

Was
Darwin
Wrong?



A Revolution in Palaeontology

by Gert Korthof

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"Fossils are isolated points in Deep Time that cannot be connected"

"Without cladistics, palaeontology is no more of a science than the one that proclaimed that Earth was 6,000 years old and flat - and *then* had the effrontery to claim divine sanction for this view."

"Cladistics is a way of looking at the world in terms of the pattern rather than the proces that creates the pattern."

Henry Gee is an editor for the weekly science magazine *Nature* and has been trained as a palaeontologist in the group of Colin Patterson at the Natural History Museum in London. According to Henry Gee a revolution has been going on in palaeontology. The above quotes are revolutionary statements indeed. Gee is a critic of old fashioned 'missing link' palaeontology: the well-known type of palaeontology that constructs trees of ancestors and descendants. Almost synonymous with 'the theory of evolution'.

Palaeontologists produced *narratives* and *scenarios* how some dinosaurs got wings and became birds. How some fishes got legs and evolved into land



"In search of deep time.

Beyond the fossil record to a new history of life."

by Henry Gee

The Free Press.

1999

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New Edition:

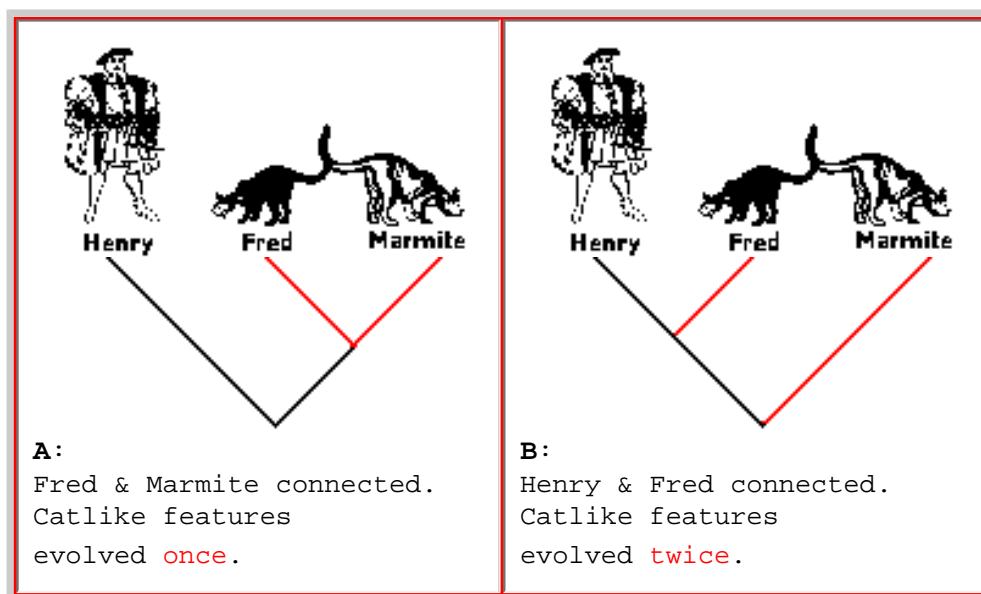
Deep Time: Cladistics, The Revolution in

Evolution. Paperback - 272 pages new edition (5 March, 2001) Fourth Estate; ISBN: 1857029879

animals. How some apes got brains and evolved into humans. (Mere the fact that the word 'story' is used in stead of 'theory' means a lot.) But fossils are isolated points in deep time says Gee, and can never be linked with certainty. The fossil evidence is unable to support evolutionary narratives. These scenario's can never be tested by experiment and so are unscientific! Traditional palaeontology is story telling. We can never be certain that *Archaeopteryx* is the missing link between birds and dinosaurs. Not surprisingly exactly these stories were often attacked by the critics of evolution! But from the lips of a mainstream scientist as Gee, these statements sound quite revolutionary. Gee attacks what once was orthodoxy! Is Gee rejecting the whole idea of common descent of all organisms? What else can palaeontologists do than constructing trees of ancestors and descendants? Does he claim that palaeontologists did everything wrong up till now? Is there anything good left in evolutionary theory? A small group started a search for a new science of palaeontology and systematics. They are now called 'cladists' and their science 'cladistics'.

What is cladism?

What cladism is, is best shown when his 2 cats and Gee himself are placed in a cladogram. In a cladogram all species are on the top row. Species are never placed on different levels. That means: no ancestors! That means: all species are des-cendants! Then a tree is drawn to connect them based on the smallest amount of change in a tree. Since the two cats are closer to each other than either is to Henry, the two cats are connected. This is shown in figure A.



