

Expert Statement (*Kenneth R. Miller*)

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Professional Background:

I earned a Bachelor of Science degree in Biology at Brown University (1970), and attended the University of Colorado on a National Defense Education Act Fellowship, earning my Ph. D. in Biology in 1974. I joined the faculty of Harvard University in 1974 as a Lecturer, and was promoted to Assistant Professor in 1976. In 1980, I accepted a position at Brown University, and was subsequently promoted to Associate Professor (1982) and Professor (1986). I am a cell biologist whose research centers on the structure and function of biological membranes and membrane proteins. I have published more than 50 research papers in scientific journals, including *Nature*, *Scientific American*, and *Cell*. I have also written a number of scientific reviews, commentary articles, and book reviews published in similar journals. Together with Joseph S. Levine, I am coauthor of a number of high school and college textbooks in general biology that are widely used throughout the United States. I am a member of the American Association for the Advancement of Science, the American Institute for Biological Sciences, and The American Society for Cell Biology, in which I chair the Education Committee.

1) The Scientific Status of Evolutionary Theory

Evolution is the process of biological change over time that has characterized life on Earth since its beginning billions of years ago. An appreciation of the sweeping nature of evolutionary change developed during the early years of the industrial revolution, when widespread excavations first began to reveal the Earth's successive geologic ages. By the end of the 18th century, pioneering scientists such as Georges Cuvier (1769-1832) had demonstrated that living things had changed dramatically over time. These discoveries led many naturalists to seek the forces that might have caused these changes. Best known may be Jean-Baptiste Lamarck (1744-1829), whose explanations for change focused on the creative power of the environment to shape the adaptations of organisms over time.

The modern theory of evolution originates in the ideas of Charles Darwin (1809-1882), who articulated his views in a series of books, the best-known of which is *On the Origin of Species* (1859). Darwin's observations convinced him that forces at work in the world today can account for the origin of new species, and documented his hypothesis with the results of years of careful observation and analysis. Darwin's ideas included a series of testable predictions regarding the character of the fossil record, the age of the earth, and the nature of inheritance (genetics). In the years following the first publication of his ideas, each of these predictions was confirmed, and Darwin's theory of evolution by natural selection earned general acceptance by the scientific community. The National Academy of Sciences, the most prestigious scientific body in the United States, summarized the scientific importance of evolution in this way:

*The concept of biological evolution is one of the most important ideas ever generated by the application of scientific methods to the natural world. The evolution of all the organisms that live on Earth today from ancestors that lived in the past is at the core of genetics, biochemistry, neurobiology, physiology, ecology, and other biological disciplines. It helps to explain the emergence of new infectious diseases, the development of antibiotic resistance in bacteria, the agricultural relationships among wild and domestic plants and animals, the composition of Earth's atmosphere, the molecular machinery of the cell, the similarities between human beings and other primates, and countless other features of the biological and physical world. As the great geneticist and evolutionist Theodosius Dobzhansky wrote in 1973, "Nothing in biology makes sense except in the light of evolution." [from *Science and Creationism*, 1999, preface]*

The enduring power of evolution as a scientific idea stems in part from the simplicity of its core propositions, all of which are strongly supported by accumulating scientific evidence. The first of these is the observation that life has changed over time. As noted earlier, the historical realization of the magnitude of such changes was one of the formative elements in Charles Darwin's original formulation of evolution. In the 20th century, a dramatic expansion of the fossil record and its attendant evidence for biological change over time has made the pattern of biological change abundantly clear.

The second core proposition of evolution is that living things share common ancestries. This is a direct inference drawn from the clear and convincing patterns of change seen in the fossil record. In cases where fossil records of living organisms are complete enough to trace the pattern of life over millions of years, the conclusion of common ancestry, also known as descent with modification, is the only reasonable inference supported by the evidence. One recent example can be seen in Bruce J. MacFadden's (2005) recent review of the fossil record of the horse, which described the common ancestry shared by this group of organisms as documented in its rich and detailed fossil history.

The third element of the theory of evolution is the proposition that biological change over time is driven by forces observable in the world today. Darwin noted that living species contain great reservoirs of diversity, and that additional diversity appears spontaneously (by mechanisms that include mutation). He argued that the interactions of organisms with their environment selected for those organisms best-suited to thrive, and that a process known as natural selection resulted. Natural selection was thought by Darwin to be the primary force driving descent with modification, or evolution. Evolutionary biologists have confirmed the process of natural selection through direct observation, but have discovered that other processes also are important in evolutionary change. These include genetic drift, the so-called founder effect, genetic recombination, transposition, and horizontal gene transfer between species.

In modern science, evolution is far more than the study of events that took place in the past. Evolution is a hard-working and productive scientific theory put into practice every day by scientists in a wide variety of fields. Evolutionary theory is used to design new drugs based on the process of natural selection, to check the spread of insects able to prey upon genetically-modified plants, and to align and identify genes and DNA sequence data in studies of organismic genomes. Evolutionary theory provides the basic rationale for the three drug HIV regimen that has prolonged hundreds of thousands of lives of AIDS patients, and is at the heart of efforts to control the spread of infectious diseases and microbial drug resistance. This makes evolution a key weapon in medicine's battles against infectious killers such as tuberculosis and malaria.

Evolution, like all scientific theories, is necessarily incomplete. Because the evidence of the Earth's past is fragmentary, natural history does not document each and every major evolutionary event in the history of life. Nonetheless, the evidence that we do have abundantly confirms Darwin's general ideas regarding evolutionary change, a point also made by the National Academy in its 1999 report:

So many intermediate forms have been discovered between fish and amphibians, between amphibians and reptiles, between reptiles and mammals, and along the primate lines of descent that it often is difficult to identify categorically when the transition occurs from one to another particular species. (Science and Creationism, 1999)

All scientific ideas are subject to change, revision, and rejection if they are contradicted by new evidence, and evolution is not an exception. Nonetheless, in nearly a century and a half of investigation, not a single piece of scientific evidence has emerged to contradict the idea that a process of evolutionary change gave rise to the species that exist today. In fact, quite the

opposite is true. Evidence from a wide variety of fields, many not even imagined during the lifetime of Charles Darwin, has shed light on the mechanism of evolutionary change and further supported the general outline of his ideas. The concept of evolution, therefore, is not controversial within science, and is generally accepted as the central idea upon which all of modern biology is based.

Evolutionary theory explains the process by which evolutionary change takes place. Darwin's general idea of evolutionary change focused on variation within species, acted upon by natural selection, as the driving force in adaptation and speciation (the formation of new species). Because his ideas were formed at a time before modern genetics, they did not include the detailed mechanisms by which variation appears and is acted upon over time. In the early part of the 20th century, a synthesis of biochemistry, genetics, and evolutionary theory emerged to produce what became known as neo-Darwinian theory. The neo-Darwinian theory successfully incorporated evolution into the rapidly advancing field of molecular genetics, and enabled scientists, for the first time, to study and to test evolution at the molecular level.

