

DARWIN'S "TREE OF LIFE"

PHYLOGENETIC TREES

In biology, a phylogenetic tree, or phylogeny, is used to show the genealogic relationships of living things. A phylogeny is not so much evidence *for* evolution as much as it is a codification of data about evolutionary history. According to biological evolution, organisms share common ancestors; a phylogeny shows how organisms are related. The tree of life shows the path evolution took to get to the current diversity of life. It also shows that we can ascertain the genealogy of disparate living organisms. This is evidence for evolution only in that we can construct such trees at all. If evolution had not happened or common ancestry were false, we would not be able to discover hierarchical branching genealogies for organisms (although textbooks do not generally explain this well). Referring to any phylogenetic tree as "Darwin's tree of life" is somewhat of a misnomer. Darwin graphically presented no phylogenies in the *Origin of Species*; the only figure there depicts differential rates of speciation. If anyone deserves credit for giving us "trees of life," it is Ernst Haeckel, who drew phylogenies for many of the living groups of animals literally as trees, as well as coining the term itself.

WELLS'S SHELL GAME

Wells uses phylogenetic trees to attack the very core of evolution — common descent. Wells claims that textbooks mislead students about common descent in three ways. First, Wells claims that textbooks do not cover the "Cambrian Explosion" and fail to point out how this "top-down" pattern poses a serious challenge to common descent and evolution. Second, he asserts that the occasional disparity between morphological and molecular phylogenies disproves com-

mon descent. Finally, he demands that textbooks treat *universal* common ancestry as unproven and refrain from illustrating that "theory" with misleading phylogenies. Therefore, according to Wells, textbooks should state that there is no evidence for common descent and that the most recent research refutes the concept entirely. Wells is completely wrong on all counts, and his argument is entirely based on misdirection and confusion. He mixes up these various topics in order to confuse the reader into thinking that when combined, they show an endemic failure of evolutionary theory. In effect, Wells plays the equivalent of an intellectual shell game, putting so many topics into play that the "ball" of evolution gets lost.

THE CAMBRIAN EXPLOSION

Wells claims that the Cambrian Explosion "presents a serious challenge to Darwinian evolution" (Wells, 2000:41) and the validity of phylogenetic trees. The gist of Wells's argument is that the Cambrian Explosion happened too fast to allow large-scale morphological evolution to occur by natural selection ("Darwinism"), and that the Cambrian Explosion shows "top-down" origination of taxa ("major" "phyla" level differences appear early in the fossil record rather than develop gradually), which he claims is the opposite of what evolution predicts. He asserts that phylogenetic trees predict a different pattern for evolution than what we see in the Cambrian Explosion. These arguments are spurious and show his lack of understanding of basic aspects of both paleontology and evolution.

Wells mistakenly presents the Cambrian Explosion as if it were a *single* event. The Cambrian Explosion is, rather, the preservation of a series of faunas that occur over a 15–20 million year period starting around 535 mil-

lion years ago (MA). A fauna is a group of organisms that live together and interact as an ecosystem; in paleontology, “fauna” refers to a group of organisms that are fossilized together because they lived together. The first fauna that shows extensive body plan diversity is the Sirius Passet fauna of Greenland, which is dated at around 535 MA (Conway Morris, 2000). The organisms preserved become more diverse by around 530 MA, as the Chenjiang fauna of China illustrates (Conway Morris, 2000). Wells erroneously claims that the Chenjiang fauna predates the Sirius Passet (Wells, 2000:39). The diversification continues through the Burgess shale fauna of Canada at around 520 MA, when the Cambrian faunas are at their peak (Conway Morris, 2000). Wells makes an even more important paleontological error when he does not explain that the “explosion” of the late Early and Middle Cambrian is preceded by the less diverse “small shelly” metazoan faunas, which appear at the *beginning* of the Cambrian (545 MA). These faunas are dated to the early Cambrian, not the Precambrian as stated by Wells (Wells, 2000:38). This enables Wells to omit the steady rise in fossil diversity over the ten million years between the beginning of the Cambrian and the Cambrian Explosion (Knoll and Carroll, 1999).