A second possibility is shown in figure B: Henry and Fred are closer related to each other than to Marmite. Obviously absurd. The point is however that we can compare all the possible trees in a quantitative way. Consider each cladogram is a hypothesis says Gee. How to chose between them? Basically with the principle of parsimony. The cat-like features are innovations. Innovations are improbable events. In figure A the cat-features originated only **once**, and in Figure B **twice**. So tree A postulates less evolutionary innovation than B. Tree A is more **parsimonious** than B. Tree A is more probable than tree B. Tree A is not automatically true, but is the best hypothesis. One doesn't need to have an evolutionary bias to conclude that. It's the principle of parsimony. An evolutionary change such as evolving new features can be considered as costs. So this method tries to find the minimum evolutionary costs of a tree. Calculating the costs of all possible trees and finding the most parsimonious tree is a type of problem that computers can solve. However Gee does not go into technical

details. Gee is an appetiser. The real meals are in the textbooks [\(1\)](#).

A tree connecting 3 species is a simple example. But the cladistic method can be extended to all species living on the Earth. It's a very powerful method with far reaching consequences for the whole field of evolutionary biology, palaeontology and systematics. Instead of cat-like features, molecular data such as proteins and DNA are being used. These data are even more suitable to be evaluated by computers (public available computer programs are available on the net).

Cladism: progress or retreat?

According to Gee cladism is a step forwards because it produces *testable* hypotheses about the relations between organisms and because cladism rejects the storytelling mode of evolutionary history as *unscientific*. However cladism could also be interpreted as a retreat because now it is impossible to know for certain whether one species is the ancestor of another (p155), once held as the ultimate goal of evolutionary science. "Classification should not be a search for ancestry and descent" (p147). Palaeontologists claimed too much. Fossil evidence has its limitations.

Maybe this situation is comparable with the evolution of Young-Earth-Creationism into Intelligent Design Movement. Attempts to prove the Bible-God are replaced by the claim that one cannot identify *who* designed the world, but one can prove *the fact of design* with mathematical rigor and by inference the existence of *some* intelligent agent (see: William Dembski). So a retreat can be progress if it involves discarding unscientific assertions.

Cladism: evolutionary assumption?

Henry Gee does not doubt common descent of all life:
"That my cat Fred and I really have a common ancestor is not in doubt" (p37).
Again and again this is repeated:
"Even though it is impossible to know for certain whether one species is the ancestor of another, we *do* know that any two organisms found on Earth must be cousins in some degree." (p155).
Common descent of organisms must be a necessary assumption of cladistics because cladograms, are based on common evolutionary innovations (the catlike features in the figures *A* and *B*) and the nodes represent hypothetical ancestors. It would make no sense to construct cladograms if one did not believe that the organisms in the cladogram share a common ancestor. Other sources confirm the existence of these assumptions, for example [An introduction to Cladistics](#) of The Museum of Paleontology of the University of California, Berkeley, UCMP, makes it very clear by listing 3 assumptions of cladistics. The first assumption is: "*Any group of organisms are related by descent from a common ancestor.*"
Far from being a non-evolutionary classification, as Michael Denton(1986) [\(5\)](#) suggested, cladism is based on evolution.

Criticism within bounds

Gee the critic. Gee the authority.

Why does Gee not discuss the evolutionary assumption? Is it reasonable to have common descent as an assumption in cladograms? Is there any direct or indirect way to justify that assumption? Are there alternative assumptions? [\(2\)](#). The critics of evolution did reject that assumption. Gee, a critic of old style palaeontology, a critic of authorities, behaves as an authority when stating: "we

do know that any two organisms found on Earth must be cousins in some degree." How does he know? Here his critical attitude stops. Henry Gee: the authority. It's amazing that the same person severely attacking stories about ancestry and descent, does not try to answer the question: if cladism presupposes evolution, how can cladism be evidence for evolution? He doesn't seem to have any interest in that question. He doesn't feel the need for justification of that assumption. Nevertheless, for those not satisfied with assumptions, it is an exciting question.

Boundaries of the assumption

One obviously cannot construct a cladogram and deny common descent *of the organisms involved in the cladogram*, but that does not mean assuming common descent of *all* life! Cladograms are computationally limited to a small number of species (up to hundreds depending on computer power (8)), so computable cladograms never cover the entire tree of life anyway. So the evolutionary assumption does not say anything about the whole tree of life. It's unnecessary to claim something about the organisms *outside* the cladogram. Just as unnecessary to claim something about the evolutionary *process* which produced the pattern in the cladogram.

Cladism: evidence for evolution?

