A CRITIQUE OF "29 EVIDENCES FOR MACROEVOLUTION" PART 1

By Ashby L. Camp

In "29 Evidences for Macroevolution," Douglas Theobald sets forth the evidence that he believes proves scientifically that all living organisms descended from "one original living species." He does so by listing what he claims are 29 potentially falsifiable predictions of the hypothesis of universal common ancestry and presenting the evidence that he believes confirms each of those predictions.

Dr. Theobald does not address the origin of the first living thing or the mechanism by which that first organism diverged into every life form that has ever existed. His thesis is expressly restricted to the affirmation of universal common ancestry. In other words, he argues that, without knowing anything about how the first life arose or how it diversified, one can still be certain that all living things descended from the same ancestor. He states in the introduction (emphasis supplied):

> In this treatise, I consider only macroevolution [which he labels a "virtual synonym" for universal common descent]. I do not consider microevolutionary theories, such as natural selection, genetic drift, sexual selection, theories of speciation, etc., *which biologists use as mechanistic theories to explain macroevolution*. Neither do I consider abiogenesis; I take it as axiomatic that an original self-replicating life form existed in the distant past.

In the conclusion, he says (emphasis supplied):

> These previous points are all proofs of macroevolution alone; the evidences and the conclusion *are independent of any explanatory mechanism*. This is why scientists call macroevolution the "fact of evolution." None of the 29 predictions directly address how macroevolution has occurred; nevertheless, *the validity of the macroevolutionary conclusion does not depend on whether Darwinism, Lamarckism, or something else is the true mechanism of evolutionary change or not. The macroevolutionary conclusion still stands, regardless*.

Dr. Theobald understandably seeks to free the claim of universal common ancestry from the debate about the sufficiency of evolutionary mechanisms, particularly the debate about neo-Darwinism. It should not go unnoticed, however, that a bare claim of universal common ancestry is compatible with *all* mechanisms of common descent, including divine direction. So if God chose to have a reptile give birth to a bird, for example, that would be consistent with an "amechanistic" argument for universal common ancestry.[1]

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[1] Dr. Theobald contradicts his claim to argue for common ancestry without regard to any particular mechanism by including in his definition of macroevolution the requirement of *gradualness*. He states,

The fact Dr. Theobald leaves the mechanism of descent completely open does not make his claim trivial. On the contrary, the claim of universal common ancestry is incompatible with the belief that God separately created more than one living thing. It therefore challenges the convictions of biblical creationists, progressive creationists, and all who believe that mankind was created separately from animals.

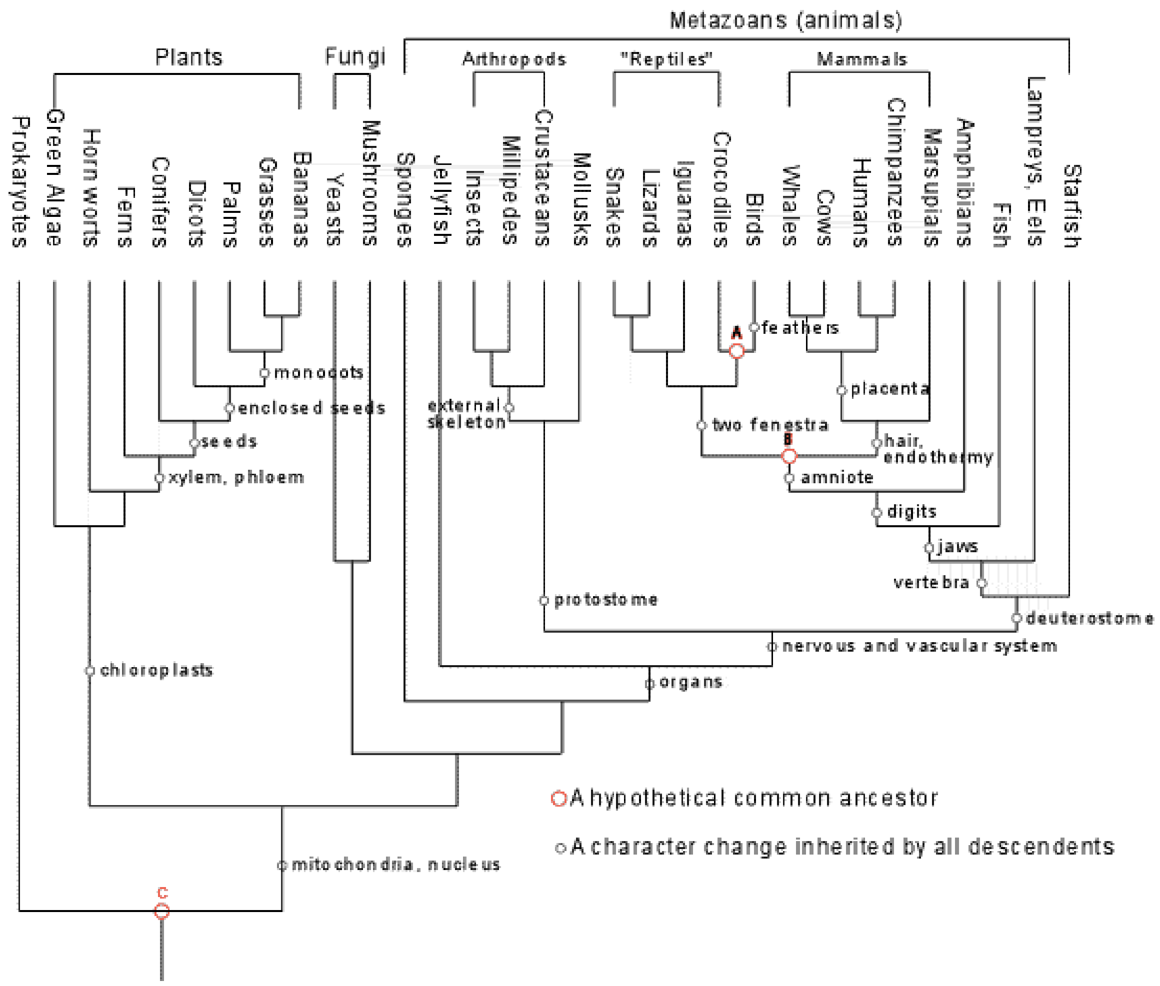
I address Dr. Theobald's predictions in the order in which he presented them. The italicized paragraphs following the predictions are quotations from his article. I quote only the prediction portion (or what I deem the relevant parts of it), not the alleged confirmations and potential falsifications. That would require me to duplicate the entire article. The accuracy of my references to the alleged confirmations or potential falsifications can be verified by consulting Dr. Theobald's article. It is available online at www.talkorigins.org/faqs/comdesc/.

