

Systematics:

Naming Organisms and Reconstructing the Evolutionary History of Life

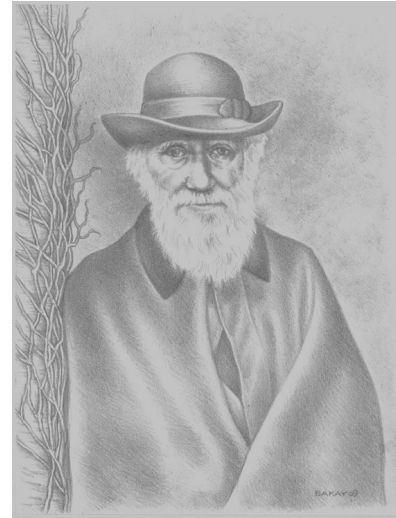
Mike Viney



Tree Fern *Psaronius brasiliensis*
Permian; Pedra de Fogo Formation
Bieland, Maranhão Province, Brazil

In the last paragraph of *The Origin of Species* Charles Darwin (1809-1882) reflects eloquently on the common ancestry of life on Earth:

“There is a grandeur in this view of life, with its several powers, having been originally breathed by the Creator into a few forms or into one; and that whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being created (Darwin, 1859/1993, pp 648-649).”



Charles Darwin c. 1881

Continuity of Life

Charles Darwin saw continuity to life through his theory of natural selection. This same continuity was echoed in the work of the German physician Rudolf Virchow (1821-1902). In 1852 Virchow hypothesized that cell division could account for cell reproduction. In his 1855 classic work *Die Cellularpathologie* he writes, “Omnis cellula e cellula” (all cells arise from cells). The Cell Doctrine is a cornerstone of modern Biology and in the light of evolution indicates common ancestry through cell division.

In adult humans each of the more than ten trillion cells can be traced back to the original unicellular zygote. The zygote itself was the product of a sperm fertilizing an egg cell. The sperm and egg cell can be traced back to the zygotes from which they arose. This simple thought experiment takes us back from one generation to the next. There exists an unbroken continuity to life; we can trace all of our cells back to the very first cells that existed on Earth. Thus, we can infer from the Cell Doctrine that all organisms can trace their cells back to the very first cell from which all life arose some 3.5 billion years ago (deDuve, 2002, pp 9-10).

Binomial Nomenclature

In science, taxonomy is the formal classification of organisms. Today, taxonomic systems strive to cluster organisms into natural hierarchical groupings based upon morphology and phylogeny. Organisms are classified using a system developed by the Swedish scientist Carolus Linnaeus (1707-1778). Prior to Linnaeus the names of organisms consisted of descriptive phrases. These phrases were called polynomials. Linnaeus was attempting to classify life on Earth in his book *Systema Naturae*, first published in 1735. Linnaeus used polynomials, but also provided a condensed two-word Latin name for each organism. This two-word system is called binomial nomenclature and is still used today.

Binomial nomenclature is used to give each organism a scientific name. The first word is the Genus (plural genera), which is always capitalized. The second word is the species and is always written in lower case. The generic and specific names are either italicized or underlined. The name for humans is *Homo sapiens*. Once the scientific name of an organism is introduced in a document it can be abbreviated thereon. The abbreviation for *Homo sapiens* is *H. sapiens*. The domestic dog is *Canis familiaris* (abbreviated *C. familiaris*).

In 1942 the famous evolutionary biologist, Ernst Mayr (1904-2005), proposed the biological species concept. A biological species is a group of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups. Identifying a species can be problematic. Breeding habits are not always known and less than 20% of living species are properly described. Many living species are described using morphology. Fossil species are defined using morphology and phylogeny.

Linnaeus grouped taxa (singular taxon) into hierarchical groups. From most specific to most general we have: species, genus, family, order, class, phylum, and kingdom. It was clear to Darwin that the pattern of hierarchical groups in the Linnaean system mirrored

the splitting pattern of evolution. After Darwin taxonomists were trying to form natural groups reflecting evolutionary history.

Classification is always changing as new fossil and molecular data are gathered. The desire to form groups based upon evolutionary relationships has led to the development of several contrasting taxonomic schools over the years. Evolutionary taxonomy, numerical taxonomy, and cladism were all developed in an attempt to uncover evolutionary relationships. All of these systems go beyond traditional taxonomy in that they strive to understand the diversity of organisms and the relationships among them. The science that studies biodiversity is called systematics. Systematics combines traditional taxonomy, phylogeny, and biogeography to understand the evolutionary history of life on Earth. Of the three competing systems mentioned above we will focus on cladism as it has become the standard for working scientists. For a discussion of all three systems see *Bringing Fossils to Life* by Donald Prothero.

