

f36 Phenetics slips from prominence

< overall similarity does not prove relatedness, statistics, phenogram vs. cladogram >

How strange is this shame of the living creature that slips away into a corner to die, convinced that he may not expect from outward nature any reverence or regard for his suffering and death! —Thomas Mann.¹

The two competing schools of the day, the “evolutionary taxonomists” [who describe gradualistic change and divergence of characteristics] and the “pheneticists” or “numerical taxonomists,” [who describe change and divergence of overall similarities] finally found one area of mutual agreement—Hennig’s approach was wrong. Each group disagreed with Hennig for different reasons, but at the 1965 meetings of the Society for Systematic Zoology leading proponents of each school, Ernst Mayr and Robert Sokal, did coin the same term of derision for Hennigian approaches—cladism.

—Vicki A. Funk and Daniel R. Brooks: Foreword *Advances in Cladistics, Proceedings of the First Meeting of the Willi Hennig Society*, 1981.²

Systematics is the scientific study of kinds and diversity of organisms and of any and all relationships among them, [whereas] taxonomy is the theoretical study of classification, including its bases, principles, procedures, and rules. —G. G. Simpson *Principles of Animal Taxonomy*, 1961.³

Willi Hennig (1913-1978)

In 1950, finding fault with phenetics, which is also known as numerical taxonomy, Hennig conceived of a systematics that later came to be called *cladistics*.



“We may conclude that perfecting the methods of measuring overall basic similarity is of no significance for phylogenetic systematics. If absolute size of the differences in form is not a reliable measure of phylogenetic kinship, we must ask whether some other way of evaluating these differences is not a better means of discovering phylogenetic criticisms.”²

Fossil assemblages, except framework reef contributors, unavoidably suffer from both taphonomic loss (missing are organisms that decomposed or dissolved) and time averaging (concentrations of organisms in sediments that were reworked by transportation or dissolution). Fossil information suffers from grouping of fossils into particular taxa by perceived phylogenetic relationship based on no consistent methodology. To redress this laxity arose, with the advent of cheapening computer costs, the school of numerical taxonomy called phenetics. This discipline centers on factor analysis of numerical data that are obtained by clearly stated methods of measurement on features of individual fossils that are sampled in fair number from collected assemblages. Its results are portrayed as a phenogram. This groups species on the basis of overall similarity and shows how these, in the measured criteria, change in time. The purity of the pheneticist method of taxonomy attracted many and, beginning in the 1950s ignoring (insect systematist)⁴ **Willi Hennig**’s cries (*Grundzüge einer Theorie der phylogenetischen Systematik*, 1950)⁵ against it, stochastically generated phylogenies began to appear as of body of seemingly unassailable fortitude. Unfortunately, factor analysis does not discriminate between phylogenies that it erects and those that evolution has generated.

Given an imperfect fossil record, a phylogeny for its members can only be a hypothesis. In this regard, the phylogenies that numerical taxonomy constructs, while practical for key building and for the nuts-and-bolts use of fossils in sedimentary mineral and fossil-fuel exploration, are almost certainly false in that its groups are likely paraphyletic or, worse, are polyphyletic. Thus, the post-Darwin ideal that phylogenies should convey the fact that its members are derived from a common ancestor is subverted.

Willi Hennig's *exposé* of phenetics in *Systematik und Phylogenese*, 1956,⁶ tore at the heart of that discipline by showing its results to be merely expedient. In 1966, an English translation (*Phylogenetic Systematics*)⁷ of his book of 1950, with additions, broadcast his premise that taxonomy (the practice of classification) should express the branching (cladistic) relationships among species *regardless* of similarity or difference. Systematics (the study of relationships among organisms) as advocated by Hennig is now called *cladistics*.⁸ The product of cladistics is a cladogram (**Figure f36.1**), which can be considered to be an *estimate* of the true phylogenetic tree. A cladogram (**Figure f36.2**) has the virtue of being a hypothesis that is clearly testable in all its parts. For example, the character "horns," in a group considered, can have the character-states "straight" and "curly," and debatable is the polarity of these character states, i.e. of the two, is curly evolved from (more derived than) straight?