These advances have led to many refinements of evolutionary theory, and to efforts to understand and define the relative contributions of scores of processes, including genetic recombination, transposition, horizontal gene transfer, gene duplication, sexual selection, and developmental mutations to the process of evolutionary change. There is considerable discussion and debate within the scientific community as to the relative importance of these and other mechanisms, and these conflicts continue to motivate vigorous research and investigation. The emergence of new scientific knowledge ensures that evolutionary theory will remain an active and productive branch of science for many years to come.

Significantly, none of these debates undermines the scientific standing of evolution itself, despite the free and open inquiry that characterizes the scientific process. In fact, each of these has added to our understanding of the ways in which evolution works, and strengthened each of the core elements of the theory.

2) *Biology* by Miller and Levine

The coverage of evolution in *Biology* by Miller and Levine (© 2004) reflects the broad consensus on evolutionary biology held by the scientific community. To biologists, evolution is the central organizing idea around which our modern concept of the life sciences is framed. As noted by the National Academy of Sciences (1998), "The scientific consensus around evolution is overwhelming."

The Pennsylvania Academic Standards for Science and Technology require students to acquire the knowledge and skills needed to explain the mechanisms of the theory of evolution. *Biology* has been written with these requirements very much in mind. Evolution occupies a prominent position in the textbook, and is explicitly dealt with in Chapters 15-18. In addition, many other parts of the text, including Chapter 29 ("Comparing Invertebrates") and Chapter 33 ("Comparing Chordates"), use the notion of common evolutionary ancestry to explain similarities of structure and function among closely related organisms. This textbook presents the student with the view of biology shared by the vast majority of working scientists in the United States and throughout the world. Evolution is presented as an explanation for the diversity of living organisms and for the rich library of fossil specimens that illustrate the natural history of life on this planet. *Biology* therefore meets the requirements of the Pennsylvania State Science Standards in every respect.

Our approach in *Biology* has been to emphasize the scientific method and the process of science. An example of this emphasis can be found in our text:

A useful theory may become the dominant view among the majority of scientists, but no theory is considered absolute truth. Scientists analyze, review, and critique the strengths and weaknesses of theories. As new evidence is uncovered, a theory may be revised or replaced by a more useful explanation. Sometimes, scientists resist a way of looking at nature, but over time new evidence determines which ideas survive and which are replaced. Thus, science is characterized by both continuity and change. (Miller and Levine, 2004. p. 15)

In line with our emphasis on critical thinking and helping students to understand the history of science, evolutionary theory is not presented to students as a completed body of work, but rather as a theoretical solution to the puzzle of life's history and diversity. Section 15-1 of our text ("The Puzzle of Life's Diversity") points out many of the facts and observations that puzzled the young naturalist Charles Darwin during and after his voyage on H. M. S. Beagle. The attempts of other naturalists of the 18th and 19th century to deal with these facts are described in section 15-2, including the first comprehensive theory of evolution, developed by Jean-Baptiste Lamarck.

Lamarck's theory, as described and illustrated on page 376, had many strengths. Among these was its success in explaining why organisms seem to be so well-adapted to their environments. Lamarckian theory also helped to explain how organisms had changed over time, as documented in the fossil record. Despite these strengths, a critical examination of his hypothesis showed

many glaring weaknesses, most notably the lack of any evidence that acquired traits can be passed on to an organism's offspring. It is against the failure of Lamarck's theory of evolution that students are first introduced to Darwin's alternative theory.

The elements of Darwin's theory of evolution are laid out on pages 378-382. Once students have had a chance to see how evolution explains the puzzle of life's diversity, the text then asks students to examine the evidence in favor of this theory. Very clearly, evolutionary theory has exceptional strengths, which is why virtually all biologists regard it as the central organizing principle of the life sciences. However, our text makes sure that students clearly understand that a level of uncertainty remains. For example, we are careful to point out that gaps in the fossil record for many species remain. Such gaps clearly reflect the incomplete nature of fossil evidence detailing the natural history of many species. However, we also point out that the fact that many such gaps have been filled since the time of Darwin is actually one of the strongest points of evidence in favor of evolution.

Gaps remain, of course, in the fossil records of many species, although a lot of them shrink every year as new fossils are discovered. These gaps do not indicate weaknesses in the theory of evolution itself. Rather, they point out uncertainties in our understanding of exactly how some species evolved. (Miller and Levine, 2004. p. 383)

The fact that so many major gaps have indeed been closed over time as fossil collections have grown, as noted by the National Academy earlier in this report, is one of the great overall strengths of the theory of evolution.

The Tentative Nature of Scientific Theory

The need for students to review and critique scientific explanations requires that textbooks clearly depict the tentative nature of scientific conclusions. We have done this time and time again, especially in sections of the text that deal with evolution. For example, we describe the uncertainty inherent in Darwin's explanation of the remarkable diversity of finches on the Galapagos Islands like this:

Could the island birds have changed over time, as populations in different places adapted to different local environments? Darwin struggled with this question for a long time. He finally decided that all these birds could have descended with modifications from a common mainland ancestor. . (Miller and Levine, 2004. p. 383)

The tentative nature of Darwin's conclusion, reflected in the language that these birds "could have descended" from a common ancestor, is reinforced by more detailed discussions of speciation later in the book (Chapter 16). Although modern evidence from molecular biology has reinforced Darwin's conclusions, and even identified the mainland species from which the island birds arose, we nonetheless describe only a "hypothetical scenario" for the evolution of the Galapagos finches [p. 408], clearly indicating the fact that our reconstruction of these historical speciation events remains incomplete, as science often is.

The sense of uncertainty, which prevails in our description of vestigial organs (only a "possibility" for their origin is claimed), and our discussion of similarities in embryology (the fraudulent drawings of Ernst Haeckel are pointed out), is essential in giving students a chance to review and critique the scientific adequacy of these explanations. As we note in the conclusion of Chapter 15, evolutionary biology is a vigorous field marked by active research and spirited debate:

"Of course, like all good science, evolutionary theory continues to change as new data are gathered and new ways of thinking arise. As you will see shortly, researchers still debate such important questions as precisely how new species arise and why species become extinct. There is also uncertainty as to how life began." . (Miller and Levine, 2004. p. 383)

Scientific theories exist to make sense of the natural world, by tying together the relationships between myriad facts and observations. In this respect, our prominent mention of continuing debate on crucial issues such as speciation and the origin of life clearly indicates that evolutionary theory remains incomplete and unfinished, highlighting some of the uncertainties of this theory, which exist side-by-side with its remarkable strengths.

