

A CRITIQUE OF "29 EVIDENCES FOR MACROEVOLUTION" PART 5

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PREDICTION 22: GENETIC CHANGE

The genetic information specifies everything about an organism and its potential. Genotype specifies possible phenotypes, therefore, phenotypic change follows genetic change. This obviously should be one of the areas where evolutionary change is seen, and genetic change is truly the most important for understanding evolutionary processes.

For the record, it is most doubtful that genetic information specifies everything about an organism. "According to a small but growing number of biologists, there is considerable evidence that genes do *not* control development." (Wells 1999, 51.) This evidence includes the following: (1) replacing an egg's genes with those of another species does not change the developmental pattern of the egg into an embryo; (2) mutations induced in developmental genes often lead to death or deformity but never alter the endpoint of embryonic development (they cannot even change the species); (3) strikingly different cell types arise in the same animal, even though all of them contain the same DNA; (4) similar developmental genes are found in animals as different as worms, flies, and mammals.

No one knows all the nongenetic factors involved in development, but they appear to include patterns in the egg cell membrane (that help to route gene products) and patterns in microtubules (microscopic fibers that are continually arranging themselves to give the cell its shape and to transport molecules within it). There is good evidence that both of these patterns are heritable apart from DNA. (Wells 1999, 52-53.) Wells concludes:

This does not mean that we now understand developmental programs. Far from it! But it is quite clear that they cannot be reduced to *genetic* programs, written in the language of DNA sequences. It would be more accurate to say that a developmental program is written into the structure of the entire fertilized egg -- including its DNA, microtubule arrays, and membrane patterns -- in a language of which we are still largely ignorant. (Wells 1999, 53.)

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then the DNA of organisms will be capable of change.
2. The DNA of organisms is capable of change.

It is not a prediction of the hypothesis of universal common ancestry that the DNA of organisms will be capable of change. Common ancestry does not even predict the existence of DNA. It has no stake in any particular mechanism of descent.

If one adds to the hypothesis the more specific claim that all organisms arose from a common ancestor by accumulated alterations of DNA, the issue is not simply whether DNA can change but whether the kinds of changes required for universal common ancestry can and did occur. From a naturalistic perspective, meaning without some kind of intelligent design or intervention, that seems impossible.

Renowned French zoologist Pierre-Paul Grasse made no secret of his skepticism:

What gambler would be crazy enough to play roulette with random evolution? The probability of dust carried by the wind reproducing Durer's "Melancholia" is less infinitesimal than the probability of copy errors in the DNA molecule leading to the formation of the eye; besides, these errors had no relationship whatsoever with the function that the eye would have to perform or was starting to perform. There is no law against daydreaming, but science must not indulge in it. (Grasse, 104.)

In 1967 a group of internationally known biologists and mathematicians met to consider whether random mutations and natural selection could qualify as the mechanism for evolution. The answer of the mathematicians was "No." In the words of Murray Eden of M.I.T., "What I am claiming is that without some constraint on the notion of random variation, in either the properties of the organism or the sequence of the DNA, there is no particular reason to expect that we could have gotten any kind of viable form other than nonsense." (Moorehead and Kaplan, 14.)

Mathematicians/astronomers Sir Fred Hoyle and Chandra Wickramasinghe concur.⁵¹ Summarizing his and Hoyle's analysis of the alleged mechanism of evolution, Wickramasinghe states:

We found that there's just no way it could happen. If you start with a simple micro-organism, no matter how it arose on earth, primordial soup or otherwise, then if you just have that single organizational, informational unit and you said that you copied this sequentially time and again, the question is does that accumulate enough copying errors, enough mistakes in copying, and do these accumulations of copying errors lead to the diversity of living forms that one sees on earth. That's the general, usual formulation of the theory of evolution. . . . We looked at this quite systematically, quite carefully, in numerical terms. Checking all the

⁵¹ Hoyle was a professor at Cambridge and the former head of the Institute of Theoretical Astronomy at that university. Wickramasinghe is the chairman of the Department of Applied Mathematics and Astronomy at University of Cardiff. They published a booklet titled *Why Neo-Darwinism Does Not Work* (Cardiff: University College Cardiff Press, 1982), which they describe as a "simple and decisive disproof of the 'Darwinian' theory." See also, Hoyle's *Mathematics of Evolution* (Memphis, TN: Acorn Enterprises, 1999).

numbers, rates of mutation and so on, we decided that there is no way in which that could even marginally approach the truth." (Varghese, 28.)