It seems to me that if constructing cladograms is to be evidence for common descent, then it is immensely important to have an objective measure of failure/success of cladogram construction. Even more important is to report in an unbiased way the successes as well as the failures of the cladogram construction. If they can't fail, what do they tell us? Will the common descent assumption be rejected if they fail? (7) Could it be that any alternative to common descent is always much more unparsimonious? Common descent as the most parsimonious assumption? For example if you didn't connect animals, plants and bacteria into one tree of life, then thousands independent origins of genes must be postulated? Why ignoring these important and exciting questions? I wished Gee had put more energy in pointing out how cladism, while depending on the assumption of evolution, still could be used to confirm evolution. Such would be the case if for example, cladistic trees based on different and independent data confirm each other, thereby giving support to the hypothetical tree as a true representation of reality and thereby confirming the initial assumption (3). Another exciting confirmation is the work of Steven Benner (6), but Gee mentions it only in passing! Benner reconstructed an ancestral molecule in the laboratory based on a cladogram and showed it was functional. Thus a hypothesis about a hypothetical ancestral molecule has been tested. This line of research is extremely important if one seeks independent confirmation of a cladogram including its evolutionary assumptions. The question remains: what happens if trees based on independent data contradict each other?

The critics of evolution

Gee ignored the critics of evolution. However they used to launch the same attacks on missing-link-palaeontology as the cladists. On one hand creationists welcomed cladism because of its radical critical attitude to Darwinist story-telling. This is clear from Phillip Johnson's (4) account of the exhibition of the London Museum of Natural History in 1979 and 1980 and the fact that he visited the late Colin Patterson, the great defender of cladism. Johnson did not tell us *what cladism is*, he only suggested cladism is doubt about the fact of evolution and

nothing more. However: Gee shows the public that cladism is more than doubt and criticism: he introduces us into the method of cladism and shows that it is a scientific method. Michael Denton (5) showed also great interest in cladistics. He interpreted cladism as the abandonment of the evolutionary view. Wrong as we have seen.

On the other hand if creationists discover that cladism *assumes* common descent of all life, they are expected to get angry! and reject it! Can creationists accept cladism? In so far creationists accept micro-evolution (most of them do), they accept common descent of *the species involved* in micro-evolutionary cladograms (2). Even a creationist would agree that tree A is more probable than tree B. Young-Earth-Creationists accept common descent for all humans. So, yes a creationist can construct micro-evolutionary cladograms. The most interesting cladogram in that respect is of course humans and apes. Are humans close to chimps and bonobos in a creationist cladogram? An what does *that* mean? It could be that the principle of parsimony rules out any theory that relies on independent creation (see: [Walter Remine](#)).

Note system

Finally a note on his nearly perfect Note system. The book has one Notes section at the end of the book, which is better than lists at the end of each chapter. The notes are identified by the page number to which they belong. This results in one continuous numbering of notes. This is useful. Further he subdivided the notes section per chapter. This is redundant but adds to its usefulness. However, Gee did not indicate the footnotes in the text itself. So he needed an alternative way of identification: he repeated the full sentence. The perfect note system is John Alcock's double index system: first alphabetise author names, add a sequence number, and use that number in the text.

Notes

1. Roderic Page & Edward Holmes(2000) *Molecular Evolution. A Phylogenetic Approach* focuses on constructing molecular trees. A must for the serious student of cladistics. The more general textbooks of evolution have chapters or paragraphs on cladistics: Monroe Strickberger(2000) *Evolution, Third Edition* discusses in addition to explaining cladistics, 9 (!) objections to cladistics. Mark Ridley(1996) *Evolution. Sec. Edition.* has a few paragraphs on methods of classification, including cladistics; Douglas Futuyma(1998) *Evolutionary Biology. Third Edition* has a good explanation of cladistics in the chapter 'Classification and Phylogeny', including some limitations of cladistic analysis.
2. Is divine creation difficult or easy? Is it an improbable or probable event? A creationist must know the answer before he can chose the most parsimonious tree. If divine creation is easy then a tree with many independent origins is the best one. Then even a million independent creations would be no problem. If divine creation is difficult then a tree with a minimum of independent origins is the best one, just like cladistics with common descent.
3. as suggested to me by Brian R. Speer (University of California Museum of Paleontology, Berkeley).
4. Phillip Johnson, *Darwin on Trial*, Chapter 11 ([reviewed](#) on this site).
5. Michael Denton(1986), *Evolution: A Theory in Crisis*, p138-139. ([reviewed](#) on this site).
6. Thomas M. Jermann, Jochen G. Opitz, Joseph Stackhouse and Stepen A. Benner "Reconstructing the evolutionary history of the artiodactyl ribonuclease superfamily", *Nature* 374, 57-59 (1995).
7. "In some genes of *Arabidopsis*, for reasons that remain obscure, the plant seems to have more in common with people than with yeast, bacteria, nematode worms

or fruit flies. There are surprisingly close homologues between humans and *Arabidopsis* in genes involved in DNA damage repair and transport." Mike Bevan of the John Innes Institute in Norwich quoted by Gail Vines, New Scientist 2 december 2000, p38.