One of the shortcomings of Darwin's formulation of the theory of evolution was its author's ignorance of the nature of biological inheritance. Darwin was not alone in this respect, of course. Like other naturalists working in the middle of the 19th century, his ideas on biological inheritance were highly speculative, and ultimately turned out to be incorrect. In our introduction to Chapter 16 we point out that:

This lack of knowledge left two big gaps in Darwin's thinking. First, he had no idea how heritable traits, such as those shown in Figure 16-1, pass from one generation to the next. Second, although variation in heritable traits was central to Darwin's theory, he had no idea how variation appeared. . (Miller and Levine, 2004. p. 393)

The emergence of modern genetics and molecular biology has helped to fill both of these gaps, as we explain in Chapter 16. As we note, natural selection can now be studied in more precise genetic terms, with the result that scientists are now able to model and study the effects of natural selection on single-gene traits, on polygenic traits, and on entire populations.

3) Language of the Dover Statement

It is my understanding that in January 2005 a statement was read to students in Dover schools which said, in part:

Because Darwin's theory is a theory, it continues to be tested as new evidence is discovered. The theory is not a fact. Gaps in the theory exist for which there is no evidence.

A theory is defined as a well-tested explanation that unifies a broad range of observations.

Intelligent Design is an explanation of the origin of life that differs from Darwin's view. The reference book "Of Pandas and People" is available for students who might be interested in gaining an understanding of what Intelligent Design actually involves.

With respect to any theory, students are encouraged to keep an open mind. The school leaves discussion of the origin of life to individual students and their families.

This statement contains a number of errors of fact, misrepresents the scientific standing of evolution, and serves, as far as I am able to tell, no scientific or educational purpose.

Calling Special Attention to Evolution

The Board statement correctly describes a theory as "as a well-tested explanation that unifies a broad range of observations," and it quite properly advises students that they should keep an open mind "with respect to any theory." Unfortunately, it disregards its own advice on these matters by calling special attention to just one scientific theory, the theory of evolution. The effect of citing evolution, and only evolution, in this way has the obvious effect of suggesting to students that the scientific support for evolution is weak, and that students should hold this particular theory up for special scrutiny.

In reality, evolutionary theory enjoys the same status as other well-tested explanations in science, and there is no rational basis for suggesting that it, and it alone, should be mentioned in the context of doubt and skepticism that pervades this statement from the Dover Board.

Misrepresenting the Meaning of a Theory

The Board statement tells students that "The theory is not a fact," and that "it continues to be tested as new evidence is discovered." Both of these statements are clearly designed to mislead students about evolution.

The Board's emphasis that evolution is not a fact might be appropriate if they had pointed out instead that *no scientific theory* is a fact, and that *all scientific theories* continued to be tested in

light of new scientific discoveries. Instead, their claim that evolution “is not a fact” is clearly designed to undermine the scientific standing of evolution by implying that if science were certain of the validity of evolutionary theory, it might some day be regarded as a fact. The important point to be made is that scientific theories don’t ever become facts; rather, scientific theories explain facts. We do not expect, by reason of analogy, that atomic theory will ever become “atomic fact,” regardless of the weight of evidence supporting it. The Board’s language clearly has the effect of promoting student misunderstanding as to the nature and validity of scientific theories.

Citing Unnamed “Gaps”

Students and teachers in Dover must be left to speculate as to what the Board might mean when it tells them that “gaps in the theory” [of evolution] “exist for which there is no evidence.” If the Board wishes to tell students that evolution, like all of science, is necessarily incomplete, this admonition might serve a useful scientific purpose. Joseph Levine and I made exactly such a statement in our textbook:

A useful theory may become the dominant view among the majority of scientists, but no theory is considered absolute truth. Scientists analyze, review, and critique the strengths and weaknesses of theories. As new evidence is uncovered, a theory may be revised or replaced by a more useful explanation. Sometimes, scientists resist a way of looking at nature, but over time new evidence determines which ideas survive and which are replaced. Thus, science is characterized by both continuity and change. (Miller and Levine, 2004. p. 15)

We pointed this out to the student-readers of our text to help them appreciate the tentative nature of all scientific knowledge. What we did not do was to argue that evolution alone should be regarded as tentative, because any such suggestion would amount to a distortion of scientific reality. Unfortunately, the Board’s statement does distort scientific reality telling students there are problems with evolutionary theory without ever stating what those problems (“gaps”) might be. Because the “gaps” are unnamed, they cannot possibly be addressed in a factual manner, even by teachers well-versed in the scientific evidence for evolution.

Misrepresenting Darwin’s Theory

The Board seems to believe that our current understanding of evolution is the same as that of Charles Darwin, and this apparently has led them to statements such as “Intelligent Design is an explanation of the origin of life that differs from Darwin’s view.” This statement implies that “Darwin’s view” of the origin of life is the one generally taught in biology classes (and textbooks), an implication that is completely incorrect.

In reality, Darwin never wrote in detail about the origin of life, beyond speculations in a personal letter to biologist Joseph Hooker that the conditions for life to appear on the early earth might have appeared in a “warm little pond.” Since Darwin also speculated (in the final sentence of *On*

the Origin of Species) that a Creator might have produced the first living things, it is not correct to tell students that Darwin had any particular view on “the origin of life.”

The Board statement also misrepresents the “intelligent design” position by defining it merely as an idea on the origin of life. In reality, “intelligent design” argues that many features of living organisms, not just the origin of life, can be attributed to an intelligent agent acting outside the laws of nature.

Leaving “the origin of life” to Students and their Families

The Dover statement contains a confusing contradiction that makes it nearly impossible to understand the Board’s educational intent for the students of Dover High School. After defining “intelligent design” as “an explanation of the origin of life,” the Board explains that it will leave “discussion of the origin of life to individual students and their families.” If “intelligent design” deals explicitly with the origin of life and if the School provides reference books (*Of Pandas and People*) presenting the “design” view of the origin of life, how can the Board possibly claim that this subject will be left to students and their families?

This internal contradiction leaves one to suspect that the Board hopes that evolutionary views of the origin of life will not be taught in classes, but that the “design” view that a supernatural designer intervened to create life on Earth will be adopted by students.

4) “Intelligent Design” as a Scientific Alternative to Evolution

"Intelligent Design Theory" is a new anti-evolution movement that has been presented as an alternative to an older formulation known as "creation science." It differs from the older movement in that it maintains a studied neutrality on the scientific evidence from geology and astronomy on the ages of the earth and the universe, and seems to accept the fossil record. It argues, however, that an unnamed "designer" must have been responsible for much of the process, although it presents no evidence for the actions of such a designer. This means that "intelligent design" is an entirely negative concept, since the case for "design" is made entirely by assembling a selection of arguments that call the validity of evolutionary mechanisms into question.