The method is not confined to the study of organisms. For example, linguistic (meme) evolution (as Darwin himself realized) is analogous to biological (gene) evolution (**Footnote f36.1**).

The present reality is that a cladistic presentation of phylogeny is a requirement for publication in peer reviewed scientific journals. Even so, away from its leaves, the sparseness of a cladogram and its "black box" derivation alienates those who would see ancestors and those artistically fleshed out. □

Figure f36.1⁹ Comparison of a phenogram with a cladogram, based on the hypothetical states of four taxa. The phenogram is constructed from the total number of character states shared by any pair of taxa, whereas the cladogram is constructed only from the derived-character states (marked by primes) shared by pairs of taxa. The character state transitions are marked on the cladogram.

Note that the evolutionary tree implied by all shared characters (phenogram) radically differs from that implied by only shared derived characters (cladogram).

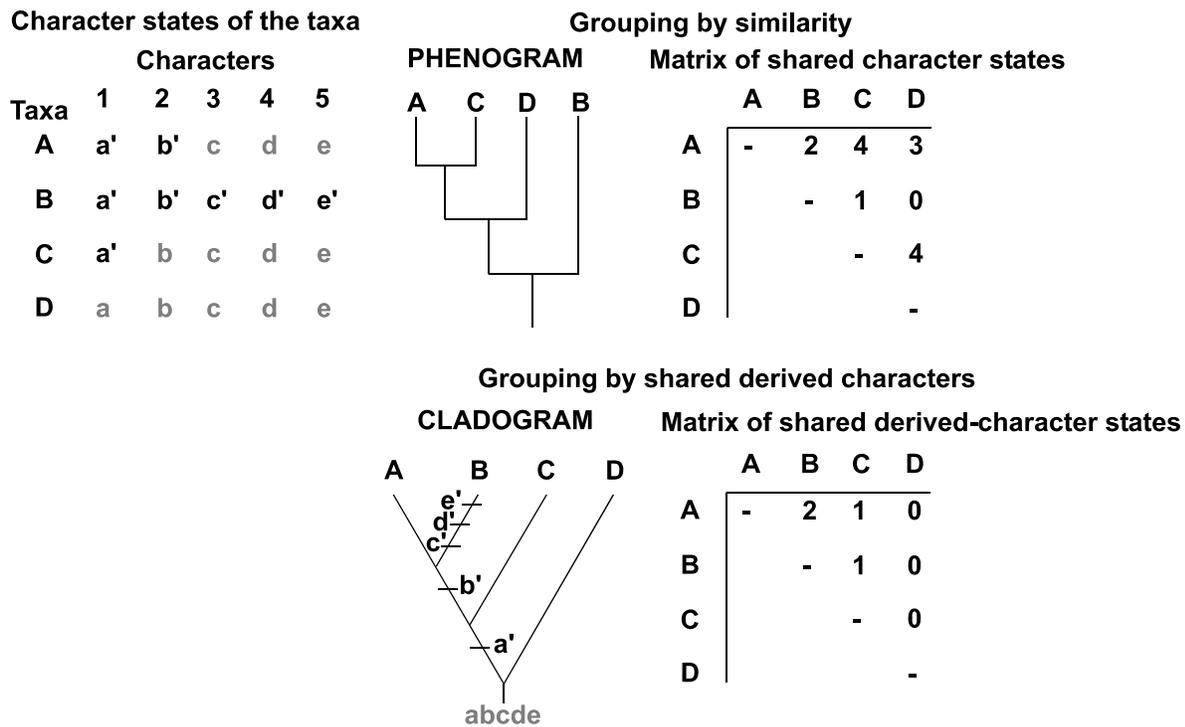
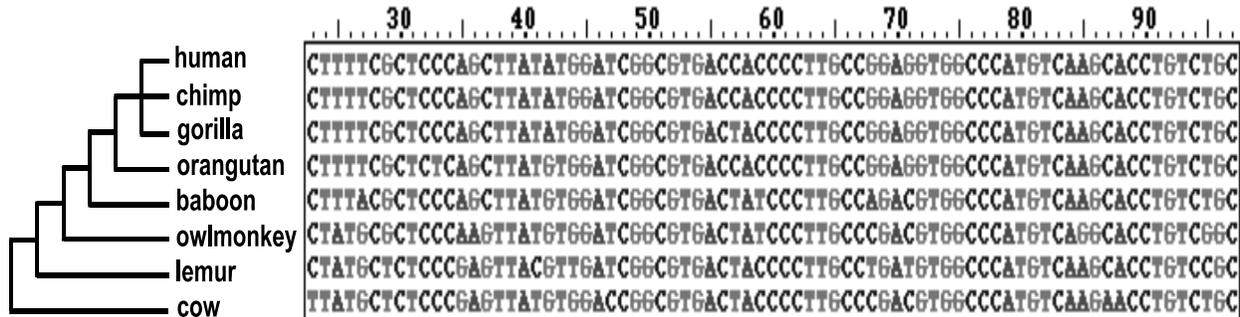