Cladistics & the Tree of Life

Multiple lines of evidence, including morphological data, biochemistry, and DNA sequencing support that all organisms are genetically related. A single branching tree of life or phylogeny connects all living and extinct forms of life. Evolutionary relationships between organisms are established through cladistic analysis of morphological data and molecular phylogeny reconstruction.

The German Entomologist Willi Hennig (1913-1976) developed cladistics or phylogenetic systematics in the 1950's. Cladistics became well known when Hennig's 1950 *Phylogenetic Systematics*, originally published in German, was translated to English in 1966 (Prothero, 1998, p. 46). Cladistics is a school of taxonomy that establishes evolutionary relationships based upon shared derived characteristics or evolutionary novelties. Using cladistic analysis, paleontologists will construct a cladogram, which is a branching diagram that shows evolutionary relationships between organisms. Three definitions are important for understanding how a cladogram is constructed.

Shared primitive characters or traits (symplesiomorphies) are characteristics shared by all members of the group being compared. Shared derived characters or traits (synapomorphies) are characters shared by only some members of the group. Shared derived traits represent evolutionary novelties that are unique to the immediate lineage being considered. Primitive and derived characters are defined by the problem being solved. For example, hair and mammary glands would be derived characters at the class level for mammals, but a primitive character at the level of mammalian orders or families (Prothero, 1998, p.48). An outgroup is an organism which is only distantly related to the others and is placed on the cladogram as a comparison.

Constructing a Simple Cladogram

Let's construct a simple cladogram for plants to better understand cladistics (Johnson & Raven, 2001, p. 328). In Table 1, the traits for the out-group are marked with a zero. Traits not found in the outgroup are considered derived traits and are marked with a 1.

Constructing a Cladogram for Plants

Organisms	Derived Traits		
	Vascular tissue	Seeds	Flowers
Mosses (out)	0	0	0
Pine trees	1	1	0
Flowering plants	1	1	1
Ferns	1	0	0
Total	3	2	1

Table 1

Starting with a diagonal line, the out-group is placed on the first branch (Fig 1). Just past the first branch, the most common derived trait is listed; in this case vascular tissue is composed of tube-like cells. The branching point or node on a cladogram marks the point where shared derived characters arose. Next, the second most common derived trait is determined, which in this case is seeds. Ferns lack seeds and are thus placed on the second branch. The third most common derived trait is flowers. Conifers do not have flowers and are thus placed on the third branch. Flowering plants are placed at the end.

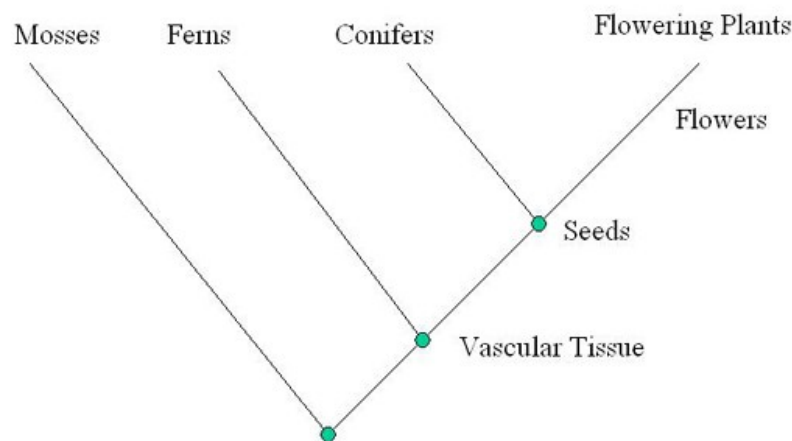


Figure 1

Monophyletic Groups

Cladograms show the closeness of relationships or how recently two groups shared a common ancestor. The distances between nodes are relative not absolute, so a cladogram is not an evolutionary tree. The cladogram, supported by unique shared derived characters, shows only that two taxa, branching from a common node, are closely related sister groups. A sister group consists of two lineages sharing a common ancestor from which no other lineages have sprung. Three kinds of cladistic groupings are recognized. A monophyletic group or clade arise from a single ancestor and include all the living and fossil descendants of that ancestor (Benton, 2005, p. 32). Many familiar groups are monophyletic such as the phylum Chordata or subphylum Vertebrata. The members of a clade or monophyletic group share at least one derived character. A goal of cladistic

analysis is to identify monophyletic groups because they are natural groups, true to phylogeny. Many traditional classifications include non-monophyletic groupings, although they are avoided whenever possible.

