Why Intelligent Design Fails

A Scientific Critique of the New Creationism

Edited by Matt Young and Taner Edis

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Darwin's Transparent Box

The Biochemical Evidence for Evolution

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MICHAEL J. BEHE is perhaps best known as the author of *Darwin's Black Box* (1996). But I know Mike Behe as a biochemist and a scientific colleague; we are both interested in DNA structures. I first heard of Behe more than 20 years ago, when I was a graduate student in a biophysical chemistry group and Behe had co-authored a paper about a form of DNA called Z-DNA (Behe and Felsenfeld 1981). (The paper was famous, to some of us, because it meant Z-DNA might be more likely to occur within living cells.) In 1997, one of my students told me about a biochemistry professor who had written a book showing that complicated biochemical systems were "intelligently designed" and could not have evolved. I had no idea that the book was written by the same Michael Behe.

Both Phillip Johnson and Behe claim that none of the reviewers of *Darwin's Black Box* found fault with the science. "The reviewers say what I knew they would say: Behe's scientific description is accurate, but his thesis is unacceptable because it points to a conclusion that materialists are determined to avoid," claims Johnson (Dembski and Kushiner 2001, 38). In the same edited volume Behe agrees with this claim: "the reviewers are not rejecting design because there is scientific evidence against it, or because it violates some flaw of logic. Rather I believe they find design unacceptable because they are uncomfortable with the theological ramifications of the theory" (100).

Interested readers should look carefully through some of the reviews of Behe's book and decide for themselves whether his statement is true. (See,

for example, Coyne 1996, Orr 1997, Doroit 1997, Ussery 1999.) More-recent discussions on both sides of the topic appear in the April 2002 issue of *Natural History* and Pennock's (2001) edited collection. Kenneth Miller (1999) argues that Behe's irreducible complexity fails the biochemistry test. Miller, like Behe, is a Catholic. But contrary to Behe, Miller rejects intelligent design as a scientific theory because there is scientific evidence against it and also because of flawed logic; his arguments are by no means the result of his opposition to the theological implications.

Reduction of Irreducibly Complex Biochemical Systems

I have a stake in this issue: I also have written a review of Behe's book (Ussery 1999) and was critical of his science. I will explain why.

Behe (1996) defines an irreducibly complex (IC) system 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. An irreducibly complex system cannot be produced directly" (39). As an example of IC, Behe uses the mousetrap and claims that it needs all five components in order to function. Take away any one component, and it will not work. Before we even get into the specific examples, the mousetrap analogy itself has problems (see chapter 2). In fact, a competition has been held to develop mousetraps with fewer than the "necessary" five components, and there are many examples of mousetraps consisting of fewer parts—including some with only a single piece (Ruse 2003, 313).

Biochemistry has many IC systems, says Behe, and he uses as an example the cilium, which consists of about 250 proteins. (See Miller 1999, 140–43, for a discussion of various reduced forms of cilia.) Behe also mentions the bacterial flagellum, which is a simplified bacterial version of the cilium with about 40 proteins, as another example of an IC system. Since the flagellar system is smaller and perhaps more tractable, I will spend time here examining it in more detail.

To begin, let us consider how many parts are needed. If something is to be irreducible, then it makes sense to agree on the minimum number of components that will allow the system to function. Exactly how many parts are minimally required for the bacterial flagellum? There are two parts to this question. First, at face value, Behe says that only three IC parts are essential for function. But each of these parts is made of proteins. The second, related question, is how many proteins are essential to make a functioning flagellum. The number of proteins is much easier to quantify and verify, whereas an IC part

is more difficult to nail down. So let us try to answer the more tractable second question first and then go back to the first.