Joseph Levine and I did not include "design" theory in our textbook because it has not won acceptance from a significant portion of the scientific community. Indeed, ours is the same position taken by Dr. Bruce Gordon of Baylor University, one of the leaders of the design movement, and the first person to head a program devoted to intelligent design at a major American university. As Dr. Gordon writes, "In particular, the theory [of intelligent design] has been prematurely drawn into discussions of public science education, where it has no business making an appearance without broad recognition from the scientific community that it is making a worthwhile contribution to our understanding of the natural world" (Gordon, 2001). We agree. Until "design" passes scientific scrutiny, it has no place in science classrooms or textbooks.

"Intelligent design" advocates often cite the complexity of living cells as a reason to invoke the hypothesis of design. While this may seem to account for any unexplained problem in biology, it does so only by abandoning the scientific method and making "design" the solution to every such problem. An explanation of this sort, which can explain any conceivable evidence, in fact explains nothing. Since the "design" explanation is not testable, it falls outside the realm of science, and places it in the realm of theology, where non-natural explanations are an accepted part of the explanatory landscape. Theological explanations may be correct, of course (as when I believe that a loving God hears my prayers and acts in my life to answer them), but they cannot be tested by the methods of science — and therefore they are not science.

Dr. Bruce Alberts, President of the National Academy of Sciences, clearly had this in mind when he characterized his position on "intelligent design" in a letter to the New York Times:

In fact, the majestic chemistry of life should be astounding to everyone. But these facts should not be misrepresented as support for the idea that life's molecular complexity is a result of "intelligent design." To the contrary, modern scientific views of the molecular organization of life are entirely consistent with spontaneous variation and natural selection driving a powerful evolutionary process.

In evolution, as in all areas of science, our knowledge is incomplete. But the entire success of the scientific enterprise has depended on an

insistence that these gaps be filled by natural explanations, logically derived from confirmable evidence. Because "intelligent design" theories are based on supernatural explanations, they can have nothing to do with science. (letter to NY Times, February 12, 2005)

Alberts' position on "design" has recently been supported by John H. Marburger III, director of President Bush's Office of Science and Technology Policy:

Speaking at the annual conference of the National Association of Science Writers, Marburger fielded an audience question about "Intelligent Design" (ID), the latest supposedly scientific alternative to Charles Darwin's theory of descent with modification. The White House's chief scientist stated point blank, "Intelligent Design is not a scientific theory." And that's not all -- as if to ram the point home, Marburger soon continued, "I don't regard Intelligent Design as a scientific topic." (Chris Mooney, "Intelligent Denials", The American Prospect Online, Feb 22, 2005.)

The Biochemical Challenge to Evolution

One of the principal claims made by adherents of intelligent design is that they can detect the presence of "design" in complex biological systems. As evidence, they cite a number of specific examples, including the vertebrate blood clotting cascade, the eukaryotic cilium, and most notably, the eubacterial flagellum (Behe 1996a, Behe 2002).

Of all these examples, the flagellum has been presented so often as a counter-example to evolution that it might well be considered the "poster child" of the modern anti-evolution movement. To anti-evolutionists, the high status of the flagellum reflects the supposed fact that it could not possibly have been produced by an evolutionary pathway.

There is, to be sure, nothing new or novel in pointing to a complex or intricate natural structure, and professing skepticism that it could have been produced by the "random" processes of mutation and natural selection. Nonetheless, the "argument from personal incredulity," as such sentiment has been appropriately described, has been a weapon of little value. Anyone can state at any time that *they* cannot imagine how evolutionary mechanisms might have produced a certain species, organ, structure. Such statements, obviously, are personal, and not scientific.

The hallmark of the intelligent design movement, however, is that it purports to rise about the level of personal skepticism. It claims to have found a *reason* why evolution could not have produced a structure like the bacterial flagellum, a reason purportedly based on sound, solid scientific evidence.

Why does the intelligent design movement regard the flagellum as unevolvable? Because it is said to possess a quality known as "irreducible complexity." Irreducibly complex structures, we are told, could not have been produced by evolution, or, for that matter, by any natural process. They do exist, however, and therefore they must have been produced by something.

That something could only be an outside intelligent agency operating beyond the laws of nature — an intelligent designer. That, simply stated, is the core of the new argument from design, and the intellectual basis of the intelligent design movement.

The great irony of the flagellum's increasing acceptance as an icon of anti-evolution is the fact that research had demolished its status as an example of irreducible complexity almost at the very moment it was first proclaimed.

The flagellum was cited in *Darwin's Black Box* (Behe 1996a) a book by Michael Behe that employed it in a carefully-crafted anti-evolution argument. Building upon William Paley's well-known "argument from design," Behe sought to bring the argument two centuries forward into the realm of biochemistry. Like Paley, Behe appealed to his readers to appreciate the intricate complexity of living organisms as evidence for the work of a designer. Unlike Paley, however, he claimed to have discovered a scientific principle that could be used to prove that certain structures could not have been produced by evolution. That principle goes by the name of "irreducible complexity."

An irreducibly complex structure is defined as ". . . a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning." (Behe 1996a, 39):

"An irreducibly complex system cannot be produced directly by numerous, successive, slight modifications of a precursor system, because any precursor to an irreducibly complex system that is missing a part is by definition nonfunctional. Since natural selection can only choose systems that are already working, then if a biological system cannot be produced gradually it would have to arise as an integrated unit, in one fell swoop, for natural selection to have anything to act on." (Behe 1996b)

Living cells are filled, of course, with complex structures which have only recently become accessible to scientific observation and study, and whose detailed evolutionary origins are therefore not known. Therefore, in fashioning an argument against evolution one might pick nearly any cellular structure, the ribosome for example, and claim — correctly — that its origin has not been explained in detail by evolution.

The utility of the bacterial flagellum is that it seems to rise above this "argument from ignorance." By asserting that it is a structure "in which the removal of an element would cause the whole system to cease functioning" (Behe 2002), the flagellum is presented as a "molecular machine" whose individual parts must have been specifically crafted to work as a unified assembly. The existence of such a multipart machine, it is argued, provides genuine scientific proof of the actions of an intelligent designer.

In the case of the flagellum, the assertion of irreducible complexity means that a minimum number of protein components, perhaps 30, are required to produce a working biological function. By the logic of irreducible complexity, these individual components should have no function until all 30 are put into place, at which point the function of motility appears. What this

means, according to the argument, is that evolution could not have fashioned those components a few at a time, since they do not have functions that could be favored by natural selection. As Behe (2002) wrote: ". . . natural selection can only choose among systems that are already working," and an irreducibly complex system does not work unless all of its parts are in place. The flagellum is irreducibly complex, and therefore, it must have been designed.