I appreciate the civility with which Dr. Theobald argued his case and hope that my response is in kind. I also appreciate his candor in acknowledging that "science can never establish 'truth' or 'fact' in the sense that a scientific statement can be made that is formally beyond question." (That may seem obvious to those attuned to the philosophy of science, but I suspect it will come as a surprise to many.) So however much weight one assigns to the evidences adduced by Dr. Theobald, they cannot "prove" universal common ancestry in the sense of rendering its rejection illogical.[2] That being said, the focus of this response is on the weight to which the evidences are entitled.

I include here for convenient reference Dr. Theobald's Figure 1, which he labels "The standard phylogenetic tree."

"Macroevolution, as I will use it, is the theory of common descent with *gradual* modification" (emphasis supplied). He states further that "[g]radualness concerns genetically probable organismic changes between two consecutive generations, i.e., those changes that are within the range of normal variation observed within modern populations." There is no reason to believe that the range of variation observed within modern populations can account for the creation of new organs, structures, and systems as required by the hypothesis of universal common ancestry. In restricting the mechanism of macroevolution to observable degrees of genetic variation, Dr. Theobald lets in the back door the very debate about mechanism that he tossed out the front. He thereby assumes the burden of proving that accumulated observable variation can account for universal common ancestry. Since he makes no attempt to meet that burden but rather repeatedly disavows the relevance of any particular mechanism of modification, I assume he did not intend to specify accumulated observable variation as the mechanism of macroevolution, despite what his definitions may suggest.

[2] This limitation is evident, from a philosophical perspective, by the fact the evidences, if offered as formal proofs, are in the form "If A (universal common ancestry), then B; B therefore A." This argument is a non sequitur, known more specifically as the fallacy of affirming the consequent.



PREDICTION 1: THE FUNDAMENTAL UNITY OF LIFE

According to the theory of common descent, modern living organisms, with all their incredible differences, are the progeny of one single species in the distant past. In spite of the extensive variation of form and function among organisms, several fundamental criteria characterize all life. Some of the macroscopic properties that characterize all of life are (1) replication, (2) information flow in continuity of kind, (3) catalysis, and (4) energy utilization (metabolism). At a very minimum, these four functions are required to generate a physical historical process that can be described by a phylogenetic tree.

If every living species descended from an original species that had these four obligate functions, then all living species today should necessarily have these functions. Most importantly, they should have inherited the structures that perform these functions. The genealogical relatedness of all life predicts that organisms should be very similar in the particular mechanisms and structures that execute these basic life processes.

The alleged prediction and fulfillment are:

(1) If universal common ancestry is true, then all organisms will have one or more traits in common.

(2) All organisms have one or more traits in common.

Unless one inserts an additional premise imposing a limit on the degree to which descendants can vary (which would require specification of a mechanism of descent), the claim of common ancestry does not require that all of the descendants share one or more traits. There is no *logical* reason why completely novel organisms could not arise in one or more lineages. Absent specification of a mechanism of descent, which Dr. Theobald purposefully avoids, there is no way to tether the traits of the descendants to those of the common ancestor.

The belief that evolution predicts biologic universals is "one of evolution's major illusions." (ReMine, 92.) As Walter ReMine says:

> First, evolution does not predict that life would arise precisely once on this planet. If there were two or more unrelated systems of life, then evolutionary theory would effortlessly accommodate that situation.[3]
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> Second, even if life originated precisely once, then evolutionary theory would still not predict biologic universals. Shortly after life's origin, nothing prevented life from branching and leading separate lineages to higher life forms entirely lacking the known biologic universals.
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> Third, evolutionary loss and replacement processes could prevent biologic universals. If one organism is a distant ancestor to another, then nothing in evolution predicts the two must share similarities. If evolution were true, then distant ancestors and descendants (as well as sister groups) can be totally different.
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> Evolution never did predict biologic universals, it merely accommodated them. (ReMine, 92-93.)

Biophysicist Cornelius G. Hunter concurs. He writes:

> There is yet another reason that the universality of the genetic code is not strong evidence for evolution. Simply put, the theory of evolution does not predict the genetic code to be universal (it does not, for that matter, predict the genetic code at all). In fact, leading evolutionists such as Francis Crick and Leslie Orgel are surprised that there aren't multiple codes in nature.

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[3] Dr. Theobald assumes a single origin of life, so this comment is beyond the scope of his paper. I include it to provide context for the remainder of the quote.

> Consider how evolutionists would react if there were in fact multiple codes in nature. What if plants, animals, and bacteria all had different codes? Such a finding would not falsify evolution; rather, it would be incorporated into the theory. For if the code is arbitrary, why should there be just one? The blind process of evolution would explain why there are multiple codes. In fact, in 1979 certain minor variations in the code were found, and evolutionists believe, not surprisingly, that the variations were caused by the continuing evolution of the universal genetic code. Of course, it would not be a problem for such an explanation to be extended if it were the case that there were multiple codes. There is nothing wrong with a theory that is comfortable with different outcomes, but there is something wrong when one of those outcomes is then claimed as supporting evidence. If a theory can predict both A and not-A, then neither A nor not-A can be used as evidence for the theory. When it comes to the genetic code, evolution can accommodate a range of findings, but it cannot then use one of those findings as supporting evidence. (Hunter, 38.)

The fact some leading evolutionists believe early life forms were biochemically distinct from modern forms confirms that evolution does not predict biologic universals. Robert Shapiro, for example, entertains the possibility of finding living relics of an original protein-based life form that lacked DNA and RNA. (Shapiro, 293-295.) Likewise, A. G. Cairns-Smith thinks that descendants of ancient crystalline clay organisms may be all around us. He states: "Evolution did not start with the organic molecules that have now become universal to life: indeed I doubt whether the first organisms, even the first evolved organisms, had any organic molecules in them at all." (Cairns-Smith, 107.)

On the other hand, ReMine argues that biologic universals *are* a prediction of his message theory of creation, which "says all life was constructed to look like the unified work of a single designer." (ReMine, 94.) So evolution does not predict the unity of living things, but at least one theory of creation does.