In his attempt to make the Cambrian Explosion seem instantaneous, Wells also grossly mischaracterizes the Precambrian fossil record. In order to argue that there was not enough time for the necessary evolution to occur, Wells implies that there are no fossils in the Precambrian record that suggest the coming diversity or provide evidence of more primitive multicellular animals than those seen in the Cambrian Explosion (Wells, 2000:42–45). He does this not by producing original research, but by selectively quoting paleontological literature on the fossil record and

claiming that this proves that the fossil record is complete enough to show that there were no precursors for the Cambrian Explosion animals. This claim is false. His evidence for this “well documented” Precambrian fossil record is a selective quote from the final sentence in an article by Benton et al. (2000). While the paper’s final sentence does literally say that the “early” parts of the fossil record are adequate for studying the patterns of life, Wells leaves out a critical detail: the sentence refers not to the Precambrian, but to the *Cambrian and later times*. Even more ironic is the fact that the conclusion of the paper directly refutes Wells’s claim that the fossil record does not support the “tree of life.” Benton et al. (2000) assessed the completeness of the fossil record using both molecular and morphological analyses of phylogeny. They showed that the *sequence of appearance* of major taxa in the fossil record is consistent with the pattern of *phylogenetic relationships* of the same taxa. Thus they concluded that the fossil record is consistent with the tree of life, entirely opposite to how Wells uses their paper.

Wells further asserts that there is no evidence for metazoan life until “just before” the Cambrian explosion, thereby denying the necessary time for evolution to occur. Yet Wells is evasive about what counts as “just before” the Cambrian. Cnidarian and possible arthropod embryos are present 30 million years “just before” the Cambrian (Xiao et al., 1998). There is also a mollusc, *Kimberella*, from the White Sea of Russia (Fedonkin and Waggoner, 1997) dated approximately 555 million years ago, or 10 million years “just before” the Cambrian (Martin et al., 2000). This primitive animal has an uncalcified “shell,” a muscular foot (Fedonkin and Waggoner, 1997), and a radula inferred from “mat-scratching” feeding patterns surrounding fossilized individuals (personal observation; Seilacher, pers.

comm.). These features enable us to recognize it as a primitive relative of molluscs, even though it lacks a calcified shell. There are also Precambrian sponges (Gehling and Rigby, 1996) as well as numerous trace fossils indicating burrowing by wormlike metazoans beneath the surface of the ocean's floor (Seilacher, 1994; Fedonkin, 1994). Trace fossils demonstrate the presence of at least one ancestral lineage of bilateral animals nearly 60 million years "just" before the Cambrian (Valentine et al., 1999). Sixty million years is approximately the same amount of time that has elapsed since the extinction of non-avian dinosaurs, providing plenty of time for evolution. In treating the Cambrian Explosion as a single event preceded by nothing, Wells misrepresents fact — the Cambrian explosion is *not* a single event, *nor* is it instantaneous and lacking in any precursors.

Continuing to move the shells, Wells invokes a semantic sleight of hand in resurrecting a "top-down" explanation for the diversity of the Cambrian faunas, implying that phyla appear first in the fossil record, before lower categories. However, his argument is an artifact of taxonomic practice, not real morphology. In traditional taxonomy, the recognition of a species implies a phylum. This is due to the rules of the taxonomy, which state that if you find a new organism, you have to assign it to all the necessary taxonomic ranks. Thus when a new organism is found, either it has to be placed into an existing phylum or a new one has to be erected for it. Cambrian organisms are either assigned to existing "phyla" or new ones are erected for them, thereby creating the effect of a "top-down" emergence of taxa.

Another reason why the "higher" taxonomic groups appear at the Cambrian Explosion is because the Cambrian Explosion organisms are often the first to show features that allow us to relate them to living groups. The

Cambrian Explosion, for example, is the first time we are able to distinguish a chordate from an arthropod. This does not mean that the chordate or arthropod lineages evolved then, only that they then became recognizable as such. For a simple example, consider the turtle. How do you know a turtle is a turtle? By the shell. How would you recognize the ancestors of the living turtle, before they evolved the shell? That is more complicated. Because its ancestors would have lacked the diagnostic feature of a shell, ancestral turtles may be hard to recognize (Lee, 1993). In order to locate the remote ancestors of turtles, other, more subtle, features must be found.

