

f35 Cladistics < derived characters >

Taxa once touted as ancestral are really not ancestral, for a variety of empirical reasons.
To learn [this] proves sometimes a troubling experience akin to loss of religious faith.
—Gary Nelson.²

In Darwinian evolution the characteristics of an organism can be argued to be modifications of the characteristics of a single ancestor species. The wing of a bird can reasonably be the modified foreleg of a bipedal reptile and the feathers the modified scales of that ancestor.³ Which modification is important to the classification of life depends on the taste of the classifier. Most people would agree that feathers make the bird. But a disagreeable observer might argue that reduction of fingers by fusion and loss via vestigial splints on the forelimb is more diagnostic.

In neo-Darwinian evolution, mutations introduce or delete characters. The group of all creatures that are more closely related among themselves with respect to derived (new by mutations) characters than they are to others is called a *clade* (*ade* in this word is pronounced *aid*). In *cladistics* (*ad* in this word is pronounced *add*), a taxon is defined as a group of organisms (or taxa) with an ancestral taxon (species) unique to itself, or is a group composed of all descendants of one ancestral species. These “real” taxa are monophyletic (**Figure f35.1**) (not paraphyletic or polyphyletic).

A clade *reduced-digits* could include birds and horses. Most would find (excluding from consideration mythical Pegasus) that an unreasonable grouping. A forelimb-with-three-digits is so of birds and primitive horses as *Plagiolophus*. However, horse digits have hooves which character is advanced over five-toed mammals of which the first, as *Eozostrodon*, were clawed. Horses belong to a clade *reduced-digits and hooves* that does not include birds. As to feathers, these are modified reptilian scales. Birds could include unrelated ancestral stocks of scaly reptiles which evolved feathers. So Birds could be a polyphyletic class and not a clade which by definition is monophyletic.

Deciding on what is or is not a clade is not easy. How some agreed-to clades of vertebrates can be arranged is shown in **Figure f35.2**. The nested arrangement is called a cladogram. The cladogram shows the least number of evolutionary steps that must have built upon each other to account for the diversity of named groups. These groups, not necessarily of the same hierarchal level, are chosen to be inclusive enough to keep their number small.

In what respects is the portrayal of a phylogenetic tree as a cladogram different from the traditional?

A Darwinian phenogram (**Figure f35.3**) is constructed so that its branches, when traced upward, link organisms in the order in which they evolved from each other. Branching indicates divergence of species and bundles of these are given hierarchal names (Kingdoms, ... , species). A branch's thickness at any time horizon is drawn to show the relative abundance of species in the hierarchal groups portrayed. Also, unique characters evolved in single lineages and trends within groups are usually labeled. However, not labeled is what justifies a branching in the tree and the placement of the point (time) of a branching is hypothetical.

A neo-Darwinian cladogram is stylized in the way that a subway map is different from a road map. In a subway map, absolute space is sacrificed so as to show most simply the order of station stops on lines that lead from terminuses. In a cladogram, absolute time is sacrificed so as to lay out most simply the order of inherited characteristics beginning with those that are unique and most recent and working back. Hierarchal ranks are not considered. What can be reconstructed by the parsimonious search back through candidate ancestors at ever more ancient levels is the *order* in which *derived characteristics* evolved in extant and extinct organisms. Clades are distinguish with the economy of ignoring primitive characters that ancestors *necessarily* shared. Evolutionary change within groups cannot be shown if branching has not led from it. Only derived characters (states) reliably establish

natural (monophyletic) groups (clades). This is so as a derived character will be present only in direct descendants. Loss of a derived character is not necessarily a problem given its setting (Dollo's rule).

For living organisms, cladistics enables cook-book ways to reveal descent from genetic codes (**Footnote f35.1**). For fossils, cladistic methods for paleontologist are not so simple: Groups investigated are those that conventional phylogenetic studies have indicated. These groups include fossil *and* living organisms. Their clear-cut features, called characters, are listed only if "judged" to be a derived (a mutationally evolved) character among others of the group and a chosen out-group. A computer program then sorts the individuals by their listed characters to produce a cladogram.

