# Disclosure

of things evolutionists don’t want you to know

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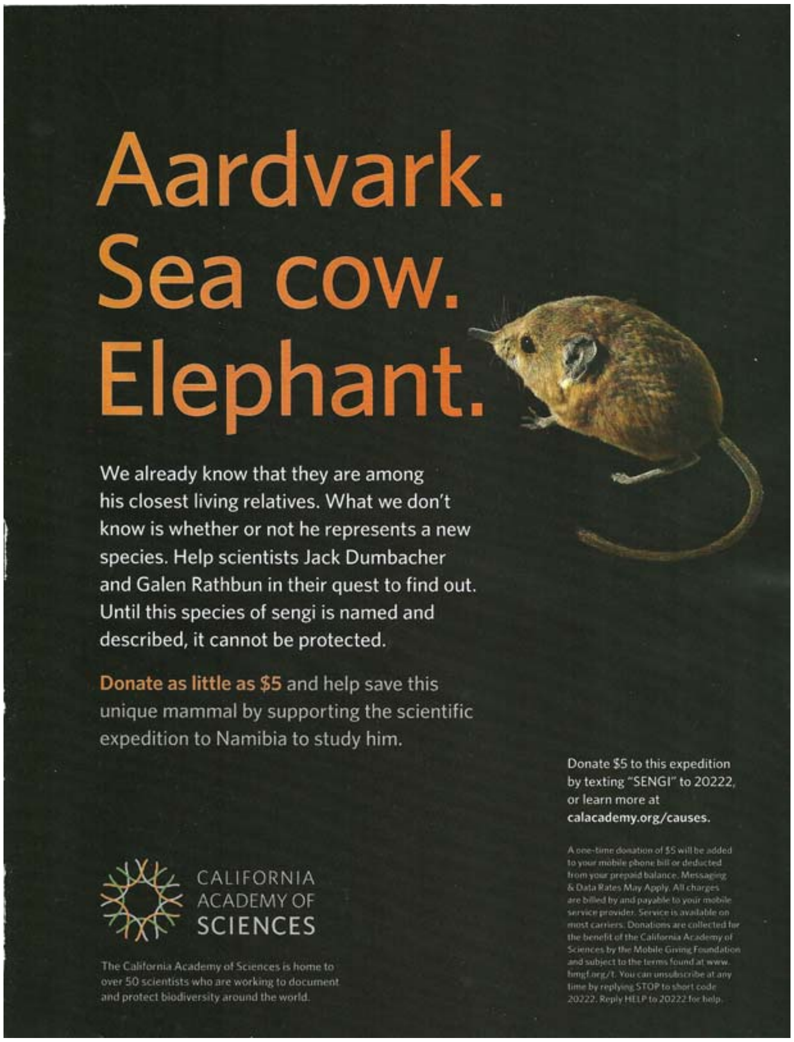
# FOOLISH RELATIONSHIPS

***Cladistics can produce some really foolish relationships.***

Traditionally, our April feature article is an April Fool parody to celebrate National Theory of Evolution Day (April 1). Last month, however, the California Academy of Sciences ran a full-page ad that is even sillier than any parody we could write. We swear to you that this ad is not an April Fool joke. It’s real. Go to their web site and let them beg you for money! They need $10,000 by April 30. (They only had about $500 on April 2.)



Aardvark.
Sea cow.
Elephant.

We already know that they are among his closest living relatives. What we don’t know is whether or not he represents a new species. Help scientists Jack Dumbacher and Galen Rathbun in their quest to find out. Until this species of sengi is named and described, it cannot be protected.

**Donate as little as $5** and help save this unique mammal by supporting the scientific expedition to Namibia to study him.

Donate $5 to this expedition by texting “SENGI” to 20222, or learn more at **calacademy.org/causes.**

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CALIFORNIA
ACADEMY OF
SCIENCES

The California Academy of Sciences is home to over 50 scientists who are working to document and protect biodiversity around the world.

The sentence following the word “elephant” is, “We already know that they are among his closest living relatives.” We can’t think of anything more foolish than saying that the little sengi in the picture is more closely related to a sea cow or an elephant than it is to a mouse.