Similarly, before the Cambrian Explosion, there were lots of "worms," now preserved as trace fossils (i.e., there is evidence of burrowing in the sediments). However, we cannot distinguish the chordate "worms" from the mollusc "worms" from the arthropod "worms" from the worm "worms." Evolution predicts that the ancestor of all these groups was wormlike, but which worm evolved the notochord, and which the jointed appendages? In his argument, Wells confuses the identity of the individual with how we diagnose that identity, a failure of logic that dogs his discussion of homology in the following chapter. If the animal does not have the typical diagnostic features of a known phylum, then we would be unable to place it and (by the rules of taxonomy) we would probably have to erect a new phylum for it. When paleontologists talk about the "sudden" origin of major animal "body plans," what is "sudden" is not the appearance of animals with a particular body plan, but the appearance of animals that *we can recognize* as having a particular body plan. Overall, however, the fossil record fits the pattern of evolution: we see evidence for worm-like bodies first, followed by variations on the worm theme. Wells seems to ignore a growing body

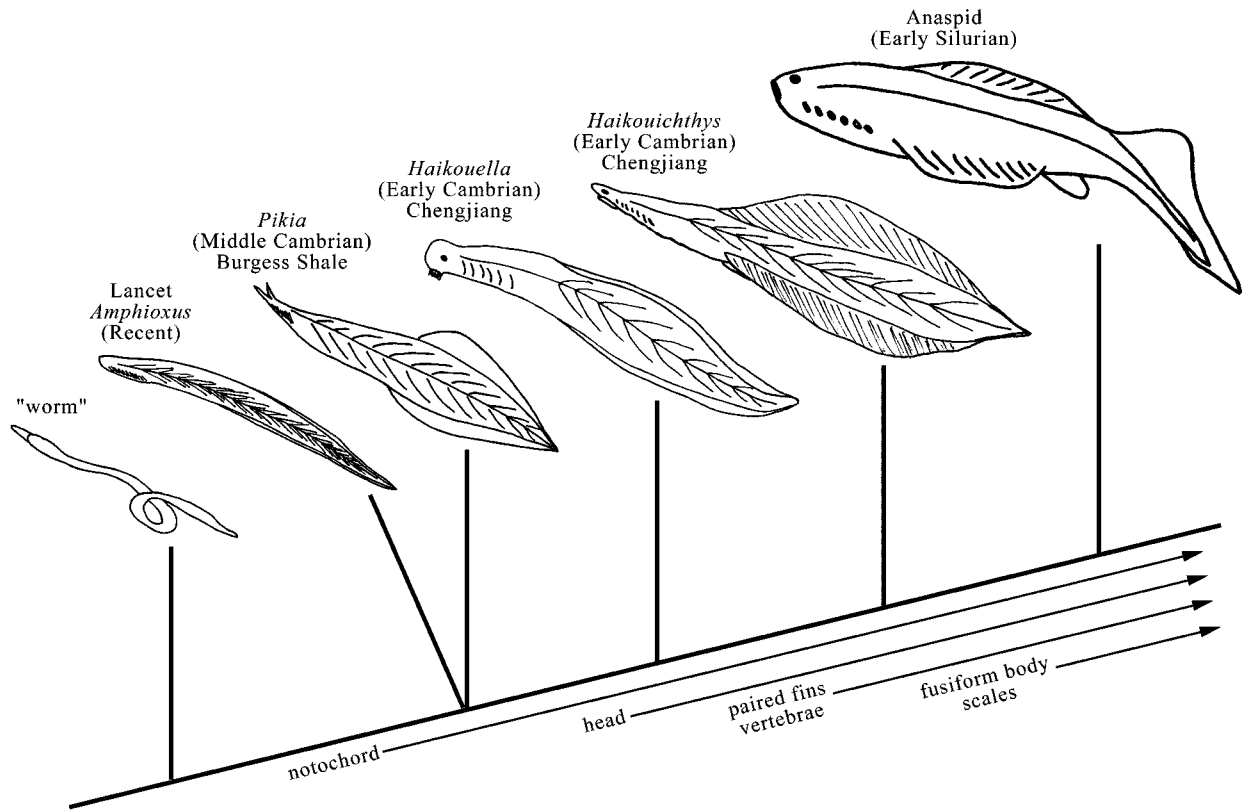


Figure 3. Stepwise evolution of vertebrate features as illustrated by living and fossil animals.

