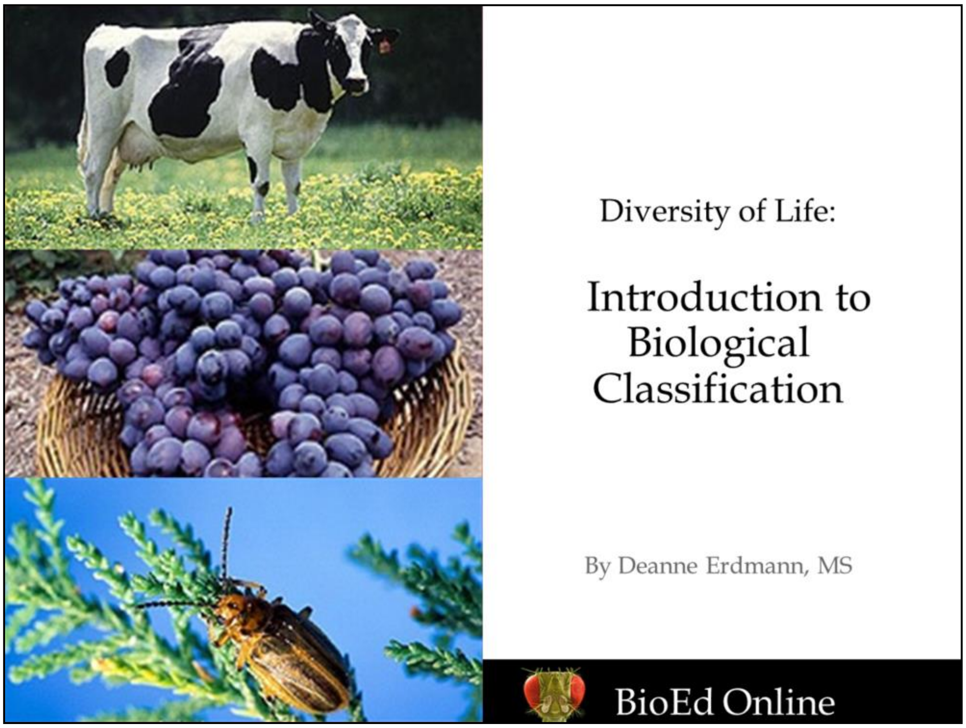

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Why Do We Classify Organisms?

To understand how and why organisms function the way they do, and how they interact with one another, we must observe patterns in development and evolution. Think about the scope of the Life Science Content Standards: understanding the cell; molecular basis of heredity; biological evolution; interdependence of organisms, matter, and energy; organization in living systems; and behavior of organisms. Classification is a scientific approach to grouping organisms based on current knowledge gathered from all of these fields.

It is more important to understand how and why classification systems are organized than to memorize each individual level. Classification systems encompass a wide, dynamic body of knowledge that is being modified continually.

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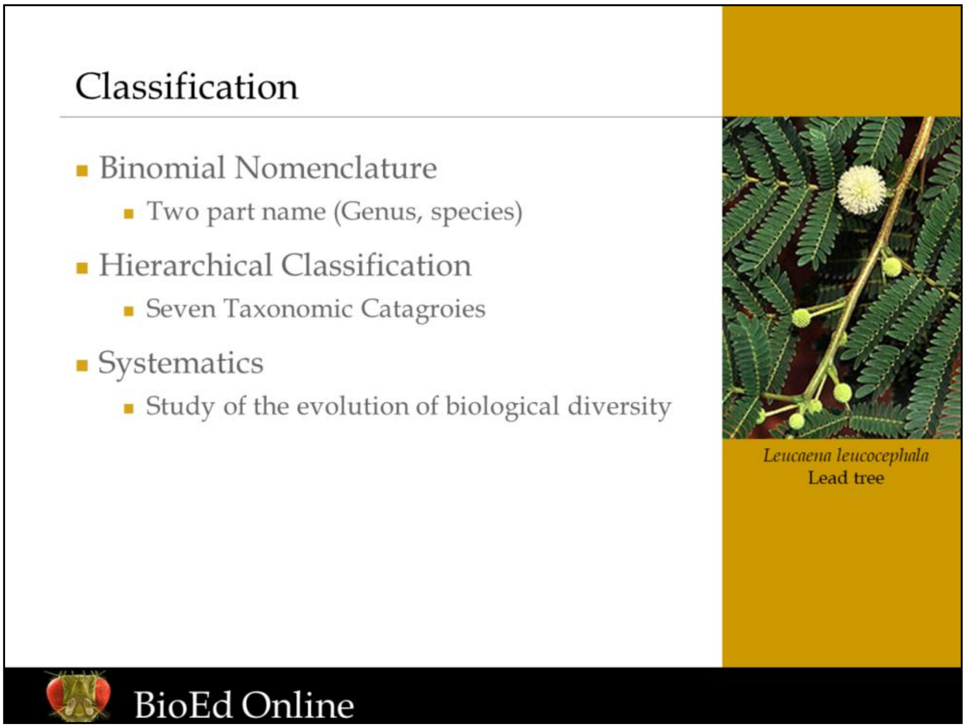

