

No waves of intelligent design

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In PNAS, Phillips (1) attempts to explore the evolution of dynein, a major motor protein of the eukaryotic cytoskeleton, using different hydrophobicity scales, and comes to several dramatic conclusions. The results of this analysis are taken to indicate that self-organized criticality (SOC) is integral to evolutionary optimization, that evolution of all proteins occurs, primarily, via positive selection, that this pervasive positive selection is shaped by “water waves” traveling along proteins, and even that the optimization in protein evolution stems from intelligent design. However, the actual observations reported in the article do not appear to support or even to be compatible with any of these far-reaching conclusions.

What the paper effectively reports, is the existence of relatively long-range patterns of hydrophobicity in proteins, particularly, in dyneins. These patterns show periodicity, especially, in the heptad repeat regions that form coiled structures in the dynein stalks (2). The appearance of periodic hydrophobicity patterns in repetitive protein structures, certainly, is not surprising; furthermore, self-similarity, or fractal properties, are necessarily discernible in such structures. Such self-similarity brings the analogy to SOC (3), leading to the suggestions that SOC is the “magic wand” of protein physics and evolution (4). Generally, however, the presence of such patterns is a natural consequence of the structural organization of proteins, whereby certain proportions and quasi-periodic distributions of hydrophobic and hydrophilic amino acid residues are essential for the formation of individual structural elements, such as β -sheets and α -helices, and for globular domain folding (5). Ultimately, the patterns of amino acid residue distribution and, accordingly, hydrophobicity were shaped by selection. Does this, however, refute the neutral theory of molecular evolution and imply pervasive positive

selection? Not at all. The simplest argument against this interpretation is the conservation of the structures and, accordingly, the hydrophobicity patterns of numerous proteins across hundreds of millions and even billions of years of evolution. Dynein, in particular, is conserved in all eukaryotes and retains the key structural elements and underlying sequence motifs throughout 1.5 billion years or so since the last common eukaryotic ancestor (6); hence the conservation of the hydrophobicity patterns that is apparent, in particular, in plots shown by Phillips (1). There is no reason to believe that the patterns of hydrophobicity in protein sequences are maintained by positive selection for functionally important “water waves” as opposed to the well-characterized purifying selection eliminating mutations that perturb the protein fold and hence are deleterious. Moreover, neutral evolutionary processes, in the form of constructive neutral evolution, can provide for the emergence of complex domain architectures, such as that of dynein, as well as multimeric protein complexes (7–9). Positive selection leading to functional innovations is rare in the evolution of most proteins, especially, highly conserved ones, such as dynein.

In summary, it is unfortunate when observations on simple patterns in biological sequences are overinterpreted to overthrow the fundamental tenets of evolutionary biology. Invoking intelligent design in an attempt to buttress unjustified generalizations on evolution is non sequitur writ large.

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The authors declare no competing interest.

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