

A CRITIQUE OF "29 EVIDENCES FOR MACROEVOLUTION" PART 2

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PREDICTION 6: ANATOMICAL VESTIGIAL STRUCTURES

Some of the more renowned evidences for evolution are the explanations it provides for nonfunctional or rudimentary vestigial characters, both anatomical and molecular. Throughout macroevolutionary history, functions necessarily have been gained and lost; thus, we predict vestigial structures, which are structural evidence of lost functions. Since there is no apparent reason for their existence, nonfunctional characters of organisms are especially puzzling. So are rudimentary structures, which have different and relatively minor functions compared to the same more developed structures in other organisms. Consequently, evolutionary explanations for vestigial characters are strong proofs.

Explanations are not evidence; they are attempts to explain evidence. So the first and last sentences of the quoted paragraph are at best overstatements. The question is whether the evidence of "vestigial" structures favors the explanation of universal common ancestry, and if so, how strongly.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then some organisms will have structures the function of which was lost or diminished in the course of the organism's evolutionary history ("vestiges" of the organism's evolutionary history).
2. Some organisms have structures the function of which was lost or diminished in the course of the organism's evolutionary history.

Vestigial structures are not a necessary result of all possible mechanisms of universal common descent. They are understandable within a neo-Darwinian framework of random mutation and natural selection, but since Dr. Theobald has chosen to argue for common ancestry without regard to any mechanism of descent, he cannot offer as evidence data that can be explained only by particular mechanisms of descent.

Moreover, even neo-Darwinism does not demand vestigial structures; it simply accommodates them. They can exist or not exist with equal ease under the theory and can appear with any frequency. Any result can be explained by appeal to the randomness of mutation and the uncertainty of the selective pressures that were at work in any given lineage.

In any event, vestigial structures provide no support for the claim of universal common ancestry. A bona fide vestigial structure says only that the organism in which it is found descended from an earlier organism that possessed the structure in fully

functional form. It says nothing about how that earlier organism came to exist, whether it descended from a universal common ancestor, descended from one of many independently created organisms, or was itself created independently.¹⁵ Since vestigial structures can arise in unconnected lineages as well as in lineages that are rooted in a common ancestor, they do not count as evidence for universal common ancestry.

Of course, the identification of bona fide vestigial structures is fraught with difficulty. Dr. Theobald defines a vestigial character as "a character that *for all intents and purposes* has no *obvious* or *important* function, yet is structurally *similar* to functional characters in other species" (emphasis supplied). He elaborates: "If the character appears reduced and rudimentary compared to the same structure in other organisms, and the structure has obvious important functions in the majority of other organisms, then it is considered a vestigial structure."

The problems are illustrated by Dr. Theobald's use of the human coccyx (which he describes as "the four fused tail vertebrae of humans") as an example of a vestigial structure. It has long been known that the coccyx serves as a point of attachment for ligaments and several important muscles. So why think the coccyx was not specially designed by a Creator to fulfill that function?

The answer, from Dr. Theobald's definition, is twofold. First, the function of the coccyx must be judged "unimportant" (given that the function is obvious). That, however, is a grossly subjective assessment. It is also clearly theological. How does one determine when a function is important enough to make it plausible that a Creator would specially design a structure to fulfill it?

This particular trap is avoided if vestigial structures are defined as those that have *no* function (rather than those that have no *important* function). But that definition stumbles over the fact one can never really be certain that an apparently functionless structure is really functionless. It may be that we lack the knowledge necessary to appreciate its function. As S. R. Scadding pointed out 20 years ago:

I would suggest that the entire argument that vestigial organs provide evidence for evolution is invalid on two grounds, one practical, the other more theoretical. The practical problem is that of unambiguously identifying vestigial organs, i.e., those that have no function. The analysis of Wiedersheim's list of vestigial organs points out the difficulties. . . . Wiedersheim could list about one hundred in humans; recent authors usually list four or five. Even the current short list of vestigial structures in humans is questionable. . . . (Scadding, 173.)¹⁶

¹⁵ Creationists, for example, agree that bona fide vestigial structures exist, but they believe those structures are strictly the result of degenerative changes within created kinds (e.g., blind salamanders and fish, flightless birds and beetles).

¹⁶ Scadding's more theoretical objection is that one cannot arrive scientifically at the negative assertion that an organ has no function.

Second, the coccyx must be judged "similar" to a functional structure in another organism. But how similar must the structures be and how is that similarity to be measured? It is a vague concept that can be shaped easily by one's presuppositions. Moreover, there is no reason why a Creator could not adapt similar designs for different purposes. To conclude that one structure is too similar to another to have been separately designed to fulfill a function requires an assumption about the Creator's *modus operandi*. It is, therefore, a theological assessment.