Biophysicist Spetner has likewise concluded that the probability of getting the necessary mutations through random copying errors is far too small to make neo-Darwinism a feasible explanation for all the diversity of life. A summary of his argument is available at http://www.creationresearch.org/creation_matters/97/cm9707.html#Not by Chance. See also, Spetner's "Evolution, Randomness, and Hashkafa" at <http://members.nbci.com/torahscience/evol1.htm>.

In any event, the fact the DNA of organisms is capable of change does nothing to advance the claim of universal common ancestry. That datum is fully compatible with the claim that multiple lineages were created independently and endowed with a degree of genetic adaptability.

PREDICTION 23: MORPHOLOGICAL CHANGE

Cladistic classification, and thus, phylogenetic reconstruction, is largely based on the various distinguishing morphological characteristics of species. Macroevolution requires that organisms' morphologies have changed throughout evolutionary history; thus, we should observe morphological change and variation in modern populations.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then morphological change and variation will be observable in modern populations.
2. Morphological change and variation are observable in modern populations.

Again, it is not a prediction of the hypothesis of universal common ancestry that morphological change and variation will be observable in modern populations. The hypothesis does not predict any particular mechanism of diversification. Thus, populations could be morphologically uniform and change in one generation outside our viewing frame. There is not even a requirement that the mechanism of universal common ancestry still be operating today.

If one adds to the hypothesis the more specific claim that all organisms arose by a continuing process of selection from morphological variation within existing populations, it raises the issue of the source of the continuing variations on which selection supposedly operated.⁵² That leads straight to the preceding discussion. The revised hypothesis also raises the issue of the nature of the selection and its adequacy for accomplishing the results attributed to it.

⁵² As philosopher of biology Paul Nelson notes, "Whether [favorable] variations have, or could have, occurred are factual questions to which selection is helpless to speak." (Nelson, 63.)

In any event, the morphological changes and variations that are observed in modern populations certainly do not justify the conclusion of universal common ancestry. They are fully compatible with the claim that multiple lineages were created independently and endowed with a degree of genetic adaptability. In fact, the experimental data suggest that there are natural limits to the extent to which species can change.

As science commentator Jeremy Rifkin (and many others) has noted:

The fruit fly has long been the favorite object of mutation experiments because of its fast gestation (twelve days). X rays have been used to increase the mutation rate in the fruit fly by 15,000 percent. All in all, scientists have been able to "catalyze the fruit fly evolutionary process such that what has been seen to occur in *Drosophila* (fruit fly) is the equivalent of many millions of years of normal mutations and evolution." Even with this tremendous speedup of mutations, scientists have never been able to come up with anything other than a fruit fly. More important, what all these experiments demonstrate is that the fruit fly can vary within certain upper and lower limits but will never go beyond them. (Rifkin, 134.)

The same holds true for the extensive genetic experiments done on *E. coli* bacteria. According to geneticists Lane Lester and Ray Bohlin:

The study of bacteria has been profoundly at the center of studies of mutations. This is because they reproduce rapidly, producing large populations and large numbers of mutants. They are also easily maintained and their environments are easily manipulated in the laboratory. Despite all their advantages, never has there arisen in a colony of bacteria a bacterium with a primitive nucleus. Never has a bacterium in a colony of bacteria been observed to make a simple multicellular formation. Although hundreds of strains and varieties of *Escherichia coli* have been formed, it is still *Escherichia coli* and easily identifiable as such. (Lester and Bohlin, 88.)

PREDICTION 24: FUNCTIONAL CHANGE

One of the major differences between organisms is their capacity for various functions. The ability to occupy one niche over another is invariably due to differing functions. Thus, functional change must be extremely important for macroscopic macroevolutionary change.

Presumably, the alleged prediction and fulfillment are:

1. If universal common ancestry is true, then the acquisition of new capabilities will be observable in modern populations.

