THE COUNTER-CREATIONISM HANDBOOK

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win's black box, the biochemical challenge to evolution" by Michael Behe. http://www.don-lindsay-archive.org/creation/behe.html; Miller, K.R. 1999. *Finding Darwin's God*, Chap. 5; Shanks, N., and K.H. Joplin. 1999. Redundant complexity. http://www.asa3.org/ASA/topics/Apologetics/POS6-99ShenksJoplin.html; TalkOrigins Archive. n.d.b. Irreducible complexity and Michael Behe. http://www.talkorigins.org/faqs/behe.html; Ussery, D. 1999. A biochemist's response to "The biochemical challenge to evolution." http://www.cbs.dtu.dk/staff/dave/Behe.html.

CB200.1: Bacterial flagella are irreducibly complex.

Bacterial flagella and eukaryotic cilia are irreducibly complex (see CB200). *Since nonfunctional intermediates cannot be preserved by natural selection, these systems can only be explained by intelligent design.* (Behe 1996a, 59–73)

1. This is an example of argument from incredulity (see CA100) because irreducible complexity can evolve naturally (see CB200). Many of the proteins in the bacterial flagellum or eukaryotic cilium are similar to each other or to proteins for other functions. Their origins can easily be explained by a series of gene duplication events followed by modification and/or co-option, proceeding gradually through intermediate systems different from and simpler than the final flagellum.

One plausible path for the evolution of flagella goes through the following basic stages (keep in mind that this is a summary, and that each major co-option event would be followed by long periods of gradual optimization of function):

a. A passive, nonspecific pore evolves into a more specific passive pore by addition of gating protein(s). Passive transport converts to active transport by addition of an ATPase that couples ATP hydrolysis to improved export capability. This complex forms a primitive type III export system.

b. The type III export system is converted to a type III secretion system (T3SS) by addition of outer membrane pore proteins (secretin and secretin chaperone) from the type II secretion system. These eventually form the P- and L-rings, respectively, of modern flagella. The modern type III secretory system forms a structure strikingly similar to the rod and ring structure of the flagellum (Blocker et al. 2003; Hueck 1998).

c. The T3SS secretes several proteins, one of which is an adhesin (a protein that sticks the cell to other cells or to a substrate). Polymerization of this adhesin forms a primitive pilus, an extension that gives the cell improved adhesive capability. After the evolution of the T3SS pilus, the pilus diversifies for various more specialized tasks by duplication and subfunctionalization of the pilus proteins (pilins).

d. An ion pump complex with another function in the cell fortuitously becomes associated with the base of the secretion system structure, converting the pilus into a primitive protoflagellum. The initial function of the protoflagellum is improved dispersal. Homologs of the motor proteins MotA and MotB are known to function in diverse prokaryotes independent of the flagellum.

e. The binding of a signal transduction protein to the base of the secretion system regulates the speed of rotation depending on the metabolic health of the cell. This imposes a drift toward favorable regions and away from nutrient-poor regions, such as those found in overcrowded habitats. This is the beginning of chemotactic motility.

f. Numerous improvements follow the origin of the crudely functioning flagellum. Notably, many of the different axial proteins (rod, hook, linkers, filament, caps) originate by duplication and subfunctionalization of pilins or the primitive flagellar axial structure. These proteins end up forming the axial protein family.

The eukaryotic cilium (also called the eukaryotic flagellum or undulipodium) is fundamentally different from the bacterial flagellum. It probably originated as an outgrowth of the mitotic spindle in a primitive eukaryote (both structures make use of sliding microtubules and dyneins). Cavalier-Smith (1987; 2002) has discussed the origin of these systems on several occasions.

2. The bacterial flagellum is not even irreducible. Some bacterial flagella function without the L- and P-rings. In experiments with various bacteria, some components (e.g., FliH, FliD [cap], and the muramidase domain of FlgJ) have been found helpful but not absolutely essential (Matzke 2003). One third of the 497 amino acids of flagellin have been cut out without harming its function (Kuwajima 1988). Furthermore, many bacteria have additional proteins that are required for their own flagella but that are not required in the "standard" well-studied flagellum found in *E. coli*. Different bacteria have different numbers of flagellar proteins (in *Helicobacter pylori*, for example, only thirty-three proteins are necessary to produce a working flagellum), so Behe's favorite example of irreducibility seems actually to exhibit quite a bit of variability in terms of numbers of required parts (Ussery 1999).

Eukaryotic cilia are made by more than 200 distinct proteins, but even here irreducibility is illusive. Behe (1996a) implied and Denton (1986) claimed explicitly that the common 9 + 2 tubulin structure of cilia could not be substantially simplified. Yet functional 3 + 0 cilia, lacking many microtubules as well as some of the dynein linkers, are known to exist (K. R. Miller 2003, 2004).

3. Eubacterial flagella, archebacterial flagella, and cilia use entirely different designs for the same function. That is to be expected if they evolved separately, but it makes no sense if they were the work of the same designer.

Further Reading: Dunkelberg, P. 2003. Irreducible complexity demystified. http://www.talkdesign.org/faqs/icdmyst/ICDmyst.html; Matzke, N. J. 2003. Evolution in (brownian) space. http://www.talkdesign.org/faqs/flagellum.html; Musgrave, I. 2000. Evolution of the bacterial flagella. http://www.health.adelaide.edu.au/Pharm/Musgrave/essays/flagella.htm; Ussery, D. 1999. A biochemist's response to "The biochemical challenge to evolution." http://www.cbs.dtu.dk/staff/dave/Behe.html.

with Nicholas Matzke

CB200.2: Blood clotting is irreducibly complex.

The biochemistry of blood clotting is irreducibly complex, indicating that it must have been designed. (Behe 1996a, 74–97)

1. The blood clotting systems appears to be put together by using whatever long polymeric bridges are handy. There are many examples of complicated systems made from components that have useful but completely different roles in different components. The co-opting of parts with different functions gets around the "challenge" of irreducible complexity evolving gradually.