Classification

Classification systems attempt to solve the problem of providing meaningful groupings of organisms. The Swedish scientist, Carolus von Linnaeus, is credited with introducing binomial nomenclature and hierarchical classification as an organized way of naming and describing organisms and their relationships to one another. Binomial nomenclature refers to the use of a two-part name for each species (one name designating genus and one designating species).

Linnaeus described a hierarchical classification system using seven taxonomic categories, or taxa (Kingdom, Phylum, Class, Order, Family, Genus, Species). Beginning with species, each category becomes progressively more comprehensive. For example, while the leopard, tiger and domestic cat all belong to different genera, they are grouped together in the same family.

Taxonomy is the science of classification. When taxonomic systems include hypothesized evolutionary relationships among groups, the field generally is referred to as Phylogenetics. Systematics is a larger field involving classifying organisms based on their phylogenetic relationships. Systematics can be thought of as the study of biological diversity and how that diversity evolved. In a sense, Charles Darwin introduced systematics in his revolutionary work, *The Origin of Species.* He wrote, “The natural system is founded on descent with modification; that the characters which naturalists consider as showing true affinity between any two or more species, are those which have been inherited from a common parent, and, in so far, all true classification is genealogical” (Darwin, 1859).

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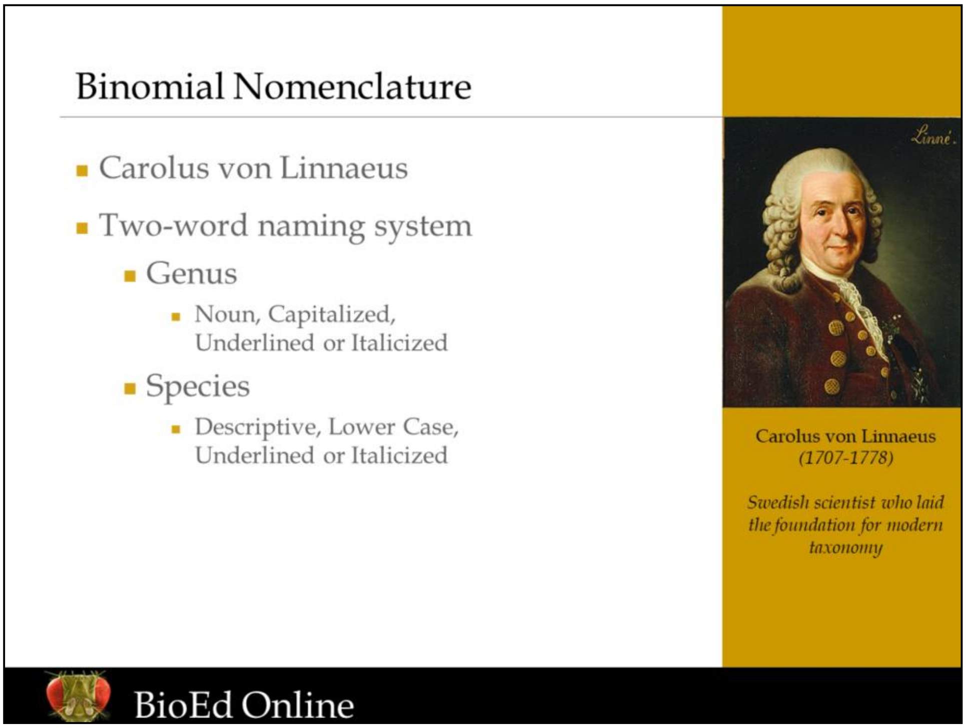

