

Debating Design

From Darwin to DNA

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Notes on Contributors

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James Barham was trained in classics at the University of Texas at Austin and in the history of science at Harvard University. He is an independent scholar who has published some dozen articles on evolutionary epistemology, the philosophy of mind, and the philosophy of biology in both print and electronic journals, including *BioSystems*, *Evolution and Cognition*, *Rivista di Biologia*, and *Metanexus.net*. His work consists of a critique of the mechanistic and Darwinian images of life and mind, as well as an exploration of alternative means of understanding value, purpose, and meaning as objectively real, natural phenomena, in both their human and their universal biological manifestations. He is working on a book to be called *Neither Ghost nor Machine*.

the critical element that distinguishes the empirical sciences from other forms of knowledge: the requirement that scientific hypotheses be empirically falsifiable. Scientific hypotheses cannot be consistent with all possible states of affairs in the empirical world. A hypothesis is scientific only if it is consistent with some but not other possible states of affairs not yet observed in the world, so that it may be subject to the possibility of falsification by observation. The predictions derived from a scientific hypothesis must be sufficiently precise that they limit the range of possible observations with which they are compatible. If the results of an empirical test agree with the predictions derived from a hypothesis, the hypothesis is said to be provisionally corroborated; otherwise, it is falsified.

The requirement that a scientific hypothesis be falsifiable has been called by Karl Popper the *criterion of demarcation* of the empirical sciences, because it sets apart the empirical sciences from other forms of knowledge. A hypothesis that is not subject to the possibility of empirical falsification does not belong in the realm of science. See F. J. Ayala, "On the Scientific Method, Its Practice and Pitfalls," *History and Philosophy of Life Sciences* 16 (1994): 205–40.

29. This point has been made in sensuous prose by John Updike in his recent *Toward the End of Time* (New York: Knopf, 1997), p. 214: "It makes sense: all those blazing suns, red and swollen or white and shrunk or yellow like our moderate own, blue and new or black and collapsed, madly spinning neutron stars or else all-swallowing black holes denser yet, not to mention planets and cinderlike planetoids and picturesque clouds of glowing gas and dark matter hypothetical or real and titanic streaming soups of neutrinos, could scarcely be expected to converge exactly upon a singularity smaller, by many orders of magnitude, than a pinhead. The Weyl curvature, in other words, was very very *very* near zero at the Big Bang, but will be much larger at the Big Crunch. But, I ignorantly wonder, how does time's arrow know this, in our trifling immediate vicinity? What keeps it from spinning about like the arrow of a compass, jumping broken cups back on the table intact and restoring me, if not to a childhood self, to the suburban buck I was when still married." The mystery of aging and ultimate personal demise receive, in Updike's view, but little help from considerations of the immensity and endurance of the physicist's universe.

I sometimes make the same point by rephrasing a witticism that I once heard from a friend: "In the matter of the value and meaning of the universe, science has all the answers, except the interesting ones."

The Flagellum Unspun

The Collapse of "Irreducible Complexity"

Kenneth R. Miller

Almost from the moment *On the Origin of Species* was published in 1859, the opponents of evolution have fought a long, losing battle against their Darwinian foes. Today, like a prizefighter in the late rounds losing badly on points, they've placed their hopes on one big punch – a single claim that might smash through the overwhelming weight of scientific evidence to bring Darwin to the canvas once and for all. Their name for this virtual roundhouse right is "Intelligent Design."

In the last several years, the Intelligent Design (ID) movement has attempted to move against the standards of science education in several American states, most famously in Kansas and Ohio (Holden 1999; Gura 2002). The principal claim made by adherents of this view is that they can detect the presence of "Intelligent 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 counterexample to evolution that it might well be considered the "poster child" of the modern anti-evolution movement. Variations of its image (Figure 5.1) now appear on web pages of anti-evolution groups such as the Discovery Institute, and on the covers of "Intelligent Design" books such as William Dembski's *No Free Lunch* (Dembski 2002a). 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 an anti-evolutionist 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 sentiments have been appropriately described, has been a weapon of little value in the anti-evolution movement. Anyone can state at any time