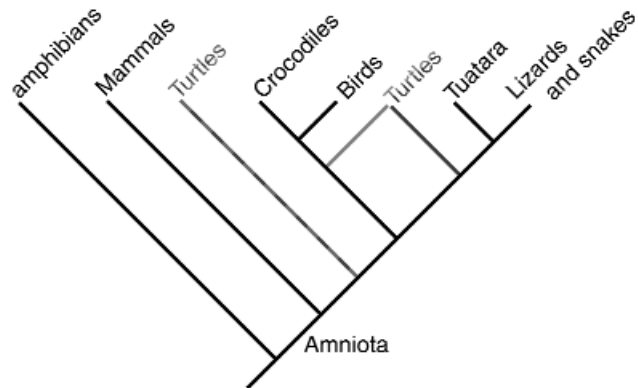
of literature showing that there are indeed organisms of intermediate morphology present in the Cambrian record and that the classic “phyla” distinctions are becoming blurred by fossil evidence (Budd, 1998, 1999; Budd and Jensen, 2000).

Finally, the “top-down” appearance of body-plans is, contrary to Wells, compatible with the predictions of evolution. The issue to be considered is the practical one that “large-scale” body-plan change would of course evolve before minor ones. (How can you vary the lengths of the beaks before you have a head?) The difference is that, many of the “major changes” in the Cambrian were initially minor ones. Through time they became highly significant and the basis for “body-plans.” For example, the most primitive living chordate *Amphioxus* is very similar to the Cambrian fossil chordate *Pika*. Both are basi-

cally worms with a stiff rod (the notochord) in them. The amount of change between a worm and a worm with a stiff rod is relatively small, but the presence of a notochord is a major “body-plan” distinction of a chordate. Further, it is just another small step from a worm with a stiff rod to a worm with a stiff rod and a head (e.g., *Haikouella*; Chen et al., 1999) or a worm with a *segmented* stiff rod (vertebrae), a head, and fin folds (e.g., *Haikouichthys*; Shu et al., 1999). Finally add a fusiform body, fin differentiation, and scales: the result is something resembling a “fish” (Figure 3). But, as soon as the stiff rod evolved, the animal was suddenly no longer just a worm but a chordate — representative of a whole new phylum! Thus these “major” changes are really minor in the beginning, which is the Precambrian–Cambrian period with which we are concerned.

CONGRUENCE OF PHYLOGENIES BASED ON DIFFERENT SOURCES OF DATA

Wells also points to the occasional lack of congruence between molecular- and morphology-based phylogenies as evidence against common descent. (Molecular phylogenies are based on comparisons of the genes of organisms.) Wells omits the fact that the discrepancies are frequently small, and their causes are largely understood (Patterson et al., 1993; Novacek, 1994). Although not all of these discrepancies can yet be corrected for, most genetic and morphological phylogenies are congruent for 90% of the taxa included. For example, all phylogenies, whether morphological or molecular, consider all animals bearing amniotic eggs to be more closely related to one another than to amphibians. Within this group, all reptiles and birds are more closely related to each other than they are to mammals. Finally, birds and crocodiles are more closely related to each other than to lizards, snakes, and the tuatara (Gauthier et al., 1988; Gauthier, 1994). The only group whose placement varies for both molecular and morphology data sets is turtles. This is due to a phenomenon called “long branch attraction” or the “Felsenstein Zone” (Huelsenbeck and Hillis, 1993). Long branch attraction is caused when an organism has had so much evolutionary change that it cannot be easily compared to other organisms, and due to the nature of the methodology used to evaluate phylogeny, it can appear to be related to many possible organisms (Felsenstein, 1978; Huelsenbeck and Hillis, 1993). This is the case for turtles. Turtles are so morphologically and genetically different from the rest of the reptiles that they are hard to place phylogenetically (Zardoya and Meyer, 2001). Still, researchers have narrowed down the possible turtle relationships to



"Traditional" turtle relationship based on morphological data (e.g. Gregory, 1946; Gauthier et al., 1988; Gauthier, 1994; Lee, 1997).
"Odd" turtle relationship based on molecular data (Zardoya and Meyer, 1998; 2001).
"Odd" turtle relationship based on morphological data (Rieppel and deBraga, 1996; deBraga and Rieppel, 1997; Rieppel and Reiz, 1999).
"Traditional" turtle position based on "total evidence" combined analysis of molecular and morphological data (Eernise and Kluge, 1993).