A paraphyletic group is a taxon that includes some but not all of the descendants of a common ancestor (Prothero, 1998, p. 422). In a paraphyletic group some of the descendants have lost the derived trait. The class Reptilia is a well-known paraphyletic group. Reptiles most likely arose from a common ancestor, but the group excludes birds (class Aves), which are descended from reptiles. The term evolutionary grade is sometimes used to denote a paraphyletic group. The class Reptilia has been replaced by the class Sauropsida, which is monophyletic because it includes birds.

A polyphyletic group is a taxon that includes groups from two unrelated lineages (Prothero, 1998, p. 423). In a polyphyletic group the apparent derived character is actually the result of convergent evolution and the common shared ancestor does not possess the feature. Grouping elephants, hippos, and rhinos into pachyderms is an example of a polyphyletic grouping (Benton, 2005, pp 31-32). Combining mammals and birds based upon the characteristic of being warm-blooded represents a polyphyletic grouping.

Cladograms are Testable

Cladistics has become the major tool for scientists studying evolutionary relationships and has had a profound affect on traditional classification systems. Cladistics changed the focus from finding ancestors to analyzing patterns of shared specializations. The power of a cladogram and the reason for its success is that it is a scientific hypothesis that can be tested by looking at additional character states or additional taxa (especially outgroups) (Prothero, 1998, p. 49).

Molecular Phylogenetics

Extinct and extant organisms in The Tree of Life are connected to one another by their genomes. Thus, molecules record evolution and can be used to establish the degree of

relationship between different organisms. Molecular phylogeny consists of constructing patterns of evolutionary relationships by comparing the proteins and nucleic acids of different organisms.

Multiple methods are used to compare the distances between sequenced nucleic acids (DNA and RNA) or proteins. A molecular tree of relationships is produced from the aligned gene or protein sequences. The idea that molecules may mutate at a predictable rate has led to the concept of the molecular clock. Thus differences in molecular structure can be turned into time of divergence (Benton, 2005, pp 34-35). Molecular phylogeny reconstructions represent an independent approach to discovering phylogeny because they use genetic comparisons instead of morphological differences as in cladistic analyses.

In many cases, molecular phylogenetics has confirmed evolutionary histories inferred by traditional phylogenetic methods (Lewin, 1997, p. 53). In other instances it has been at odds with morphological techniques. Molecular phylogenetics has even solved problems for which morphological techniques had no answer. Molecular phylogenetics has influenced the classification and evolutionary histories of many organisms. Molecular data broke up the Kingdom Monera, provided evidence in support of the endosymbiotic theory for the origin of eukaryotic organelles, unraveled the origin of Australian song birds, and helped to uncover the evolutionary history of humans and other apes as well as change their family taxa (Lewin, 1997, pp. 19-85).

Molecular data support a growing body of evidence for the importance of horizontal or lateral gene transfer. Horizontal gene transfer or HGT is known to be important in the evolution of prokaryotes (Bacteria & Archaea). HGT may also be a significant evolutionary factor for unicellular eukaryotes. So, the vertical gene transfer supposed by a tree of life analogy is not the whole story. Some scientists argue that an evolutionary web or net reticulating from the three domains of Bacteria, Archaea, and Eukarya would be a more useful analogy for the evolution of life than a tree. Dr. W. Ford Doolittle points

out that while some evolutionary relationships are tree-like; many others are not (Lawton, 2009, p. 39).

The Great Chain of Being & the Tree of Life

In the time of Linnaeus, scholars attempted to group organisms from the simplest to the most complex in a hierarchy that reflected the fixed orderliness of creation. In so doing, they were trying to discover anatomical clues that linked life into a Great Chain of Being; revealing the pattern of divine creation. Today we still look for similarities and differences in form and structure (morphology) and use some of the same basic taxonomic methods. Since the time of Linnaeus, much has been added to human knowledge regarding relationships among life-forms that inhabit Earth. We have greater awareness of the history of life on Earth as it is revealed by the fossil record, extinction, mechanisms for evolution, geologic changes in Earth's crust as well as the patterns and molecules that guide inheritance. In our time, scholars attempt to recover evolutionary history using cladistic analysis of morphological data and molecular phylogeny reconstruction. In so doing, we are striving to recover The Tree or web of Life, a phylogeny connecting all living and extinct forms of life on Earth.

Bibliography

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The pencil sketch of Charles Darwin used in this paper is by Michele Bakay. The drawing was inspired by an 1881 photograph of Darwin standing on the veranda at Down House taken by Elliot and Fry of London. Darwin was seventy-two when the photograph was taken. The photograph is housed in the Darwin Archive at Cambridge University Library (Berra, 2009, p. 79).

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Hermanophyton taylorii
Jurassic; Morrison Fm; Brushy Basin Member
East McElmo Creek, Cortez, Colorado