8. According to Stewart Robert Hinsley, cladograms can be produced with Phylip and MEGA from DNA data representing well in excess of 100 species on a 4 year old PC. Larger data sets have been used by professionals (e.g. the angiosperm tree of Soltis and Soltis, from the late 1990's).

Further Reading

- Three important (positive) reviews of *In Search of Deep Time*:
 1. Kevin Padian: "[What the media don't tell you about evolution](#)". Scientific American Feb 2000, pp82-83. An important and approving 2-page review by a palaeontologist.
 2. Peter J. Bowler: "[Life's Sometimes Artful Arrangement](#)". American Scientist March-April 2000. "cladism depends on the notion of common ancestry".
 3. David M Irwin: "[Dead branches on the tree of life](#)". *Nature* **403**, 480-481, 03 February 2000. (subscription necessary for Nature online) gives a nice summary. (approves the book)
- [Introduction to Cladistics](#) from The Museum of Paleontology of the University of California, Berkeley: "Cladistics is a particular method of hypothesizing relationships among organisms based on the idea that members of a group share a common evolutionary history".
- Trisha Gura: "[Bones, molecules ... or both?](#)", *Nature* **406**, 230-233 (2000). Evolutionary trees constructed by studying biological molecules often don't resemble those drawn up from morphology. Can the two ever be reconciled?
- [Profile of Henry Gee](#), Nature magazine.
- Henry Gee: [Evolution: Down with species](#). Nature Science *update*. 19 April 2000.
- Henry Gee (Editor): *Shaking the Tree : Readings from Nature in the History of Life*, Paperback - 411 pages (May 2000) University of Chicago Press. A collection of articles from 'Nature'.
- Henry Gee: [Why have sex?](#). The steamy sex lives of birds could be part of a serious evolutionary game. Nature Science Update, 20 July 2000
- Henry Gee: [Evolution: getting a head](#). Nature Science *update*. 4 August 2000.
- Henry Gee: [Evolution: Shaking the family tree](#), Nature Science Update, 1 February 2001.
- Henry Gee: [A journey into the genome: what's there](#), Nature Science Update, 12 February 2001.
- Henry Gee: "Palaeontology: Return to the planet of the apes", *Nature* **412**, 131-132 (2001). (news and views)
- Henry Gee: "Biogeochemistry: That's life? *Nature* **416**, 28 (2002) 7 March 2002. (news and views)
- Henry Gee: [Two cheers for extinction](#) *Nature* **416**, 28 March 2002 (Nature Science Update, free access).
- Henry Gee: [Early bird ate seeds](#), *Nature*, **418**, July 25 2002 (Nature Science Update, free access).
- Henry Gee: [Face of yesterday](#), on the dramatic discovery of a seven- million-year-old hominid. *The Guardian*, July 11, 2002. This article is typical for Gee. It shows how he thinks about missing links. (there are more articles of Gee in The Guardian).
- Henry Gee: [Fossil boosts trees-down start for flight](#), *Nature*, 23 January 2003 (Nature Science Update, free access).
- Henry Gee: [Evolution: Ending incongruence](#) *Nature* **425**, 782 (23 Oct 2003)

News and Views. (Recovering the true evolutionary history of a group of organisms is now possible with higher reliability).

- Henry Gee (2004) *Jacob's Ladder: The History of the Human Genome*, Foruth Estate, 272 pp. Is reviewed by Andrew Berry in *Nature* **429**, 133 (13 May 2004).
- Henry Gee (2004) [The Tyranny of Design](#), *Nature*, Published online: 07 July 2004. How could sophisticated mechanisms such as the flagellar motor or the adaptive immune system have evolved without some guiding hand? Henry Gee finds his answer to the argument of Intelligent Design in the lamprey.
- Olaf R. P. Bininda-Emonds (2004) "Phylogenetic Supertrees: Combining Information To Reveal The Tree Of Life" (Computational Biology). Kluwer Academic Pub. (This difference in strategy has allowed for the exciting possibility of larger, more complete phylogenies than are otherwise currently possible, with the potential to revolutionize evolutionarily-based research.) [11-11-2004]
- Henry Gee (2004) *The Science of Middle-Earth*. Cold Spring Press: 2004. 256 pp. To be published in the UK by Souvenir Press. Reviewed in *Nature*, **432**, 674 - 675 [09 December 2004].

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