Not every paleontologist is happy with the present trend of organizing museum displays of fossils to indicate how contemporaries of a group differ by some being more derived than others. Alan Craig complains, and Stanley Friesen⁴ would agree: "What is wrong with naming groups, especially stem-groups, that we all have to use all the time? Moreover, I am genetically much closer to my first cousin than to my descendants a thousand generations down the line, and the logical conclusion of a Russian-doll [Matryoshka-doll] type of classification is that I am a blue-green alga."⁵ His grumble is that he feels more comfortable with grades than clades. The difference is that the recognition of grades of evolution, as the advance of feathers over scales, separates *out* groups of organisms whereas in cladistics the separation is *within* a group of organisms. The appearance of feathers allows birds is shown in a phenogram as an ongoing class distinct from scaly reptiles. The class of scaly reptiles from which they stemmed can go extinct or continue in its own different evolutionary directions. In this context, Class Birds could be polyphyletic (more than one scaly reptile species can have evolved feathers). In a cladogram, the appearance of the character feathers is shown to define the clade *birds* nested in the clade *scaly-reptiles*. In this context, the clade *birds* is monophyletic (has only one ancestor species) and if more than one species of scaly reptile evolves feathers each would be a different *feathered reptile* clade within the clade *scaly-reptiles*.

Indeed, grades degrade. Consider, the coelacanth that the taxonomy of grades relegates to a minor, faltering, side branch to the ray-finned fishes which have gloriously evolved. However, when viewed cladistically from the top down, the clade *fishes* is seen to contain a monophyletic subclade to which we belong with tetrapods, lung fishes, and coelacanths, that is of equal status, surely, to the subclade of ray-finned fishes that for all their diversity are still in water.

A Darwinian phenogram by the placement of hierarchal named groups, their durations, and divisions, tells a story of evolution that can be read from the bottom up. A neo-Darwinian cladogram lists *all* the groups (taxa), extant and extinct, that it addresses, as external nodes (leaves) at the top of a tree. Limbs to these branch from internal nodes in the tree. Each internal node is empty of any exhibit of a complete organism (all such physical exhibits are leaves) and it or the limb leading to it is merely tagged with the derived character(s) that justifies it and, in a pure cladogram, these are *not* descriptions of a named hierarchal group (class, family, etc.).

Away from the leaves that can be fully described, the extreme sparseness and arcane nature of what is detailed within a cladogram does *not* make for exciting story telling. In *The Ancestor's Tale*, 2004.⁶ Richard Dawkins charmingly has leaves tell their tales in the order of concestors (nodes) down from our leaf. But note, the concestors at nodes cannot be described and so, nor is the tale told by them.

Discomfort with a cladogram can be in the misguided looking for a story reading of it from the bottom up. Read that way, if you look again at **Figure f35.2**, reading characteristics along limbs (as there are no exhibits of full organisms) you would first see yourself as a waterproof (amniote) egg. Yes, you are a member of the clade *waterproof-egg*. Now, reading up the wrong branching limb, you might not realize (not being a biologist who knows what uric acid is) that you are not on the evolutionary path to yourself until, having sequentially rejected the branchings that lead to a turtles leaf, a lizards & snakes leaf, and a crocodiles leaf, you reach the branching point (node) beyond which are feathers. No you do not belong to the clade *feathers*. Returning to waterproof-egg you read

up the other branching limb, the one that you did not before. Ah, the clade *hair and mammary* is the one to which you belong. Enclosed in this, in nesting-doll style, is the clade *live-birth*. You do belong to this clade which includes a pouched-mammals leaf (which includes kangaroos, koala, echidna, and the like) and a more derived placental-mammals leaf (which includes you). This bewildering experience is because you read the neo-Darwinian cladogram as you would have a Darwinian phenogram. At the bottom of the cladogram there is no indication of what organisms are considered beyond that they will be born from waterproof eggs. The organisms are listed only at the top of the cladogram. You should have read the cladogram from the top down. In the cladogram, individuals or groups of individuals distinguished from each other are leaves at twig ends. Select any one, and the number of character changes between it and the putative root of the tree indicates how derived it is—with the limitation that the number of branching points (nodes) cannot be more than the number of members (leaves) in the group, and evolutionary change that may have otherwise accrued between nodes is not shown however great this be. Upon reading the list of the named animal types at the top of the cladogram, you recognize that your navel (belly button), and not your enormous gluteus maximus and swollen head (surely a weakness of the cladogram representation), places you in the clade *placenta*. Reading down that branch you discover that your clade is within the clade that includes thin-bummed and small brained marsupials because the animal groups, whose branches (two in this example) join at that point, are of individuals born already hatched (live birth). Proceeding further you find that this clade is within the clade of animals all of which have hair and mammary glands, and so on. This is also an efficient way a cladogram can be constructed: from the top down. When complete, the cladogram is a tree in which clades (taxa) are arranged in a nested ascent. Clades are defined to branching points (nodes) on the tree. As such, each clade (taxon) is uniquely defined by shared characteristics not found in ancestors leading to it. By the way they are distinguished, the nodes do not have the familiar taxonomic names that are used in Darwinian phenograms although sometimes (**Figure f35.4**) these can be appended. For example, in the American Museum of Natural History, NYC, is a hall in which representatives of distinctive groups of mammals and non-mammalian synapsids (mammallike reptiles) are cladistically ordered. The nested clades are numbered 1 through 6, and one is guided to examine the exhibits in that order. This walk, that way, through a cladogram-come-phenogram (neo-Darwinian-come-Darwinian) phylogenetic tree guarantees maximal bewilderment as this forces the wrong concept that the ancestors to clades are on display as they would be in a traditional phylogenetic tree. A cladogram requires first an overview of the list of all types that are included. A traditional (Darwinian) phylogenetic tree (phenogram) announces, *mutatis mutandis*, at the bottom the ancestral group that will diversify and follows gradualistic change along limbs that branch from ancestral types.⁶ For sensible neo-Darwinian questions to suggest themselves, best first examine the representative mammals of clade 6. In what evolved characters do these differ from the more inclusive clade 5 to which they also belong? Clade 4 includes all the foregoing groups and additional groups one of which is Primates. Surprise! And so on.⁷

