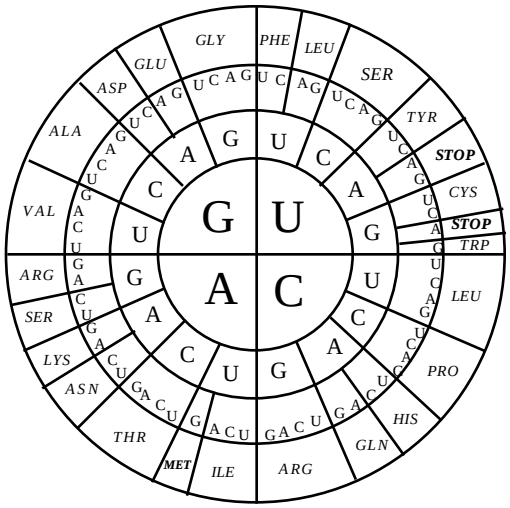
DI Fails Again to "Crack" the Code

Kenneth R. Miller

On October 10, 2001, the folks at the Discovery Institute paid me the unexpected compliment of producing a long press release crafted specifically to reply personally to my defense of comments made in the PBS Evolution series. It's nice to be noticed!

One of the PBS programs had noted that living organisms share a universal genetic code, a claim that the Discovery Institute (DI) immediately labeled as "false" and misleading. Their objections were based on the discovery, over the past 20 years, that a number of genetic systems, especially those in mitochondria, have slight differences from the standard genetic code found in most textbooks. This means that the genetic code, according to the Institute, is not universal, and "does not provide 'powerful evidence' that all living things 'evolved on a single tree of life'" For the Discovery Institute, this was doubtless the opening they had hoped to find in order to make credible charges of scientific inaccuracy against the PBS series. In their viewer's guide they wrote triumphantly:



(Above) The Standard Genetic Code

> "So the first hard evidence that we are given for Darwin's tree of life turns out to be false."

Unfortunately for the credibility of the Discovery Institute, a close examination of the evidence indicated that it was their own claims that were false, not those of the evolution series. These errors were detailed in a brief document I released on September 25, 2001. Their new press release, "A Reply to Kenneth Miller on the Genetic Code," is a carefully-crafted response designed to defend DI scholars against my analysis of their original accusations. Once again, however, they've exposed nothing so much as their own shallow understanding of science and their remarkable abilities to ignore clear and powerful evidence for evolution, no matter where it is found.

I challenged their assertions that the genetic code is not universal by emphasizing how widely the basic molecular elements of the genetic machinery are shared across the kingdoms of life. I wrote that:

> Despite the DI rhetoric, living organisms do indeed share a common mechanism that copies and translates heritable genetic information. All living organisms translate the genetic code using ribosomes, tiny protein-building factories, they all translate it with the aid of small molecules called transfer RNA, they all read it in the same direction, and they all read it in the same way, translating the code 3 letters at a time into sequences of amino acids, the building blocks of proteins. **[Miller, 9/25/01]**

In their rebuttal, did they challenge the accuracy of any of these statements? Absolutely not — because all of these things are true. Instead, they made three very different, subtle, and carefully-targeted assertions of misrepresentation:

The Discovery Institute charges that:

1. Miller completely misrepresents Knight et al.'s composite phylogeny of genetic codes.

2. Variant genetic codes are not analogous to the differences between dialects of the same language.

3. Miller's references to biotechnology do not accurately represent the experimental literature on variant genetic codes.

We'll take them one at a time:

I) "Misrepresentation of Knight *et al.'s* composite phylogeny of genetic codes"

The Discovery Institute challenged my assertion that the slight differences in the codes of certain organisms occur in "regular patterns" that strongly support the notion of common descent. Here's what I had written:

> The variations from the standard code occur in regular patterns that can be traced directly back to the standard code, which sits at the center of the diagram. What this means is that these slight variations of the code provide powerful — and unexpected — confirmation of the evolution of the code from a single common ancestor. **[Miller, 9/25/01]**

According to Mark Edwards, who apparently wrote the DI rebuttal, I made a serious mistake when I said that the code variations supported the notion of common ancestry. In support of their position, they cited a 2001 study from Laura Landweber's lab at Princeton (Knight *et al*, 2001), and made reference to "Figure 2" of that paper. Figure 2 is a summary of the genetic code differences in various organisms, which I included in my original critique of the DI charges.