How many proteins are necessary to make a flagellum? According to Behe (1996),

> The bacterial flagellum, in addition to the proteins already discussed [200 proteins for the most complicated cilia] requires about forty other proteins for function. Again the exact roles of most of these proteins are not known, but they include signals to turn the motor on and off; "brushing" proteins to allow the flagellum to penetrate through the cell membrane and cell wall; proteins to assist in the assembly of the structure; and proteins to regulate the production that make up the flagellum. (72–73)

"About forty" is vague if we are trying to figure out the minimum number of proteins. A good place to start is to look through some of the more than 100 completely sequenced bacterial genomes (anonymous 2003a) to see how many flagellar proteins are found in various genomes. Perhaps we can find a lower bound.

The common and well-studied bacterium *E. coli* strain K–12 has 44 flagellar proteins. Another bacterium, such as *Campylobacter jejuni*, has only 27 flagellar proteins. So perhaps 27 is the lower limit? But what if we find a bacterium with even fewer flagellar proteins? Can Behe's theory of irreducible complexity tell us what to expect for the lower limit? Maybe 25 proteins are necessary. On the other hand, if people report finding a bacterium that has only 23, then we need to have a careful look through the genome to see if they have missed two flagellar proteins somewhere. This makes sense: if something is irreducibly complex, then by definition *all* of the parts must be essential. If we could figure out the minimum number of proteins essential for function, the "IC number" for a given biochemical system, then it might be possible to say that Behe's idea of IC can be a useful tool for biologists looking at complete bacterial genomes. How can we determine the IC number for the bacterial flagellum? According to Behe (1996), "because the bacterial flagellum is composed of at least three parts—a paddle, a rotor, and a motor—it is irreducibly complex" (72). Evidently, only three parts are needed, but how many proteins? I have posed this question to several ID advocates and have been told that Behe is clear that you need only three parts. If each part could be made of a single protein, then evidently only three proteins are necessary. That is, an irreducibly complex flagellum can, in principle, be reduced to a mere three essential proteins.

This sounds strange. Upon closer examination, it seems that Behe is say-

ing, on the one hand, that you cannot reduce the complex forty-protein machine of a bacterial flagellum, but, on the other hand, you can perhaps find something that is still functional but has lost about 90 percent of its protein components. That is, we could go from about forty proteins to only three essential proteins—one each for a paddle, a motor, and a rotor. So if we look at the problem in terms of the number of proteins, the irreducibly complex argument makes predictions that can easily be tested by looking at genomic sequences and are wildly different from what is observed.

But what about Behe's argument that a bacterial flagellum, consisting now of a mere three proteins, is still irreducibly complex since it will no longer be functional if you remove any one of the components? Behe's three parts are nice descriptions, but published scientific reviews of bacterial flagella classify the flagellar protein components into *six* functional categories, not three: regulatory proteins, proteins involved in assembly, flagellar structural components, flagellar proteins of unknown function, sensory transduction components, and chemoreceptors (Macnab 1992).

All three of Behe's IC parts fall into the third category, structural components. Thus, when Behe talks about the three IC parts of the flagellum, he is referring to only one of the six categories of flagellar proteins defined in the literature; proteins from the other five categories are not part of his IC system (that is, they are not part of the paddle, rotor, or motor). These proteins might be important for function, but you could remove them or replace them with other proteins handy in the cell, and the system would still function. Some bacteria, for example, have only half as many flagellar proteins as other bacteria.

For consistency, let us consider the three parts Behe describes as irreducibly complex. Behe claims that such an IC biochemical system could not have possibly evolved, since you need all three functions (paddle, rotor, and motor) simultaneously for proper function. But what if you already had each of the three components lying around, doing other functions in the cell, and then put them together? This idea can be tested by having a closer look at the components of the three different systems: are they unique to the flagellar system, or could they be used in other, non-IC biological systems?

The paddle consists of a set of proteins called flagellin, which will self-assemble; that is, if you take individual copies of the protein and mix them together, they will spontaneously polymerize to form the paddle (Yonekura et al. 2002). In practice, you need only one or a very few proteins, but the question is whether there is evidence that this protein could have evolved. I found some pertinent references in the *Journal of Molecular Evolution*, which Behe

complains deals mainly with (mere) sequence comparison. (See, for example, Harris and Elder 2002.)