Of course, the biochemical similarity of living things fits easily within a creation framework. As biochemist Duane Gish explains:

> A creationist would also expect many biochemical similarities in all living organisms. We all drink the same water, breathe the same air, and eat the same food. Supposing, on the other hand, God had made plants with a certain type of amino acids, sugars, purines, pyrimidines, etc.; then made animals with a different type of amino acids, sugars, purines, pyrimidines, etc.; and, finally, made man with a third type of amino acids, sugars, etc. What could we eat? We couldn't eat plants; we couldn't eat animals; all we could eat would be each other! Obviously, that wouldn't work. All the key molecules in plants, animals, and man had to be the same. The metabolism of plants, animals, and man, based on the

> same biochemical principles, had to be similar, and therefore key metabolic pathways would employ similar macromolecules, modified to fit the particular internal environment of the organism or cell in which it must function. (Gish, 277.)

As for the alleged fulfillment, I do not doubt that all living things have carried out the basic functions of life in similar ways, but there are many organisms, past and present, about which we know nothing. It is impossible to be certain that none of these organisms is (or was) biochemically unique (witness the speculations of Shapiro and Cairns-Smith). The claim that all organisms have one or more traits in common is true in the sense that all living things necessarily have the traits by which life is defined, but that is simply a tautology -- living things all have the traits of living things.

PREDICTION 2: A "NESTED" HIERARCHY OF SPECIES

As you can see from the phylogeny in Figure 1, the predicted pattern of organisms at any given point in time can be described as "groups within groups." This nested hierarchical organization of species contrasts sharply with the continuum of "the great chain of being" and the continuum predicted by Lamarck's theory of organic progression. Few other natural processes would predict a nested hierarchical classification. Real world examples that cannot be classified as such are elementary particles (which are described by quantum chromodynamics), the elements (whose organization is described by quantum mechanics and illustrated by the periodic table), the planets in our Solar System, books in a library, or specially designed objects like buildings, furniture, cars, etc. That certain organisms merely are similar to each other is not enough to support macroevolution; the nested classification pattern that satisfies the macroevolutionary process is very specific.

The alleged prediction and fulfillment are:

(1) If universal common ancestry is true, then organisms will be classifiable in a nested hierarchy.

(2) Organisms are classifiable in a nested hierarchy.

It is not a corollary of the hypothesis of common descent that organisms will have features by which they can be classified as groups within groups. Common descent can explain or accommodate nested hierarchy (though not without difficulty in the specific case of neo-Darwinism), but it does not predict it. There are mechanisms of descent from a common ancestor that would yield a different pattern. If common descent can yield either nested hierarchy or something else, then the presence of nested hierarchy does not count as evidence of common descent.

Hunter puts it this way:

> It has been known since Aristotle that species tend to cluster in a hierarchical pattern, and in the eighteenth century Linnaeus saw it as a reflection of the Creator's divine plan. Obviously this pattern does not force one to embrace evolution. Also, Darwin's law of natural selection does not predict this pattern. He had to devise a special explanation -- his *principle of divergence* -- to fit this striking pattern into his overall theory. To be sure, evolution can accommodate this hierarchical pattern, but the pattern is not necessarily implied by evolution. (Hunter, 108.)

Even a mechanism of descent that includes branching events does not ensure a nested pattern. As ReMine explains:

> The pattern of descent depends on the extent that evolved characters are later lost. Suppose losses are significant, and characters are replaced at a high rate. Then there is no reason to expect a nested pattern. Descendants could be totally different from their distant ancestors and sister groups, with little or no semblance of nested similarities linking them. (ReMine, 343.)
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> Evolution does not predict a hierarchical pattern. Simple processes of loss, replacement, anagenesis, transposition, unmasking, or multiple biogenesis would prohibit such a pattern. Since hierarchical patterns (such as cladograms or phenograms) are not predicted by evolution they are not evidence for evolution. (ReMine, 444.)

In fact, nested hierarchy raises some difficult issues within a neo-Darwinian framework. As Michael Denton observes:

> In the final analysis the hierarchic pattern is nothing like the straightforward witness for organic evolution that is commonly assumed. There are facets of the hierarchy which do not flow naturally from any sort of random undirected evolutionary process. If the hierarchy suggests any model of nature it is typology[4] and not evolution. How much easier it

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[4] "Typology" views organisms as variations of *distinct* archetypes. See, Denton (1986), 93-118. With reference to nested hierarchy, Denton writes:

> The sort of evolution [pre-Darwinian typologists] conceived was the creative derivation of all the members of a class from the hypothetical archetype which existed in the mind of God. When typologists drew up branching tree diagrams to illustrate the relationships between different species, this did not imply that the members of a class had been derived by natural descent from a common ancestor. None of the nodes or branches of such trees had any real empirical existence; they were 'links' but only in an abstract and ideal sense. As Agassiz in his essay on classification maintained:
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> > *What we call branches expresses, in fact, a purely ideal connection between animals, the intellectual conception which unites them in creative thought.* It seems to me that the more we examine the true significance of this kind of

> would be to argue the case for evolution if all nature's divisions were blurred and indistinct, if the *systema naturalae* was largely made up of overlapping classes indicative of sequence and continuity. (Denton 1986, 136-137.)

The notion that the nested hierarchy of organisms is incompatible with creation is based, not on science, but on the unprovable theological assumption that if God created life he would do it in some other way. As biologist Leonard Brand explains:

> The hierarchical arrangement of life illustrated in Fig. 9.6 has been used by Futuyma (1983) and others as evidence that life must have evolved. They believe that if life were created, the characteristics of different organisms would be arranged chaotically or in a continuum, not in the hierarchy of nested groups evident in nature. If we think of that concept as a hypothesis, how could it be tested? Actually, to state how a Creator would do things and then show that nature is or is not designed that way is an empty argument. Such conjecture depends on the unlikely assumption that we can decide what the Creator would be like and how he would function. (Brand, 155.)

It may be that the nested hierarchy of living things simply is a reflection of divine orderliness. It also may be, as Walter ReMine suggests, that nested hierarchy is an integral part of a message woven by the Creator into the patterns of biology. (See, e.g., ReMine, 367-368, 465-467.) The point is that the hierarchical nature of life can be accommodated by creation theory as readily as by evolution. Accordingly, "[i]t is not evidence for or against either theory." (Brand, 155.)