> In their caption to Figure 2, Knight et al. note explicitly that variant codes have arisen "repeatedly and independently in different taxa." This pattern of convergent variation has generated much discussion in the primary literature. If these are indeed convergent changes, they do not provide evidence of common descent at all, but rather would be misleading similarities that, taken by themselves, generate a false history of the organisms in question. **[Discovery Institute, 10/10/01]**

This statement is a perfect example of the Discovery Institute's tendency to miss the scientific point in just about any study that provides support for evolution. What Knight *et al* actually wrote in their caption was "Note that the same few changes have taken place repeatedly and independently in different taxa." This statement refers to their observation that the same very slight changes have occurred repeatedly in different groups of organisms. For example, Knight *et al* write that:

> Sometimes the same change recurs in different lineages: for instance, the UAA and UAG codons have been reassigned from Stop to Gln in some diplomonads , in several lineages of ciliates and in the green alga Acetabularia acetabulum. **[Knight *et al*, 2001]**

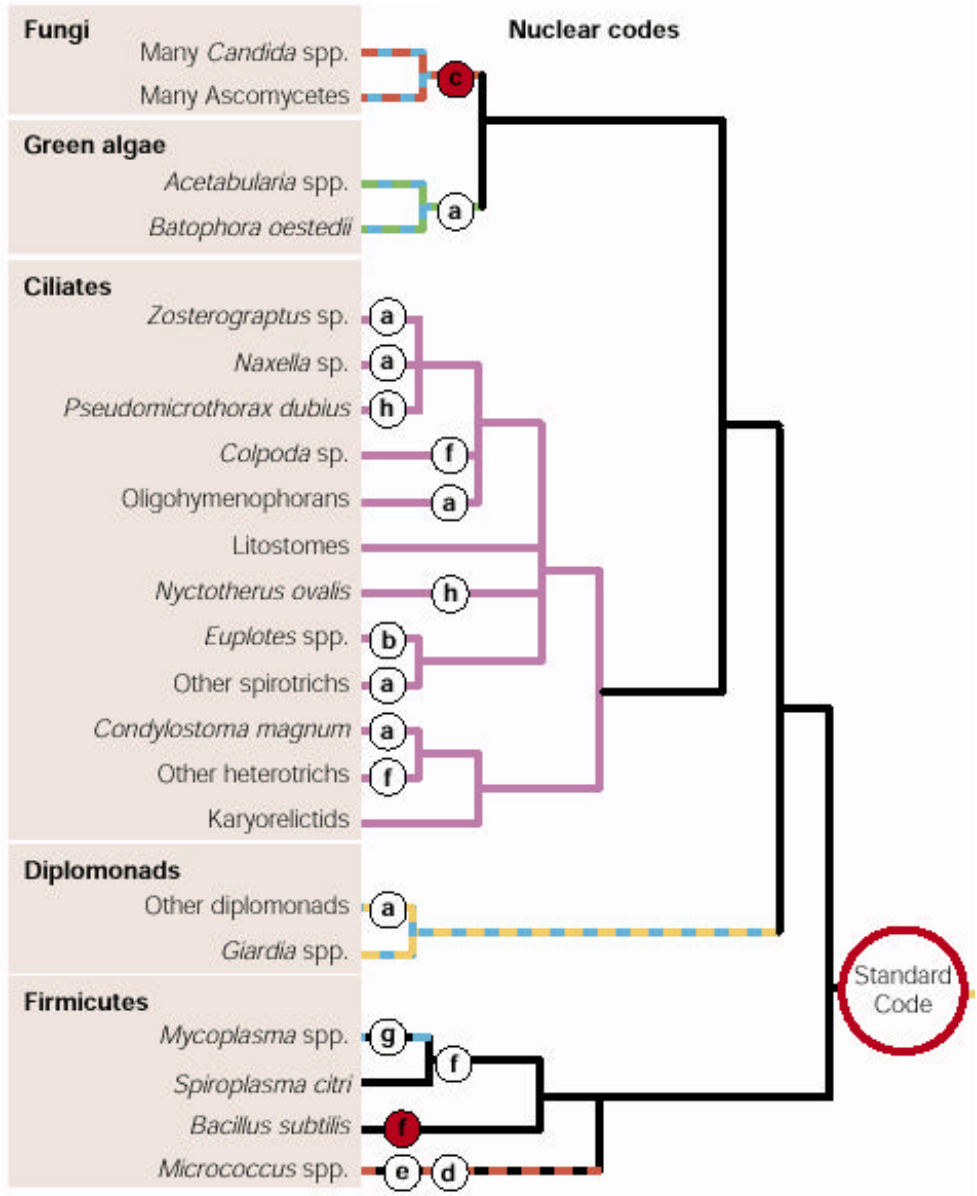
A dose of realism is in order here. Noticeably absent from the Discovery Institute's writings on this subject are any hints of the *actual* nature of the variations in the genetic code which they find so interesting. Why? I suspect that reason is simple. It's because the data support Darwin.