Figure 4. Amniote relationships based on different sources of data. Note that the only group whose position varies is turtles.

a few possibilities (Rieppel and deBraga, 1996; Lee, 1997; deBraga and Rieppel, 1997; Zardoya and Meyer, 1998; Rieppel and Reiz, 1999; Rieppel, 2000; Figure 4), and none of these claim turtles are mammals. The uncertainty over the precise placement of turtles with respect to other groups, however, does not mean that they did not evolve. Unfortunately, genes can never be totally compared to morphology since genetic trees cannot take fossil taxa into account: genes don't fossilize. No diagnostic tool of science is perfect. The imperfections in phylogenetic reconstruction do not make common ancestry false. Besides, are these extremely technical topics really appropriate for introductory textbooks?

Instead of clearly discussing these actual phylogenetic issues, Wells invents one that isn't even real. He cites a 1998 paper that placed cows phylogenetically closer to whales than to horses, calling that finding “bizarre” (Wells, 2000:51). Yet this is not “bizarre” at all; it was *expected*. All the paleontological and molecular evidence points to a whale

origin within artiodactyls, and further to the fact that artiodactyls (cows, deer, antelopes, pigs, etc.) are not more closely related to perissodactyls (horses, rhinos, and the tapir) than they are to whales (Novacek, 1992, 2001). Wells makes this statement smugly, as if to suggest that everyone should think that this sounds silly. Unfortunately, it is Wells's criticism that is silly.

THE UNIVERSAL COMMON ANCESTOR

Finally, Wells cites the “failure” of molecular phylogeny to clarify the position of the Universal Common Ancestor as proof that there is no common ancestry for any of life. Here, Wells mixes up the different scales of descent in order to tangle the reader in a thicket of phylogenetic branches. He is