Here's why they ran such a foolish ad:

> Academy scientists Galen Rathbun and Jack Dumbacher are working to document and describe a new species of sengi in Namibia. Initial DNA analysis from a markedly unique sengi suggests that it is genetically distinct from other sengis in the region. The pair of scientists must travel to Namibia and survey the desert habitat where the "mystery" sengi was first spotted to gather more information about the sengi. If, as the Academy scientists suspect, this sengi turns out to be a new species, it will be the smallest sengi known. It is also likely to be among the rarest.
>
> There are currently only 17 known species of sengi. The classification of a new species would significantly add to the biodiversity found in this unique group of mammals as well as provide a better understanding of the evolution of our distant mammalian relatives. The more we are able to understand about evolution and biodiversity, the better equipped we can be to protect and save our natural world.
>
> By describing and naming this new species, the scientists can begin the process of garnering protection for the animal. [1]

We MUST send these scientists to Africa "to protect and save our natural world!" ☺ If this little mammal goes extinct, we won't ever be able to understand the evolution of our mammalian relatives. What a tragedy that would be!

How did these scientists become such fools? It's all because of a taxonomy based on cladistics.

## Taxonomy

The creationist Linnaeus originated the biological classification system (called "taxonomy" by scientists) used today. His goal was simply to group plants and animals in a logical way to make it easier to organize information about them in order to make it easier to study them. What he did was no different than a grocery store manager deciding how to stock the shelves to make it easy for shoppers to find what they need. But what is a logical grouping to one person might not be logical to another person. That's why you may find it hard to locate the items on your shopping list if you go to a different grocery store.

Classification is simply a matter of opinion. Linnaeus did a pretty good job, in most people's opinion; but not perfect. So, occasionally plants and animals have been reclassified by consensus of modern biologists.

The opinion of twentieth century biologists was that plants and animals are similar because of common ancestry. This evolutionary assumption has led to two problems. One problem is that it has led to circular reasoning. That is, plants and animals were classified on the basis of presumed ancestry. Then, the classification was used as proof that those plants and animals did have that presumed ancestry.

Another serious problem arose when geneticists got involved. Living things with the closest common ancestor should be the most genetically similar. Therefore, it seemed that the biological classification method could be made "more accurate" by using genetic comparisons rather than observable physical characteristics. This led to some foolish conclusions, such as a sengi being more closely related to a sea cow than a mouse. But let's not get ahead of ourselves. Let's continue methodically down the historical path that led to such a foolish conclusion.

Try to think like an evolutionist. You have no doubt that all life evolved from a common ancestor. Therefore, you are absolutely convinced that creatures that share a close common ancestor will be the most closely related on a genetic level. If a genetic analysis produces a surprising new relationship, then the previous classification must have been the result of human error. Some sort of bias, or incorrect logic, must have contaminated the previous results. The only solution is to replace unreliable human reasoning with the impartial analysis of a computer using well-defined rules. But there is a fatal flaw.

## 65 Love Affair

Most people think computers are objective and unbiased. You feed the data in, and get the results out, no matter what they are. The computer doesn't care about ramifications and lets the chips fall where they may. While it is true that the computer is unbiased, the computer programmer might not be.

In 1965, I was a member of a Boy Scout Explorer post sponsored by the local IBM office. There was a high school dance coming up. Some of us computer nerds had a great idea. The notion of computer dating was just beginning. So, we got all the boys and girls to fill out questionnaires and submitted the data to one of the IBM engineers to match us up. After the initial result, we suggested some changes. After two or three more tries, the computer came up with the "right" pairings. Remarkably, we were all paired with the prettiest girls. It was clear evidence (to us) that the computer got it right.

The computer really is unbiased; but the programmer isn't. The computer blindly follows the rules; but it is the programmer who makes the

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[1] http://www.calacademy.org/join/causes/

rules. Which chromosomes should be compared, and how should they be compared? It's the programmer's decision. If the programmer doesn't like the results, he makes different decisions and runs the program again.

## Cladistics

The modern way to classify plants and animals is to use cladistics.

> Cladistics: a system of biological taxonomy that defines taxa uniquely by shared characteristics not found in ancestral groups and uses inferred evolutionary relationships to arrange taxa in a branching hierarchy such that all members of a given taxon have the same ancestors [2]

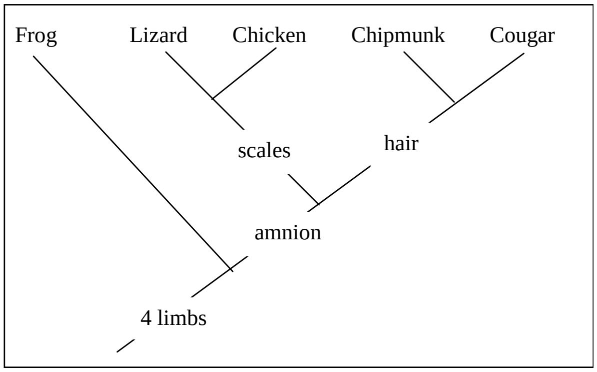
It is apparent from the definition that the process is based on the presumption of evolution. Naturally, it will produce a result consistent with evolution (or die trying).