A grade is composed of species that have certain defining characters in common. A clade is a group of species that have derived character(s), the first of which appeared in their common ancestor.

Because almost all paleontologists today are engaged in presenting their findings in terms of cladograms, the precise use of the Linnaean terms higher than family is rapidly being abandoned for the practical reason that, in the light of cladistics, their informational value has lessened (**Footnote f35.2**). Even so, a new species, if it is to be formally named, must be placed in a Linnaean scheme. To fit, a new species may require reorderings, subdivisions of, and additions of groups to an existing Linnaean classification scheme. However, whether, for example, a clade inclusive of all ornithischian species is an order, or a suborder, has no bearing on the construction of a cladogram. Furthermore, instability would escalate if a Linnaean formal name were devised for every limb in the deluge of (always tentative) cladograms that are now seeing publication. The justification for a cladogram is that the organization of data in it is a testable hypothesis. No special review of it, beyond that, is required. Omitted or incomplete data matrixes allow the duplicitous to be spotted.⁸

Of the estimated 100 million species in the world, completing “Adam’s task” to name each, although speeded by the Linnaeus’s hierarchal method laid out in *Systema Naturae*, 1735, has succeeded in naming less than three percent. “It is said that some of Charles Darwin’s own collection still languishes on shelves in England awaiting names,” Jack Hitt (uncertainly) tells us.⁹ Using fast DNA identification and cladistics, “The All-Species Inventory” (a globally accessible database), a project for identifying life from “the bottom of the Marianas Trench to the top of a rainforest canopy” originated by Kevin Kelly and Stewart Brand, is invested to complete most of Adam’s task in this generation. □

Figure f35.2

A cladogram of amnions represented by Mammalia orders, class Birds, and Sauropsida orders.

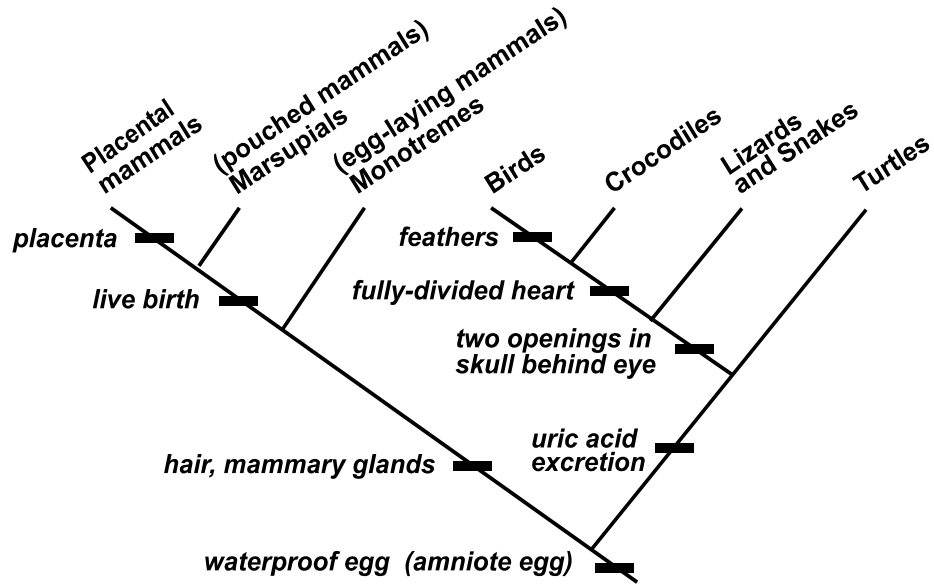


Figure f35.3 (left)

A phenogram of class Mammalia.