The assertion that cellular machines are irreducibly complex, and therefore provide proof of design, has not gone unnoticed by the scientific community. A number of detailed rebuttals have appeared in the literature, and many have pointed out the poor reasoning of recasting the classic argument from design in the modern language of biochemistry (Coyne 1996; Miller 1996; Depew 1998; Thornhill and Ussery 2000). I have suggested elsewhere that the scientific literature contains counter-examples to any assertion that evolution cannot explain biochemical complexity (Miller 1999, p. 147), and other workers have addressed the issue of how evolutionary mechanisms allow biological systems to increase in information content (Schneider 2000; Adami, Ofria, & Collier 2000).

The most powerful rebuttals to the flagellum story, however, have emerged from the steady progress of scientific work on the genes and proteins associated with the flagellum and other cellular structures. Such studies have now established that the entire premise by which this molecular machine has been advanced as an argument against evolution is wrong — the bacterial flagellum is not irreducibly complex. As the evidence has shown, nature is filled with examples of "precursors" to the flagellum that are indeed "missing a part," and yet are fully-functional. Functional enough, in some cases, to pose a serious threat to human life.

Certain pathogenic bacteria attack human cells by means of specialized protein secretory systems that inject protein toxins into the cells of their hosts. The type III secretory system (TTSS) is such an example, allowing gram negative bacteria to translocate proteins directly into the cytoplasm of a host cell (Heuck 1998). The proteins transferred through the TTSS include a variety of truly dangerous molecules, some of which are known as "virulence factors," and are directly responsible for the pathogenic activity of some of the most deadly bacteria in existence (Büttner and Bonas 2002; Heuck 1998).

Molecular studies of proteins in the TTSS have revealed a surprising fact — the proteins of the TTSS are directly homologous to the proteins in the basal portion of the bacterial flagellum. As Heuck (1998) has pointed out, these homologies extend to a cluster of closely-associated proteins found in both of these molecular "machines." On the basis of these homologies, McNab (1999) has argued that the flagellum itself should be regarded as a type III secretory system. Extending such studies with a detailed comparison of the proteins associated with both systems, Aizawa has seconded this suggestion, noting that the two systems "consist of homologous component proteins with common physico-chemical properties" (Aizawa 2001). It is now clear, therefore, that a smaller subset of the full complement of proteins in the flagellum makes up the functional transmembrane portion of the TTSS.

Stated directly, the TTSS does its dirty work using a handful of proteins from the base of the flagellum. From the evolutionary point of view, this relationship is hardly surprising. In fact, it is to be expected that the opportunism of evolutionary processes would mix and match proteins

to produce new and novel functions. According to the doctrine of irreducible complexity, however, this should not be possible. If the flagellum is indeed irreducibly complex, then removing just one part, let alone 10 or 15, should render what remains "by definition nonfunctional." Yet the TTSS is indeed fully-functional, even though it is missing most of the parts of the flagellum. The TTSS may be bad news for us, but for the bacteria that possess it, it is a truly valuable biochemical machine.

The existence of the TTSS in a wide variety of bacteria demonstrates that a small portion of the "irreducibly complex" flagellum can indeed carry out an important biological function. Since such a function is clearly favored by natural selection, the contention that the flagellum must be fully-assembled before any of its component parts can be useful is obviously incorrect. As a result, the principal biochemical argument for intelligent design, the contention that the bacterial flagellum is irreducibly complex, has failed.

As I noted in an article for *Natural History* magazine (Miller 2002), similar analyses can be described for each of the other systems proposed as examples of intelligent design. The evolution of the vertebrate blood clotting cascade, for example, has been described in detail by Hanumanthaiah *et al* (2002), Davidson *et al* (2003) and Jiang and Doolittle (2003). The evolution of antibody-based adaptive immunity, one of the most complex systems in the body, has been elucidated as well. This work has taken place in many laboratories, and representative reports have appeared in papers by Lewis and Wu (2000), Market and Papavasiliou (2003), DuPasquier *et al* (2004), Zhou *et al* (2004), and Klein and Nikolaidis (2005). In addition, Nonanka and Yoshizaki (2004) were able to show how evolution produced the complement system, a complex and important part of the body's defenses against infection.

More generally, Long *et al* (2003) have reviewed the origin of new genes with novel functions, and have described 22 examples of such genes. Krem and DiCera (2002) have described the ways in which evolution produces that complex cascade-like pathways that function in signaling pathways associated with functions from blood clotting to signal transduction in development. Intelligent design bases its critique of evolution on the claim that new information cannot be produced by Darwinian mechanisms, and yet this claim has been repeatedly disproved by observations of novel pathways and enzymes that have arisen in the recent past. Prijambada *et al* (1995) described the ways in which Darwinian mechanisms produced nylonase, a new enzyme that breaks down the synthetic polymer nylon. Despite the claims of "design" advocates to the contrary, the ability of living organisms to respond to environmental change by evolution is truly remarkable. Bacteria have even been able to evolve new pathways to break down 2,4-dinitrotolulene, the explosive compound in TNT (Johnson *et al*, 2002).

The Informational Challenge to Evolution

At first glance, William Dembski's case for intelligent design seems to follow a distinctly different strategy in dealing with biological complexity. His recent book, *No Free Lunch* (Dembski 2002a), lays out this case, using information theory and mathematics to show that life is the result of intelligent design. Dembski makes the assertion that living organisms contain what he calls "complex specified information" (CSI), and claims to have shown that the

evolutionary mechanism of natural selection cannot produce CSI. Therefore, any instance of CSI in a living organism must be the result of intelligent design. And living organisms, according to Dembski, are chock-full of CSI.

Dembski's arguments, couched in the language of information theory, are highly technical and are defended, almost exclusively, by reference to their utility in detecting information produced by human beings. These include phone and credit card numbers, symphonies, and artistic woodcuts, to name just a few. One might then expect that Dembski, having shown how the presence of CSI can be demonstrated in man made objects, would then turn to a variety of biological objects. Instead, he turns to just one such object, the bacterial flagellum.

Dembski offers his readers a calculation showing that the flagellum could not have possibly have evolved. Significantly, he begins that calculation by linking his arguments to those of Behe, writing: "I want therefore in this section to show how irreducible complexity is a special case of specified complexity, and in particular I want to sketch how one calculates the relevant probabilities needed to eliminate chance and infer design for such systems" (Dembski 2002a, p. 289). Dembski then tells us that an irreducibly complex system, like the flagellum, is a "discrete combinatorial object." What this means, as he explains, is that the probability of assembling such an object can be calculated by determining the probabilities that each of its components might have originated by chance, that they might have been localized to the same region of the cell, and that they would be assembled in precisely the right order. Dembski refers to these three probabilities as P_{orig} , P_{local} , and P_{config} , and he regards each of them as separate and independent (Dembski 2002a, p. 291).