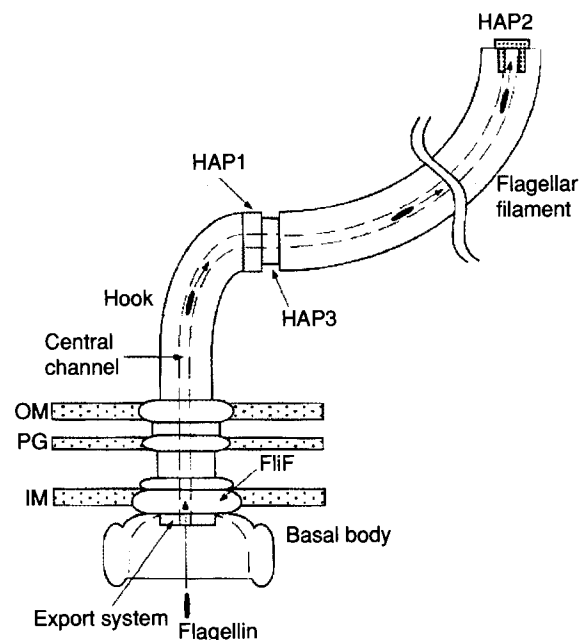


FIGURE 5.1. The eubacterial flagellum. The flagellum is an ion-powered rotary motor, anchored in the membranes surrounding the bacterial cell. This schematic diagram highlights the assembly process of the bacterial flagellar filament and the cap-filament complex. OM = outer membrane; PG = peptidoglycan layer; IM = cytoplasmic membrane. (From Yonekura et al. 2000.)

that he or she cannot imagine how evolutionary mechanisms might have produced a certain species, organ, or structure. Such statements, obviously, are personal – and they say more about the limitations of those who make them than they do about the limitations of Darwinian mechanisms.

The hallmark of the Intelligent Design movement, however, is that it purports to rise above 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 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 the anti-evolutionist movement is that fact that research had demolished its status as an example of irreducible complexity almost at the very moment it was first proclaimed. The purpose of this chapter is to explore the arguments by which the flagellum’s notoriety has been achieved, and to review the research developments that have now undermined the very foundations of those arguments.

THE ARGUMENT’S ORIGINS

The flagellum owes its status principally to *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 raised the argument to a new level, claiming 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). Why would such systems present difficulties for Darwinism? Because they could not possibly have been produced by the process of evolution:

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)

The phrase “numerous, successive, slight modifications” is not accidental. The very same words were used by Charles Darwin in the *Origin of Species* in describing the conditions that had to be met for his theory to be true. As Darwin wrote, if one could find an organ or structure that could not have been formed by “numerous, successive, slight modifications,” his “theory would absolutely break down” (Darwin 1859, 191). To anti-evolutionists, the bacterial flagellum is now regarded as exactly such a case – an “irreducibly complex system” that “cannot be produced directly by numerous successive, slight modifications.” A system that could not have evolved – a desperation punch that just might win the fight in the final round, a tool with which the theory of evolution might be brought down.

THE LOGIC OF IRREDUCIBLE COMPLEXITY

Living cells are filled, of course, with complex structures whose detailed evolutionary origins are 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.

Such arguments are easy to make, of course, but the nature of scientific progress renders them far from compelling. The lack of a detailed current explanation for a structure, organ, or process does not mean that science will never come up with one. As an example, one might consider the question of how left-right asymmetry arises in vertebrate development, a question that was beyond explanation until the 1990s (Belmonte 1999). In 1990, one might have argued that the body's left-right asymmetry could just as well be explained by the intervention of a designer as by an unknown molecular mechanism. Only a decade later, the actual molecular mechanism was identified (Stern 2002), and any claim one might have made for the intervention of a designer would have been discarded. The same point can be made, of course, regarding any structure or mechanism whose origins are not yet understood.

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 therefore 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 thirty, are required to produce a working biological function. By the logic of irreducible complexity, these individual components should have no function until all thirty are put into place, at which point the function of motility appears. What this means, of course, 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 wrote, "natural selection can only choose among systems that are already working" (Behe 2002), 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. Case closed.

ANSWERING THE ARGUMENT

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 counterexamples to any assertion that evolution cannot explain biochemical complexity (Miller 1999, 147), and other workers have addressed the issue of how evolutionary mechanisms allow biological systems to increase in information content (Adami, Ofria, and Collier 2000; Schneider 2000).

The most powerful rebuttals to the flagellum story, however, have not come from direct attempts to answer the critics of evolution. Rather, they 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 we will see, the flagellum – the supreme example of the power of this new "science of design" – has failed its most basic scientific test. Remember the claim that "any precursor to an irreducibly complex system that is missing a part is by definition nonfunctional"? 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.