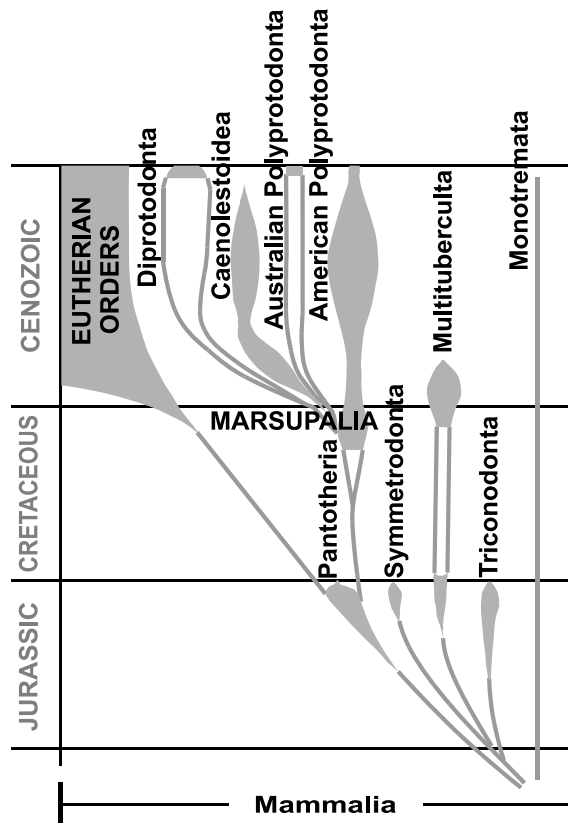
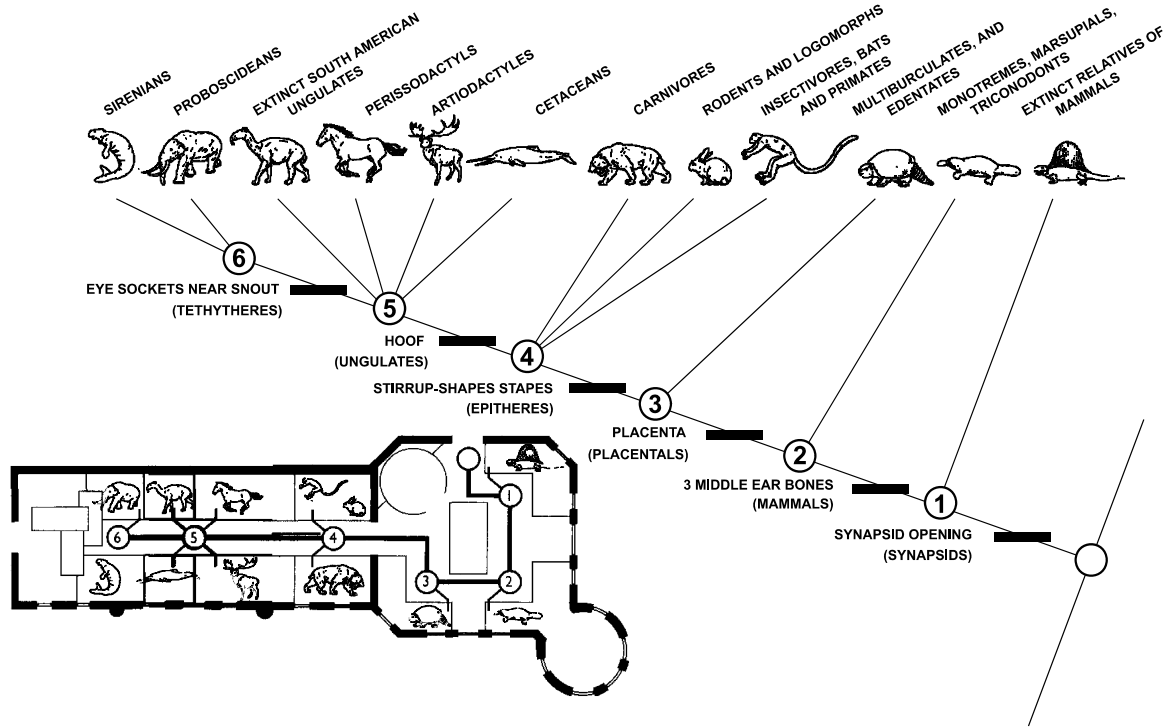