In his recent book, Hunter spotlights the metaphysical nature of such arguments. After citing comments by evolutionists about various alleged vestigial structures, he writes:

Behind this argument about why the patterns in biology prove evolution lurks an enormous metaphysical presupposition about God and creation. If God made the species, then they must fulfill our expectations of uniqueness and good engineering design. We might say that God was supposed to have optimized the design of each species. Evolutionists have no scientific justification for these expectations, for they did not come from science. They are part of a personal religious belief and as such are not amenable to scientific debate. In fact, evolutionists rely on a rather narrow metaphysical target in their attacks on creation. The evolutionist's notion of God and divine creation is, for many people, just a straw man -- an overly simplified metaphysic that conveniently supports their views. (Hunter, 49.)

The suggestion that universal common ancestry would be falsified by finding "vestigial structures" in an organism that were not present in that organism's alleged ancestors, as depicted in the standard phylogeny, is incorrect (in that it is based on a false premise). To use one of Dr. Theobald's examples, if a fish species were discovered with a relatively small, nonfunctional leg or pelvis, it would only be labeled a "vestigial structure" if that species was judged to have "evolved back" from a tetrapod (i.e., if its branch on the phylogeny was relocated). Otherwise, it would be hailed as an example of a nascent structure, that is, a structure that is on its way "in" rather than on its way "out." Rather than being the death knell of common descent, it would be touted as evidence that tetrapods evolved from fish. Dr. Theobald sorely underestimates the flexibility of the theory he is asserting.

In fact, the absence of nascent structures poses a problem for neo-Darwinian common descent. If, as Dr. Theobald says, "functions necessarily have been gained and lost" throughout evolutionary history, why does one find evidence only of degeneration? As Wise says:

The absence of [nascent] organs would seem to argue that although we have evidence of degeneration from an earlier, more optimal design, we lack evidence of a move toward a new optimal design. It would seem that

if an Intelligent Designer created optimal designs *in the past* and life's history has been a move away from that optimum, the presence of vestigial organs and the absence of nascent organs would be better explained by intelligent design than by evolutionary theory. (Wise, 223.)

PREDICTION 7: MOLECULAR VESTIGIAL CHARACTERS

Vestigial characters should also be found at the molecular level. Humans do not have the capability to synthesize ascorbic acid (otherwise known as Vitamin C), and the unfortunate consequence can be the nutritional deficiency called scurvy. However, the predicted ancestors of humans had this function (as do all animals except primates and guinea pigs). Therefore, we predict that humans, primates, and guinea pigs should carry evidence of this lost function as a molecular vestigial character.

Just for the record, it is not true that all animals except primates and guinea pigs have the ability to synthesize ascorbic acid. That ability is lacking in some species of fish, birds, and bats and is present in some species of primates.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then some organisms will have genes the function of which was lost in the course of the organism's evolutionary history.
2. Some organisms have genes the function of which was lost in the course of the organism's evolutionary history.

Since this is the concept of vestigial structure applied to genes, the preceding response is largely applicable. Vestigial genes are not a necessary result of all possible mechanisms of universal common descent, and since Dr. Theobald has chosen to argue for common ancestry without regard to any mechanism of descent, he cannot offer as evidence data that can be explained only by particular mechanisms of descent.

Moreover, even neo-Darwinism does not demand vestigial genes; it simply accommodates them. If they did not exist, it would mean that an incapacitating mutation never occurred or never occurred in an environment that was selectively neutral in terms of the gene's function. If they did exist, it would mean the opposite. Any result can be fit within the scheme.

In any event, vestigial genes provide no support for the claim of universal common ancestry. A bona fide vestigial gene says only that the organism in which it is found descended from an earlier organism that possessed the gene in functional form. It says nothing about how that earlier organism came to exist, whether it descended from a universal common ancestor, descended from one of many independently created organisms, or was itself created independently.

Consider Dr. Theobald's primary example, the L-gulano-g-lactone oxidase gene, which is one of the genes required for the synthesis of vitamin C. Assuming this is a bona fide pseudogene in humans, meaning a nonfunctional version of a gene that was functional at some point in the human lineage, it says nothing about the origin of the ancestor that possessed the functioning gene. That ancestor could have been independently created or could have descended from a creature that had been independently created. So this entire line of argument cannot do what Dr. Theobald needs it to do.

As with other vestigial structures, it is difficult to identify bona fide vestigial genes. We simply do not know enough to be able to declare definitively that any given series of nucleotides has absolutely no function. As molecular biologist Pierre Jernstrom recently noted:

Pseudogenes are often referred to in the scientific literature as nonfunctional DNA, and are regarded as junk. But more scientists are now conceding that this is far from true for many pseudogenes. Failure to observe pseudogenes coding for a product under experimental conditions is no proof that they never do so inside an organism. It is also impossible to rule out protein expression based solely on sequence information, as DNA messages can be altered by, e.g., editing the transcribed RNA, skipping parts of the sequence, etc. Moreover, the inability to code for a protein useful to an organism hardly exhausts other possible functions pseudogenes may have. (Jernstrom, 15.)

