National Center for Science Education

Defending the Teaching of Evolution in the Public Schools

Issue 16 (Volume 5, Number 2 - Summer 1985) http://www.ncseweb.org/resources/articles/4661_issue_16_volume_5_number_2_4_10_2003.asp

Creation/Evolution

— page 1 —

New Proteins Without God's Help William M. Thwaites

Creationists seem to be proud of their calculations that supposedly show how thermodynamics and probability prevent the chance formation of biologically useful macromolecules such as enzymes. Their "evidence" usually consists of quotations from such authors as Hubert P. Yockey, who agrees that catalytically active proteins cannot occur by chance. Yockey (1977a and b), looking at fully evolved proteins, says that their information content is too high for their chance formation.

Creationists do their own calculations to show that the chance formation of biologically useful proteins is impossible. These calculations almost always involve the erroneous assumption that each of the many amino acid positions in a protein must be filled by the one particular amino acid suitable for that position. Since there are twenty different amino acids available for each position, the chance of randomly getting a string of 200 amino acids all in the right order is $(1/20)^{200}$. If you plug this expression into a calculator, it will tell you that it equals essentially zero. Thus, the creationists say, you can't get such a protein by a chance ordering of amino acids. As Duane Gish of the Institute for Creation Research (ICR) put it (1976), "The time required for a single catalytically active protein molecule to arise by pure chance would be billions of times the assumed age of the earth."

But proteins, even modern highly evolved specialized proteins, are not built with that degree of specificity. What's more, many proteins show in their structure that they were built of smaller subunit sequences of amino acids (Doolittle, 1981) or they have a simple metalo-organic core that could have functioned alone as a primitive precursor of today's complex enzyme. So the creationist calculations give an answer of zero probability because the creationists make at least two major errors in their assumptions: they assume a degree of specificity that has not been shown to exist in real proteins, and they insist that newly formed proteins must be as efficient as their older and highly evolved counterparts.

We've been trying to explain all this to the protein "experts" at ICR for the last seven years. We have told them that new proteins could indeed form from the random ordering of amino acids. We have warned them that their calculations were based on faulty assumptions and soon someone would document the natural formation of a new protein from the random association of amino acids.

Now it has happened! Not one, but two, new proteins have been discovered. In all probability new proteins are forming by this process all the time, but this seems to be the first documentation of this phenomenon. The newly discovered proteins are enzymes that break down some of the byproducts produced during nylon manufacture. Since nylon first came into commercial production in 1940, we know that the new enzymes have formed since that time.

When the enzymes were first discovered about 1975 (Kinoshita, *et al*, 1981), it was at first thought the new enzymes arose through the modification of preexisting enzymes that had similar functions. To test this notion, the discoverers looked to see if the other enzymes in the same organism would react to antibodies made against the new enzymes. But by this criterion the new enzymes were unique. Antibodies against them found nothing similar with which to react among the array of other enzymes in the organism.

Again it was reasoned that if the new enzymes were just old enzymes with minor changes to allow digestion of nylon byproducts, they should retain at least a slight amount of activity with their original substrates. But the new enzymes had no activity on biologically derived molecules having similar chemical structures. So, by this attribute as well, the new enzymes were seen to be unique.

It seemed that if the new enzymes were indeed derived from randomly ordered amino acids, they would be very inefficient compared to the usual highly evolved enzyme, since the new enzymes would not have had billions of years of natural selection to reach a pinnacle of biological perfection. It has been shown that one of the new enzymes (the linear oligomer hydrolase) has about 2% of the efficiency demonstrated by three other enzymes that perform similar reactions with biologically derived substrates (Kinoshita, *et al*). Thus, by this criterion, as well as the others, the enzyme appears to be newly formed.

— page 3 —

More recently, another analysis (Ohno, 1984) added further evidence that at least one of the proteins was formed from an essentially random sequence of amino acids. This evidence is a little bit more difficult to understand since its comprehension involves some understanding of how the genetic code works. I'll just have to refer readers who do not have this background to an explanation such as Suzuki, *et. al*, 1976. It appears that the DNA that formed the gene was somewhat unusual since it could be "read" without finding a "stop" word in any of the three "reading frames." It can be shown that such DNA sequences could easily occur through the well-known process of duplication. The DNA sequence suggests that a simple "frame-shift" mutation could have brought about the chance formation of at least this one enzyme. "Frame-shift" mutations are known for forming totally new and essentially random arrays of amino acids since the code is "read" in a new reading frame. Usually the proteins that are formed by frame-shift mutations are totally useless sequences of amino acids that have no structural, antigenic, or enzymatic relationship to the original protein. This time, however, the new protein was useful. Being useful, it was retained by natural selection and was

finally discovered by biochemists who noticed a bacterium that could live on industrial waste.

All of this demonstrates that Yockey (1977a and b), Hoyle and Wickramasinghe (1981), the creationists (Gish, 1976), and others who should know better are dead wrong about the near-zero probability of new enzyme formation. Biologically useful macromolecules are not so information-rich that they could not form spontaneously without God's help. Nor is help from extraterrestrial cultures required for their formation either. With this information in hand, we can wonder how creationists can so dogmatically insist that life could not have started by natural processes right here on earth.

References

Doolittle, R. 1981. "Similar Amino Acid Sequences: Chance or Common Ancestry?" *Science* 214:149-159.

Gish, D. 1976. "The Origin of Life: Theories on the Origin of Biological Order." *ICR Impact* #37.

Hoyle, F., and N. C. Wickramasinghe. 1981. Evolution from Space. J. M. Dent, London.

Kinoshita, S., T. Terada, T. Taniguchi, Y. Takene, S. Masuda, N. Matsunaga, H. Okada. 1981. "Purification and Characterization of 6-Aminohexanoic-Acid-Oligomer Hydrolase of *Flavobacterium sp.* K172." European Journal of Biochemistry 116:547-551.

Ohno, S. 1984. "Birth of a Unique Enzyme from an Alternative Reading Frame of the Preexisted, Internally Repetitious Coding Sequence." *Proceedings, National Academy of Sciences* 81:2421-2425.

Suzuki, D. T., A. J. F. Griffiths, R. C. Lewontin. 1976. *An Introduction to Genetic Analysis*. W. H. Freeman and Co., San Francisco.

Yockey, H. P. 1977a. "A Calculation of the Probability of Spontaneous Biogenesis by Information Theory." *Journal of Theoretical Biology* 67:377-398.

Yockey, H. P. 1977b. "On the Information Content of Cytochrome c." Journal of Theoretical Biology 67:345-376.

Dr. Thwaites is a professor of biology at San Diego State University where he conducts a two-model creation-evolution course. He has debated creationists on various occasions.

© Copyright 1985 by William M. Thwaites