Binomial Nomenclature

Early naturalists identified plants and animals by observable structural similarities and referred to organisms using long complicated phrases. This was known as the "polynomial system." In this system, a plant might be described by phrases of 12 or more words. It is not surprising that polynomial names could become very complex and were often misinterpreted when translated from one language to another.

In the 1700s, Carolus von Linnaeus, sometimes referred to as the Father of Classification, described a binomial system, which was published in his early work, *System Naturae* (1735). Although he created the two-word system as a short-cut for users of this work, the system was rapidly adopted as a manageable way of naming species.

In the binomial nomenclature system, **genus** and **species**—just two names—replace the long string of words used in the polynomial system. The meaning of words can differ from language to language and from country to country. For example, in Great Britain, the word "buzzard" refers to an organism Americans call a hawk. For this reason, scientific names are written in Latin to maintain a uniform system of naming across all languages.

In the binomial system, **genus** is always a noun, underlined (or italicized), and capitalized; **species** is a descriptive term, underlined (or italicized), and not capitalized. Some examples of binomial names include: *Quercus rubra* (red oak), *Panthera pardus* (leopard), or *Homo sapiens* (human).

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Hierarchical Classification

Carolus von Linnaeus created a hierarchical classification system using seven taxonomic categories, or taxa (Kingdom, Phylum, Class, Order, Family, Genus, Species). These categories are based on shared physical characteristics, or phenotypes, within each group. Beginning with kingdom, each successive level of classification becomes more and more specific. Organisms within the same order have more in common with one another than organisms within the same class. For example, all species of bears are mammals, but not all mammals are bears. A useful pneumonic tool to help students remember the hierarchical classification system is: "King Phillip Came Over For Green Soup," with the first letter of each word representing each category, beginning with kingdom and ending with species.

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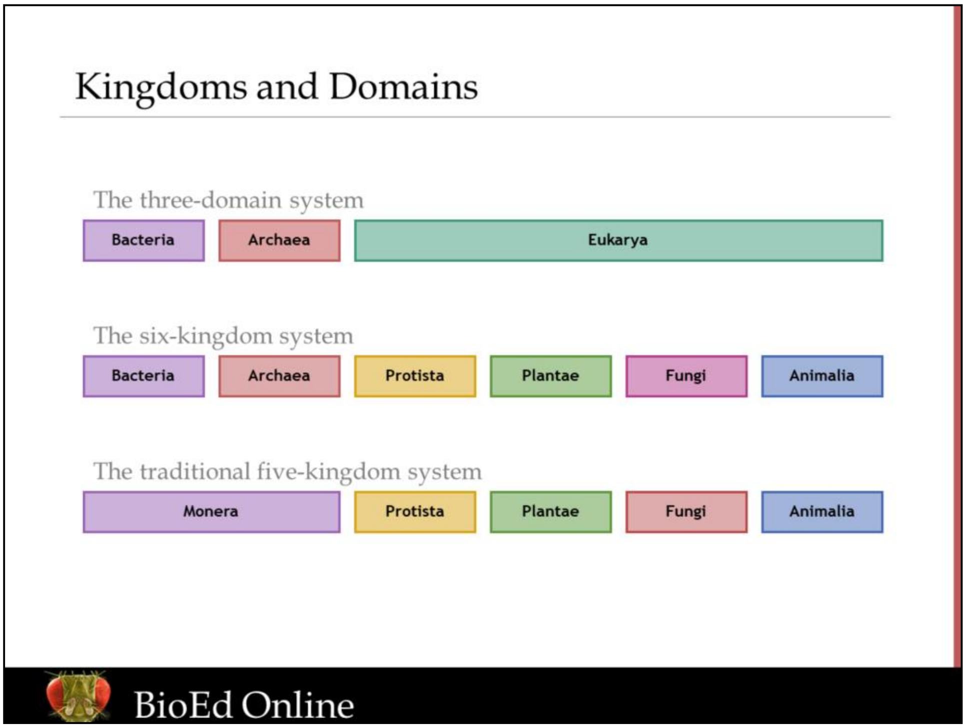