The process appears to be completely objective—but it isn't.

## Whiting's Example

Dr. Michael F. Whiting is a well-known (in biological circles) expert in insect evolution at Brigham Young University. [3]

He gave a televised BYU Forum Address on May 24, 2005, in which he explained how cladistics works. Sixteen minutes into the lecture he produced this cladogram, and explained how he produced it.

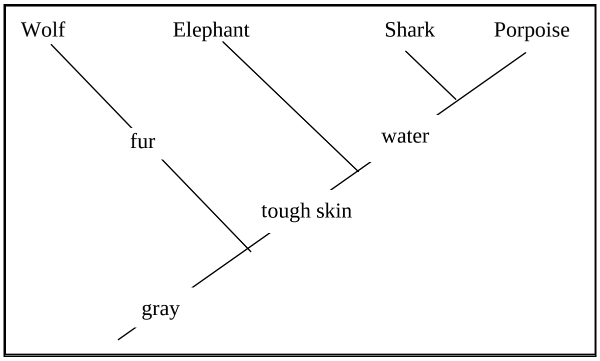


He started with the chicken, chipmunk, and cougar. Remember that the definition of cladistics included the phrase, "shared characteristics not found." Chipmunks and cougars have hair, but chickens don't share that characteristic. Therefore, they are more closely related to each other than they are to chickens.

Then he added the lizard. Lizards have scales. Although we generally think of chickens as having feathers, they do have scales on their feet. So, the lizard is closely related to the chicken.

Then he added the frog. The frog doesn't have hair or scales. Furthermore, their eggs don't have an amnion. But all have four limbs.

So, in his simple example, it all works out nicely, consistent with evolution. The chicken is closely related to the lizard because birds evolved from dinosaurs. It all looks so objective and clear. It seems like it should always work, no matter who does it or how you start. So, since it is April, let's try to do it, and make fools of ourselves.



Let's start with shark, porpoise, and elephant. The shark and porpoise share the characteristic that they live in the water. The elephant doesn't. So, the shark and the porpoise are most closely related.

Now we add the wolf. It has fur, rather than tough leathery skin. But all four are gray. It is all very logical, but it must be wrong because it doesn't match the evolutionists' expectations. Whales and porpoises were supposed to have evolved from a land mammal, not a shark. Our foolish mistake was thinking that living in the water was more important than having mammary glands. And why was that a mistake? It was a mistake because it didn't agree with evolutionary theory. Of course, the evolutionary consensus might change. If evolutionists decide that it is more likely that mammary glands evolved twice (one on land, and once in the water), and whales and porpoises did not evolve from a land mammal, then we will be proved right after all.

## Genetic Cladistics

Whiting's example used physical characteristics rather than genetic similarity. But it doesn't work any better at the genetic level.

> One of the most pervasive challenges in molecular phylogenetics is the incongruence between phylogenies obtained using different

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[2] http://www.merriam-webster.com/dictionary/cladistics
[3] http://whitinglab.byu.edu/MFW.htm

> data sets, such as individual genes. [4]

Let's translate that into plain English. A "phylogeny" is a family tree. If you build a family tree comparing one particular gene, you will get a different family tree than if you used a different gene. Using different genes give "incongruent" (in other words, conflicting) results.

Why does this happen?

> Analytical factors affecting phylogenetic reconstruction include the choice of optimality criterion, limited data availability, taxon sampling and specific assumptions in the modelling of sequence evolution. [5]

In plain English, here are their four excuses why it doesn't always work. (In fact, it doesn't ever work, but they don't want to admit that.)

First, there is "the choice of optimality criterion." In other words, if you choose to compare the wrong thing (like living in water rather than having breasts) you will get the wrong answer.

Second, there is "limited data availability." This is a good general purpose excuse. "We weren't stupid—we just didn't have all the facts. We did the best we could with the limited information available to us."

Third, there is "taxon sampling." They can't compare everything, so they have to compare a few representative samples. "If the samples turn out not to be truly representative, it's not our fault."

Finally, "specific assumptions" regarding how evolution actually works. Remember, they are trying to prove what they already believe. If their assumption about how evolution happened is wrong (and it is), then their conclusion will be wrong.

As if these four excuses weren't enough, they have another backup excuse.