Dr. Theobald's claim that "specially designed objects like buildings, furniture, cars, etc." cannot be classified in a nested hierarchy requires elaboration. In terms of mere classification, it is incorrect. Buildings and vehicles have both been used as examples of nesting (Ridley 1993, 52-54; Fastovsky and Weishampel, 51-53; Brand, 165-166). According to Mark Ridley:

> Any set of objects, whether or not they originated in an evolutionary process, can be classified hierarchically. Chairs, for instance, are independently created; they are not generated by an evolutionary process: but any given list of chairs could be classified hierarchically, perhaps by dividing them first according to whether or not they were made of wood, then according to their colour, by date of manufacture, and so on. The fact that life can be classified hierarchically is not, in itself, an argument for evolution. (Ridley 1985, 8.)

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group, the more we shall be convinced that they are not founded upon material relations. [*emphasis added*] (Denton 1986, 132.)

PREDICTION 3: CONVERGENCE OF INDEPENDENT PHYLOGENIES

If there is one true historical phylogenetic tree, all separate lines of evidence should converge on the same tree, our standard phylogenetic tree.

The alleged prediction and fulfillment are:

(1) If universal common ancestry is true, then phylogenies constructed from any comparisons of organisms will "converge" on the standard phylogenetic tree.

(2) Phylogenies constructed from comparisons of certain biological molecules in organisms "converge" on the standard phylogenetic tree.

There is an obvious disconnect between the alleged prediction and fulfillment. The fulfillment refers to only one basis of comparison (biological molecules), not all bases of comparison, and it refers to only some comparisons on the selected basis (some biological molecules), not all comparisons.

The alleged prediction could, of course, be amended to conform to the statement of fulfillment. The important point is that it is not a prediction of the hypothesis of common ancestry that phylogenies[5] constructed from comparisons of biological molecules will match phylogenies constructed from comparisons of morphology. This is obvious from the fact molecular and morphological phylogenies often are inconsistent, and yet the hypothesis of common descent is not considered falsified. The discordant data are simply accommodated by the theory.

The conflict between molecular and morphological phylogenies is a notorious problem in systematics. In fact, it was the focus of a recent article in *Nature*, subtitled: "Evolutionary trees constructed by studying biological molecules often don't resemble those drawn up from morphology. Can the two ever be reconciled, asks Trisha Gura." (Gura, 230.) Ms. Gura states in the article:

> When biologists talk of the 'evolution wars', they usually mean the ongoing battle for supremacy in American schoolrooms between Darwinists and their creationist opponents. But the phrase could also be applied to a debate that is raging within systematics. On one side stand traditionalists who have built evolutionary trees from decades of work on species' morphological characteristics. On the other lie molecular systematists, who are convinced that comparisons of DNA and other

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[5] Strictly speaking, these are not "phylogenies" but "phenograms" and "cladograms." "[A] lineage is a recognizable line of ancestry with identifiable ancestors and descendants. A *phylogeny* is merely discrete segments of lineage connected to an identifiable tree-structure of ancestry." (ReMine, 259.) A "phenogram" is a tree-structured diagram based on the overall similarities between the objects being classified. A "cladogram" is a tree-structured diagram based on the distribution of particular characters throughout the objects being classified. Neither phenograms nor cladograms specify ancestors, whereas a true phylogeny does. (ReMine, 265-268.) I am aware that most writers do not observe these distinctions, but they are still worth keeping in mind.

> biological molecules are the best way to unravel the secrets of evolutionary history. . . .
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> Battles between molecules and morphology are being fought across the entire tree of life. Perhaps the most intense are in vertebrate systematics, where molecular biologists are challenging a tradition that relies on studies of fossil skeletons and the bones and soft tissue of living species. . . .
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> So can the disparities between molecular and morphological trees ever be resolved? Some proponents of the molecular approach claim there is no need. The solution, they say, is to throw out morphology, and accept their version of the truth. "Our method provides the final conclusion about phylogeny," claims Okada. Shared ancestry means a genetic relationship, the molecular camp argues, so it must be better to analyse DNA and the proteins it encodes, rather than morphological characters that can end up looking similar as a result of convergent evolution in unrelated groups, rather than through common descent. But morphologists respond that convergence can also happen at the molecular level, and note there is a long history of systematists making large claims based on one new form of evidence, only to be proved wrong at a later date. (Gura, 230, 232.)

These conflicts have long been recognized. In 1986, biochemist Christopher Schwabe wrote:

> Molecular evolution is about to be accepted as a method superior to paleontology for the discovery of evolutionary relationships. As a molecular evolutionist I should be elated. Instead it seems disconcerting that many exceptions exist to the orderly progression of species as determined by molecular homologies; so many, in fact, that I think the exception, the quirks, may carry the more important message. (Schwabe, 280.)

The incongruities of the molecular evidence led Schwabe to conclude that there were *multiple evolutionary trees* stemming from many separate origin-of-life events. In other words, he thought the evidence favored the existence of different genealogies instead of a unique one, i.e., polyphyletic evolution rather the traditional view of monophyletic evolution (universal common ancestry). He opined, "The quirks that will not submit to the neo-Darwinian hypothesis are telling us that life had countless origins and that the chemistry of the origins of life has produced the diversity that has become a substrate for the evolution of biological complexity." (Schwabe, 282.)

Two years earlier, Schwabe and Gregory Warr were equally blunt in their criticism of molecular phylogenies. They saw the field of molecular evolution as being mired in subjectivity driven by an *a priori* commitment to universal common ancestry. They wrote:

> We believe that it is possible to draw up a list of basic rules that underlie existing molecular evolutionary models:
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> 1. All theories are monophyletic, meaning that they all start with the *Urgene* and the *Urzelle* which have given rise to all proteins and all species, respectively.
> 2. Complexity evolves mainly through duplications and mutations in structural and control genes.
> 3. Genes can mutate or remain stable, migrate laterally from species to species, spread through a population by mechanisms whose operation is not fully understood, evolve coordinately, splice, stay silent, and exist as pseudogenes.
> 4. Ad hoc arguments can be invented (such as insect vectors or viruses) that can transport a gene into places where no monophyletic logic could otherwise explain its presence.
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> This liberal spread of rules, each of which can be observed in use by scientists, does not just sound facetious but also, in our opinion, robs monophyletic evolution of its vulnerability to disproof, and thereby its entitlement to the status of a scientific theory.
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> The absolute, explicit and implicit, adherence to all the monophyletic principle and consequently the decision to interpret all observations in the light of this principle is the major cause of incongruities as well as for the invention of all the genetic sidestepping rules cited above. (Schwabe and Warr, 467.)