THE TYPE III SECRETORY APPARATUS

In the popular imagination, bacteria are "germs" – tiny microscopic bugs that make us sick. Microbiologists smile at that generalization, knowing that most bacteria are perfectly benign, and that many are beneficial – even essential – to human life. Nonetheless, there are indeed bacteria that produce diseases, ranging from the mildly unpleasant to the truly dangerous. Pathogenic, or disease-causing, bacteria threaten the organisms they infect in a variety of ways, one of which is by producing poisons and injecting them directly into the cells of the body. Once inside, these toxins break down and destroy the host cells, producing illness, tissue damage, and sometimes even death.

In order to carry out this diabolical work, bacteria not only must produce the protein toxins that bring about the demise of their hosts, but also must efficiently inject them across the cell membranes and into the cells of their hosts. They do this by means of any number of specialized protein secretory systems. One, known as the type III secretory system (TTSS), allows 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

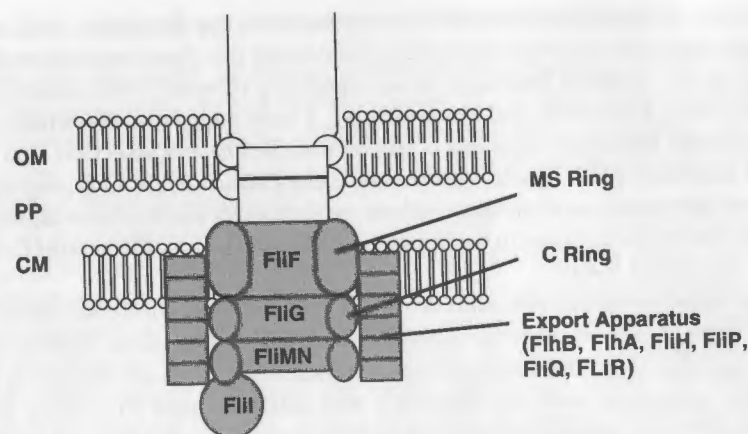


FIGURE 5.2. There are extensive homologies between type III secretory proteins and proteins involved in export in the basal region of the bacterial flagellum. These homologies demonstrate that the bacterial flagellum is not "irreducibly complex." In this diagram (redrawn from Heuck 1998), the shaded portions of the basal region indicate proteins in the *E. coli* flagellum homologous to the Type III secretory structure of *Yersinia*. OM = outer membrane; PP = periplasmic space; CM = cytoplasmic membrane.

factors," that are directly responsible for the pathogenic activity of some of the most deadly bacteria in existence (Heuck 1998; Büttner and Bonas 2002).

At first glance, the existence of the TTSS, a nasty little device that allows bacteria to inject these toxins through the cell membranes of their unsuspecting hosts, would seem to have little to do with the flagellum. However, 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 figure 5.2 (Heuck 1998) shows, 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, 163). 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 in order 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 ten or fifteen, 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. Because 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. What this means is that the argument for intelligent design of the flagellum has failed.

COUNTERATTACK

Classically, one of the most widely repeated charges made by anti-evolutionists is that the fossil record contains wide "gaps" for which transitional fossils have never been found. Therefore, the intervention of a creative agency – an intelligent designer – must be invoked to account for each gap. Such gaps, of course, have been filled with increasing frequency by paleontologists – the increasingly rich fossil sequences demonstrating the origins of whales are a useful example (Thewissen, Hussain, and Arif 1994; Thewissen et al. 2001). Ironically, the response of anti-evolutionists to such discoveries is frequently to claim that things have only gotten worse for evolution. Where previously there had been just one gap, as a result of the transitional fossil there are now two (one on either side of the newly discovered specimen).

As word of the relationship between the eubacterial flagellum and the TTSS has begun to spread among the "design" community, the first hints of a remarkably similar reaction have emerged. The TTSS only makes problems worse for evolution, according to this response, because now there are two irreducibly complex systems to deal with. The flagellum is still irreducibly complex – but so is the TTSS. So now there are two systems for evolutionists to explain instead of just one.

Unfortunately for this line of argument, the claim that one irreducibly complex system might contain another is self-contradictory. To understand this, we need to remember that the entire point of the design argument, as exemplified by the flagellum, is that only the entire biochemical machine, with all of its parts, is functional. For the Intelligent Design argument to

stand, this must be the case, since it provides the basis for their claim that only the complete flagellum can be favored by natural selection, not any of its component parts.