The possibility of an undiscovered function has become even greater with the recent sequencing of the human genome. Though humans may have as many as 300,000 proteins, it turns out that they have only about 30,000 genes.¹⁷ Thus, the genome is even more complex than previously believed. As J. Craig Venter of Celera Genomics explained in the press conference announcing the sequencing of the human genome:

[O]ur understanding of the human genome has changed in the most fundamental ways. The small number of genes -- some 30,000 -- supports the notion that we are not hard wired. We now know the notion that one gene leads to one protein, and perhaps one disease, is false.

One gene leads to many different protein products that can change dramatically once they are produced. We know that some of the regions that are not genes may be some of the keys to the complexity that we see in ourselves. We now know that the environment acting on our biological

¹⁷ There is some uncertainty about this number, but the fact two competing teams came up with roughly the same estimate (30,000 - 40,000) supports its accuracy. A recent letter published in *Cell* argues that the figure is too low. While Michael Cooke, one of the authors of the letter, believes 30,000 is too low, "he estimates the total is probably not more than 60,000," which is only slightly less amazing. Researchers who came up with the original figure are sticking with it. Daniel Q. Haney, "Researchers Question Report on Genes," *Washington Post* (August 23, 2001) online at www.washingtonpost.com/wp-srv/aponline/20010823/aponline170150_000.htm.

steps may be as important in making us what we are as our genetic code. (Bethell, 52.)

When asked immediately after the press conference about Venter's suggestion that one gene could give rise to ten proteins, James Watson (of DNA fame) said, "Some genes can give rise to 50 different proteins." (Bethell, 56.) As summed up by the Washington Post, "The way these genes work must therefore be far more complicated than the mechanism long taught." (Bethell, 52.)

Indeed, the evolutionists' claim that pseudogenes are still present and recognizable tens of millions of years after they supposedly ceased functioning suggests that they serve some kind of purpose. Otherwise, they should have been removed or altered beyond recognition by the accumulation of mutations. Jerlstrom writes:

The persistence of pseudogenes is in itself evidence for their activity. This is a serious problem for evolution, as it is expected that natural selection would remove this type of DNA if it were useless, since DNA manufactured by the cell is energetically costly. Because of the lack of selective pressure on this neutral DNA, one would expect that 'old' pseudogenes would be scrambled beyond recognition as a result of accumulated random mutations. Moreover, a removal mechanism for neutral DNA is now known. (Jerlstrom, 15.)

Granting the possibility that pseudogenes have a function, the claim that they are a vestige of evolutionary history reduces to the notion that a Creator would not fulfill a function in one organism by using a series of nucleotides that are similar to a series of nucleotides that fulfill a different function in another organism. That, however, is a theological argument. Hunter makes the point well:

A pseudogene is a DNA sequence that resembles a gene but appears to be nonfunctional. In evolutionary lore, these are vestigial organs at the molecular level. And just as the vestigial organ argument for evolution relies on the assumption of full knowledge about the organism, so too the pseudogene argument assumes that we can be sure they are not useful. They are assumed to be the byproduct of useless, but not terribly harmful, mutations. Gray writes:

Further analysis shows that this gene is a pseudogene, i.e., it looks like a real gene, but it is not expressed due to a mutation in the gene itself. Now we could argue that in God's inscrutable purpose he placed that vitamin C synthesis look-alike gene in the guinea pig or human DNA or we could admit the more obvious conclusion, that humans and primates and other mammals share a common ancestor.

Here Gray makes a negative theological argument. He seems comfortable in assuming just what God would have done when it comes to designing the genotype. Gray states unequivocally that the pseudogene is a result of mutation, but this is nothing more than evolutionary speculation. More important, he then claims that God obviously would not have an inscrutable purpose for having the nonstandard gene there. For our purposes the point is not that pseudogenes do or do not have function or that God must have or must not have designed them. The point is simply that, like evolutionists, theistic evolutionists need Darwin's negative theology. (Hunter, 168-169.)

Even if one could be certain that a gene was functionless (a pseudogene) and had been rendered such by a specific mutation, finding that same gene and mutation in another species would not mean that those species had descended from a common ancestor. The same gene could have been inactivated by the same mutation occurring independently. The evolutionists' reply that this suggestion is too improbable to take seriously depends on the assumption that the mutation in question occurs randomly. But if there is (or was) a mechanism of mutation that favors certain locations in the gene, the odds against an independent occurrence of the mutation drop according to the strength of that bias.