In 1993, Patterson, Williams, and Humphries scientists with the British Museum, reached the following conclusion in their review of the congruence between molecular and morphological phylogenies:

> As morphologists with high hopes of molecular systematics, we end this survey with our hopes dampened. Congruence between molecular phylogenies is as elusive as it is in morphology and as it is between molecules and morphology. . . .
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> Partly because of morphology's long history, congruence between morphological phylogenies is the exception rather than the rule. With molecular phylogenies, all generated within the last couple of decades, the situation is little better. Many cases of incongruence between molecular phylogenies are documented above; and when a consensus of all trees within 1% of the shortest in a parsimony analysis is published (e.g. 132, 152, 170), structure or resolution tends to evaporate. (Patterson and others, 180.)

Citing many recent examples, Laura Maley and Charles Marshall wrote in 1998: "Animal relationships derived from the new molecular data sometimes are very different from those implied by older, classical evaluations of morphology. Reconciling these differences is a central challenge for evolutionary biologists at present." (Maley and Marshall, 505.) An important issue is the nature of the assumptions under which this reconciliation will be pursued.

The following year, biologist Carl Woese, an early pioneer in constructing rRNA-based phylogenetic trees, wrote: "No consistent organismal phylogeny has emerged from the many individual protein phylogenies so far produced. Phylogenetic incongruities can be seen everywhere in the universal tree, from its root to the major branchings within and among the various taxa to the makeup of the primary groupings themselves." (Woese, 6854.)

It should be noted that molecular phylogenies are constructed on the basis of certain evolutionary assumptions. The tree that is presented is chosen from a forest of alternatives, typically on the assumption of maximum parsimony. That is, the tree that is selected is the one that reflects the least amount of presumed evolutionary change. But if the assumption of maximum parsimony fails to fit the data, it can be jettisoned in favor of another. (Hunter, 40-41.)[6] The availability of such ad hoc adjustments for resolving incongruities makes the claim of falsifiability an illusion. Any result can be accommodated by the theory by revising one or more of the underlying assumptions.

Even if a morphological phylogeny was matched closely by multiple molecular phylogenies, that would not prove that the groups in question descended from a common ancestor.[7] The molecular differences could be linked to the morphological differences for some other reason. Hunter illustrates the point this way:

> Penny[8] obtained his trees by culling those that were most parsimonious -- that is, he selected the trees that showed the least amount of evolutionary change to represent the history of life. The first problem is that Penny's method works perfectly fine on things we know did not come about via Darwinian evolution. For example, Penny's method would also

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[6] By appealing to molecular phylogenies, Dr. Theobald is appealing implicitly to their assumption about the manner of descent. However reasonable any given assumption may be from a neo-Darwinian perspective, Dr. Theobald's stated objective is to establish universal common descent without regard to any explanatory mechanism. He is thus precluded from assuming particular mechanisms of descent (e.g., one that excludes widespread lateral gene transfers) to make his case.

[7] Of course, to have relevance for Dr. Theobald's thesis of *universal* common ancestry, the analyses would need to include all groups of living things.

[8] "David Penny reconstructed the phylogeny for a group of eleven species, using five protein molecules. The proteins were used one at a time, independently of the other four, yet they suggested similar phylogenies." (Hunter, 40.) Hunter points out that "though Penny found the trees to be 'very similar,' there were significant differences. For example, some of his trees show the dog relatively far from the human (nine species out of a possible ten), whereas others show the dog relatively close to the human (three species distant out of ten)." (Hunter, 40.)

> claim that automobiles evolved from one another. Consider a group of vehicles, beginning with a small economy car and increasing in size to larger cars and to minivans and large-sized vans. One could quantify several aspects of the vehicle designs, such as tire size, steering mechanism, engine size, number of seats and so forth. Presupposing the evolutionary paradigm and searching for parsimonious relationships, we would find that most of the design measures suggest the same relationship. The smaller vehicles have smaller tires, manual steering, smaller engines, and fewer seats. The larger vehicles have larger tires, power steering, larger engines, and more seats. In other words, the groupings suggested by the different design measures (tire size, steering mechanism, engine size, etc.) tend to be similar. But of course, the family of automobiles did not evolve from one another via random mutations. The groupings of the design measures are a natural result of engineering and have nothing to do with Darwinian evolution. How then can Penny's results provide "strong support" for evolution? (Hunter, 40.)

As Gish explains, it would not be surprising from a creation perspective to find that biochemical similarities increase in relation to other similarities of the creatures being compared. He writes:

> We know, for instance, that man is more similar to a chimpanzee than he is to a bat; that he is more similar to either a chimpanzee or a bat than he is to a crocodile or a flea. Man, chimpanzee, and the bat are mammals. The creationist would expect, therefore, that his protein, DNA, and RNA molecules, those macromolecules that are among the most important molecules in metabolism, would be more similar to those of the chimpanzee and to those of the bat than to those of the crocodile or the flea. . . . Creationists believe that all normal genes, the genes that account for the normal, healthy differences in plants and animals, were created. Each basic type of plant and animal was created with a sufficient genetic potential or variability (or gene pool, as geneticists say) to permit sufficient variability within the circumscribed boundaries of each kind, in order to adapt to various environments and conditions. (Gish, 277-278.)

Biologist Leonard Brand concurs. "Anatomy is not independent of biochemistry. Creatures similar anatomically are likely to be similar physiologically. Those similar in physiology are, in general, likely to be similar in biochemistry, whether they evolved or were designed." (Brand, 156.) He makes the same point with specific reference to phylogenies based on cytochrome c.

> An alternate, interventionist hypothesis is that the cytochrome c molecules in various groups of organisms are different (and always have been different) for functional reasons. Not enough mutations have occurred in these molecules to blur the distinct grouping evident in Fig. 10.1 [the cytochromes percentage of sequence difference matrix]. . . . If

> we do not base our conclusions on the *a priori* assumption of megaevolution, all the data really tell us is that the organisms fall into nested groups without any indication of intermediates or overlapping of groups, and without indicating ancestor/descendant relationships. The evidence can be explained by a separate creation for each group of organisms represented in the cytochrome c data. (Brand, 158-159.)

Of course, failure to discern a relationship between morphology and a particular biological molecule does not prove the nonexistence of such a relationship. It may mean simply that the relationship is beyond our present understanding. The possibility of our ignorance is obvious, but even if it was not, earlier proclamations that most DNA is functionless "junk" illustrate the point. "Recent research has begun to show that many of these useless-looking sequences do have a function." (Walkup, 19.)