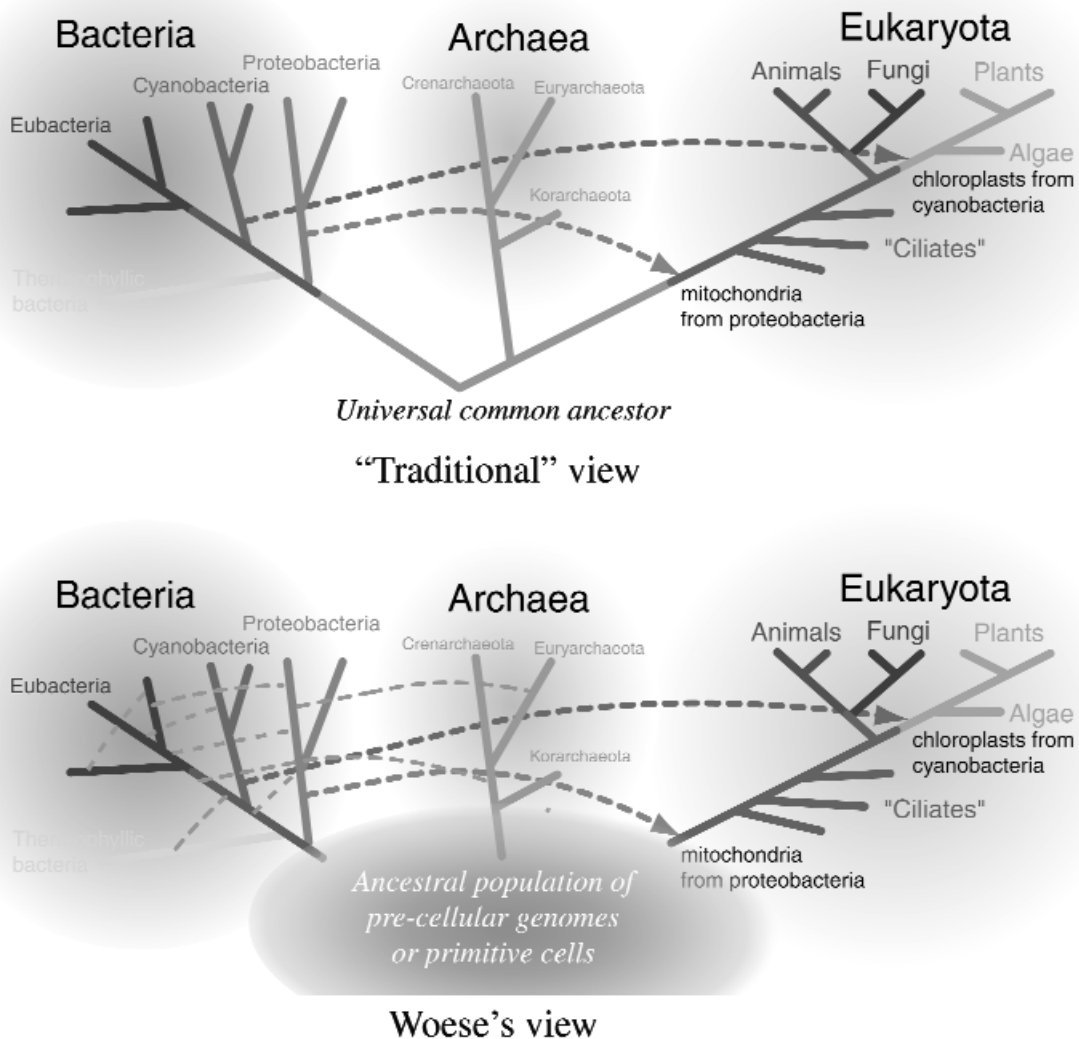


Figure 5. The traditional view of phylogenetic relationships for the three “domains” of life compared to Woese’s view. Note that the only difference lies in whether there is a single “root” at the base of the tree. Regardless, eukaryotes, archaeans, and bacteria all share a common ancestor on both, although Woese does posit a greater degree of lateral transfer for single-celled organisms.

attacking the notion that life originated with one population, and that all life can trace its ancestry back to that population, the Universal Common Ancestor (UCA). The problem has been that it is hard to determine relationships when there is nothing to compare to. How do you compare “not life” to “life”? We have no fossils of the earliest forms of life, and the high degree of genetic change that has occurred in the 3.8 billion years since the early stages of life make it nearly impossible to reconstruct the “original” genetic code. This does not invalidate the concept of common ancestry; it just makes it difficult and potentially impossible to untangle the lineages. And this does not mean that there is not one real lineage: the inability to determine the actual arrangement of “domains” at the base of the tree or to characterize the UCA does not make the UCA any less real than the inability to characterize light unambiguously as either a wave or a particle makes light unreal.

Some authors (e.g., Woese, 1998) go further and suggest that there is no “UCA”; rather, they suggest, life arose in a soup of competing genomes. These genomes were constantly exchanging and mixing, and thus cellular life may have arisen multiple times. Wells misrepresents the statements of those scientists to make it look as if they are questioning the entirety of common ancestry, when what they question is just the idea of a *single* common ancestor at the base of life. Further, when some suggest that we should abandon the search for the UCA, they do not mean that they don’t think it existed. They mean only that it may be a waste of time to try to find it given the current technology and methods at our disposal. Regardless of the status of a UCA, which is at the base of the tree of life, the entire debate has nothing to do with the branches of the tree — the shared descent of eukaryotes, of animals, or common descent among vertebrates, arthro-

pods, or angiosperms (Figure 5). That is still *a lot* of evolution that Wells’s inaccurate attack on the idea of a UCA does nothing to dispel.

WHAT THE TEXTBOOKS SAY

The concept of common ancestry is at the core of evolution. The very idea that different species arise from previous forms via descent implies that all living things share a common ancestral population at some point in their history. This concept is supported by the fossil record, which shows a history of lineages changing through time. Because evolution is the basis for biology, it would be surprising if any textbook teaching contemporary biology would portray common descent other than matter-of-factly.