This approach overlooks the fact that the last two probabilities are actually contained within the first. Localization and self-assembly of complex protein structures in prokaryotic cells are properties generally determined by signals built into the primary structures of the proteins themselves. The same is likely true for the amino acid sequences of the 30 or so protein components of the flagellum and the approximately 20 proteins involved in the flagellum's assembly (McNab 1999; Yonekura *et al* 2000). Therefore, if one gets the sequences of all the proteins right, localization and assembly will take care of themselves.

According to Dembski, evolution could still not construct the 30 proteins needed for the flagellum. His reason is that the probability of their assembly falls below what he terms the "universal probability bound." According to Dembski, the probability bound is a sensible allowance for the fact that highly improbable events do occur from time to time in nature. To allow for such events, he agrees that given enough time, any event with a probability larger than 10^{-150} might well take place. Therefore, if a sequence of events, such as a presumed evolutionary pathway, has a calculated probability less than 10^{-150} , we may conclude that the pathway is impossible. If the calculated probability is greater than 10^{-150} , it's possible (even if unlikely).

When Dembski turns his attention to the chances of evolving the 30 proteins of the bacterial flagellum, he makes what he regards as a generous assumption. Guessing that each of the proteins of the flagellum have about 300 amino acids, one might calculate that the chances of getting just one such protein to assemble from "random" evolutionary processes would be 20^{-300} ,

since there are 20 amino acids specified by the genetic code. Dembski, however, concedes that proteins need not get the *exact* amino acid sequence right in order to be functional, so he cuts the odds to just 20^{-30} , which he tells his readers is "on the order of 10^{-39} " (Dembski 2002a, p. 301). Since the flagellum requires 30 such proteins, he explains that 30 such probabilities "will all need to be multiplied to form the origination probability" (Dembski 2002a, p. 301). That would give us an origination probability for the flagellum of 10^{-1170} , far below the universal probability bound. This is presented as proof that flagellum couldn't have evolved, and therefore must be the product of design.

In contrast to this confident conclusion, a careful analysis of the way in which Dembski calculates the probability of an evolutionary origin for the flagellum shows how little biology actually stands behind those numbers. His computation calculates only the probability of spontaneous, random assembly for each of the proteins of the flagellum. Having come up with a probability value on the order of 10^{-1170} , he assures us that he has shown the flagellum to be unevolvable. This conclusion, of course, fits comfortably with his view that "The Darwinian mechanism is powerless to produce irreducibly complex systems..." (Dembski 2002a, p. 289).

However complex Dembski's analysis, the scientific problem with his calculations is almost too easy to spot. By treating the flagellum as a "discrete combinatorial object" he has shown only that it is unlikely that the parts of flagellum could assemble spontaneously. Unfortunately for his argument, no scientist has ever proposed that the flagellum or any other complex object evolved that way. Dembski, therefore, has constructed a classic "straw man" and addressed it away with an irrelevant calculation.

By treating the flagellum as a discrete combinatorial object he has assumed in his calculation that no subset of the 30 or so proteins of the flagellum could have biological activity. As we have already seen, this is wrong. Nearly a third of those proteins are closely related to components of the TTSS, which does indeed have biological activity. A calculation that ignores that fact has no scientific validity.

More importantly, Dembski's willingness to ignore the TTSS lays bare the underlying assumption of his entire approach towards the calculation of probabilities and the detection of "design." *He assumes what he is trying to prove.*

According to Dembski, the detection of "design" requires that an object display complexity that could not be produced by what he calls "natural causes." In order to do that, one must first examine all of the possibilities by which an object, like the flagellum, might have been generated naturally. Dembski and Behe, of course, come to the conclusion that there are no such natural causes. But how did they determine that? In fact, this "conclusion" is an unsupported assumption upon which all of his calculations depend. Suppose that there are such causes, but one simply happened not to think of them? Dembski actually seems to realize that this is a serious problem. He writes: "Now it can happen that we may not know enough to determine all the relevant chance hypotheses. Alternatively, we might think we know the relevant chance hypotheses, but later discover that we missed a crucial one. In the one case a design inference could not even get going; in the other, it would be mistaken" (Dembski 2002a, p. 123 (note 80)).

What Dembski is telling us is that in order to "detect" design in a biological object one must first come to the conclusion that the object *could not* have been produced by any "relevant chance hypotheses" (meaning evolution). Then, and only then, are Dembski's calculations brought into play. Stated more bluntly, what this really means is that the "method" first involves *assuming the absence* of an evolutionary pathway leading to the object, followed by a calculation "proving" the impossibility of spontaneous assembly. This faulty *a priori* reasoning is exactly the sort of logic upon which the new "science" of intelligent design has been constructed.

Not surprisingly, scientific reviewers have not missed this point — Dembski's arguments have been repeatedly criticized on this issue and on many others (Orr 2002; Charlesworth 2002; Padian 2002).

The Origin of Biological Information

Arguments in favor of "design" are often predicated on the statement that living organisms contain large quantities of biological information (which is true) and that no natural process can account for the presence of this information (which is false). They then conclude that the existence of such information is evidence for design.

Such arguments ignore a wealth of research and scholarship on the origins of biological information. In reality, evolutionary mechanisms that can generate increased complexity and biological information are very well understood, and are described in many research papers. Adami *et al* (2000) described a carefully-controlled model system in which increases in information are driven by repeated rounds of reproduction, mutation, and selection, the same forces that drive evolutionary change in nature. Adami's system mimics the evolutionary process in remarkable detail, as highlighted in a 2003 article in *Nature* (Lenski *et al* 2003). Thomas Schneider of the National Institutes of Health has come to similar conclusions with respect to information based in nucleic acids (Schneider 2000).

Specific experiments on a variety of living organisms have shown that information does indeed arise through distinctly Darwinian mechanisms. The supporting evidence includes a number of studies on gene duplication (Brown *et al*, 2003; Ohta, 2003; Lynch & Conery, 2000; Hughes & Freeman, 2003), as well as experiments in which organisms have responded to adverse environmental conditions by increasing the information content of their DNA (Lenski, 1995; Papadopoulos *et al*, 1999; Riehle *et al*, 2001).

The origin of biological information, as nearly all of these scientists have pointed out, is explained by the mechanism of evolution itself. Variation in the information content of living organisms arises by means of mutations, a few of which increase information content. Natural selection then chooses those variations best-suited to the environment, "fixing" the increased information in the genome. The energetic price that such increases in information entail is considerable, but is fully accounted by the great cost of unsuccessful variants in the struggle for existence. To pretend otherwise, as the intelligent design movement has, is unfortunate and misleading.

5) *Of Pandas and People* – a Brief Analysis

Of Pandas and People (Kenyon & Davis, 1993), which pretends to be an open, objective examination of the pros and cons of evolutionary biology, is actually nothing of the sort. It is, instead, a collection of half-truths, distortions, and outright falsehoods that attempts to misrepresent biology and mislead students as to the scientific status of evolutionary biology.

