14(3):547-560. doi:10.1128/CMR.14.3.547-560.2001