As in the case of possible functions for pseudogenes, we simply do not know enough to assess definitively the odds against the independent occurrence of inactivating mutations (because we lack complete knowledge of all past and present mechanisms of mutation). So even conclusions about common ancestry that are based on the presence of similar, bona fide pseudogenes must remain tentative.¹⁸

For example, molecular biologist Michael Brown believes there is evidence for the existence of either viral or enzymatic activity that creates mutations. He writes:

So I think there is a mechanistic process that has produced many of the Pseudogenes that we have, rather than a random process. If the Pseudogene is truly defective and if the mutations are truly found in patterns (not random), then the idea that it's a common mechanism is possible. Viruses have enzymes that, under the same conditions, do repeatable reactions.

If the DNA in Humans, Chimps, Monkeys, etc., are very similar, then if they are all infected by the same virus, would we expect the virus to do the same thing in the different species? I think so.¹⁹

¹⁸ For a fuller and more technical discussion of these and other issues, see the articles by Gibson, Walkup, and Woodmorappe (2000) listed in the bibliography. These articles are also available online at www.grisda.org/origins/21091u.htm, www.answersingenesis.org/home/area/magazines/tj/tjv14n2_junk_dna.pdf, and www.answersingenesis.org/Home/Area/Magazines/tj/docs/tj14_3-jw_pseudo.pdf, respectively.

The point is not that Brown's opinion necessarily is correct but that it (or something analogous) may be correct. Our understanding is just too rudimentary to permit us to say with certainty that similar pseudogenes were not caused independently by a nonrandom mechanism.

The fact some pseudogene-derived phylogenies disagree is consistent with the suggestion that something other than common descent is involved in the phenomenon. Phylogenies based on several pseudogene sequences have yielded conflicting results with regard to the human-chimp-gorilla trichotomy. (Woodmorappe 2000, 62-63.) Of course, evolutionists have ways of accommodating these discordant data, but their presence remains noteworthy.

PREDICTION 8: ONTOGENY AND DEVELOPMENT OF ORGANISMS

Embryology and developmental biology have provided some fascinating insights into evolutionary pathways. Since the cladistic morphological classification of species is generally based on derived characters of adult organisms, embryology and developmental studies provide a nearly independent body of evidence.

The ideas of Ernst Haeckel greatly influenced the early history of embryology; however, his ideas have been superseded by those of Karl Ernst van Baer, his predecessor. Van Baer suggested that the embryonic stages of an individual should resemble the embryonic stages of its ancestors (rather than resembling its adult ancestors, a la Haeckel). The final adult structure of an organism is the product of numerous cumulative developmental processes; for species to evolve, there necessarily must have been change in these developmental processes. The modern developmental maxim is the inverse of Haeckel's biogenetic law. "Phylogeny recapitulates Ontogeny," not the opposite. Walter Garstang stated even more correctly that ontogeny creates phylogeny. What this means is that once given knowledge about an organism's ontogeny, we can confidently predict certain aspects of the historical pathway that was involved in this organism's evolution (Gilbert 1997, pp. 912-914). Thus, embryology can provide confirmations and predictions about evolution.

Two different concepts seem to be mixed here. On the one hand, there is the suggestion that descendant ontogenies tend to recapitulate ancestral ontogenies (Garstang's notion of paleogenesis). This is the claim that all vertebrates, for example, are very similar at an early stage of embryological development, with noticeable differences coming only in later stages. The more closely related the species being compared, the longer their embryos will develop similarly. The more distantly related the species, the sooner their embryos will diverge in appearance.

¹⁹ These comments are from an email posted at Dr. Brown's website (<http://www.mhrc.net/pseudogene.htm>).

On the other hand, there is the suggestion that the embryos of organisms develop in ways that exhibit aspects of the organism's evolutionary history.²⁰ Thus, Dr. Theobald points to the fact certain reptile jaw bones and marsupial middle ear bones develop from the same embryological structures as evidence that the middle ear bones of mammals evolved from the jaw bones of reptiles.

The alleged prediction and fulfillment under the first concept are:

1. If universal common ancestry is true, then all ontogenies will begin similarly, and the ontogenies of more closely related species will remain similar longer than will the ontogenies of more distantly related species.
2. All ontogenies begin similarly, and the ontogenies of more closely related species remain similar longer than do the ontogenies of more distantly related species.

The alleged prediction and fulfillment under the second concept are:

1. If universal common ancestry is true, then certain aspects of an organism's evolutionary history will be exhibited in its ontogeny.
2. Certain aspects of an organism's evolutionary history are exhibited in its ontogeny.

There is nothing about the hypothesis of universal common ancestry that requires any particular manner of reproduction, let alone one in which embryos either recapitulate the ontogenies of their ancestors or pass through stages representative of their evolutionary history. Common ancestry can accommodate such phenomena, but it certainly does not predict it. And if it does not predict the phenomena, it cannot be falsified by their absence or confirmed by their presence.