Textbooks treat the concept of common descent in basically the same way as do scientists; they accept common ancestry of living things as a starting point, and proceed from there. Phylogenies thus appear in many places in a text, which makes it very hard to evaluate exactly how textbooks “misrepresent” biological evolution using trees. Most texts show a phylogeny in chapters discussing systematics and taxonomy. In this section there is usually a tree of “kingdom” or “domain” relationships, which may be what Wells considers a tree showing “universal” common ancestry; unfortunately, his discussion is too vague for a reader to be sure whether that is what he is referring to. Many textbooks show additional, more detailed trees in their discussions of different taxonomic groups. In terms of textbook presentations, then, there is no single “Darwin’s tree of life” presented in some iconic state, but many various phylogenies shown in the appropriate sections of most books. Textbooks also present trees in the chapters on processes and mechanisms of evolution, in the “Origin of life” or “History of life” chapters, and in chapters dealing with individual taxonomic groups.

| Book | Darwin's "Tree of Life" | | | |
|---|-------------------------|-------------------|-------------------|----------------|
| | //pages | //words | mentions Cambrian | Wells's grade |
| Schraer, W. D. and H. J. Stolze. 1999. <i>Biology: The Study of Life</i> , seventh edition. Prentice-Hall, Upper Saddle River, NJ. 944p. | 3/4 (1) | 148 | No | F |
| Johnson, G. B. 1998. <i>Biology: Visualizing Life</i> . Holt, Rinehart & Winston, Orlando. 895p. | (8) | NA ¹ | Yes | F ² |
| Biggs, A., C. Kapinka, and L. Lundgren. 1998. <i>Dynamics of life</i> . Glencoe/McGraw Hill, Westerville, OH. 1119p. | 1 (15) | 105 | Yes | F ³ |
| Miller, K. R. and J. Levine. 2000. <i>Biology</i> , fifth edition. Prentice-Hall Upper Saddle River, NJ. 1114p. | 1(10) | 302 | Yes* | F ⁴ |
| Starr, C. and R. Taggart. 1998. <i>Biology: The Unity and Diversity of Life</i> , eighth edition. Wadsworth Publishing Company, Belmont CA. 920p. | (31) | NA ⁵ | Yes | F ⁶ |
| Guttman, B. S. 1999. <i>Biology</i> . WCB/McGraw-Hill, Boston. 1175p. | 1 (24) | 1111 ⁷ | No | F |
| Mader, S. 1998. <i>Biology</i> , sixth edition. WCB/McGraw-Hill, Boston. 944p. | (15) | NA ⁸ | Yes | F ⁹ |
| Raven, P. H. and G. B. Johnson. 1999. <i>Biology</i> , fifth edition. WCB/McGraw-Hill Boston. 1284p. | (19) | NA | No | F |
| Campbell, N. A., J. B. Reese, and M. G. Mitchell. 1999. <i>Biology</i> , fifth edition. Benjamin Cummings, Menlo Park, CA. 1175p. | NA ¹⁰ | NA ¹⁰ | Yes | D |
| Futuyma, D. 1998. <i>Evolutionary Biology</i> . Sinauer Associates, Sunderland, MA. 761p. | 1+ ¹¹ | >200 | Yes | D |

1. Johnson contains no specific section for a "tree of life"; some phylogenies appear in the text.
2. Johnson discusses the rapid origin of major animal body plans in the Cambrian, though he does not call it an "explosion." A "D" would be a more appropriate grade.
3. Wells grade is an "F"; however, the book discusses the Cambrian in the "History of life" section (p. 406), although it does not explicitly call it "explosion." A "D" may be a more appropriate grade on Wells's scale.
4. The text explicitly discusses the "Cambrian Explosion" by name on p. 601; it also discusses problems with rooting the universal tree on p. 326. A "D" would be a more appropriate grade, perhaps even a "D+."
5. Much like Campbell et al., Starr and Taggart integrate phylogenies throughout the text and use them to structure the diversity of life section.
6. The text discusses the Cambrian, although it does not refer explicitly to an "explosion." A "D" would be a more appropriate grade.
7. Guttman devotes one paragraph to describing what phylogenetic trees are. Trees appear throughout the book when discussing evolutionary relationships of different organisms.
8. There is no single "tree of life" section in the text. Phylogenetic method is discussed in detail in the "Classification" chapter (chapter 28; p. 491–506) and phylogenetic trees appear throughout the text.
9. The Cambrian is discussed in the "History of life" section (chapter 20; p. 333) but is not called an "explosion". A "D" may be a more appropriate grade.
10. Phylogenetic trees are integrated throughout Unit 5 (p. 490–665), and there is no single treatment of the "tree" in the evolution chapter.
11. Futuyma has a section titled "Tree of life" in the "History of life" chapter; however, phylogenetic trees appear throughout the book.