However, if the flagellum contains within it a smaller functional set of components such as the TTSS, then the flagellum itself cannot be irreducibly complex – by definition. Since we now know that this is indeed the case, it is obviously true that the flagellum is not irreducibly complex.

A second reaction, which I have heard directly after describing the relationship between the secretory apparatus and the flagellum, is the objection that the TTSS does not tell us how either it or the flagellum evolved. This is certainly true, although Aizawa has suggested that the TTSS may indeed be an evolutionary precursor of the flagellum (Aizawa 2001). Nonetheless, until we have produced a step-by-step account of the evolutionary derivation of the flagellum, one may indeed invoke the argument from ignorance for this and every other complex biochemical machine.

However, in agreeing to this, one must keep in mind that the doctrine of irreducible complexity was intended to go one step beyond the claim of ignorance. It was fashioned in order to provide a rationale for claiming that the bacterial flagellum could not have evolved, even in principle, because it is irreducibly complex. Now that a simpler, functional system (the TTSS) has been discovered among the protein components of the flagellum, the claim of irreducible complexity has collapsed, and with it any “evidence” that the flagellum was designed.

THE COMBINATORIAL ARGUMENT

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 he 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 then offers his readers a calculation showing that the flagellum could not 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, 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 have been 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, 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 probably true for the amino acid sequences of the thirty or so protein components of the flagellum and the approximately twenty 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.

To the ID enthusiast, however, this is a point of little concern. According to Dembski, evolution still could not construct the thirty 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 argues 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 is possible (even if unlikely).

When Dembski turns his attention to the chances of evolving the thirty 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 chance 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, 301). Since the flagellum

requires thirty such proteins, he explains that thirty such probabilities “will all need to be multiplied to form the origination probability” (Dembski 2002a, 301). That would give us an origination probability for the flagellum of 10^{-1170} , far below the universal probability bound. The flagellum could not have evolved, and now we have the numbers to prove it. Right?

ASSUMING IMPOSSIBILITY

I have no doubt that to the casual reader, a quick glance over the pages of numbers and symbols in Dembski’s books is impressive, if not downright intimidating. Nonetheless, the way in which he 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 “[t]he Darwinian mechanism is powerless to produce irreducibly complex systems” (Dembski 2002a, 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 the flagellum could assemble spontaneously. Unfortunately for his argument, no scientist has ever proposed that the flagellum, or any other complex object, evolved in that way. Dembski, therefore, has constructed a classic “straw man” and blown 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 thirty 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 to 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, such as 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? What is the scientific method used to support such a conclusion? Could it be that their assertions of the lack of natural causes simply amount to an unsupported personal belief? Could it be that there are such causes but that they 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, 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, naturally, 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. Incredibly, this a priori reasoning is exactly the sort of logic upon which the new “science of 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 (Charlesworth 2002; Orr 2002; Padian 2002).

DESIGNING THE CYCLE

In assessing the design argument, therefore, it only *seems* as though two distinct arguments have been raised for the unevolvability of the flagellum. In reality, those two arguments, one invoking irreducible complexity and the other specified complex information, both depend upon a single scientifically insupportable position – namely, that we can look at a complex biological object and determine with absolute certainty that none of its component parts could have been first selected to perform other functions. Now the discovery of extensive homologies between the type III secretory system and the flagellum has shown just how wrong that position was.

When anti-evolutionary arguments featuring the bacterial flagellum rose to prominence, beginning with the 1996 publication of *Darwin’s Black Box* (Behe 1996a), they were predicated upon the assertion that each of the protein components of the flagellum was crafted, in a single act of design, to fit the specific purpose of the flagellum. The flagellum was said to be unevolvable because the entire complex system had to be assembled first in order to produce any selectable biological function. This claim was broadened to include all complex biological systems, and to assert further that science would never find an evolutionary pathway to any of these systems. After all, it hadn’t so far, at least according to one of the principal advocates of “design”:

There is no publication in the scientific literature – in prestigious journals, specialty journals, or books – that describes how molecular evolution of any real, complex, biochemical system either did occur or even might have occurred. (Behe 1996a, 185)

As many critics of intelligent design have pointed out, that statement is simply false. Consider, as just one example, the Krebs cycle, an intricate biochemical pathway consisting of nine enzymes and a number of cofactors that occupies center stage in the pathways of cellular metabolism. The Krebs cycle is "real," "complex," and "biochemical." Does it also present a problem for evolution? Apparently it does, according to the authors of a 1996 paper in the *Journal of Molecular Evolution*, who wrote:

"The Krebs cycle has been frequently quoted as a key problem in the evolution of living cells, hard to explain by Darwin's natural selection: How could natural selection explain the building of a complicated structure in toto, when the intermediate stages have no obvious fitness functionality? (Melendez-Hevia, Wadell, and Cascante 1996)

Where Intelligent Design theorists threw up their hands and declared defeat for evolution, however, these researchers decided to do the hard scientific work of analyzing the components of the cycle and seeing if any of them might have been selected for other biochemical tasks. What they found should be a lesson to anyone who asserts that evolution can act only by direct selection for a final function. In fact, nearly all of the proteins of the complex cycle can serve different biochemical purposes within the cell, making it possible to explain in detail how they evolved:

In the Krebs cycle problem the intermediary stages were also useful, but for different purposes, and, therefore, its complete design was a very clear case of opportunism. . . . the Krebs cycle was built through the process that Jacob (1977) called "evolution by molecular tinkering," stating that evolution does not produce novelties from scratch: It works on what already exists. The most novel result of our analysis is seeing how, with minimal new material, evolution created the most important pathway of metabolism, achieving the best chemically possible design. In this case, a chemical engineer who was looking for the best design of the process could not have found a better design than the cycle which works in living cells. (Melendez-Hevia, Wadell, and Cascante 1996)

Since this paper appeared, a study based on genomic DNA sequences has confirmed the validity of its approach (Huynen, Dandekar, and Bork 1999). By contrast, how would Intelligent Design have approached the Krebs cycle? Using Dembski's calculations as our guide, we would first determine the amino acid sequences of each of the proteins of the cycle, and then calculate the probability of their spontaneous assembly. When this is done, an origination probability of less than 10^{-400} is the result. Therefore, applying "design" as a predictive science would have told both groups of researchers that their ultimately successful studies would have been fruitless, since the probability of spontaneous assembly falls below the "universal probability bound."

We already know, however, the reason that such calculations fail. They carry a built-in assumption that the component parts of a complex

biochemical system have no possible function beyond serving the completely assembled system itself. As we have seen, this assumption is false. The Krebs cycle researchers knew better, of course, and were able to produce two important studies describing how a real, complex, biochemical system might have evolved – the very thing that design theorists once claimed did not exist in the scientific literature.

THE FAILURE OF DESIGN

It is no secret that concepts like "irreducible complexity" and "Intelligent Design" have failed to take the scientific community by storm (Forrest 2002). Design has not prompted new research studies, new breakthroughs, or novel insights on so much as a single scientific question. Design advocates acknowledge this from time to time, but they often claim that this is because the scientific deck is stacked against them. The Darwinist establishment, they say, prevents them from getting a foot in the laboratory door.

I would suggest that the real reason for the cold shoulder given "design" by the scientific community – particularly by life science researchers – is that time and time again its principal scientific claims have turned out to be wrong. Science is a pragmatic activity, and if your hypothesis doesn't work, it is quickly discarded.

The claim of irreducible complexity for the bacterial flagellum is an obvious example of this, but there are many others. Consider, for example, the intricate cascade of proteins involved in the clotting of vertebrate blood. This has been cited as one of the principal examples of the kind of complexity that evolution cannot generate, despite the elegant work of Russell Doolittle (Doolittle and Feng 1987; Doolittle 1993) to the contrary. A number of proteins are involved in this complex pathway, as described by Behe:

When an animal is cut, a protein called Hagemann factor (XII) sticks to the surface of cells near the wound. Bound Hagemann factor is then cleaved by a protein called HMK to yield activated Hagemann factor. Immediately the activated Hagemann factor converts another protein, called prekallikrein, to its active form, kallikrein. (Behe 1996a, 84)

How important are each of these proteins? In line with the dogma of irreducible complexity, Behe argues that each and every component must be in place before the system will work, and he is perfectly clear on this point:

[N]one of the cascade proteins are used for anything except controlling the formation of a clot. Yet in the absence of any of the components, blood does not clot, and the system fails. (Behe 1996a, 86)

As we have seen, the claim that every one of the components must be present in order for clotting to work is central to the "evidence" for design. One of

those components, as these quotations indicate, is factor XII, which initiates the cascade. Once again, however, a nasty little fact gets in the way of Intelligent Design theory. Dolphins lack factor XII (Robinson, Kasting, and Aggeler 1969), yet their blood clots perfectly well. How can this be, if the clotting cascade is indeed irreducibly complex? It cannot, of course, and therefore the claim of irreducible complexity is wrong for this system as well. I would suggest, therefore, that the real reason for the rejection of "design" by the scientific community is remarkably simple – the claims of the Intelligent Design movement are contradicted time and time again by the scientific evidence.