> Data sets composed of genes showing heterogeneity in mode of sequence evolution may also compound bias rather than resolve the true history. Furthermore, because current tests are not always reliable, it has been difficult to estimate incongruence. [6]

If you are unlucky enough to pick genes that evolved differently (that is, they had a heterogeneous mode of sequence evolution), you will get the wrong answer.

Finally, they did admit that the method is "not always reliable." Actually, it is never reliable. Since they get so many incongruent (that is, contradictory) results, it is really hard to tell how bad the method really is.

They compared eight different kinds of yeasts using different genes and different rules, and came up with the 12 different, "robustly supported alternative" evolutionary relationships shown below. We realize that the printing may be too small for you to read; but that isn't important. The point is that the method gives 12 different results, depending upon which genes it compares, and what rules it uses to compare them.

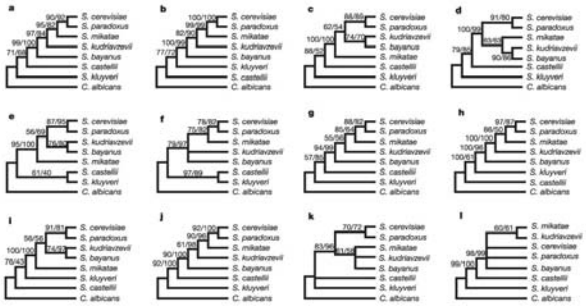

FIGURE 1. Single-gene data sets generate multiple, robustly supported alternative topologies. [7]

We didn't have to search very hard to find an article with contradictory evolutionary relationships. The professional scientific literature is full of examples. In fact, that's the reason why Rokas and associates wrote the article. They were looking for a method of comparing genes that gives reasonable, consistent results. In their words,

> To systematically investigate the degree of incongruence, and potential methods for resolving it, we screened the genome sequences of eight yeast species and selected 106 widely distributed orthologous genes for phylogenetic analyses, singly and by concatenation. [8]

In other words, they wanted to find out how bad the method really is ("the degree of incongruence") and try to figure out a way to fix it. (Of course, they had to suggest a way to fix it. If they didn't, they would never have gotten their paper published.) So, they picked eight species of yeast to analyze.

We should point out that it is entirely possible, even likely, that these eight varieties of yeast might actually have a common ancestor. Microevolution does really happen. They are trying to prove that the method works for microevolution, and expand their conclusion to macroevolution (which is a fundamentally different

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[4] Rokas *et al.*, *Nature*, 23 October 2003, "Genome-scale approaches to resolving incongruence in molecular phylogenies", pp. 798 - 804

[5] *ibid.*

[6] *ibid.*

[7] *ibid.*

[8] *ibid.*

thing that microevolution). Ironically, the process doesn't even work for the real process of microevolution, so there isn't any reason to believe it works for the mythical process of macroevolution. But, we are getting ahead of ourselves again.

Let's get back to their method. They selected 106 genes that they believed to be unrelated ("orthologous"). They tried to produce a family tree (a "phylogenetic analysis") using single genes. Then they tried using combinations of genes.

They eventually found that if they used enough genes, they got consistent results (for the genes they picked, and these particular species of yeast). Here is their official conclusion.

> **Implications for resolution of phylogenies**
>
> Our results show that there is widespread incongruence between phylogenies recovered from individual genes. Therefore reliance on single or a small number of genes has a significant probability of supporting incorrect relationships for the eight yeast taxa. Perhaps surprisingly, none of the factors known or predicted to cause phylogenetic error could systematically account for the observed incongruence, suggesting that there may be no good predictor of the phylogenetic informativeness of genes. However, regardless of the source of incongruence, concatenation of a sufficient number of unlinked genes (≥20 genes in this study) yields the species tree with remarkable support. [9]

In other words, using a single gene, or just a few genes, will almost certainly give the "wrong" answer. Furthermore, there is no way to tell, in advance, how to pick genes that will give the "right" answer.

Of course, they could not have gotten the paper published if their conclusion was, "We tried as hard as we could, but we couldn't solve the problem." Fortunately for them, they finally came up with "a species tree with remarkable support." The fact that it is "remarkable" to find a way to get the genetic data to agree with itself speaks volumes. Their solution was to average the heck out of the data, and rely on regression to the mean. That amounts to little more than ignoring all the differences.

If evolution were really true, then it should not matter much which genes are compared. But, as we recently showed you, the Y chromosomes of chimps and humans are radically different. [10] If the method gives different answers every time, it can't possibly give you "the one correct answer" because there are multiple different answers. But even if the method does give the same answer every time, it might be consistently wrong.

To see why averaging the data gives consistent results, and why consistency isn't proof of correctness, we have to go back to school.