The cytochrome c data on which Dr. Theobald relies present some puzzles from a neo-Darwinian perspective. First, the cytochromes of all the higher organisms (yeasts, plants, insects, fish, amphibians, reptiles, birds, and mammals) exhibit an almost equal degree of sequence divergence from the cytochrome of the bacteria *Rhodospirillum*. In other words, the degree of divergence does not increase as one moves up the scale of evolution but remains essentially uniform. The cytochrome c of other organisms, such as yeast and the silkworm moth, likewise exhibits an essentially uniform degree of divergence from organisms as dissimilar as wheat, lamprey, tuna, bullfrog, snapping turtle, penguin, kangaroo, horse, and human. (See matrices in Brand, 157 and Davis and Kenyon, 37.)

Why would the sequence divergence of cytochrome c between bacteria and horses be the same as the divergence between bacteria and insects? The presumed evolutionary lineage from the ancestral cell to a modern bacterium differs radically from the presumed evolutionary lineage from the ancestral cell to a modern horse, both of which differ radically from the presumed evolutionary lineage from the ancestral cell to a modern insect. How could a uniform rate of divergence have been maintained through such radically different pathways? According to Michael Denton, a molecular biology researcher, "At present, there is no consensus as to how this curious phenomenon can be explained." (Denton 1998, 291.)

Moreover, the notion that the rates of divergence remain uniform regardless of evolutionary pathway does not fit all of the cytochrome c data. For example, referring to Dr. Theobald's Figure 1 (reproduced above), lampreys, carp, and bullfrogs allegedly shared a common ancestor above the node labeled "vertebra." Since that time, the branch leading to carp and bullfrogs evolved independently of the branch leading to lampreys. If the rates of cytochrome c divergence remain uniform regardless of evolutionary pathway, then the degree of sequence variance between the cytochrome c of lampreys and carp would be essentially the same as the degree of variance between the cytochrome c of lampreys and bullfrogs. That is not the case. The variance between the cytochrome c of lampreys and carp is 12%, whereas the variance between lampreys and bullfrogs is 20%. (See matrix in Davis and Kenyon, 37.)

Second, the sequences of cytochrome c sometimes differ inversely to the presumed evolutionary proximity of the organisms being compared. For example, turtles and rattlesnakes, both being reptiles, are presumed to have shared a common ancestor with each other more recently than they shared a common ancestor with humans. So the evolutionist would expect the cytochrome c of a rattlesnake to be more similar to that of a turtle than to that of a human. That, however, is not the case. The cytochrome c of the rattlesnake varies in 22 places from that of the turtle but only in 14 places from that of a human. (See matrix in Brand, 134.)

Humans and horses, both being placental mammals, are presumed to have shared a common ancestor with each other more recently than they shared a common ancestor with a kangaroo (a marsupial). So the evolutionist would expect the cytochrome c of a human to be more similar to that of a horse than to that of a kangaroo. Yet, the cytochrome c of the human varies in 12 places from that of a horse but only in 10 places from that of a kangaroo. (See matrix in Brand, 134.)

Such discrepancies between traditional phylogenies and those based on cytochrome c are well known. Even Ayala could only bring himself to say that "[t]he overall relations agree *fairly well* with those inferred from the fossil record and other sources" (emphasis supplied). (Ayala, 68.) He then acknowledged:

> The cytochrome c phylogeny disagrees with the traditional one in several instances, including the following: the chicken appears to be related more closely to the penguin than to ducks and pigeons; the turtle, a reptile, appears to be related more closely to birds than to the rattlesnake, and man and monkeys diverge from the mammals before the marsupial kangaroo separates from the placental mammals. (Ayala, 68.)

PREDICTION 4: POSSIBLE MORPHOLOGIES OF PREDICTED COMMON ANCESTORS

Any fossilized animals found should conform to the standard phylogenetic tree. Every node shared between two branches represents a predicted common ancestor; thus there are ~30 common ancestors predicted from the tree shown in Figure 1. Our standard tree shows that the bird grouping is most closely related to the reptilian grouping, with a node linking the two (A in Figure 1); thus we predict the possibility of finding fossil intermediates between birds and reptiles. The same reasoning applies to mammals and reptiles (B in Figure 1). However, we predict that we should never find fossil intermediates between birds and mammals.

The alleged prediction and fulfillment are:

(1) If universal common ancestry is true, then all fossilized animals will "conform"[9] to the standard phylogenetic tree.

(2) All fossilized animals "conform" to the standard phylogenetic tree.

Universal common ancestry affirms only that all creatures descended from the same ancestor. There is nothing about that affirmation that requires conformity to the standard phylogenetic tree. A phylogenetic tree is merely a diagram that reflects current evolutionary thinking about the relationships of the taxa included. Branches are arranged on the tree on the assumption of evolution and according to perceived similarities in selected traits.[10] The relationships of some branches are viewed more dogmatically than the relationships of others, but none of the branches are set in stone.

Since phylogenies are by nature provisional, the suggestion that the hypothesis of common descent would be falsified by "[a]ny finding of mammal/bird intermediates" is mistaken. Should a strikingly birdlike mammal be discovered, the standard tree simply

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[9] By "conform" to the standard phylogenetic tree, Dr. Theobald appears to mean having traits that are definitive of two taxa that are shown on the phylogeny as ancestral and descendant (e.g., reptiles and birds). Nonconformity to the standard phylogenetic tree is having traits that are definitive of two taxa that are shown on the phylogeny as having arisen independently of each other (e.g., birds and mammals).

[10] Brand is worth quoting at length here.