Figure f35.4¹⁰

A cladogram of living mammal orders and groups of their extinct relatives

This cladogram is the inspiration for the floor plan (inset) of the 1994 re-opened Fossil Mammal halls in the American Museum of Natural History, NYC (with sterile curation that ignores William Blake’s 1799 maxim: “The wisest of the Ancients considered what is not too Explicit as the fittest for Instruction, because it arouses the faculties to act”).¹¹



Footnote f35.1 *Phylogenetic Trees Made Easy*, 2001, is Barry G. Hall’s highly useable “how-to” manual for molecular biologists that proceeds as:¹²

1. Identify a protein or DNA sequence of interest.
2. Identify other sequences that are related to the sequence of interest and obtain electronic files of those sequences.
3. Align the sequences.
4. Using the resulting alignment, generate a phylogenetic tree.
5. Print (and perhaps publish) the results.

Comment

A cladogram is constructed by attention to the order of character-state pairs: judged-to-be-derived / judged-to-be ancestral, that branch from and justify a node in the phylogenetic tree that is constructed. Cladograms are best read from the “leaves” back to the “root.” Computer programs can start formal map construction in many (black box, for most users) ways and at any place in a data set. However, a person who attempts to construct a cladogram with pencil and paper begins by grouping leaves and then grouping these and so on back to a root. In effect, one works back in time.

Significantly, from cladistic studies comes an awareness of how common “living” fossils are, and have been. This realization is not so forcefully gained from the study of traditional phylogenetic trees.

Footnote f35.2 Cladistic analyses and the realities of developmental biology

Generations of systematists have studied amniote phylogeny at diverse genealogical levels, and its broad outlines ... antedates the Theory of Descent. [However,] ... during the first two-thirds of this century, there was little thought given to what constituted evidence for phylogenetic relationships. The origins of the major extant lines ... have become clearer in the post-Hennigian era.

—*The Tree of Life* Coordinator and Editor: David R. Maddison.¹³

Cladistic analyses of differences in the nucleotide sequence of segments of DNA have converged on the view that, genetically, people bear a particularly close evolutionary relationship to chimpanzees, while gorillas and orangutans arose along separate evolutionary lines.

Is this now well established DNA version of kinships in agreement with other cladistic analyses?

(No) Cladistic analysis of *skeletal traits of apes* places people in one clade separate from chimpanzees, gorillas, and orangutans.

(No) Cladistic analysis that *includes skeletal measurements of baboons and several other African monkeys and the apes*, places humans with orangutans in one clade and chimpanzees and gorillas in another.

(Yes) Cladistic analysis of *197 measurements of muscles, nerves, blood vessels, and connective tissue from various modern primates* finds clades that correspond to the established DNA version.

Evidently, the characteristics chosen for cladistic analysis can greatly influence the outcome.

Homeobox genes control the general shape of the fetal body. These genes also trigger a series of biological processes that foster the growth of integrated sections of the skeleton rather than the development of individual bones.

For example, C. Owen Lovejoy has found two homeobox genes that regulate the growth of both the vertebrate forearm and all fingers except the thumb, and two others that participate only in thumb growth. Even subtle alterations of these genes or their protein products at various times could be implicated in the evolution of disparate hand proportions typical of modern primates and of our fossil ancestors. Changes that then occur to other parts are possible add-on consequences not controlled by a homeobox gene. For example, of the robust australopithecines, a homeobox gene change may have orchestrate the greatly expanded chewing teeth at the back of the mouth. A consequent was the allowed formation, Melanie A. McCollum has proposed, of many *other* of their distinctive skull features.

Until anthropologists become familiar with developmental biology and understand how complex chains of molecular processes form the bones and soft tissues that coalesce into bodies, Tim D. White (codiscoverer of the famous 3.2-million-year-old human ancestor ‘Lucy’) admits that new fossil finds will “continue to be assigned to unique rather than established species—so evolutionary trees have gotten downright bushy.”

Timothy G. Bromage concurs: “We can’t solve debates over Neandertals or any other human ancestors using anatomical characteristics that are subjectively defined and don’t have a clear relationship to evolutionary history ... Let’s examine bones with a fresh perspective on biology and life history.”¹⁴ For example, laser ablation stable isotope analysis of enamel of 4 molars of adult *Paranthropus (Australopithecus) robustus* (1.8 million years old, Swartkrans, South Africa) reveal omnivorous (not specialist, as formerly assumed) seasonal diets of C3 forest foods (as fruits and leaves) and (lean-time?) savanna C4 foods (as grasses & sedges or the flesh of animals that ate these).¹⁵