A complete critique of the many problems with *Pandas* would take almost as many pages as the book itself, but here are a few points of special concern:

The Age of the Earth

Pandas claims to be a book that seeks to examine the “timeless question of biological origins.” A truly scientific attempt to do exactly this would begin by examining the age of the earth and reviewing the scientific techniques used by geologists to determine the ages of rocks and fossils. Curiously, *Pandas* does nothing of the sort. In fact, not a word can be found anywhere in *Pandas* regarding the age of the earth or geological ages recognized by earth scientists. Ignoring the age of the earth while attempting to teach students natural history makes about as much sense as trying to teach American history without telling students that the American revolution began in 1775, which is to say, no sense at all.

Why does *Pandas* make this striking omission? Its authors have never been willing to say why they ignore such a crucial part of earth history, but I suspect that the answer is simple. If they were to bring authentic scientific evidence regarding earth history into play, it would immediately become clear to readers that the ages of rocks and fossils support, in dramatic fashion, the evolutionary history of life that geologists have recognized for many decades. Because this important mass of scientific evidence is at odds with their anti-evolutionary thesis, they choose to ignore it. They are free to do this, of course, but students who might attempt to use *Pandas* as a scientific textbook will be rightly baffled by its attempts to teach natural history without a time scale, and will surely ask their teachers what science can tell us about the geologic time scale. *Pandas* ignores this most basic question, perhaps because it does not like the answer that science provides.

The Fossil Record

Pandas seriously misrepresents the nature of the fossil record. For example, on pages 99-100 the authors of *Pandas* have written:

Intelligent design means that various forms of life began abruptly through an intelligent agency, with their distinctive features already intact - fish with fins and scales, birds with feathers, beaks, and wings, etc. Some scientists have arrived at this view since fossil forms first appear in the rock record with their distinctive features intact, rather than gradually developing.

Actually, a close examination of the fossil record supplies scores of examples that show the

gradual appearance of a wide variety of physical adaptations, including, for example, the vertebrate limb. *Pandas* wishes to claim that abrupt appearances of critical features (which might be taken to support design) characterize the fossil record. Unfortunately, this contention does not square with the facts. The earliest known fish, for example, were quite different from the fish we recognize today. The earliest fossil forms lacked many of the characteristics possessed by fish today, including jaws, paired limbs and bony internal skeletons, and yet *Pandas* wishes to tell students that fish (and all fossil forms) appear in the fossil record "with their distinctive features intact."

To take another example, strong fossil evidence indicates that the first land vertebrates evolved from lobe-finned fish. One of the very first land vertebrates, a species known *Acanthostega gunnari*, illustrates the point. *Acanthostega*, although clearly a land-dwelling animal, retained an unmistakable sign of its aquatic ancestry: internal gills. No other amphibian possesses internal gills, and the gills preserved in key *Acanthostega* fossils make it clear that *Acanthostega* could breathe with its gills underwater, just like a fish, and could also breathe on land, using lungs. In other words, it was a true "transitional form." This first amphibian-like tetrapod was, as evolution would have predicted, more fish-like than any tetrapod to follow. As the discoverers of one of the most detailed *Acanthostega* fossils wrote: "Retention of fish-like internal gills by a tetrapod blurs the traditional distinction between tetrapods and fishes" (Coates & Clack, 1991).

Pandas implies that fossils such as these have never been discovered. If *Pandas'* goal was to engage students with authentic data, rather than to raise doubts and questions in the minds of its readers, it would surely present and discuss these fossil forms. Instead, it offers students a generalization that such fossils do not exist. Unfortunately, that generalization is wrong.

More recently, in 1997 paleontologists Edward B. Daeschler and Neil Shubin discovered a fossilized fin so well-preserved that its soft parts could be seen outside its underlying bony skeleton. The fin contained eight well-defined, recognizable digits. Incredibly, this fish had a fin with fingers, eight in number, just like the digits of *Acanthostega*. In other words, the limbs of land vertebrates did not appear suddenly (as if designed). They began to appear gradually, in the ancestors of land vertebrates, as if they evolved. (Daeschler & Shubin, 1997). This evidence directly contradicts the "design" claim that such key morphological features appear fully-formed and complete.

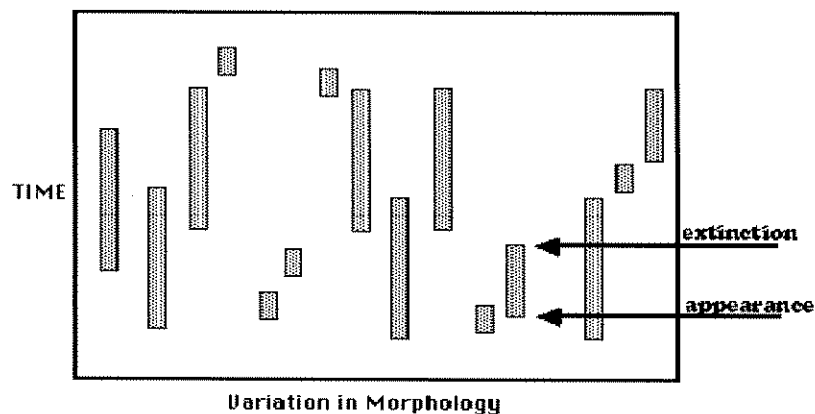
More Misrepresentations of the Fossil Record

On Page 95 of *Pandas*, Figure 4-2 attempts to show the abrupt appearance of most phyla in the Cambrian Period of geological history. Curiously, the diagram is a *schematic*, not a genuine diagram in which the individual phyla would be labeled and identified. Why not show the actual phyla and their names? I believe the reason is very simple. If the phyla were all labeled, the authors would not be able to make the suggestion that they do now, which is that most important groups of organisms alive today can trace their origins to this period, nor would they be able to pretend that all multicellular animal life first appeared in the Cambrian. In fact, if the dominant forms of plant and animal life on land were included in such a diagram (flowering plants and insects, respectively), students would learn that these organisms appeared hundreds of millions of years *after* the time shown in the graph. Furthermore, all of the great unicellular phyla (found

in the kingdoms Eubacteria, Archaeobacteria, and Protista) precede the Cambrian by hundreds of millions of years. And finally, the animals of the Cambrian were preceded by abundant soft-bodied animals known as Ediacaran fauna, which date at least a hundred million of years back into the Precambrian. Unfortunately, the readers of *Pandas* will never learn these facts because the authors are so intent on pretending that all major groups of organisms originated at just one period of time. And that is simply not true.