## Little School on the Prairie

Suppose you go to one of the small towns in western Nebraska. Suppose this town has only one school with a total of thirty students in grades 1 through 12. It is likely that some of these students have brothers and/or sisters in the school. In this part of the country children tend not to move far from parents, so it is likely some of the students have cousins in the school. As a scientist, it is your job to figure out which of the students are most closely related. You want to come up with a method that will tell you which students are siblings, which are cousins, and which aren't related at all.

First, you compare them using just a single characteristic. You look at each student's hair color and decide which students are most closely related based on hair color alone. Then you examine eye color and group the students, but you don't get the same results. So then you measure ear shape, and get yet a third, different result. You try again using nose shape, lip shape, teeth, complexion, and body mass index. Every time you get different results.

It is clear that using a single characteristic just won't tell you which students are related. So, you try using five characteristics in combination. You try hair color, eye color, ear shape, nose shape, and body mass index. Then you try hair color, eye color, ear shape, nose shape, and complexion. Success at last! Both combinations of five characteristics give almost identical results! Of course you get consistent results because the average of the four common characteristics outweighs the contribution of the one different characteristic.

If you average enough characteristics, you will get a consistent result. The method will consistently tell you that the same students are related to each other. But that doesn't mean those students really are related to each other. If you try the same method on a single class of unrelated students in a big city school, it will consistently pick out the siblings and cousins, even if none of them are closely related. Comparisons of individual genes (and individual proteins, for that matter) suggest different evolutionary relationships. Comparisons of large groups of genes suggest a consistent evolutionary

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[9] *ibid.*

[10] *Disclosure*, February 2010, "Why, Oh Y?", http://www.scienceagainstevolution.org/v14i5n.htm

relationship; but that consistency isn't significant—the consistency is simply a result of the law of averages.

## Ape Men

We have seen that cladistics analysis of varieties of yeast give inconsistent results (unless you combine all the results together into a meaningless average). We encourage you to read the scientific literature and discover for yourself that this is a common occurrence. You will discover passages like this one.

> Despite tremendous progress in recent years, phylogenetic reconstruction involves many challenges that create uncertainty with respect to the true historical associations of the taxa analysed. One of the most notable difficulties is the widespread occurrence of incongruence between alternative phylogenies generated from single-gene data sets. Incongruence occurs at all taxonomic levels, from phylogenies of closely related species to relationships between major classes or phyla and higher taxonomic groups.[11]

You have probably seen multiple different suggested relationships between the supposed ape men ("hominids," in scientific terms). Ten years ago we showed you six different cladistic analyses of how our alleged human ancestors were related.[12] They are still trying to get the method to work.

> Parsimony-based cladistic analyses are useful in deciphering relationships within the hominid family tree, despite their shortcomings.[13]

This quote tells us more about wishful thinking than scientific reality. Cladistic analysis is useful if it supports the scientist's opinion. If it doesn't, it is because the method has shortcomings.

## Foolish Blind Faith

Despite the known shortcomings of cladistics analysis, some people will believe it no matter how foolish the conclusion. If a cladistics analysis says that a sengi is more closely related to an aardvark, sea cow, or elephant, than it is to a mouse, who can argue with that? IT'S SCIENCE! You can't argue with science, can you?

# Book Review

## What Darwin Got Wrong

***Here is our mixed review of a book written by evolutionists against the theory of evolution.***

Last month we were excited to read in *New Scientist* that evolutionists were about to publish a book questioning the power of natural selection.[14] Naturally, we pre-ordered it, and it arrived just after we published last month's newsletter. Now we have read it, and we can tell you about it.

Here's our conclusion for those readers who don't have the patience to read our whole review of What Darwin Got Wrong by Jerry Fodor and Massimo Piattelli-Palmarini: It presents a unique argument proving that natural selection cannot be responsible for the diversity of all life forms on Earth. It is particularly compelling given the fact that the authors do not believe in creation or intelligent design. Unfortunately, the book is difficult to read, as you will discover from the quotes in this review. So, if you don't have the patience to read our entire book review, which explains their argument in simpler terms, then there is no chance you will have the patience to read the whole book. ☺

## Prefatory Comments

Just so you know where they are coming from, the authors begin by saying,

> In fact, we both claim to be out-right, card-carrying, signed-up, dyed-in-the-wool, no-holds-barred atheists. We therefore seek thoroughly naturalistic explanations of the facts of evolution, although we expect that they will turn out to be quite complex, as scientific explanations often are.[15]

This is the first hint that they don't have any explanation for how evolution could have happened. They just know that Darwin was wrong.