2. The acquisition of new capabilities is observable in modern populations.

It is not a prediction of the hypothesis of universal common ancestry that the acquisition of new capabilities will be observable in modern populations. The hypothesis does not predict any particular mechanism of diversification. Thus, the capabilities of populations could be constant within our viewing frame. There is not even a requirement that the mechanism of universal common ancestry still be operating.

But more importantly, the functional changes observed in species do nothing to advance the claim of universal common ancestry. They are fully compatible with the claim that multiple lineages were created independently and endowed with a degree of genetic adaptability.

Interestingly, most if not all of the functional changes observed in species point away from random mutation as the explanation. They do so in two ways. First, some of the changes are produced by a *loss* of information. That raises the question of how the information that was lost arose in the first place. Spetner writes:

We have seen that there are some point mutations that, under the right circumstances, do give the organism an advantage. There are point mutations that make bacteria resistant to antibiotics. There are some that make insects resistant to insecticides. There are some that increase quantitative traits in farm plants and animals. But all these mutations reduce the information in the gene by making the protein less specific. They add no information, and they add no new molecular capability. Indeed, all mutations studied destroy information. None of them can serve as an example of a mutation that can lead to the large changes of macroevolution.

The neo-Darwinian would like us to believe that large evolutionary changes can result from a series of small events if there are enough of them. But if these events all lose information they can't be the steps in the kind of evolution the [neo-Darwinian theory] is supposed to explain, no matter how many mutations there are. Whoever thinks macroevolution can be made by mutations that lose information is like the merchant who lost a little money on every sale but thought he could make it up on volume. (Spetner, 159-160.)

Second, some of the changes appear to be nonrandom responses to the environment, suggesting that the genome was "set up" for an adaptive change to be triggered by a cue from the environment. (See, Spetner, 175-208.) That raises the question of how the genome came to be in that prepared state.

The 1982 study by Barry Hall cited by Dr. Theobald provides a good illustration. Hall prepared a strain of *E. coli* that lacked a gene necessary for the metabolizing of

lactose. But in the presence of lactose, *two mutations* were found in the same bacterium (one to a dormant and previously unknown structural gene and the other to its control gene) that in combination permitted it to metabolize lactose. By Hall's calculation, he should have had to wait 100,000 years to see these double mutations, but in the presence of lactose he found about 40 of them in a few days. "These results suggest that lactose in the environment induced these mutations." (Spetner, 188.) Spetner observes:

Darwinian evolutionists see the nonrandom interpretation of these experimental results as obviously incorrect because they contradict the neo-Darwinian dogma. I, on the other hand, see this interpretation as confirming, on the bacterial level, the nonrandom variation indicated by many examples in plants and animals -- examples that Darwinian evolutionists have largely ignored because they do not fit in. Resistance to the nonrandom-variation interpretation stems from a refusal to abandon the Darwinian agenda that evolution must confirm that life arose and developed spontaneously. With that agenda, nonrandom adaptive variation, arising from an environmental signal turning ON an already present set of genes, is hard to account for. . . .

The several examples cited above indicate that the phenomenon, if it is indeed vindicated, may be widespread in bacteria. Just as these bacteria contain "cryptic" genes which encode for enzymes that are needed in some environments, so I suggest that other organisms also may have latent parts of their genome dedicated to be adaptive to a certain set of environmental conditions that may arise. The environment can then supply a cue that will turn ON the latent section that will make the organism adaptive. (Spetner, 191-192.)⁵³

PREDICTION 25: EARTH'S STRANGE PAST AND THE FOSSIL RECORD

A very general conclusion made from the theory of common descent is that life, as a whole, was different in the past. The predicted evolutionary pattern is that the farther back we look back in time, the more different life should appear from the modern biosphere. More recent fossils should be more similar to contemporary life forms than older fossils.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then life forms will differ increasingly from modern forms as one moves down the fossil record.
2. Life forms differ increasingly from modern forms as one moves down the fossil record.

⁵³ Spetner describes two other kinds of nonrandom variations of phenotype, one that is heritable and one that is not. (Spetner, 192-197.)