> The process used in constructing phylogenetic trees begins with the collection of data on the characteristics of the groups being studied. If we study the relationships between several orders of mammals, we compare many characters of these orders, perhaps beginning with tooth and skeletal anatomy to determine which orders have canine teeth and which have a complete postorbital bar behind the eyes. Many additional characters would be added. Then we tell the computer to compare these groups, to determine the similarities (homologies) between them, and to generate phylogenetic trees.
>
> Determining which characteristics are primitive (ancestral) and which are derived is called polarization. This is usually accomplished by including an outgroup in the analysis for comparison. The outgroup is a group that is closely related to but is outside of the groups that are being studied. For example, a study of the orders of mammals might use reptiles as an outgroup. The mammalian order with the fewest differences from the outgroup is considered the most primitive order, closest to the common ancestor of mammals. (Brand, 162-163.)
>
> When we first put the data into the computer, it does not produce a tree; it has no way to determine which one of the groups is the ancestor or closer to the ancestor. It can only produce an uprooted tree, showing which groups are more similar (D in Fig. 10.4). An outgroup must be added before it can produce a tree. However, we have no reason to introduce an outgroup unless we first assume evolution of the two groups from a common ancestor. A study of mammals, using reptiles as the outgroup, is based on the assumption that they both evolved from a common ancestor. If we make that assumption, then the computer looks for the order of mammals with the most characters in common with the outgroup. Now the computer makes the mammalian group the root of the tree that it can construct. It cannot even construct a tree unless the researcher first makes the assumption of megaevolution by adding an outgroup. (Brand, 164.)

would be modified to accommodate the new creature, after wrangling over its placement in the schema.

The ease with which this precise adjustment could occur was illustrated two decades ago, when "[t]he reality of the 'mammal-bird,' a hypothetical common ancestor of birds and mammals, [was] a contentious issue in modern systematics." (Mike Benton, 18.) Brian Gardiner's cladistic analysis indicated that birds were most closely related to mammals, which relationship was supported by two Cambridge scientists' analysis of molecular data. That view was readily accepted by some, even to the point that one French paleontologist "published a restoration of the hypothetical common ancestor between birds and mammals -- a sort of warm-blooded, hairy/feathery climbing insect eater!" (Mike Benton, 18.) Branches can be rearranged, even between mammals and birds, without skipping a beat in terms of commitment to common ancestry.

Of course, the discovery of a strikingly birdlike mammal would not necessarily force a shift in thinking about the relationship of mammals and birds (a placing of their branches next to each other). The birdlike features could be attributed to convergent evolution. Many organisms are believed by evolutionists to have evolved similar traits independently. (In fact, some experts believe that the birdlike features of dromaeosaurids, the dinosaurs considered by most experts to be the sister group to birds, arose independently rather than by inheritance from the ancestor of birds.) If the mammal's birdlike traits were judged to be the result of convergent evolution, the species would be shown on the phylogenetic tree as a subset or side branch of mammals that was unrelated to birds.

The shift in thinking over the last 30 years about the relationship of dinosaurs and birds is an example of a generally accepted phylogenetic adjustment, albeit at a lower taxonomic level. From the publication of Gerhard Heilmann's *The Origin of Birds* in 1926, it was a matter of textbook orthodoxy that birds were more closely related to thecodonts (an order of reptiles) than to theropods (a suborder of a different order of reptiles). Thus, the discovery in 1964 of the birdlike theropod *Deinonychus* was contrary to phylogenetic expectations. Today, however, the standard phylogeny shows birds more closely related to theropods than to thecodonts.

The assertion that all fossilized animals conform to the standard phylogenetic tree is unprovable, because one can never be sure that all fossilized animals have been discovered. But more importantly, the premise turns out to be merely a restatement of the claim of nested hierarchy. It adds nothing to the case for common ancestry.

Conformity and nonconformity to the standard phylogenetic tree are defined in the article in terms of "intermediates." It is stated that, given the standard phylogeny, one would expect "intermediates" between reptiles and birds and between reptiles and mammals (because these pairs are shown as sharing hypothetical common ancestors, A and B in Figure 1), but one would not expect "intermediates" between mammals and birds. It is then alleged that the fossils conform to this expectation, and thus "conform to the standard phylogenetic tree," in that "intermediates" have been found between reptiles and birds (citing mainly dromaeosaurids) and between reptiles and mammals (citing synapsids) but not between mammals and birds.

But according to the definition of "intermediate" given in the article, dromaeosaurids are *not* reptile-bird intermediates and synapsids are *not* reptile-mammal intermediates. An "intermediate form" is defined as "[a] fossil or modern species that displays characters *definitive* of two or more different taxa" (emphasis supplied). Dromaeosaurids do not display characters that are *definitive* of both reptiles and birds (which is why they are not considered birds), and synapsids do not display characters that are *definitive* of both reptiles and mammals (which is why they are not considered mammals).

On the other hand, under the given definition, *all* taxa qualify as "intermediates" between themselves and the taxa in which they are shown as nested.[11] For example, *all* mammal species, including all monotremes and marsupials, are reptile-mammal "intermediates" because they all possess the traits that are definitive of both Reptilia and Mammalia.[12] That is, they are all amniotes with the definitive traits of Mammalia. (Reptilia is defined simply as amniotes that are not birds or mammals [Carroll, 193].) Likewise, *all* bird species, including the Kiwi (called an "honorary mammal"), are reptile-bird "intermediates" because they all possess the traits that are definitive of both Reptilia and Aves.

But if taxa are intermediate by virtue of being nested, the existence of intermediates is not a separate argument for common ancestry. It is the argument of nested hierarchy under a different label. And if there are no intermediates between non-nested taxa, that means only that nested hierarchy is a pattern to which there are no known exceptions. As previously explained, that result could be accommodated by the theory of common descent, but it is not evidence for it.

In citing dromaeosaurids as reptile-bird intermediates and mammal-like reptiles as reptile-mammal intermediates, Dr. Theobald is apparently defining "intermediates" as organisms that are morphologically between alleged ancestors and descendants (rather than using the specified definition of organisms that possess the *definitive* traits of the two relevant taxa). But if intermediates can occur by definition only between alleged ancestors and descendants, then they can occur by definition only in conformity to the phylogenetic tree.

Consider the striking similarities between some marsupials and placentals. If the consensus were that a marsupial wolf evolved into a placental wolf, then the marsupial wolf would qualify as an intermediate under the definition being considered. That is, it

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[11] Theobald's definition thus approaches that of Cracraft, who wrote, "Each species, then is an intermediate in some sense of the word; all species possess primitive and derived characters." (Cracraft, 146.)

[12] Figure 1 is misleading here in that it uses the label "Reptiles" only for diapsids. Anapsida, the group believed to have given rise to both diapsids and synapsids (and eventually mammals), is a subclass of Reptilia.

would be morphologically between its alleged ancestor (an earlier marsupial) and descendant (the placental wolf). But since the consensus (which is reflected in the standard phylogeny) is that marsupial wolves and placental wolves arose independently, the marsupial wolf cannot qualify as a marsupial-placental intermediate, whatever its morphology. Conformity with the standard phylogeny is guaranteed by the definition.

