

Kenneth Miller refutes Intelligent Design - or does he?

(Biologist Kenneth Miller is an important ID opponent. He is interviewed widely on ID and was an important expert witness in the Kansas ID trial. Below are Miller's criticisms of two main arms of Intelligent Design theory Michael Behe's Irreducible Complexity and William Dembski's Complex Specified Information. *Comments on Miller's criticisms and why they fail to persuade are included in italics.* I strongly suggest viewing the half hour Quick Time video of the Japanese Team who unravelled the molecular construction of the flagellum on <http://www.nanonet.go.jp/english/mailmag/2004/files/011a.wmv> or at least the 2 minute version at <http://www.arn.org/docs/mm/flagellarassembly-1.mov>)

The full text of Miller's argument may be found at <http://www.millerandlevine.com/km/evol/design2/article.html>

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.

(Miller admits that there are many molecular cellular complexes for which no detailed theoretical evolutionary origin has been proposed.)

By asserting that the flagellum 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 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.

(This is a false deduction from Irreducible Complexity. IC does not forbid subsets of components of molecular machines being utilised in other molecular machines. IC simply asserts that there are multiple interacting components, the individual parts of which have no independent function.)

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.

Molecular studies of proteins in the Type Three Secretory System of some bacteria have revealed that the proteins of the TTSS are exactly the same as the proteins in the base portion of the bacterial flagellum.

It is now clear that a smaller subset of the full complement of proteins in the flagellum makes up the functional transmembrane portion of the TTSS. The TTSS is a truly valuable biochemical machine.

From the evolutionary point of view, this relationship is hardly surprising.

(It is also not surprising to ID theorists. It indicates that one subset of the Flagellum structure is useful in another context. This is what happens with human designs. It supports rather than refutes Intelligent

Design.)

According to the doctrine of irreducible complexity, however, this should not be possible.

(The use of the word "doctrine" is to taint ID as a religious concept.)

The existence of the TTSS demonstrates that a small portion of the "irreducibly complex" flagellum can carry out an important biological function. Since such a function is clearly favoured 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.

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.

The flagellum contains within it a smaller functional set of components, the TTSS, so the flagellum itself cannot be irreducibly complex by definition. It is obviously true that the flagellum is not irreducibly complex.

Until we have produced a step-by-step account for the evolutionary derivation of the flagellum, one may indeed invoke the argument from ignorance for this and every other complex biochemical machine.

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 couldn't 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.

(IC was constructed to provide clear examples of why Darwin's slow small steps could not function to evolve the bacterial flagellum. The TTSS is a useful machine using a definite subset of the structures in the flagellum. There is no agreement amongst biologists which came first, the TTSS or the flagellum. This does not explain at all why Miller believes without evidence that the flagellum or the TTSS arose by slow small steps. We simply have two giant leaps instead of one. The logic of IC does not forbid the use of functional multiple protein complexes that are subsets of molecular machines being utilised as parts of other molecular machines. This is exactly what intelligent agents do.)

On Dembski Miller writes

Dembski offers a calculation showing that the flagellum could not have possibly have evolved and therefore possess what he calls Complex Specified Information (SCI).

According to Dembski, evolution could 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."

Mathematically, if a sequence of events, such as a presumed evolutionary pathway, has a calculated probability less than 10 to the power of -150, we may conclude that the pathway is impossible.

Estimating 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 to the power of -300, since there are 20 amino acids specified by the genetic code.

Dembski, however, concedes that proteins (*may not necessarily*) need not get the exact amino acid sequence right in order to be functional, so he cuts the odds to just 20 or 30 (*essential unique amino acids in sequence*), which reduces the improbability (*for the spontaneous formation of one protein*) to about 10 to the power of -39 (Dembski 2002a, 301).

Since the flagellum requires 30 such proteins, Dembski explains (*uncontroversially*) that 30 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 to the power of -1170, far below the universal probability bound. The flagellum couldn't have evolved, and now we have the numbers to prove it. Right?

The way in which Dembski calculates the probability of an evolutionary origin for the flagellum shows how little biology actually stands behind those numbers.

By treating the flagellum as a discrete combinational object he has shown that it is unlikely (impossible) that the parts flagellum could assemble spontaneously.

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 blown it away with an irrelevant calculation.

(On the other hand, no scientist has ever proposed any feasible detailed scenario for how any complex object evolved.)

The scientific problem with his calculations is almost too easy to spot. By treating the flagellum as a discrete combinational object he has shown only that it is unlikely that the parts flagellum could assemble spontaneously.

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.

(Miller accuses Dembski of building straw dummies. Miller's insistence that ID states with "absolute certainty that none of its component parts could have been first selected" is a straw dummy. The universal probability bound is not Dembski's concoction. A probability below 10 to the power of -150 is impossible not just improbable. Miller fails to realise that the necessary existence of only 4 interacting specified protein

sequences of 30 amino acids for any process would cross the universal probability bound. No reputable biologist argues that any form of life as we know it could conceivably exist without at least a few hundred specified proteins. Miller feels that the existence of TTSS, which has around 10 highly specified proteins interacting to perform a process useful to natural selection falsifies ID. Note though that the generous probability of even the TTSS arising without design is 10 to the power of -390, or in other words absolutely impossible.

Dr Dembski has been criticised for "not being a scientist - only a mathematician". Mathematics is the mother of physics. Miller uses clever words to make the impossible seem possible. Unfortunately for him, probability theory is no respecter of persons.)