Even if one could rightly claim these as predictions of the hypothesis of universal common ancestry, they are too general to be scientifically meaningful. How does one measure objectively the similarities of various ontogenies? What specific aspects of an organism's evolutionary history will be reflected in its ontogeny and why those aspects and not others?

And even if these ambiguities could be nailed down, views about "closely related species" and "evolutionary history" are tentative. So if all other avenues of accommodating the embryological data should fail, the option of revising phylogenies is always available. Falsifiability is again merely an illusion.

As for the first concept, the claim that ontogenies of organisms begin similarly and then progressively diverge in accordance with their alleged evolutionary proximity is false. Developmental biologist Jonathan Wells explains:

²⁰ In saying that one can "predict" certain aspects of an organism's evolutionary history from its ontogeny, Dr. Theobald means that the embryos of organisms develop in ways that exhibit aspects of the organism's evolutionary history. This is clear from what he cites as fulfillment.

Although it is true that vertebrate embryos are somewhat similar at one stage of their development, at earlier stages they are radically dissimilar. After fertilization, animal embryos first undergo a process called cleavage, in which the fertilized egg divides into hundreds or thousands of separate cells. During cleavage, embryos acquire their major body axes (e.g., anterior-posterior, or head to tail, and dorsal-ventral, or back to front). Each major group of animals follows a distinctive cleavage pattern; among vertebrates, for example, mammals, birds, fishes, and reptiles cleave very differently.

Animal embryos then enter the gastrulation stage, during which their cells move relative to each other, rearranging themselves to generate basic tissue types and establish the general layout of the animal's body. The consequences of this process are so significant that embryologist Lewis Wolpert has written that "it is not birth, marriage, or death, but gastrulation which is truly the important event in your life" (Wolpert 1991, 12). Like cleavage patterns, gastrulation patterns vary markedly among the major groups of animals, including the different classes of vertebrates (Elinson 1987).

Only after gastrulation do the embryos of mammals, birds, fishes and reptiles begin to resemble each other. In the pharyngula stage, every vertebrate embryo looks vaguely like a tiny fish, with a prominent head and a long tail. (Wells 1998, 59.)

Reviewing the notion that "during their ontogenies the members of twin taxa follow the same course up to the stage where they diverge into separate taxa," embryologist Wolfgang Dohle wrote:

Everybody who is even slightly acquainted with ontogenetic facts knows that there are hundreds of examples to which this theorem does not apply. In many polychaete and prosobranch genera one species develops through a planktonic larva, whereas another species has direct development. The telolecithal cephalopod eggs cleave in a bilateral manner without any similarity to the spiral cleavage of other related Mollusca. Triclad eggs have a blastomeric anarchy, whereas the adults very closely resemble the polyclads which show spiral cleavage. This list could easily be elongated. (Dohle, 285.)

Wells points out that this ontogenetic pattern of early differences followed by similarities and then differences again "is quite unexpected in the context of Darwinian evolution." He adds, "Instead of providing support for Darwin's theory, the embryological evidence presents it with a paradox." (Wells 2000, 99.) Of course, attempts are being made to explain the paradox by proposing that early development evolves more easily than expected, but as Wells notes, "it is clear that [these proposed

explanations] start by *assuming* Darwinian evolution, then read that back into the embryological evidence." (Wells 2000, 99.)

Of course, this is the exact opposite of basing evolutionary theory on embryological evidence. If one were to start with the evidence and then follow Darwin's reasoning about the implications of development for evolution, one would presumably conclude that the various classes of vertebrates are *not* descended from a common ancestor, but had separate origins. Since this conclusion is unacceptable to people who have already decided that Darwin's theory is true, they cannot take the embryological evidence at face value, but must re-interpret it to fit the theory. (Wells 2000, 101.)

Even if one ignores the paradoxical hourglass pattern of vertebrate ontogenies (the fact they start out looking very different, converge in appearance midway through development, and then increasingly diverge toward adulthood) and focuses only on the latter half of development, common ancestry is not the only explanation for the gradual divergence of different species. As Brand explains:

[A] home builder builds the foundation first (homes that look very different when complete can have similar foundations) and adds the unique features of the home later. An engineer attempting to design the developmental stages of all these organisms would very possibly find that it is most efficient to follow a basic plan for all and add special features later in the process, as needed for each animal. (Brand, 150.)

In addition, if Dr. Theobald's assertion that "[t]he final adult structure of an organism is the product of numerous *cumulative* developmental processes" (emphasis supplied) is correct, then organisms that are thought to be more evolutionarily derived would take longer to develop. But as Wise points out, that is not the case. "[O]rganisms that are thought to be more evolutionarily derived don't seem to have longer development." (Wise, 216.)