It is not a prediction of the hypothesis of universal common ancestry that life forms will differ increasingly from modern forms as one moves down the fossil record. Of course, if all life forms arose from a common ancestor, then there necessarily was a period of diversification. But an "amechanistic" theory of universal common ancestry says nothing about how quickly modern forms were achieved, and it does not require a fossil record of that diversification to have been made, preserved, or discovered.

In other words, if the fossil record began with modern forms, that fact alone would not falsify the hypothesis of universal common ancestry. The proponent of common ancestry could make the same kind of argument that is made currently regarding the "Cambrian Explosion," i.e., massive diversification went undocumented or undiscovered. See, e.g., Meyer, Nelson, and Chien, "The Cambrian Explosion: Biology's Big Bang," <http://www.discovery.org/articleFiles/PDFs/Cambrian.pdf>.

But more importantly, universal common ancestry is not the only possible explanation for why life forms differ increasingly from modern forms as one moves down the fossil record. In fact, the types of differences that are seen actually weigh against the claim of universal common ancestry. As paleontologist Wise points out:

As one goes back in time, organismal groups tend not to converge in morphology, but remain distinct. Most major groups remain identifiable by modern characters and distinct from their supposed ancestors all the way back to their oldest fossil representatives. This would seem to imply that the branching event of one major group from another never did occur. (Wise, 219-220.)

So, at best, the increasing divergence from modern life forms that is observed as one moves down the fossil record can be claimed to support evolution only within a multitude of major groups, not evolution from a universal common ancestor. And even that claim is weak, as significant gaps exist in alleged fossil lineages within all the major groups. I have elsewhere attempted to point out some of the gaps in purported mammal lineages, which are considered an evolutionary showcase (see, "Reappraising the Crown Jewel," <http://www.trueorigin.org/therapsd.htm>).⁵⁴

Some creationists explain the change in life forms in the fossil record by proposing that God created new species intermittently over vast ages. Biblical creationists, however, believe the fossil order is largely an artifact of a complex and unique cataclysmic process, the details of which are obscured by its uniqueness and by our ignorance of the ancient biosphere. Wise writes:

⁵⁴ For one committed to universal common ancestry, no gaps, however large or numerous, are sufficient to put a claim of descent in doubt. Gaps are assumed to be merely the absence of evidence, not evidence of the absence of lineages. Creationists, however, are committed to the proposition that numerous kinds of living things were created independently. From their perspective, gaps can be an indication that hypothesized lineages are imaginary.

The general features of the fossil record that *are* explained by evolutionary theory are at least as well explained by other theories. The existence of a Creator who introduced organisms on earth in a particular order could explain the general change in organisms through the record, but so could the effect of a global flood as it successively sampled from a biogeographically zoned distribution of organisms. The general change in organisms through time can be predicted by any one or all of these three theories (macroevolution, progressive creation, global deluge). On the other hand, the rarity or absence of evidence for transitions between major groups and the fact major groups do not converge on one another as one goes back in the fossil record seem to argue that major groups were introduced in the fossil record only *after* they were fully formed. This is more consistent with creative order and global deluge theories than with macroevolutionary theory. As for the linear relationship of species similarity above and below a particular level in the geologic column, this can be just as well explained by global deluge theory or progressive creation theory as it is by macroevolution. In deluge theory, different species are found in different pre-flood environments and get mixed with species from adjacent environments, providing the species similarity relationship. Continual introduction of species whether by evolution or creation would produce the same relationship. In short, all fossil-record order can be at least as well explained by order of creation decided by creative fiat or ocean-to-land burial of organisms in a diverse world overcome by global deluge as it is by macroevolution. (Wise, 226.)⁵⁵

PREDICTION 26: STAGES OF SPECIATION

The most useful definition of species (which does not assume evolution) for sexual metazoans is the Biological Species Concept: species are groups of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups (Mayr 1942).

If branching of existing species into new species occurred gradually in the past, we should see all possible degrees of speciation or genetic isolation today, ranging from fully interbreeding populations, to partially interbreeding populations, to populations that interbreed with reduced infertility or with complete infertility, to completely genetically isolated populations.