Kingdoms and Domains

In the 18th Century, organisms were considered to belong to one of two kingdoms, Animalia or Plantae. As biologists gathered more information about the diverse forms of life on Earth, it became evident that the two-kingdom system did not accurately reflect relationships among different groups of organisms, and the number of kingdoms increased. In 1969, Robert Whittaker proposed a five-kingdom system consisting of monerans, protists, fungi, plants and animals. In the last few years, comparative studies of nucleotide sequences of genes coding for ribosomal RNA and other proteins have allowed biologists to recognize important distinctions between bacteria and archaebacteria. The graphic on this slide illustrates the phylogenetic relationships drawn from this information using a three-domain and a six-kingdom arrangement, compared to the traditional five kingdom system.

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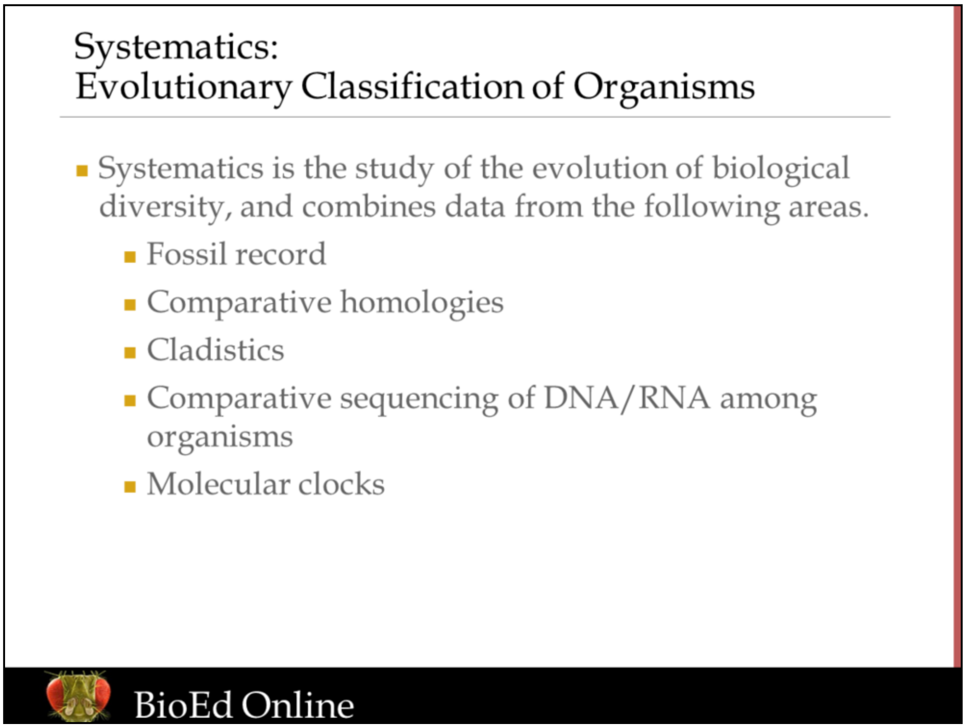

Systematics: Evolutionary Classification of Organisms

Evolutionary classification, or phylogenetics, creates classification that represents hypothesized relationships among groups of organisms. Systematists use a combination of fossil records, comparative anatomy, cladistical analyses and molecular data to understand the patterns of relationships among organisms.

The **fossil record** is an accumulation of all fossils found within layers of sedimentary rock and helps to reconstruct a geological time scale. Fossils are the remnants or impressions of organisms that lived in the past.