As for the second concept, the claim that "certain aspects" of an organism's evolutionary history are exhibited in its ontogeny (such as the alleged evolution of the mammalian middle ear from reptile jaw bones) is nothing more than an opinion. Common descent is not the only explanation for the fact separate structures in adults of different species develop from an analogous embryological structure. It is certainly possible for a designer to fabricate different structures from similar elements. A manufacturer, for example, can make the tops of one kind of footwear and the laces of another from the same nylon.

The notion that God would not employ an ontogeny in which the middle ear bones of mammals develop from the embryological structure that is analogous to that from which reptile jaw bones develop is a theological assessment. Those who reject that assessment are rightly unimpressed by evidence that draws its weight from it.

Moreover, it is unclear in what sense the ontogenetic development of mammalian middle ear bones from a structure analogous to that from which certain reptile jaw bones develop can be said to exhibit the evolution of the mammalian middle ear from the reptile jaw. The evolutionary claim is that the quadrate and articular bones of the reptilian jaw were (on two separate occasions) gradually transformed into ear ossicles through many random steps, each of which provided a significant enough advantage to be established in the population. There is no need, however, for the intermediate stages of an embryo's development to be progressively advantageous, as they are part of a directed development program that unfolds in a protective environment. The two thus seem quite unrelated.

PREDICTION 9: PRESENT BIOGEOGRAPHY

Because species divergence happens not only in the time dimension, but also in spatial dimensions, common ancestors originate in a particular geographical location. Thus, the spatial and geographical distribution of species should be consistent with their predicted genealogical relationships. The standard phylogenetic tree predicts that new species must originate close to the older species from which they are derived. Closely related contemporary species should be close geographically, regardless of their habitat or specific adaptations. If they are not, there had better be a good explanation, such as extreme mobility (cases like sea animals, birds, human mediated distribution, etc.), continental drift, or extensive time since their divergence. In this sense, the present biogeographical distribution of species should reflect the history of their origination.

A reasonable nonevolutionary prediction is that species should occur wherever their habitat is. However, macroevolution predicts just the opposite – there should be many locations where a given species would thrive yet is not found there, due to geographical barriers (Futuyma 1998, pp. 201-203).

The standard phylogenetic tree does not "predict that new species must originate close to the older species from which they are derived." A phylogeny is simply a diagram that depicts current evolutionary thinking about the genealogical relationships of the taxa included. It does not address questions of geographical proximity.

It is unclear (at least to me) what is being claimed here. On the one hand, there is the suggestion that the geographical distribution of species should be consistent with their believed (not "predicted") genealogical relationships. Thus the statement, "Closely related contemporary species should be close geographically, regardless of their habitat or specific adaptations."

On the other hand, there is the suggestion in the second quoted paragraph that only macroevolution (which Dr. Theobald labels a "virtual synonym" for universal common descent) can explain why some species live only in certain areas, despite the existence of similar habitat elsewhere. This point relates solely to the location of "given species," not to their distance from "closely related contemporary species."

It is not spelled out how these two propositions translate into support for the hypothesis of universal common ancestry. Presumably they are to be merged into something like the following: only universal common ancestry can explain the fact groups of similar species are often restricted to a particular geographic region. In that case, the alleged prediction and fulfillment can perhaps best be expressed as:

1. If universal common ancestry is true, then groups of similar species will often be restricted to a particular geographic region.
2. Groups of similar species are often restricted to a particular geographic region.

The fact groups of similar species are often restricted to a particular geographic region is not evidence of universal common ancestry. At best, it suggests that the similar species arose in that region from a common ancestor. It says nothing about whether that regional common ancestor descended from a universal common ancestor, descended from one of many independently created organisms, or was itself created independently. It therefore does not do what Dr. Theobald needs it to do.

In fact, the degrees of evolution suggested by biogeography are quite limited. As biologist L. James Gibson notes, "Geographical distributions indicate common ancestry only for lower taxonomic categories. Endemic groups are most common at the Family level or lower. Few Orders are endemic to a particular region. Thus common ancestry is suggested primarily among members of families and genera."²¹

Wise makes the point this way:

There are two sorts of biogeographical evidences. One type is the claim that very similar species are often found near one another, as if they evolved from one another. This type of biogeography, which I call *microbiogeography*, has many supporting examples. Microbiogeography is evidence for microevolution (the evolution of populations) and the origin of species, however, *not* for macroevolution of the origin of major groups. What I call *macrobiogeography* is the claim that major types of organisms tend to be associated with one another.

There are very few examples of macrobiogeographical evidences for macroevolution, and none of them is very strong. (Wise, 223.)

The best known claim of macrobiogeographical evidence is the one cited by Dr. Theobald -- the concentration of marsupials in Australia. But as Wise explains, "there are several reasons that marsupials in Australia are actually a poor example."

First, all marsupials are not in Australia. The Virginia opossum of North America, for example, is a marsupial. It is thought to have come from

²¹ From L. James Gibson, "Creation and Evolution: A Look at the Evidence" (available at <http://origins.swau.edu/papers/evol/gibson/default.html>).