Sequence comparison is where the clearest evidence for evolution lies, and that is precisely where Behe does not look. I cannot overemphasize two points: first, evolution selects organisms, not complicated biochemical systems (Lewontin 2001, Mayr 2002). Second, proteins do not evolve. Rather, they are made from mRNA, which comes from the DNA sequence. Most proteins do not last very long; eventually they get chopped up and recycled to make new proteins. What is passed on from one generation to the next and what must change for evolution to happen is the DNA sequence.

I work in a bioinformatics group where every day we look at DNA, RNA, and protein sequences. I specialize in studies of bacterial genomes that have been sequenced, doing whole genome analysis. So, for me, it is very easy to have a look at the flagellin protein. As an example, one *E. coli* version of this protein consists of 595 amino acids, coded for by 1785 base pairs. How does this sequence compare to flagellin proteins in other organisms? A computer search yielded hundreds of hits, ranging from identical matches (595 out of 595 residues) for the same protein to proteins with only 193 out of 359 amino acids matching (this was from *Salmonella enterica*, which is a bacterium closely related to *E. coli*). Thus, there is a lot of variation; more than three-fourths of the sequence can be different, yet the function is still conserved.

There is good reason for this variation. The flagellar paddles stick out from the bacterium and are a prime target for the immune system if a bacterium is living inside an animal (Eaves-Pyles et al. 2001). If the flagellin sequence does not vary, the immune system, which remembers the last time it saw a flagellum, will always kill the bacterium. This is just basic natural selection. In fact, there is quite a bit of variation of flagellin, even within the same bacterium (Meinersmann and Hiett 2000). Evolution by natural selection goes on within both the bacterium and the immune system (ironically, another of Behe's irreducibly complex systems). The immune system works by generating lots of different antibodies, and then those that work are selected for, just as in Darwinian evolution (Clark 1995).

The flagellin protein is about 400 amino acids in length, and its structure can be found on the Internet, along with a link to the three-dimensional structure of the protein (Samatey et al. 2000, 2001). Interested readers can visit this web site and download the structure, rotate the molecule, and explore the available options. The function of a protein (or RNA or DNA molecule) is determined by its shape or structure. Thus, we could have two proteins with very different sequences, but if they fold into the same shape, they might

have exactly the same function. It is this principle that must be understood in order to explain how we can have such large variation in sequence yet maintain the function of the protein. We can also have a very few, seemingly small changes, which have drastic effects on the function of the protein, if those changes are in the right place.

Let us now discuss the second of the three components, the rotor. It was hard to tease out the difference between the rotor components of the flagellum versus the motor part; the two are very much intertwined. There are, however, two different proteins responsible for the rotor: FliG is the rotor protein in a simple lateral flagellum, while the FliM and FliN proteins are responsible for rotors in the polar flagellum (McClain et al. 2002). A search for sequences similar to the FliG protein from *E. coli* in other bacteria found hundreds of sequences in other organisms, ranging from perfect matches to proteins containing less than a third of the amino acids in common. Once again, here is an example of large sequence variation, providing a large source of material for natural selection to choose from.

The third and final component is the flagellar motor. According to a recent review, "We know a great deal about motor structure, genetics, assembly, and function, but we do not really understand how it works. We need more crystal structures" (Berg 2002, n.p.). In my opinion, we need to better understand how this system works before we can consider evolutionary pathways.

I found a few interesting articles, however, with respect to Behe's claim of the irreducible complexity of the three components of the flagellum. For example, there may be only a loose coupling between the proton-driven motor and the rotation of the flagellum (Oosawa and Hayashi 1986). So perhaps the idea of an IC flagellum as some sort of distinct and self-contained unit is oversimplified. This reference, incidentally, was published in 1986, or 10 years before the publication of *Darwin's Black Box*.

Consider also the recent finding that we can mix and match different motors—that is, we can take a motor that is driven by sodium ions and substitute it for a functional flagellar motor that is driven by protons instead of sodium ions (Asai et al. 2003). Lots of motors in the bacterial cell do various other functions, so the flagellar motor did not have to come out of the blue at the same time as the whole flagellar complex.