Homologies are similarities among species attributed to the inheritance of a feature from a common ancestor. Important information about common ancestry can be discovered by comparing different organisms' anatomical, embryological and molecular homologies. A classic example of homologous structures is the comparison of the basic groups of bones in the forelimbs of different groups of vertebrates (whale, alligator, penguin and human). Although each forelimb is adapted for a different use, the bones are formed in the same way during embryological development, suggesting descent from a common ancestor.

Cladistics is based on the idea that members of a group share a common evolutionary history and are more closely related to members within their group than to other organisms. These groups are recognized as sharing unique, derived features not present in distant ancestors. A cladogram is a branching diagram that illustrates hypothesized relationships based on shared, derived characteristics.

Comparative sequencing: Scientists also can compare DNA and RNA sequences among different organisms to unravel evolutionary relationships and common ancestry. These sequences can be used in comparison studies to determine phylogenetic relationships that can not be compared between morphological or fossil data. Ribosomal RNA, chloroplast DNA, and mitochondrial DNA have proven particularly useful in these kinds of studies.

Molecular clock studies compare sequences of macromolecules (proteins and nucleic acids) among species, assuming that these macromolecules evolve at constant rates throughout time, and for different lineages. Changes in sequences (nucleotide or amino acid substitutions, or mutations) are used to develop ideas about the evolutionary divergence of species. The molecular clock hypothesis has been a powerful technique for determining evolutionary events of the remote past for which the fossil record and other evidence is lacking or insufficient. The reliability of this hypothesis is currently under debate in the scientific community.

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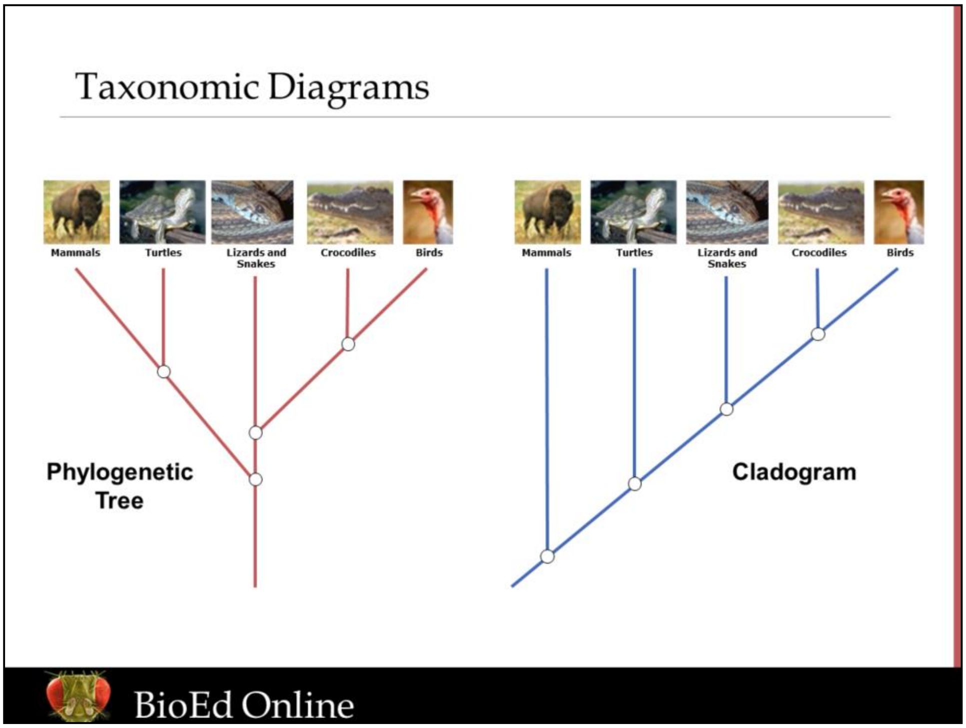

Taxonomic Diagrams

Sometimes, biologists group organisms into categories that represent common ancestries, not just physical similarities. Early naturalists used physical characteristics and later, fossil data, attempting to represent evolutionary relationships among organisms. Today, modern classification systems use fossil data, physical characteristics and DNA/RNA information to draw increasingly more accurate branching diagrams.

