

A3.2 Classification and cladistics

Unity and diversity—Organisms

Additional higher level: 3 hours

Guiding questions

- What tools are used to classify organisms into taxonomic groups?
- How do cladistic methods differ from traditional taxonomic methods?

Additional higher level

Note: There is no SL content in A3.2.

A3.2.1—Need for classification of organisms

Classification is needed because of the immense diversity of species. After classification is completed, a broad range of further study is facilitated.

- **Classification** of organisms is needed because of the immense diversity of species
 - Classification involves grouping organisms based on shared traits and evolutionary origins
 - It is vital because it helps organize information about species, reveals relationships between them, enables clear scientific communication, & facilitates a broad range of further studies

A3.2.2—Difficulties classifying organisms into the traditional hierarchy of taxa

The traditional hierarchy of kingdom, phylum, class, order, family, genus and species does not always correspond to patterns of divergence generated by evolution.

- Organisms have been historically classified into hierarchal **taxa** (categories)
 - Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species
 - Do KeeP Pond Clean Or Frog Gets Sick
- There are difficulties associated with traditional classification:
 - Evolution is a gradual process but the traditional hierarchy of taxa forces organisms into fixed groups that may not accurately represent how the patterns of biodiversity were produced
 - The taxa are arbitrarily created by humans & there are no biological guidelines for deciding how much evolutionary divergence is needed to create a new taxon
 - Different traits are used to classify organisms, which leads to differences of opinion between the scientific community

NOS: A fixed ranking of taxa (kingdom, phylum and so on) is arbitrary because it does not reflect the gradation of variation. Cladistics offers an alternative approach to classification using unranked clades. This is an example of the paradigm shift that sometimes occurs in scientific theories.

- A fixed ranking of taxa (kingdom, phylum and so on) is arbitrary because it does not reflect the gradation of variation
- Cladistics offers an alternative approach to classification using unranked clades, serving as a paradigm shift in **taxonomy** (the science of classifying organisms)

A3.2.3—Advantages of classification corresponding to evolutionary relationships

The ideal classification follows evolutionary relationships, so all the members of a taxonomic group have evolved from a common ancestor. Characteristics of organisms within such a group can be predicted because they are shared within a clade.

- The ideal classification follows evolutionary relationships, so all the members of a taxonomic group have evolved from a common ancestor
- There are advantages to classifying organisms based on evolutionary relationships instead of traits
 - It **reduces the arbitrariness** of choosing which trait is most important for classifying organisms & instead provides **one consistent organizing principle** for classification: grouping organisms according to their positions in the branching history of life
 - This does not eliminate judgement, because some factors (e.g. hybridization, horizontal gene transfer) make it more difficult to understand common ancestry, but it enhances objectivity
 - It helps scientists **explain** similarities between organisms rather than merely identify them
 - **Predictions** can be made about the characteristics of organisms within shared groups
 - It directly reflects the process of evolution that produces biodiversity

A3.2.4—Clades as groups of organisms with common ancestry and shared characteristics

The most objective evidence for placing organisms in the same clade comes from base sequences of genes or amino acid sequences of proteins. Morphological traits can be used to assign organisms to clades.

- A **clade** is a group of organisms containing **one common ancestor & all of its descendants**
 - The size of a clade can be large or small, depending on the common ancestor of interest
- **DNA/RNA or amino acid sequences** are the most objective evidence used for placing organisms in the same clade because they provide large amounts of heritable, measurable, & comparable info
 - Organisms with **fewer** sequence differences share a **more recent** common ancestor
 - Organisms with **more** sequence difference share a **more distant** common ancestor
- Other types of evidence, including morphological traits, can be used to assign organisms to clades
 - For example, morphology can be used to establish evolutionary relationships through homologous & analogous traits

A3.2.5—Gradual accumulation of sequence differences as the basis for estimates of when clades diverged from a common ancestor

This method of estimating times is known as the “molecular clock”. The molecular clock can only give estimates because mutation rates are affected by the length of the generation time, the size of a population, the intensity of selective pressure and other factors.

- After two populations diverge from a common ancestor, their lineages independently accumulate mutations in their DNA/RNA or amino acid sequences
 - The number of sequence differences increase with time & can be used to estimate when clades diverged from a common ancestor (this method of estimation is known as the **molecular clock**)
- The molecular clock assumes that mutation rates are constant, which is not true because mutation rates are affected by many factors:
 - **Generation time:** the average age of parents when their offspring are born
 - **Shorter** generation times (e.g. bacteria reproduce every few minutes) **increase** mutation rates
 - **Longer** generation times (e.g. humans reproduce in their 20s-30s) **decrease** mutation rates
 - **Population size:** affects how the frequency of the mutation changes with time
 - Small population sizes increase the probability of changes in mutation frequency
 - **Intensity of selection pressure:** depending on whether the mutation is beneficial, harmful, or neutral, selection pressures may increase, decrease, or maintain the frequency of the mutation
 - Thus, selection pressures affect the probability that a mutation will remain in a lineage & contribute to sequence differences between populations

A3.2.6—Base sequences of genes or amino acid sequences of proteins as the basis for constructing cladograms

Examples can be simple and based on sample data to illustrate the tool.