THE FLAGELLUM UNSPUN

In any discussion of the question of "Intelligent Design," it is absolutely essential to determine what is meant by the term itself. If, for example, the advocates of design wish to suggest that the intricacies of nature, life, and the universe reveal a world of meaning and purpose consistent with an overarching, possibly Divine, intelligence, then their point is philosophical, not scientific. It is a philosophical point of view, incidentally, that I share, along with many scientists. As H. Allen Orr pointed out in a recent review:

Plenty of scientists have, after all, been attracted to the notion that natural laws reflect (in some way that's necessarily poorly articulated) an intelligence or aesthetic sensibility. This is the religion of Einstein, who spoke of "the grandeur of reason incarnate in existence" and of the scientist's religious feeling [that] takes the form of a rapturous amazement at the harmony of natural law. (Orr 2002).

This, however, is not what is meant by "Intelligent Design" in the parlance of the new anti-evolutionists. Their views demand not a universe in which the beauty and harmony of natural law has brought a world of vibrant and fruitful life into existence, but rather a universe in which the emergence and evolution of life is expressly made impossible by the very same rules. Their view requires that behind each and every novelty of life we find the direct and active involvement of an outside Designer whose work violates the very laws of nature that He had fashioned. The world of Intelligent Design is not the bright and innovative world of life that we have come to know through science. Rather, it is a brittle and unchanging landscape, frozen in form and unable to adapt except at the whims of its designer.

Certainly, the issue of design and purpose in nature is a philosophical one that scientists can and should discuss with great vigor. However, the notion at the heart of today's Intelligent Design movement is that the direct intervention of an outside designer can be demonstrated by the very existence of complex biochemical systems. What even they acknowledge

is that their entire scientific position rests upon a single assertion – that the living cell contains biochemical machines that are irreducibly complex. And, they assert, the bacterial flagellum is the prime example of such a machine.

Such an assertion, as we have seen, can be put to the test in a very direct way. If we are able to find contained within the flagellum an example of a machine with fewer protein parts that serves a purpose distinct from motility, the claim of irreducible complexity is refuted. As we have also seen, the flagellum does indeed contain such a machine, a protein-secreting apparatus that carries out an important function even in species that lack the flagellum altogether. A scientific idea rises or falls on the weight of the evidence, and the evidence in the case of the bacterial flagellum is abundantly clear.

As an icon of the anti-evolutionist movement, the flagellum has fallen.

The very existence of the type III secretory system shows that the bacterial flagellum is not irreducibly complex. It also demonstrates, more generally, that the claim of "irreducible complexity" is scientifically meaningless, constructed as it is upon the flimsiest of foundations – the assertion that because science has not yet found selectable functions for the components of a certain structure, it never will. In the final analysis, as the claims of Intelligent Design fall by the wayside, its advocates are left with a single remaining tool with which to battle against the rising tide of scientific evidence. That tool may be effective in some circles, of course, but the scientific community will be quick to recognize it for what it really is – the classic argument from ignorance, dressed up in the shiny cloth of biochemistry and information theory.

When three leading advocates of Intelligent Design were recently given a chance to make their case in an issue of *Natural History* magazine, they each concluded their articles with a plea for design. One wrote that we should recognize "the design inherent in life and the universe" (Behe 2002), another that "design remains a possibility" (Wells 2002), and the third "that the natural sciences need to leave room for design" (Dembski 2002b). Yes, it is true. Design does remain a possibility, but not the type of "Intelligent Design" of which they speak.

As Darwin wrote, there is grandeur in an evolutionary view of life, a grandeur that is there for all to see, regardless of their philosophical views on the meaning and purpose of life. I do not believe, even for an instant, that Darwin's vision has weakened or diminished the sense of wonder and awe that one should feel in confronting the magnificence and diversity of the living world. Rather, to a person of faith it should enhance the sense of the Creator's majesty and wisdom (Miller 1999). Against such a backdrop, the struggles of the Intelligent Design movement are best understood as clamorous and disappointing double failures – rejected by science because they do not fit the facts, and having failed religion because they think too little of God.

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