Presumably, the alleged prediction and fulfillment are:

⁵⁵ Wise would be the first to admit that there are questions for which current deluge theories lack answers, but that is true for all explanations of earth history. For a more detailed discussion of one flood model, see Brand, 171-179, 209-318. Some worthwhile online resources are Austin and others, "Catastrophic Plate Tectonics: Global Flood Model of Earth History," <http://www.icr.org/research/as/platetectonics.html>; Brand and Florence, "Stratigraphic Distribution of Vertebrate Fossil Footprints Compared with Body Fossils," <http://www.grisda.org/origins/09067.htm>; Wise, "Punq Eq Creation Style," <http://www.grisda.org/origins/16011.htm>; and Gibson, "Fossil Patterns: A Classification and Evaluation," <http://www.grisda.org/origins/23068.htm>.

1. If universal common ancestry is true, then all the stages of the process of speciation will be observable today.

2. All the stages of the process of speciation are observable in species today.

Gradual branching of species into new species is not an element of the hypothesis of universal common ancestry, as that hypothesis says nothing about the mechanism of descent. Rather, it is an element of the more specific hypothesis of neo-Darwinism. Since Dr. Theobald purports to establish universal common ancestry apart from any particular mechanism of descent, he cannot assume a particular mechanism of descent in making his case.

Moreover, the hypothesis of universal common ancestry does not require that its processes be continuing and thus does not require that all its stages be present today. So even if the hypothesis of universal common ancestry entailed speciation, it could accommodate a failure to observe the various stages of that process.

But most importantly, evidence of speciation does nothing to advance the claim of universal common ancestry. Speciation is fully compatible with the claim that multiple lineages were created independently and endowed with a degree of genetic adaptability. The fact one species can give rise to another similar species does not mean there are no limits to the process, that a bacterium can give rise to a human. On the contrary, the experimental data cited previously suggests the opposite.

One need not be a creationist to question the extrapolation from speciation to universal common ancestry. As Brand notes, "Some scientists are beginning to doubt that the microevolutionary process extrapolated over time is adequate to produce more significant changes. They suggest that larger scale evolution must involve a different mechanism than microevolution and that it happens rapidly. (Ridley 1993, p. 523-525)." (Brand, 120.)

PREDICTION 27: SPECIATIONS

The standard phylogenetic tree illustrates countless speciation events; each common ancestor also represents at least one speciation event. Thus we should be able to observe actual speciation, if even only very rarely. Current estimates from the fossil record and measured mutational rates place the time required for full reproductive isolation in the wild at ~3 million years on average (Futuyma 1998, p. 510). Consequently, observation of speciation in nature should be a possible but rare phenomenon. However, evolutionary rates in laboratory organisms can be much more rapid than rates inferred from the fossil record, so it is still possible that speciation may be observed in common lab organisms (Gingerich 1983).

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then speciation will be observable today in laboratory organisms.
2. Speciation is observable today in laboratory organisms.

The preceding claim was that snapshots of the various stages of speciation will be present in nature. This claim is that one or more speciation events can be induced in a laboratory.

The response is the same. Dr. Theobald impermissibly assumes a particular mechanism of descent in arguing for an "amechanistic" theory of common ancestry. Moreover, the hypothesis of universal common ancestry does not require that its processes be continuing, so even if it entailed speciation, it could not be falsified by a failure to induce speciation in a laboratory.

Most importantly, however, evidence of speciation does nothing to advance the claim of universal common ancestry. Speciation is fully compatible with the claim that multiple lineages were created independently and endowed with a degree of genetic adaptability.

PREDICTION 28: MORPHOLOGICAL RATES OF CHANGE

Observed rates of evolutionary change in modern populations must be greater than or equal to rates observed in the fossil record.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then the calculated rates of evolutionary change in modern populations will be greater than or equal to the calculated rates of evolutionary change in the fossil record.
2. The calculated rates of evolutionary change in modern populations are greater than or equal to the calculated rates of evolutionary change in the fossil record.

It is not a prediction of the hypothesis of universal common ancestry or the more specific hypothesis of neo-Darwinism that the rates of evolutionary change in modern populations will be equal to or greater than the rate believed to have prevailed in the past. The hypothesis says nothing about the constancy of the rate of evolutionary change.

So if rates of change in modern populations were not sufficient to generate all living things from a universal common ancestor, it would not falsify the hypothesis. It simply would be assumed that the rate had slowed down.