> We close these prefatory comments with a brief homily: we've been told by more than one of our colleagues that, even if Darwin was substantially wrong to claim that natural selection is the mechanism of evolution, nonetheless we shouldn't say so. Not, anyhow, in public. To do that is, however inadvertently, to align oneself with the Forces of Darkness,

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[11] Rokas *et al.*, *Nature*, 23 October 2003, "Genome-scale approaches to resolving incongruence in molecular phylogenies", pp. 798 - 804

[12] *Disclosure*, January 2000, "Human Evolution", http://www.scienceagainstevolution.org/v4i4f.htm

[13] White, *Science*, 2 October 2009, "*Ardipithecus ramidus* and the Paleobiology of Early Hominids", page 64

[14] *Disclosure*, March 2010, "Natural Selection Shocker", http://www.scienceagainstevolution.org/v14i6n2.htm

[15] Fodor and Piattelli-Palmarini, What Darwin Got Wrong, 2010, Profile Books Ltd ., page xiii

> whose goal it is to bring Science into disrepute. Well, we don't agree. We think the way to discomfort the Forces of Darkness is to follow the arguments wherever they may lead, spreading such light as one can in the course of doing so. What makes the Forces of Darkness dark is that they aren't willing to do that. What makes Science scientific is that it is. [16]

We have several things to say about this.

First, it is an explicit admission that there are evolutionists who believe it is right to hide the truth from the public. All criticism of Darwin must be suppressed.

Second, if being unwilling to follow the facts wherever they lead makes one unscientific, then the evolutionists who are trying to suppress the science against evolution are being unscientific.

The authors then summarize their general approach.

> For example, we will run a line of argument that goes like this: there is at the heart of adaptationist theories of evolution, a confusion between (1) the claim that evolution is a process in which *creatures with adaptive traits are selected* and (2) the claim that evolution is a process *in which creatures are selected for their adaptive traits*. We will argue that: Darwinism is committed to inferring (2) from (1); that this inference is invalid (in fact it's what philosophers call an "intensional fallacy"); and that there is no way to repair the damage consonant with commitment to naturalism, which we take to be common ground. Getting clear on all this will be a main goal of the book.
>
> Why, you may reasonably ask, hasn't this tangle of connections been remarked upon before? [17] [italics theirs]

This tangle of connections has been remarked upon, frequently, by creationists. They call it "circular reasoning" rather than "intensional fallacy," but it is the same thing. How do Fodor and Piattelli-Palmarini answer their own question?

> But, of course, everybody is busy and you can't read everything. Nor can we. [18]

If they had read things written by the Forces of Darkness (censored by evolutionists), they would have know this has often been remarked upon before. ☺

## SKINNER AND DARWIN

The premise of their book is that Darwin got wrong what Skinner got wrong. This makes perfect sense to the book's authors because they know what Skinner got wrong; but we suspect the general public isn't as familiar with Skinner or his learning theory as the authors are. Therefore, the general public is likely to get lost right off the bat.

Comparing Darwin to Skinner smacks of a shady debating technique called "guilt by association." The fact that Skinner was wrong certainly does not prove that Darwin was wrong.

Although guilt by association isn't valid, it isn't completely without merit. Consider this analogy: A man goes to a doctor complaining of certain symptoms. The doctor has previously cured another patient with nearly identical symptoms. Just because the second patient has many of the same symptoms of the first patient, it does not prove that the second patient has the same disease and can be cured the same way. It would be irresponsible of the doctor to assume the second patient has the same disease without doing further tests. On the other hand, it would be just as irresponsible for the doctor not to consider the possibility that the second patient has the same disease and test for it.

The authors of the book recognize that Skinner's theory and Darwin's theory are remarkably similar. They know that Skinner's theory is wrong because Skinner made a logical mistake. This suggested to them that Darwin may have made the same mistake. Rather than simply assuming that Darwin's theory is wrong, they carefully examined Darwin's theory to see if Darwin made the same mistake, and came to the conclusion that he did.

It is tempting for us to explain in detail how Skinner's theory is similar to Darwin's. But, if we do that, we can't avoid falling into the same pit that the book falls into. You could very easily get lost in the details. So, we will give you a simple comparison and encourage you to read the book for more details.

Skinner's theory of learning is based on the notion that an animal is born with a mind that is a blank slate. Random events happen to the animal, which have good or bad results. The animal remembers the results, and learns to do things with good results and avoid doing things with bad results.

For example, a bear cub goes for his first walk. In the process, he randomly steps on sharp stones and smooth stones. The sharp stones hurt his paws, but the smooth stones don't. Therefore, he learns to walk on the smooth stones and avoid the sharp stones.