South America, not Australia. Thus, not all similar organisms *are* in the same area. Second, in the fossil record marsupials are known from every continent. Third, marsupials are the oldest fossil mammals known from Africa, Antarctica and Australia -- in that order. The fossil record seems to show a migration of marsupials from somewhere around the intersection of the Eurasian and African continents and then a survival in only the continents farthest from their point of origin (South America and Australia). The same major groups of marsupials (opossums) are found in both South America and Australia. Macroevolutionists claim that these major groups of marsupials are together because they evolved from a common ancestor, but the evidence can be at least as well explained as similar organisms (fit for similar environments and with similar capabilities) traveling more or less together to similar environments. (Wise, 223.)

All of Dr. Theobald's other examples involve endemic groups at lower taxonomic categories (species of lungfishes, ratite birds, leptodactylid frogs, alligators, giant salamanders, magnolias, cacti, and pineapples). Of course, creationists of all stripes accept speciation or diversification within created kinds (understanding that both "species" and "created kinds" are nebulous concepts).

Dr. Theobald acknowledges that species of alligators, giant salamanders, and magnolias occur half a world apart, but he still counts them as "close" species because it is hypothesized that Eastern North America and East Asia were once close together. There are many other seemingly anomalous geographical occurrences of the same or similar species that are explained with speculative hypotheses.²²

The flexibility of biogeography is well illustrated by the fact it was used as support for evolution prior to the acceptance of plate tectonics and continental drift. As ReMine explains:

One reason for this erosion [in the assessment of the importance of biogeography as evidence for evolution] was the 1960's development of plate tectonics and continental drift. This development radically changed the picture, and forced evolutionists to rapidly restructure biogeographical ideas away from the fixed continents axiom of Darwin and Wallace. The biogeographers tried to reconcile their data with the new concepts of movable paleogeography. The plasticity of evolutionary biogeography was nakedly revealed by its ability to suddenly adapt to the dramatic shift in geologic understanding. (ReMine, 437.)

²² For example, three of the four species of tapirs are restricted to Latin America (southern Mexico to Brazil), whereas the fourth species inhabits Burma, Thailand, Malaya, and Sumatra. Giant tortoises are found on the Galapagos islands and on the island of Aldabra (near Madagascar). Species of coelacanths are known only in Indonesia and the western Indian Ocean. Lungless salamanders live in the Western Hemisphere and southern Europe. The list could be extended easily.

Though biogeography has from the earliest days of the theory been touted as strong evidence for evolution, Nelson and Platnick wrote in 1981: "We conclude, therefore, that biogeography (or geographical distribution of organisms) has not been shown to be evidence for or against evolution in any sense." (Nelson and Platnick, 223.) Perhaps that explains why "Mark Ridley has an entire chapter on biogeography in his evolution textbook [see bibliography] but does not use biogeography as one of his evidences for evolution." (Hunter, 184 n.64.)

The assertion in the second quoted paragraph that under nonmacroevolutionary theories species should exist wherever there is suitable habitat for them is groundless. It not only ignores the room nonmacroevolutionary theories can leave for microevolution and ignores the complexity of factors that can shape the distribution of species, it is apparently based on a theological presupposition. Hunter is again worth quoting on the subject:

And for Michael Ruse, God cannot be reconciled with the facts of biogeography, so we must turn to evolution. He argues, "Given an all-wise God, just why is it that different forms appear in similar climates, whereas the same forms appear in different climates? It is all pointless without evolution." According to Edward Dodson and Peter Dodson, if God created the species, then they should be distributed uniformly around the globe. They write, "had all species been created in the places where they now exist, then amphibian and terrestrial mammals should be as frequent on oceanic islands as on comparable continental areas. Certainly, terrestrial mammals should have been created on these islands as frequently as bats were." It is remarkable how often evolutionists feel free to dictate what God should and shouldn't do. (Hunter, 113.)

Finally, the suggestion that universal common ancestry would be falsified by finding elephants or amphibians on remote islands is incorrect. Their presence would be explained in a way consistent with evolutionary convictions. Ideas of continental drift, land bridges, human involvement, storm rafts, unknown swimming ability, some form of hitchhiking, etc. would be invoked and judged more likely than the alternative. In fact, many amphibians exist on many islands, and their presence is not viewed as a threat to the evolutionary hypothesis.

PREDICTION 10: PAST BIOGEOGRAPHY

Past biogeography, as recorded by the fossils that are found, must also conform to the standard phylogenetic tree. As on [sic] example, we conclude that fossils of the hypothetical common ancestors of South American marsupials and Australian marsupials should be found dating from before these two landmasses separated.