Finally, what about fossil evidence of ancient flagella? Behe has claimed that an IC system somehow negates the fossil record as evidence for evolution:

> The relevant steps in biological processes occur ultimately at the molecular level, so a satisfactory explanation of a biological

> phenomenon . . . must include a molecular explanation. . . . Anatomy is, quite simply irrelevant. So is the fossil record. It does not matter whether or not the fossil record is consistent with evolutionary theory, any more than it mattered in physics that Newton's theory was consistent with everyday experience. (Behe 1994, n.p.)

A new theory must agree with established scientific theories if it is to be widely accepted. For example, statistical mechanics predicts the macroscopic classical thermodynamics that it replaces. Similarly, Einstein's theories predict Newtonian behavior when objects are not going too fast. Surely Behe's IC system must do the same: it must be in agreement with what we observe in the fossil record, which for bacteria goes back more than 3.5 billion years (Fortey 1997, Schopf 1999, Knoll 2003). Or are we supposed to accept only present life forms as evidence?

Of course, there are lots of complicated biochemical systems in bacteria today, but the big question is whether they have always been there, as placed by an intelligent designer, or if in fact bacterial cells have slowly changed over time from simpler systems to more-complex systems. Even if we allow for bacteria to divide once a day (*E. coli* can divide every 20 minutes), there are an awful lot of replications between now and 3 billion years ago.

Behe suggests that the intelligent designer might have put all the necessary genes into the first organism. But what we see in the laboratory is that, if an organism has extra genes (genes that are not being used), they accumulate mutations fairly quickly and soon become unusable. Within a few years, the genes of bacteria would become corrupted and disappear from the bacteria's gene pool. But Behe seems to think this would not happen, even over very long periods of time. Does he think that the intelligent designer created the first cell and then sat around and waited for 3.5 billion years for humans to come along? Maybe he is right, maybe not, but this theory does not sound like science.

In summary, all three of the irreducible components of the flagellum could have evolved independently, and the flagellum could have evolved from a combination of the three independent parts rather than suddenly being created by an intelligent designer. Such coevolution is one of several alternative mechanisms for evolution of Behe's irreducibly complex biochemical systems. Similar arguments show that Behe's three other IC systems (blood clotting, the proteosome, and the immune system) consist of reducible components that could have evolved (Miller 1999, Ussery 1999, Thornhill and Ussery 2000). As a general principle, complex biochemical systems can arise from simple precursors (Ptashne and Gann 2002).

Extraordinary Claims, Anemic Evidence

Behe (1996) makes an extraordinary claim—that finding design in biochemistry "is so unambiguous and so significant that it must be ranked as one of the greatest achievements in the history of science" (232). Furthermore, the discovery of IC biochemical systems overthrows Darwinian evolution by natural selection: "It is a shock to us in the twentieth century to discover, from observations science has made [of IC systems] *that the fundamental mechanisms of life cannot be ascribed to natural selection*, and therefore were designed. But we must deal with our shock as best we can and go on. The theory of undirected evolution is dead, but the work of science continues" (Behe 1994, n.p., emphasis added).

What evidence does Behe offer to support his extraordinary claim that life is designed and that "the fundamental mechanisms of life cannot be ascribed to natural selection"? First is his argument that complex systems such as the bacterial flagellum are IC and hence cannot have evolved. But as I have shown, there are indeed plausible mechanisms that can explain the evolutionary origin of the flagellum. (See chapter 6 for additional details.)