Figure 6. Evaluation of Wells's grading of Textbook Icon #2, "Darwin's Tree of Life." Parenthetical notations indicate the number of phylogenetic trees shown in the book.

This is because phylogenetic trees are not part of the “evidence for evolution,” but rather graphical representations of the history, genealogy, and taxonomy of life. No textbook misrepresents the methods that are used to construct trees or the trees themselves, although some trees contain out-of-date relationships and occasionally incorrect identifications of organisms pictured in them. When textbooks cover the Cambrian period, the rapid appearance of many body plans is discussed not as a “paradox” for evolutionary theory, but as an interesting event in the history of life — which is how paleontologists and evolutionary biologists consider it.

WELLS’S EVALUATION

Overall, Wells’s grading system for this “icon” is so nebulous that it is hard to figure out exactly how he evaluated the textbooks at all. The “Universal Common Ancestor” is far different from the “Cambrian Explosion.” These deal with very different places in the “tree of life” as well as very different issues in evolution. Wells’s grades seem largely based on presentations of “common ancestry.” For example, according to Wells, if the textbook treats common ancestry as “fact,” then it can do no better than a D. In order to get a C or better, a book must also discuss the “top-down” nature of the Cambrian explosion as a “problem” for evolution; if a book only mentions the Cambrian Explosion, it gets a D. Here Wells does not even apply his grading scheme consistently (Figure 6). For example, Wells chastises textbooks (Miller and Levine’s in particular) for not discussing the Cambrian Explosion, yet most of the textbooks he reviews actually mention it (Figure 6) and Miller and Levine devote an entire page (p. 601) to it. Many of the reviewed textbooks discuss the Cambrian period in the history of life sections, but do not specifically call it an

“explosion.” These discussions usually mention that it was a “rapid” origin of animal groups. Does Wells actually require that the book *explicitly* mention the “Cambrian Explosion” by name? If so, it should have been specified in the criteria. Or is it that he only looked for “Cambrian Explosion” in the notoriously spotty indexes of the textbooks? A reevaluation suggests that five of the books to which he gives an F should receive, even by his criteria, a D. Finally, one text (Miller and Levine’s) even mentions the confusing nature of the basal divergence of life caused by lateral transfer, yet this discussion can receive no credit in the grading. This is because although Wells considers the “phylogenetic thicket” to be extremely important to reject universal common ancestry, he apparently does not consider it important enough to account for it in his grading scheme. All of this calls into question how well Wells actually reviewed the texts he graded as well as whether his grades have any utility at all.

WHY WE SHOULD CONTINUE TO TEACH COMMON DESCENT

There is no reason for textbooks to significantly alter their presentations of common descent or phylogenetic trees. As long as biological evolution is the paradigm of biology, common descent should be taught. All living organisms that reproduce have offspring that appear similar to, but not exactly like, their parents. We can observe descent with modification every day, and like Darwin, we can confidently extrapolate that it has gone on throughout the history of life. Through this process, small differences would accumulate to larger differences and result in the evolution of diversity that we see today and throughout the history of life.

The concept of descent allows us to make testable predictions about the fossil record and

the genetics of organisms. For example, we predict that all animals sharing a common ancestor would have a similar genetic code, use the same cellular processes, and so on; these predictions are confirmed by biochemistry and genetics. In terms of fossils, we would expect to see animals with transitional morphologies in the past, as well as animals that appear similar, but not identical, to those living today. We also predict that these organisms, both past and present, can be arranged into a branching hierarchy of forms, which appears much like a genealogy. This is what the biological community considers science; this is what we should teach.

HOW TEXTBOOKS COULD IMPROVE THEIR PRESENTATIONS OF PHYLOGENY

There is always room for improvement in the presentations of the concept of common descent. Textbooks could improve by updating the phylogenies, many of which are now out-of-date. They should also remove discussions of “phenetics” (an outdated form of phylogenetic reconstruction and classification) from the phylogenetic reconstruction sections, and expand discussions of cladistics and more modern descent-based taxonomies. Finally, textbooks should make a clear distinction between molecular clocks and genetic phylogenies, something many fail to do clearly. However, to make textbooks conform to Wells’s criteria would be to misrepresent the entire life sciences and to deprive students of pedagogically useful visual representations of the unity of life.

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