The alleged prediction and fulfillment are:

1. If universal common ancestry is true, then the geographic distribution of fossil species will conform to the standard phylogenetic tree.
2. The geographic distribution of fossils conforms to the standard phylogenetic tree.

As I have pointed out, it is not a prediction of the hypothesis of universal common ancestry that organisms, past or present, will conform to the standard phylogenetic tree. Rather, the standard phylogenetic tree is a depiction of current evolutionary thinking about the genealogical relationship of the taxa included. Phylogenies are provisional, evolutionary constructs of data, including biogeography. If facts develop that make some aspect of a phylogeny untenable, adjustments will be made within the evolutionary framework and a new orthodoxy will be established.

Judging by the example given, the geographic distribution of fossil species is deemed to conform to the standard phylogenetic tree if the date and location of alleged ancestors do not render impossible the claim of descent. Thus, if Australian marsupials originated on another continent, one would expect to find marsupials on that continent prior to the time Australia is believed to have become geographically isolated.

The presence of similar marsupials in South America, Antarctica, and Australia may be evidence for the claim that the continents were at one time contiguous, but it is not evidence for the hypothesis of universal common ancestry. It is not even evidence for the claim that all Australian marsupials arose from a common ancestor.

"There is no direct evidence to document when marsupials first entered Australia." (Carroll, 431.) When they first appear in the fossil record of Australia in the late Oligocene, "the major groups had already differentiated," and "the interrelationships of the various lineages have not been satisfactorily established." (Carroll, 431, 440.) According to Carroll, marsupials may have entered Australia "at least 40 million years" before there is a record of their presence. (Carroll, 435.)

There is thus no way to tell what marsupials entered Australia or when they did so. If representatives of the major groups of Australian marsupials were included among the immigrants, Australia would at most bear witness to diversification at lower taxonomic levels.

Finding marsupial fossils in Antarctica establishes that there were once marsupials on that continent, but it says nothing about their having evolved from some nonmarsupial stock or even about their having given rise to distinct marsupial suborders. If South America, Antarctica, and Australia were once contiguous and if one hypothesized that marsupials radiated from South America into Australia (or vice versa), then one would predict that marsupials once existed in Antarctica. Finding that to be the case certainly is not "an astounding macroevolutionary confirmation."

Determining the place of origin and direction of marsupial dispersal is not a simple matter of tracking the date of known fossils (i.e., they arose in North American

and migrated to Australia). As Carroll's statement about the entry of marsupials into Australia makes clear, the absence of fossils is not necessarily evidence of the absence of marsupials.²³ That is why "[t]he place of origin and direction of dispersal of marsupials in the southern continents is subject to continuing debate." (Carroll, 431.)

The uncertainty surrounding this issue is apparent from the remarks of Clemens, Richardson, and Baverstock:

Against this background of ignorance and uncertainty, no definitive evaluation of the competing hypotheses concerning the time and place of the origin of the marsupials can be presented. Almost every continent on which marsupials have existed has been nominated as an area of origin of the group. . . .

Currently, hypotheses suggesting origin and early radiation of marsupials in the southern continents, particularly Australia, Antarctica and South America are favoured by many workers. (Clemens and others, 542.)

Under the heading "Potential Falsification," Dr. Theobald writes, "We confidently predict that fossils of recently evolved animals like apes and elephants should never be found on South America, Antarctica, or Australia (excepting, of course, the apes that travel by boat)." But finding fossil apes or elephants on one or more of those continents would not falsify universal common ancestry.

Any such find would, of course, face an extreme standard of proof in terms of both identification and dating (the more recent the date the more readily the explanation of human involvement would be accepted). Assuming the problem could not be avoided by denying the identification or dating, a devotee of common ancestry could revise his theory of continental drift or historical geography, propose temporary land bridges, reconsider when apes or elephants arose, suggest parallel or convergent evolution, etc. However problematic any of these proposals may be, they would be considered more likely than the alternative, i.e., that universal common ancestry is false.

The fact geography does not rule out the possibility that the modern horse descended from *Hyracotherium* provides no support for the claim of universal common ancestry. Assuming that *Equus* descended from *Hyracotherium*, that is merely diversification within the family Equidae. The change from *Hyracotherium* to *Equus* is trivial compared to the changes required by the theory of universal common ancestry.

Again, the claim under the heading "Potential Falsification" that it would be "macroevolutionarily devastating" to find an equid in South America before about 12 million years ago underestimates the theory's flexibility. It has great capacity for

²³ This is also apparent from the fact marsupial presence in southeastern Asia is known from only one fossil, which was reported in 1992 (see, S. Ducrocq and others).

accommodating seemingly discordant data. Various hypotheses for fitting the data within an evolutionary framework would circulate, and the issue would be considered "a problem" until a consensus was reached regarding the solution. It would not, however, be judged a threat to (and certainly not a falsification of) the evolutionary paradigm.