The general principle is that random events (for example, walking on stones) produce good

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[16] *ibid.*, page xx

[17] *ibid.*, page xv

[18] *ibid.*

and bad results (paw comfort or paw pain) which are filtered for maximum benefit. This is similar to Darwin's theory in which random differences in individuals are filtered by natural selection for maximum survival benefit.

Both theories are so obviously true that they are immediately accepted as being true and become ingrained in the scientific community. But then, the more the theories are examined, the more problems become apparent. Perhaps someone noticed an adult bear casually walking on some broken glass with no apparent signs of discomfort, which Skinner's theory can't explain. On closer examination, Skinner's theory was found to have many unexplainable contradictions. For some time the contradictions were ignored as anomalies; but eventually the fundamental flaw was discovered, and the theory was rejected.

In the same way, problems with Darwin's theory kept being discovered. The problems kept being ignored. But now there are just too many problems to ignore. It turns out that Darwin made the same mistakes Skinner made.

## MULTIPLE CAUSES

One of the mistakes Darwin made was that he tried to explain evolution in terms of a single cause—namely natural selection. The book says this over-simplification is as foolish as trying to explain Napoleon's loss at Waterloo on a single factor. They say any attempt to prove that Napoleon lost simply because the ground was muddy will fail, even if mud was a contributing factor.

Fodor and Piattelli-Palmarini recognize that natural selection alone can't possibly be responsible for all the diversity of life we see today. Since they believe in evolution, they assume that natural selection must simply be one of many factors involved; but they don't know what the other factors could possibly be. So, they wrote the book to inspire other evolutionists to stop wasting time on natural selection and look for whatever other explanations there might be.

Ironically, that's what we've been saying for fourteen years. Like Fodor and Piattelli-Palmarini, we don't propose any other solution. We merely point out that Darwin's theory of evolution is not consistent with demonstrable scientific principles and should be abandoned. Nothing can be gained by trying to prove a false theory is true.

## ARTIFICIAL SELECTION

Artificial selection is sometimes used to prove the reality of natural selection. We have occasionally said that artificial selection is simply natural selection on steroids. Natural selection would do what artificial selection does, if given enough time. Fodor and Piattelli-Palmarini disagree. They argue that the significant difference is intention. Artificial selection strives toward the goal of the breeder. The breeder intends to produce offspring that are bigger, smaller, faster, stronger, or whatever. Natural selection has no goal. That is a significant difference, in their opinion.

## FREE-RIDERS

One of their main arguments against natural selection has to do with "free-riders." Darwin called this, "correlation of growth," but the authors surprisingly never make the connection. The basic idea is that when breeding for one characteristic, another unrelated characteristic comes with it. The secondary, unintended characteristic just comes along for the free ride.

Back in the days before contact lenses, it was easy to tell who the smart kids were—they were the ones wearing glasses. ☺ Even now, the stereotypical image of a nerd is a kid wearing glasses. We aren't convinced that there actually is a connection, but for the sake of illustration, let us pretend that there is, just to explain their notion of free riders. Intelligence can provide a survival advantage; but poor vision doesn't. Intelligence is the ticket to survival; but poor vision gets a free ride along with intelligence.

Fodor and Piattelli-Palmarini argue that the existence of so many free-riders make it impossible to determine which characteristics actually improve the fitness for survival. The unintended side-effects may completely overwhelm the advantage of the primary mutation. (They would no doubt object to our use of the term, "unintended," because of their adamant denial of any intention of the primary mutation, but we can't think of any other way to say it.)

## OTHER EXPLANATIONS

Every time they refer to God, it is in connection with the Tooth Fairy. They clearly don't believe in creation. They aren't too keen on intelligent design, either. They are committed to a natural explanation. They consider natural selection to be supernatural, too.

Their argument against natural selection has to do with the fact that genes can't remember what happened to them in the past, and don't have any future aspirations. They do a good (but tedious) job of explaining why natural selection, is confined to the present, so it can't be responsible for evolution. Their explanation is very repetitious; but that may be a good thing because it might take multiple explanations for the truth of it to sink in.

Having ruled out supernatural explanations, and recognizing that natural selection is fatally flawed, they look for other explanations. Since scientists know less about prenatal development than most other areas of study, that's where they turn.

If they want a bumper sticker for their theory, we suggest, "Evolution begins at conception." Of course, that would be totally unacceptable to many evolutionists because of the obvious implications regarding abortion; but it is the most concise explanation we can give of their theory. They are favorably disposed to the notion that the environment somehow causes inheritable changes during the period of time between conception and birth. Although it is well-known that prenatal experience can influence the individual being born, it is unclear as to how much of that experience is inheritable.