What other evidence does Behe marshal to his defense? A supposed lack of published papers: "Even though we are told that all biology must be seen through the lens of evolution no scientist has *ever* published a model to account for the gradual evolution of this extraordinary molecular machine," writes Behe (1996, 72) about the flagellum. I did a quick search on PubMed and found 260 published articles that have the words "flagella" and "evolution" in the title or abstract. Not all of these articles describe mechanisms in a way that Behe might like, but at least some of them do, which is enough to negate his claim that "no scientist has ever published. . . . "

For example, consider a different irreducibly complex system, the immune system, and recent papers outlining its evolution. A whole new field, *evolutionary immunology,* has come to life since Behe's book was published in 1996. Out of the 4400 articles on "evolution and immunology" that can be found in PubMed, almost 2000 have been published since 1996. This hardly sounds like a dead, unprogressive field.

Finally, when Behe looked in the index of a fat biochemistry textbook, he found the word *evolution* hardly mentioned. Thus, he concluded, evolution is not necessary to understanding biochemistry. Using this same reasoning, we could claim that the atomic theory of matter was not true or at any rate not important since it is hardly mentioned in the index of biochemistry texts.

In summary, the evidence presented for rejection of the fossil record and natural selection and in favor of adopting a belief in a designer outside nature

(and hence outside the realm of science) is (1) definition by fiat of an IC system, (2) an absence of articles in the scientific literature describing the evolution of biochemical systems deemed to be IC, and (3) a paucity of entries for the word *evolution* in the indexes of biochemistry textbooks. This is anemic evidence for such extraordinary claims. Yet I have talked with people who advocate intelligent design, and they simply cannot understand why their manuscripts, which contain such weak and minuscule evidence, are not published in scientific journals. They claim that the journals are obviously biased against them because of the theological implications, and publication has nothing to do with the quality (or lack thereof) of their science.

The Popularity of Intelligent Design

While doing the background work for this article, I did a Google search, typed in "Behe," and got more than 30,000 web pages. Obviously this is more material than I can handle. Why is Behe's view of biochemical evidence for an intelligent designer so popular?

Michael Ruse (2003) deals with the issue of design in nature and evolution and argues that biological organisms are clearly different from the nonliving matter around us in that they are designed. So in this sense, he is in agreement with Behe. Ruse's designer, however, is evolution through natural selection, and there is no need to invoke the supernatural (an external intelligent designer outside the system). Behe wants to return to William Paley's watchmaker analogy from nearly 200 years ago: "Behe, Dembski, and their nemesis, [Richard] Dawkins, share a desire to return to the high Victorian era, when Britain ruled the waves and science and religion could never agree" (333). Behe and Dawkins are right in their arguments that nature is designed. The question is the mechanism of design rather than whether or not things are designed. I suspect Behe is so popular in part because of his appreciation of the complexity of nature. According to Ruse,

> However one might criticize Behe's conclusions, when he speaks about the inner workings of the cell, his audience senses the presence of a man who truly loves the natural world. Say what you like in criticism of Dawkins, when he writes about the echolocation mechanism of the bat or about the eye and its varieties, he reveals to his readers an uncommon delight in the intricate workings of the organic world. In this Behe and Dawkins are at one with Aristotle, John Ray, Georges Cuvier, and of course Charles Darwin. . . . All appreciate the organized complexity of the natural world. (334)

Hoimar von Ditfurth (1982) says that Christians should be amazed that the miracle of evolution occurred rather than claiming that "God is what we don't know."

In 1997, I posted a web version of my review of Behe's book. Since then, more than one-half million people have visited the web page, and I have received more than a thousand E-mails about the web review over the past 5 years. About one-third of the people who write to me like my review, whereas the other two-thirds assume I must be some sort of evil atheist because I don't agree with Behe. But I am critical of Behe's IC system because it is just plain bad science. (I do not, however, think that Mike Behe's published scientific work is bad. For example, I have recently cited one of Behe's scientific papers [2000] in an article about the relative amounts of A-DNA and Z-DNA in sequenced genomes [Ussery et al. 2002]. But publishing in a peer-reviewed journal and writing a popular book are two different things.)

In my opinion, intelligent design is not good science. Since there are practically no papers published in the peer-reviewed scientific literature on this subject, I think it makes no sense to teach it as science. Indeed, to teach it as science would be dishonest.