Figure f36.2¹⁰ In molecular biology, homologous genes sequences of different organisms can be compared to establish their genetic divergence from a putative common ancestor. For example an homologous animal gene is cytochrome c oxidase subunit IV. A snippet of this is shown here (right part of the figure below)



Starting 23 bases down from the start through to 98, genetic distance of humans to seven other animals listed are:

- human-chimp: 0 differences
- human-gorilla: 1 difference (position 57)
- human-orangutan: 2 differences (pos. 38, 47)
- human-baboon: 6 differences (pos. 27, 47, 57, 59, 68, 71)
- human-owl monkey: 11 differences
- human-lemur: 13 differences
- human-cow: 13 differences

Using the entire gene sequence, a molecular ‘family tree’ (left part of figure) was derived and this is found to agree with evolutionary biologists’ findings from comparative anatomy studies.

Footnote f36.1 Language trees may decide

Before European explorations, Oceania became settled by Polynesians. The last reached islands were such as New Zealand, 1,000 BP (unaccompanied by chickens and pigs), and Hawaii, 1,500 BP.

The diaspora into Polynesia followed upon the invention of the double-hulled canoe.

People of the Lapita (name for a characteristic type of pottery) cultural complex had reached central Polynesia by 3,200 BP. They had boated east from Near Oceania (the Solomon Islands) which they had settled by 3,600 BP.¹¹ Earlier settlements in Melanesia had allowed for trade with its people (with whom Polynesians carry forward evidence of light genetical mingling) and learning of the use of particular crop plants (yams—see **Scholium f36.1**, page 392, taro, and seedless breadfruits—vegetatively propagated from root cuttings of these mutants of wild seed-bearing breadnuts), domestic animals (chickens and pigs), and way-finding techniques (refracted ocean wave patterns), and acquisition of durable goods such as tools, pots and textiles. Where they originally came from could be Taiwan where there is archaeological evidence of Lapita culture, 5,500 BP. Was their diaspora into Oceania the last leg of a forward moving migration (J. M. Diamond’s ‘express train’ hypothesis, 1988)¹³ or from their population dispersed along the northern rim of Melanesia (J. Terrell’s ‘entangled bank’ hypothesis, 1988)¹⁴? A cladistic analysis of their languages, by Russel D. Gray and Fiona M. Jordan in 2000 favors the “express train” (so-called because according to it the 10,000-km Austronesian journey from Taiwan to Near Oceania took only about 2,100 years).¹⁵

But however languages may travel, rats unbidden voyage along with humans. Against Taiwan-origins, Lisa Matisoo-Smith in 2004 finds that DNA fragments out of ancient rat remains reveals today’s Southeast Asian rats to be but distantly related to the ancient rats, whereas the ancient DNA matches better with that from rats on islands west of New Guinea.¹⁶