So, the next best summary of their explanation is, "History did it." Creatures are the way they are because that's just how it happened. Prenatal experience and other environmental factors shaped each creature into what it is, and we can't really explain how (and there certainly isn't any "why"). The only thing that makes, "History did it," more palatable than "God did it," is the absence of God. But it seems to us that if "God did it," is an unacceptable explanation, then "History did it," is no more satisfactory.

## Our Summary

Fodor and Piattelli-Palmarini correctly recognize that natural selection is an inadequate and unscientific explanation for the diversity of life on Earth. They do not believe this because they are Christians—they aren't Christians. They are even more radical atheists than Darwin and Dawkins. They believe there is absolutely no purpose whatsoever in life. The mild suggestion of purpose in Dawkins' Selfish Gene theory, and the implication in Darwin's theory that natural selection causes things evolve upward to a goal are totally unacceptable to them.

Furthermore, they don't believe that there can be any simple, single explanation for the diversity of life on Earth. Therefore, they believe that there must be some sort of unknown, purely natural, complex combination of prenatal environmental influences that are responsible.

## Their Own Summary

We've done our best to summarize their argument. Their argument against natural selection is valid, but hard to follow. They have no positive explanation of how evolution could have occurred. But, in fairness, we will close by giving them the last word. Here are the last three paragraphs of their book.

> Surely, some of the interactions between organisms and their environments are casually implicated in the evolutionary fixation of some phenotypic traits; if that weren't so, it really would be miraculous that there are reliable correspondences between the two. But there's no obvious reason to doubt that these interactions are simultaneously structured at many levels of analysis; and it's entirely possible that the story about the aetiology of organism/environment matches may differ from one kind of phenotypic trait to another. If so, then the right answer to "What is the mechanism of the fixation of phenotypes?" would be: "Well, actually there are lots." We repeat that this is not in the least to suggest that the fixation of phenotypes is other than a deterministic, causal and lawful process through and through. No Tooth Fairy need apply. What is denied, however, is that there is a unitary theory (e.g. a unitary theory of organism-environment interactions) in terms of which most or all such phenomena are explained; or that the various kinds of accounts that explain them generally imply that there are laws of exogenous selection.
>
> Perhaps that strikes you as not much; perhaps you would prefer there to be a unified theory—natural selection—of the evolutionary fixation of phenotypes. So be it; but we can claim something Darwinists cannot. There is no ghost in our machine; neither God, nor Mother Nature, nor Selfish Genes, nor the World Spirit, nor free-floating intentions; and there are no phantom breeders either. What breeds the ghosts in Darwinism is its covert appeal to intensional biological explanations, which we hereby propose to do without.
>
> Darwin pointed the direction to a thoroughly naturalistic—indeed a thoroughly atheistic—theory of phenotype formation; but he didn't see how to get the whole way there. He killed off God, if you like, but Mother Nature and other pseudo-agents got away scot-free. We think it's now time to get rid of them too. [19]

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[19] *ibid.*, page 163

## Web Site of the Month – April 2010

*by Lothar Janetzko*

# ARE EVOLUTIONISTS FOOLING US?

**http://webpages.charter.net/jeffstueber/foolsus.HTM**

***"Evolution is that great all-encompassing paradigm that explains everything, yet lacks much explanatory power"***

This month's web site review looks at an article we found while searching the internet for an article on creation and evolution relating to April Fool's Day. Although this article was not written as an April Fool's Day joke, it really presents many interesting details regarding how evolutionists are trying to fool people into believing that evolution has all the answers regarding the origin of life.

The article begins by making an interesting observation about the verbal manipulation that is used especially in the creation/evolution debate. He points out that it is similar to what George Orwell wrote about in his famous novel 1984. In his novel, Orwell's protagonist Winston uses a "deceptive language called Newspeak to eliminate words and thoughts harmful and challenging to governmental control."

The article continues by discussing an article from the Associated Press that the web author believes to be a masterful work in propaganda. He believes that it is very important that readers understand how word subtlety is used to advance a biased evolutionist's view.

Under the title, "What's Science, What's Evolution," you will find a lengthy discussion about how these terms are used by various evolutionists.

Continuing in the article you will find a section with the title, "The False Dichotomy: Religion and Science." Here you will find an interesting discussion about what makes something a religion, and suggests evolution really just another religion.

More interesting sections follow, so just keep on reading. Sixty-four footnotes are referenced throughout the article.

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