> In short, Miller completely misrepresents the Knight et al. composite phylogeny. There is no "regular pattern" to the variant codes that maps congruently onto phylogenetic trees from other data. Thus, far from providing what Miller calls "unexpected confirmation of the evolution of the code from a single common ancestor," the pattern of variant codes represents a puzzle for a single tree of life. **[Discovery Institute, 10/10/01]**

Really? I urge readers to examine Figure 2 from the Knight *et al* paper, which was included in my 9/25/01 critique, and is included at the end of this analysis as well. As you will see, each and every variant code can be traced to the single, ancestral, standard code that sits in the center of the diagram. The interpretation that any reasonable person would draw from these data is that alterations from the standard code do indeed occur in regular patterns that strongly support the idea of descent with modification.

Let's take just one example to see how the evidence supports common descent and how the Institute deals with it. In several groups of organisms the meaning of the codons "UAA" or "UAG" has been changed from "Stop" to "Gln" (glutamine). The other 62 or 63 three-letter codon "words" in the genetic code is these organisms are unchanged from the standard code. These groups are shown in the portion of Figure

2 from the Knight *et al* (2001) paper dealing with the nuclear genetic code. As you will see, they point out seven groups in which such a change has taken place:



<u>Above</u>: Portion of Figure 2 from Knight *et al* (2001). Changes from UAA and UAG to "Stop" are marked with the letter "a."

The "pattern" I spoke of is clear. These changes occur in isolated lineages that long ago diverged from the evolutionary lines leading to most organisms, including animals and plants (which use the standard code). Remarkably, the Discovery Institute agrees that this is the case, even going so far as to use the word "lineage," which implies common descent:

> Sometimes the same change recurs in different lineages: for instance, the UAA and UAG codons have been reassigned from Stop to Gln in some

> diplomonads, in several species of ciliates and in the green alga ***Acetabularia acetabulum***. **[Discovery Institute, 10/10/01]**

So, how do they twist the data to imply that provide no evidence for descent with modification in those "different lineages?" By pretending that the data must be interpreted in a way that no scientist has ever proposed. Remember their assertions of how these data might generate "false" views of biological history:

> ... If these are indeed convergent changes, they do not provide evidence of common descent at all, but rather would be misleading similarities that, taken by themselves, generate a false history of the organisms in question.

The key phrase in this distortion is the suggestion that the code changes "taken by themselves" would "generate a false history." This is a classic example of the out-of-context reasoning of the Discovery Institute. Neither I nor the authors of the Knight *et al* (2001) paper have ever suggested that these data should be "taken by themselves," as the Institute suggests. Rather, if descent with modification is true, then these changes in the code should fit into a regular pattern consistent with the evolutionary relationships of the organisms in question. And, guess what? That is exactly what they do.

Have I misinterpreted the meaning of the data in the Knight *et al* (2001) paper? Here's what Prof. Laura Landweber of Princeton wrote when I sent her a copy of the Discovery Institute's analysis of her paper:

> That ***[the Discovery Institute's argument]*** is indeed a horrible misinterpretation, because it is clear, particularly in the tree in our paper and in others, that each nonstandard code is a subtle derivative of the standard genetic code and that all codes are derived from it. **[letter from Laura Landweber to KRM, 9/24/01]**

Steven Freeland, the second author on the paper, now at the University of Maryland, went further:

> I would therefore take a more direct line in pointing out how variation in the code, and subsequent adaptation of the code, is an exact molecular simile for the variation in finch beak morphlogy that Darwin famously drew from in order to derive his theory. The slight coding differences that we see today hint at an evolutionary plasticity that can accumulate over time into significant change, just as slight variation in beak morphology can lead to different species of bird.". **[letter from Steven Freeland to KRM, 9/24/01]**

The bottom line? The Discovery Institute's desperate attempts to argue that the genetic code provides no evidence in favor of descent with modification amount to a "horrible misinterpretation" of the actual evidence. I was correct in my 9/25/01 analysis, and NOVA's comments on the universality of the code stand up very well under scientific scrutiny.

2) "Variant genetic codes are not analogous to the differences between dialects of the same language."

Sure they are. The Discovery Institute had attacked this analogy (perhaps because it is too easily understood by a layperson) with these words:

> This is--at best--a wildly inaccurate analogy. From context and other clues, English speakers can discern that the words “center” and “centre,” or “color” and “colour,” refer to the same object. Meaning is preserved by context, and the reader moves along without a hitch. **[Discovery Institute, 10/10/01]**

This is not true, however, for other differences between American and British English, and that was my point. If I was to tell someone unfamiliar with British English that "profits from my lift business had enabled me to buy two new lorries," they wouldn't have a clue as to what I did for a living or what I had just purchased. Nonetheless, we regard the two versions of English as part of the same language on the basis of a very simple criterion — the vast majority of the words and the essential rules of grammar are identical.