After all, according to Dr. Theobald, evolutionists believe that the average evolutionary rate from historical colonization events is 616 times faster than the average

rate in the fossil record. If the theory can accommodate faster modern rates, it can also accommodate slower modern rates.

In any event, one cannot simply assume that the minor changes occurring in modern populations could continue beyond certain natural limits so as to create new orders, classes, and phyla. In fact, there is good reason for doubting that assumption. As biologists Davis and Kenyon point out:

Over the years, numerous investigations have explored the questions of whether species are "infinitely plastic," capable of unlimited change, or whether change is limited. Darwin advocated the unlimited change view. The accumulated evidence to date, however, severely questions Darwin on this. For example, the Bumpus study of birds (Chapter 2) showed a remarkable tendency for birds to vary within limits. Hermann J. Muller labored for many years conducting mutation experiments with fruit fly *Drosophila* to demonstrate unlimited change, and found the same tendency: change occurs only within definite limits. Others have tried, as well. Such attempts have all met with uniform lack of success, and ultimately died a quiet death. Hardly anyone is still trying to furnish an observable basis for Darwin's view of unlimited change. . . .

The Darwinist, however, believes species have unlimited potential for change even if scientists have not been able to experimentally produce it. Darwinian theory holds that the diversity of contemporary species arose through descent from a common ancestor. According to Darwinists, we must regard lack of experimentally induced, unlimited change as a problem in need of research, not a basis to doubt macroevolution. (Davis and Kenyon, 78-79.)

If, as asserted by Dr. Theobald (from Gingerich), a change rate of 400 darwins sustained over 10,000 years is sufficient to turn a mouse into an elephant, then the alleged average laboratory change rate of 60,000 darwins would be sufficient to accomplish that task in just under 67 years. This makes it all the more remarkable that decades of laboratory experiments have produced such meager results, nothing approaching the dramatic levels of transformation predicted by these figures. It is not surprising that "[s]ome scientists are beginning to doubt that the microevolutionary process extrapolated over time is adequate to produce more significant changes." (Brand, 120.)

Of course, estimates of rates of change in the fossil record are loaded with assumptions. One first must assume that two specimens are ancestor and descendant. Since evolutionists often insist that only sister groups can be identified, not actual ancestors, there is an additional level of speculation. One must prescribe the morphology of the hypothetical common ancestor and then quantify the degree to which it differs from the alleged descendant. One also must make assumptions about when the lineage in question split from the assumed ancestor and when the alleged descendant first arose.

PREDICTION 29: GENETIC RATES OF CHANGE

Rates of genetic change, as measured by nucleotide substitutions, must also be consistent with the rate required from the time allowed in the fossil record and the sequence differences observed between species.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then the current rate of nucleotide substitution in the nonfunctioning DNA of two species will be sufficient to account for the nucleotide differences in the nonfunctioning DNA of those species, given the assumed date of their divergence from a common ancestor.
2. The current rate of nucleotide substitution in nonfunctioning DNA of various species is sufficient to account for the nucleotide differences in the nonfunctioning DNA of those species, given the assumed date of their divergence from a common ancestor.

It is not a prediction of the hypothesis of universal common ancestry or the more specific hypothesis of neo-Darwinism that the current rate of nucleotide substitution in the nonfunctioning DNA of two species will be sufficient to account for the nucleotide differences in the nonfunctioning DNA of those species. The hypotheses say nothing about the constancy of the rate of nucleotide substitution or about the dates on which species diverged from a common ancestor.

So if the rate of substitution in modern populations were not sufficient to account for the nucleotide differences within the time prescribed, it would not falsify the hypotheses. It simply would be assumed that the rate had slowed down and/or that the date of divergence was earlier than previously believed.

In addition, the fact current substitution rates are sufficient to account for the nucleotide differences within the assumed time frames (from the alleged dates of divergence) does nothing to advance the claim of universal common ancestry. It does not even advance the claim that the particular species being compared descended from a more recent common ancestor. That must be *assumed*. A contrary assumption could easily be accommodated.