- **Cladistics** classifies organisms based on evolutionary relationships
- **Cladograms** are diagrams used to represent a hypothesis about evolutionary relationships
- DNA/RNA or amino acid sequences of proteins are the basis for constructing cladograms
 - Scientists first identify the number of sequence differences in a gene or protein found in all organisms of interest, then they group organisms with the fewest differences most closely
- Cladograms depict evidence-based hypotheses about evolutionary relationships, so new evidence may support, modify or reject the proposed relationship

NOS: Students should recognize that different criteria for judgement can lead to different hypotheses. Here, parsimony analysis is used to select the most probable cladogram, in which observed sequence variation between clades is accounted for with the smallest number of sequence changes.

- **Parsimony analysis** is a logical method that seeks the simplest complete explanation of scientific data
 - In cladistics, this means selecting the cladogram that accounts for the observed sequence variation using the smallest total number of evolutionary changes
- Parsimony does not imply choosing an inadequate but simple explanation, it means choosing the most complete explanation, given all the data, with the fewest assumptions
- However, parsimony analysis in cladistics is still falsifiable due to factors that complicate ancestral relationships, like convergent evolution

A3.2.7—Analysing cladograms

Students should be able to deduce evolutionary relationships, common ancestors and clades from a cladogram. They should understand the terms “root”, “node” and “terminal branch” and also that a node represents a hypothetical common ancestor.

- Parts of a cladogram:
 - **Root:** the base of the diagram which represents the most recent common ancestor of all organisms within the cladogram
 - Movement from the root towards terminal branches represents evolutionary divergence with time
 - **Node:** a branching point from which 2 lineages diverge (represents a hypothetical common ancestor)
 - **Branch:** represents an evolutionary lineage
 - A **terminal branch** is the end of a branch that represents the taxon (species or clade)

A3.2.8—Using cladistics to investigate whether the classification of groups corresponds to evolutionary relationships

A case study of transfer of plant species between families could be used to develop understanding, for example the reclassification of the figwort family (*Scrophulariaceae*). However, students are not required to memorize the details of the case study.

Note: When students are referring to organisms in an examination, either the common name or the scientific name is acceptable.

- Cladistics is used to investigate whether the traditional hierarchal classification corresponds to evolutionary relationships
 - For example, cladistics was used to investigate the phylogeny of plants in the figwort family (*Scrophulariaceae*) & it showed that the plants in the family are of different common ancestry (i.e. belong to different clades)
 - This led to the reclassification of some of the plants into other families

NOS: Students should appreciate that theories and other scientific knowledge claims may eventually be falsified. In this example, similarities in morphology due to convergent evolution rather than common ancestry suggested a classification that by cladistics has been shown to be false.

- Similarities in morphology due to convergent evolution rather than common ancestry suggested historical classifications that have now been falsified by cladistics

A3.2.9—Classification of all organisms into three domains using evidence from rRNA base sequences

This is the revolutionary reclassification with an extra taxonomic level above kingdoms that was proposed in 1977.

- Organisms were traditionally grouped into 2 categories: prokaryotes & eukaryotes
- Base sequences of **ribosomal RNA (rRNA)** showed that prokaryotes are composed of 2 distinct lineages, which led to the reclassification of organisms into a **new taxonomic level (domain)**
 - In 1977, scientists proposed 3 domains (eukaryotes, eubacteria, archaea) which are now widely accepted by the scientific community

Linking questions

- How can similarities between distantly related organisms be explained?
- What are some examples of ideas over which biologists disagree?

Review questions

- Define cladistics. [1]
- State **two** factors that affect mutation rates. [2]
- Outline the need to classify organisms. [2]
- Using **one** example, explain how cladistics has been used to falsify previous scientific knowledge. [2]
- Explain the difficulties of classifying organisms into the traditional hierarchy of taxa. [3]
- Describe the development of domains as a new taxonomic level. [3]
- Explain the advantages of classification corresponding to evolutionary relationships. [3]
- Outline how cladistic methods differ from traditional taxonomic methods. [3]
- Explain why cladistics was a paradigm shift in taxonomy. [5]
- Describe how scientists classify organisms into clades. [6]
- Evaluate the use of molecular clocks in estimating divergence from a common ancestor. [7]
- Describe how scientists develop cladograms to classify organisms. [8]

References

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