The assertions that there are "no morphological gaps" in the alleged dinosaur-to-bird transition and that there is an "exquisitely complete series of fossils" for the alleged reptile-to-mammal transition are debatable, to say the least. I have elsewhere tried to point out some of the limitations of those claims (see, "On the Alleged Dinosaurian Ancestry of Birds," http://www.trueorigin.org/birdevo.htm and "Reappraising the Crown Jewel," http://www.trueorigin.org/therapsd.htm).

But even if one granted that reptiles evolved into a bird and a mammal, that would not establish that reptiles and all other organisms descended from a common ancestor, which is the proposition being argued. The difference between a bacterium and a reptile, not to mention the other organisms, is considerably greater than the difference between a reptile and a bird or a reptile and a mammal. So the fact a reptile could evolve into a bird or a mammal would not mean that a bacterium could evolve into a reptile and everything else. In fact, granting that reptiles evolved into a bird and a mammal would not even establish that all birds and all mammals descended from a reptile. That would be an assumption.

PREDICTION 5: CHRONOLOGICAL ORDER OF PREDICTED COMMON ANCESTORS

Fossilized intermediates should appear in the correct general chronological order based on the standard tree. Any phylogenetic tree predicts a relative chronological order of hypothetical common ancestors and intermediates between these ancestors. For instance, in our current example, the reptile/mammal common ancestor (B) [from Figure 1] and intermediates should be older than the reptile/bird common ancestor (A) [from Figure 1] and intermediates.

The alleged prediction and fulfillment are:

(1) If universal common ancestry is true, then fossil intermediates will appear in the "general chronological order" reflected in the standard phylogenetic tree.

(2) Fossil intermediates appear in the "general chronological order" reflected in the standard phylogenetic tree;

As pointed out above, "intermediate" is defined in the article as "[a] fossil or modern species that displays characters *definitive* of two or more different taxa" (emphasis supplied). Since, under that definition, a taxon is intermediate by virtue of being nested within another, the alleged prediction is that fossils will appear in the order of nesting reflected in Figure 1. In other words, a prokaryotic organism would appear first, followed successively (in the fungi/metazoan direction) by organisms with nuclei, multicellularity, organs, nervous and vascular system, and so on up the deuterostomic and protostomic branches.

There is nothing about the hypothesis of universal common ancestry that requires organisms to have descended in the pattern depicted in the standard phylogeny. Common ancestry does not even require nested hierarchy, let alone any particular pattern of nesting. A phylogeny is simply a depiction of the order in which evolutionists believe taxa arose, not the order in which they were *required* to arise. (And even if it was believed that universal common descent could occur in only one way, that is an assertion about the mechanism of descent, a subject Dr. Theobald purposefully excluded from his case.)

Moreover, while ancestral taxa must have *existed* before any taxa that descended from them, that does not mean the appearance of their fossilized forms must correspond to that order of existence. However unlikely the claim may be, it remains possible for a proponent of common descent to assert that select taxa appear in the fossil record contrary to the order in which they came into existence.

Witness the fact dromaeosaurids, which are offered by Dr. Theobald as "reptile-bird intermediates,"[13] first appear in the fossil record some 25 million years *after* the first fossil bird. (If one accepts *Protoavis*, rather than *Archaeopteryx*, as the first fossil bird, the gap in appearance increases to about 100 million years.) Rather than disqualifying dromaeosaurids in Dr. Theobald's eyes as "reptile-bird intermediates," which he argues must appear in the order suggested by the standard phylogeny, it is simply assumed that dromaeosaurids lived tens of millions of years before there is any evidence of their existence. (The ambiguity of "*general* chronological order" prevents such nonconformities from falsifying the claim.)

This same strategy could be employed if dromaeosaurids turned up in strata older/lower than that in which synapsids first appear. That is, it could be assumed that pelycosaurs and therapsids actually predated dromaeosaurids but for some reason did not appear in the fossil record until later. So the suggestion that the hypothesis of universal common ancestry would be falsified if dromaeosaurids first appeared in the fossil record before synapsids reptiles is incorrect.

The fact synapsids appear before dromaeosaurids hardly constitutes proof (confirms the "prediction") that "fossilized intermediates" appear in the general chronological order indicated in the standard phylogeny. They are only two data points. But more importantly, one must bear in mind that Figure 1 is of necessity a simplified

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[13] Dromaeosaurids are considered a sister group to birds, meaning they are believed to have shared with birds a most recent common ancestor. They are not believed to have been in the actual lineage of birds. In fact, they possess certain specializations, such as the stiffened tail, that make them ill suited as ancestors. Of course, the presumed common ancestor of birds and dromaeosaurids is thought to have been quite dromaeosaurid-like. As already noted, dromaeosaurids do not qualify as reptile-bird intermediates according to Dr. Theobald's definition.

and fragmentary phylogeny. The picture changes significantly when the scope of inquiry is broadened.[14] According to one Harvard-trained paleontologist:

> [T]he correspondence between phylogeny and the fossil record is not as strong as it might first seem. When the order of *all* kingdoms, phyla and classes is compared with the most reasonable phylogenies, over 95 percent of all the lines are not consistent with the order in the fossil record. The only statistically significant exceptions are the orders of first appearances of the phyla of plants and the classes of vertebrates and arthropods. Yet these three lineages also order organismal groups from sea-dwellers to land dwellers. The land-plant phyla, for example, are in a simple sequence from plants that need standing water to survive (e.g., algae and bryophytes) to those that can survive extreme desiccation (e.g., the cacti). The vertebrate classes go from sea-dwellers (fish) to land/sea creatures (amphibians) to land creatures (reptiles/mammals), to flying creatures (birds). The arthropod classes go from sea-dwellers (e.g., trilobites, crustaceans) to land dwellers (e.g., insects). So it's not clear that macroevolution is a truly good explanation for the order of fossil first appearances of major groups of life. Such a radical idea as a global flood, for example, which gradually overcame first the sea and then the land, actually explains the primary order of major groups in the fossil record (sea to land) better than macroevolutionary theory. (Wise, 225-226.)

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[14] But even Figure 1, which highlights plants, vertebrates, and arthropods, is not free of incongruities. For example, the first appearance of Cnidaria, the phylum to which jellyfish are assigned, is earlier/lower than (or possibly contemporaneous with) the first appearance of Porifera, the phylum to which sponges are assigned.