Phylogenetic trees, or phylogenies, represent hypothesized evolutionary relationships among organisms and may include extinct as well as modern species. Cladograms are based only on characteristics observable in existing species. The branching patterns in a cladogram are defined by the presence of unique, evolving innovations (derived characteristics) shared by all members of the group.

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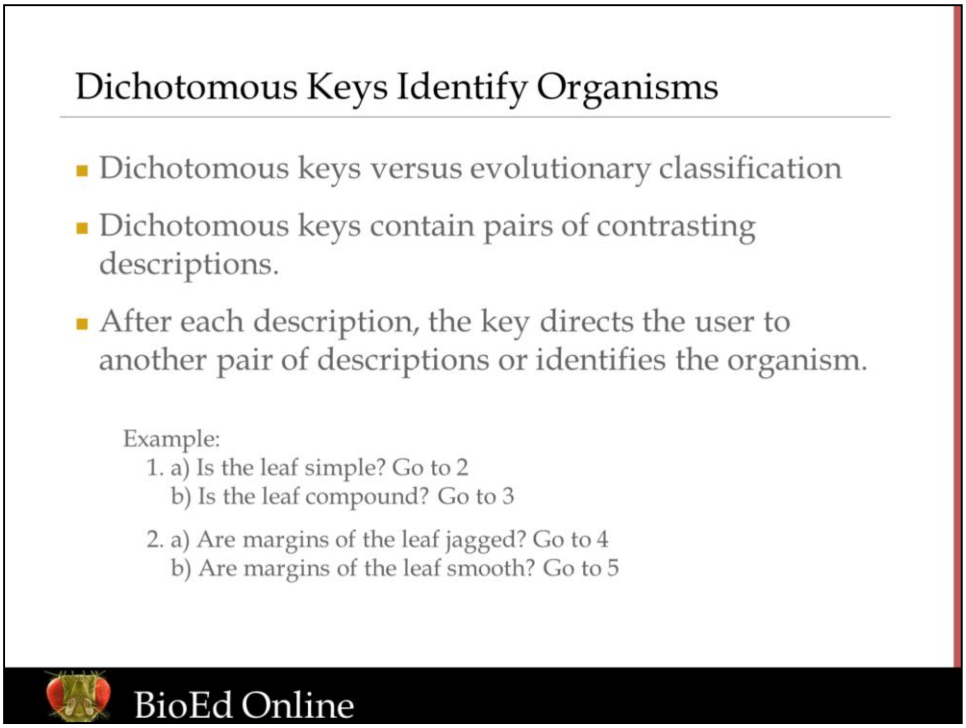

Dichotomous Keys of Identify Organisms

Identification is the process of finding the named group to which an organism belongs. Dichotomous keys are useful tools to help identify different organisms and usually are found in field guides. Identification in the field is based on features that are observable to the eye; therefore, it is important to remember that a key is an identification tool and is not synonymous with phylogenetic diagrams, which communicate hypothesized evolutionary history.

Dichotomous keys are constructed of contrasting pairs of statements. To use a dichotomous key, begin with the first pair of statements and follow the directions at the end of each statement until you reach the name of the organism you are trying to identify. With each new organism, always start at the beginning of the key (1a and 1b). The ability to use dichotomous keys is an important skill and should be incorporated into instruction throughout the year.

It is important to note that when constructing a dichotomous key, each pair of contrasting descriptions must deal with the **same** characteristic. For example the margin of the leaf might be used for the first pair of descriptors, and the shape of the leaf might be used for another pair. An **incorrect** pair of statements might be:

1a) Is the leaf heart shaped?

1b) Are the edges lobed?

References

Campbell, N. E. & Reece, J. B. (2002). *Biology* (6th ed.). Benjamin Cummings.

Thank You

- This concludes a brief review of biological classification.
- You may find additional information on this section of in the expanded content talks and in the notes below each slide in the slide library.

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