Exactly the same is true for the different versions of the genetic code. Fully 75% of the codon "words" are identical in all organisms, and even the most dramatic variants themselves differ from the standard code in no more than 5 or 6 codons (meaning that they are actually 90% identical to the standard code).

I also like the "keyboard" analogy used by Knight *et al* (2001), but had the Discovery Institute fully explained that analogy to their readers, once again they would have had to concede the central issue — namely, the principle of common ancestry. Imagine a situation where all of the traveling salesmen for a company were recalled from stations in distant regions of the world. When we examined the keyboards on their laptop computers, we discovered that all of the keyboards from the home office had the familiar QWERTY arrangement. A few of the salesmen who had been separated from the home office the longest, however, had keyboards in which a few letters had been switched or were missing. When they were analyzed, each and every one of them could be traced back to the ancestral QWERTY arrangement, modified in a variety of ways. We would quickly figure out that QWERTY came first, and the others were slight modifications of it. In other words, we'd conclude that the keyboards were related by descent with modification.

Score another point for Darwin.

3) "Miller’s references to biotechnology do not accurately represent the experimental literature on variant genetic codes."

Oh, yes, they do. I wrote:

> In fact, the entire biotechnology industry is built upon the universality of the genetic code. Genetically-modified organisms are routinely created in the lab by swapping genes between bacteria, plants, animals, and viruses. If the coded instructions in those genes were truly as different as the critics of evolution would have you believe, none of these manipulations would work. For better or for worse, they do work, and they work brilliantly. **[Miller, 9/25/01]**

What I did was to point out that if the codes were "as different as the critics of evolution would have you believe," then gene-swapping wouldn't be nearly as easy or as successful as it actually is. The Discovery Institute "rebutted" this statement by pretending that I had said something else:

> But some manipulations--namely, those involving organisms with variant codes--do not work, unless the researchers themselves intervene to ensure function. Consider, for instance, the release factor from the ciliate Tetrahymena thermophila. Release factors (in eukaryotes, these proteins are abbreviated as "eRF" to distinguish them from prokaryotic release factors) catalyze the separation of completed polypeptide chains (nascent proteins) from the ribosomal machinery. Unlike other eukaryotic release factors, however, that recognize all three stop codons (UAA, UGA, and UAG), the Tetrahymena thermophila release factor recognizes only the UGA codon as "stop." **[Discovery Institute, 10/10/01]**

Obviously, wherever differences exist, a genetic engineer must pay attention to them, as the Institute points out here. However, I *never* wrote that meaningful differences didn't exist, only that they are slight and fall into patterns that support descent with modification. None of the DI's detailed observations regarding translation in Tetrahymena deal with my contentions. The DI's best efforts to pretend that the existence of *any* translational differences between organisms spells trouble for evolution is simply false.

The Design "Alternative"

The explanation favored by the Discovery Institute for the range and diversity of life is something they call "Intelligent Design." In their criticisms of the PBS evolution series they have repeatedly argued that "Design" is an authentic scientific theory that stands on its own merits as a scientific alternative to evolution. One would think, therefore, that they would be ready to explain exactly how design explains the diversity of the genetic code more effectively than the elegant explanation of descent with modification.

I read their press releases in vain looking for details. I had hoped to learn how a designed might have chosen to alter the code in some organisms and not in others, and especially why the patterns of variation come to resemble something that we

scientists "misinterpret" as evolution. Naturally, I was disappointed. As usual, the Discovery Institute is silent on this issue. "Intelligent Design," it seems, amounts to little more than saying "Maybe a Designer Did It" for each and every fascinating pattern that appears in living organisms. It is no wonder that the scientific community has rejected "Design" again and again for the simplest of all reason — a lack of evidentiary support.

Kenneth R. Miller
Professor of Biology
Brown University
Providence, Rhode Island 02912

References:

Original Press Release: The Discovery Institute Press Release charging the *Evolution* series with false statements concerning the genetic code can be found on the web:
http://www.reviewevolution.com/press/pressRelease_FalseClaim.php

• **Robin D. Knight, Stephen J. Freeland and Laura F. Landweber (2001)** "REWIRING THE KEYBOARD: EVOLVABILITY OF THE GENETIC CODE," Nature Reviews - Genetics. 2: 49-58.

[Miller, 9/25/01] My 9/25/01 critique of the Discovery Institute's charges on the Genetic Code is available on the web at:
http://www.ncseweb.org/resources/articles/3071_km-3.pdf

[Discovery Institute, 10/10/01] The Discovery Institute Press Release responding to my 9/25/01 critique is entitled "Reply To Kenneth Miller On The Genetic Code," and is available on the web:
http://www.reviewevolution.com/press/pressRelease_ReplyMiller.php