It should be pointed out that nucleotide substitution rates in presumably nonfunctional DNA are not always in easy agreement with current phylogenies. Woodmorappe writes:

It is interesting to note that the inferred nucleotide-substitution rate in pseudogenes shows only crude correspondence with primate phylogeny, for which reason it has to be manipulated *post hoc* by up to tenfold in order to contrive an agreement between the timing of different episodes of primate evolution. (Woodmorappe 2000, 86.)

CONCLUSION

In the words of the great detective Sherlock Holmes:

"Circumstantial evidence is a very tricky thing," answered Holmes thoughtfully; "it may seem to point very straight to one thing, but if you shift your point of view a little, you may find it pointing in an equally uncompromising manner to something entirely different" . . . "There is nothing more deceptive than an obvious fact".⁵⁶

Dr. Theobald and many other bright and well-educated evolutionists are certain that the evidence of nature points ineluctably to the conclusion of universal common ancestry. I once shared that opinion of history, but having shifted my point of view, I find that the same evidence points to something entirely different.

I have explained in this paper the way Dr. Theobald's evidence looks from my perspective. I have argued that what he labels falsifiable predictions of the hypothesis of universal common ancestry are in fact mere observations that have been read back into a plastic theory and claimed as predictions. His hypothesis accommodates these observations, but since it could also accommodate contrary ones, that fact has little or no probative value. As Hunter says, "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." (Hunter, 38.)

I have shown how Dr. Theobald's evidence can be accommodated by alternative hypotheses. I have also highlighted instances where his interpretation of the evidence is driven by theological assumptions. One who rejects those underlying assumptions is justified in rejecting the conclusions that follow from them.

Since this is a critique of Dr. Theobald's article, evidence for creation has been presented only when relevant to the discussion of one of his alleged predictions. Nothing has been said about the immense difficulty in accounting for the origin of life, with its vast information content, by purely naturalistic processes.⁵⁷ And little if anything has been said about the mind-boggling complexity that exists at a variety of levels: subcellular processes and bodies, tissues, bodily organs and systems, symbiotic systems, ecosystems, and even astronomical arrangements. As Wise notes:

⁵⁶ Quoted in Denton 1986, 155.

⁵⁷ I realize that the bare hypothesis of universal common ancestry does not address the origin of life and is consistent with intelligently directed descent. But to the extent its advocates insist on strictly natural causes, it is appropriate to cite as evidence of a Creator the extreme improbability of generating life and of achieving the complexity and integration exhibited in nature.

Each of these levels features a complexity that is staggering to the human mind -- a complexity greater than any that in our experience can be produced by [a] nonintelligent natural cause. If we follow the principle of appealing only to principles that are reasonable in our experience, then the complexity of any one of these levels seems to require an appeal to an intelligent cause. However, the *total* complexity is at least the sum of the complexities of each level. If the complexity of each level suggests an intelligent cause, the total complexity screams for an intelligent cause. Macroevolutionary theory has never successfully explained the acquisition of any level of this complexity, let alone the total complexity. (Wise, 229-230.)

Likewise, little if anything has been said about the equally mind-boggling integration of these amazingly complex items and events. To quote Wise again:

As if the basic complexity of things were not enough, the integration of that complexity is truly astounding. Not only do subcellular chemical processes involve a large number of complex molecules and chemical steps, but those items and events are connected in a well-balanced and well-timed series of items and steps to produce a well-integrated process. Similarly, the workings of subcellular organelles, cells in tissues, tissues in organs, organs in systems, systems in bodies, organisms with other organisms, organisms in communities, and communities in the biosphere all show staggering integration. As with the complexity of these items and events on any given level, such a level of integration has never been observed to arise from nonintelligent natural law and process. Integration seems to argue for intelligent cause.

In addition, the integration that is so striking *within* levels is even more striking *between* levels. Not only do subcellular organelle systems and chemical processes show integration, but the chemical and organelle systems are themselves linked together, and must be for the cell to survive. Even more impressive, a similar integration exists between all levels. Once again, this level of integration is unexplained by evolutionary theory but is addressable by intelligent cause theory. (Wise, 230.)

"For since the creation of the world God's invisible qualities -- his eternal power and divine nature -- have been clearly seen, being understood from what has been made, so that men are without excuse." Rom. 1:20 (NIV)