Pandas Ignores the Issue of Extinction

Pandas shows a remarkable unwillingness to address the obvious questions raised by its own theories. For example, on page 99 (Figure 4-4) a graph showing a "face value" interpretation of the fossil record is presented. It looks something like this:



What question would any inquisitive 9th-grader ask of this graph after being instructed in "intelligent design" theory? Just this: If all organisms are *intelligently* designed, what are the forces that seem always to intervene and drive these organisms to extinction? Any theory that claims to see intelligence in these designs that have mysteriously appeared in living organisms over millions of years must also explain why these designs seem to fail nearly every time. Evolution, of course, can explain extinction quite easily. In fact, extinction is a major evolutionary mechanism. But *Pandas* avoids this embarrassing problem. Its authors cannot explain extinction, and therefore they short-change their student readers by stepping around the question.

Predictions Made in *Pandas* are Dramatically Incorrect

Pandas' predictions about future discoveries of fossils are wrong. To be sure, the text makes very few statements that could be subjected to scientific testing. However, when it does make a prediction, it fails miserably. Consider this statement from Pages 101-102:

"The absence of unambiguous transitional fossils is illustrated by the fossil record of whales. The earliest forms of whales occur in rocks of Eocene age, dated some 50 million years ago, but little is known of their possible ancestors. By and large, Darwinists believe that whales evolved from a land mammal. The problem is that there are no clear transitional

fossils linking land mammals to whales. If whales did have land-dwelling ancestors, it is reasonable to expect to find some transitional fossils. Why? Because the anatomical differences between the two are so great that innumerable in-between stages must have paddled and swam the ancient seas."

Yes, evolution predicts that there should have been transitional forms linking swimming mammals with land mammals. And their absence, *Pandas* argues, is good evidence that evolution is wrong. But in the past 20 years not one, not two, but three true intermediate forms have been discovered. Up until 1986, the oldest known fossil whale had been *Basilosaurus*, dating to about 40 million years before present (a sketch of *Basilosaurus* is shown in *Pandas*). However, fossil-hunters have now found 3 intermediates that link *Basilosaurus* to land-dwelling ancestors. They are:

Pakicetus inachus - 52 myr.

Ambulocetus natans 50 myr.

Rodhocetus kasrani 46 myr.

The actual fossil forms were described in a 1994 article in the journal *Science* (Thewissen *et al* 1994). A less technical account of these intermediate forms and their importance for understanding cetacean evolution was written by Stephen Jay Gould in *Natural History* magazine ("Hooking Leviathan By Its Past," Gould 1994).

Pandas can certainly be forgiven for not including research that appeared *after* its publication date. However, in teaching students that such intermediate forms would, indeed, could never be found, *Pandas* compounds its earlier misrepresentations of fossil history with demonstrably false prediction, a misperception of reality which has no place in authentic scientific education.

Pandas misrepresents the Molecular Evidence for Evolution

Pandas' entire Chapter 6 (on Biochemical similarities) is based on an incorrect representation of evolutionary theory. I do not know if this misrepresentation was done intentionally or out of simple misunderstanding, but either way, I would argue that the errors in this chapter are reason alone to disqualify the book from use in the science classroom.

Basically, the chapter repeatedly states that evolution predicts that amino acid sequences of key proteins (like cytochrome c) should be arranged in a linear sequence. For example, if one takes the sequences of, say, a worm, a frog, and a human, the frog sequence should be closer to the worm than the human sequence is. That is the claim that *Pandas* makes repeatedly as a "prediction" of evolutionary theory. However it is simply not true that any evolutionary biologist has ever made such a prediction (significantly, *Pandas* does not cite any references for its claims). *Pandas* then examines the data and shows that the frog and human sequences are equally distant from that of the worm. That, it argues, is contrary to the evolutionary prediction.

This is simply not true. The real story is that the fossil record clearly shows that the entire vertebrate group (including frogs and people) split off from the invertebrates (including worms)

many hundreds of millions of years ago. Therefore, the protein sequences of every animal in that group should be *equidistant* from any single invertebrate. And that is exactly what the experimental data show, as the authors of *Pandas* ought to know.

The simple fact is that this chapter misrepresents evolutionary predictions on molecular sequences, and thereby covers up the fact that the sequences stand in stunning agreement with evolution. I cannot even imagine a greater misrepresentation of fundamental data to support an incorrect conclusion.

I could go on to document further misrepresentations of scientific fact and theory in *Of Pandas and People*. However, my criticisms of this text are not unique. In fact, the many errors and misleading statements in this text were immediately recognized almost from its first publication by a variety of scientists and educators. Reviews describing the errors and misrepresentations in *Pandas* have appeared in many publications, including *Scientific American* (Beardsley 1995).

Science is an open enterprise, and scientific inquiry thrives precisely because no scientific theory or idea is ever immune from criticism, examination, or testing in the crucibles of experiment and observation. When I first opened the pages of *Pandas* and read the fine words presented by its authors in the name of free and open inquiry, I expected a text that might genuinely challenge students to examine the assumptions of what they had learned and evaluate scientific theory in an objective manner. To say that I was disappointed is to put it mildly. What I found instead was a document that contrived not to teach, but to mislead.

Pandas misstates evolutionary theory, skims over the enormous wealth of the fossil record, and ignores the sophistication of radiometric dating. How sad it would be, given the need to improve the content and rigor of science instruction in this country, for this book to be offered as part of the educational solution. There is a great deal that we do not know about the origin of life on this planet, but that does not mean that science is obliged to pretend that it knows *nothing*, or to engage in a kind of scientific relativism, pretending that all speculations about the origin of our species are equally correct. The most compelling reason to keep this book out of the biology classroom is that it is bad science, pure and simple.

Science education today faces many challenges. Our teachers must deal with an ever-changing landscape of scientific advance and technological innovation that continually changes the ground upon which they educate their students. Biology education, in particular, will be the key for many of our students as they attempt to prepare themselves for the challenges of the next century, and therefore it is especially important that teachers be supported, not hindered, in their attempts to educate students in the life sciences. The many errors and misrepresentations that inhabit the pages in *Of Pandas and People* will, quite honestly, serve to hinder teachers as they attempt to cover the stunning range and diversity of contemporary biology. I believe it is best not to burden science faculty with the needless task of overcoming the many errors and misconceptions written into this book.

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Postiglione, Christina

From: Rothschild, Eric J.
Sent: Friday, April 01, 2005 10:07 AM
To: Henson, Katherine E.
Cc: Postiglione, Christina
Subject: RE:

Tina is accumulating reports. In Ken Miller's case, he is traveling and will not be able to send us a signature page. Please craft letter to reflect that the executed signature page will be transmitted next week.

-----Original Message-----

From: Rothschild, Eric J.
Sent: Friday, April 01, 2005 9:03 AM
To: Henson, Katherine E.
Subject:

Please prepare cover letter for fed ex transmittal of plaintiffs' expert reports.

Eric Rothschild
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