

NEWS AND VIEWS

by Paul Nelson

A FACE ONLY A PALEOANTHROPOLOGIST COULD LOVE

Michael Anderson, "Fleshing out the Past: Reconstructing Fossil Faces," *Discovery* Vol. 22 (1): 11-15, 1990.

Observers and skeptics of paleoanthropology have noted that theories of human origins often seem to reflect the biases of the investigators, or prevailing intellectual fashions (Lewin, 1987), and that the theories deliver conclusions rather more certain than the scanty data at hand would really support. "Paleoanthropology reveals more about how humans view themselves," argued David Pilbeam (1978: 379), "than it does about how humans came about."

For instance, how (one might wonder) do anatomists reconstruct the faces of extinct species, known only as fossils, with -- obviously -- no preservation of soft tissues? (That such reconstructions can differ widely is well-known: witness the history of the treatment of Neanderthal fossils.) Michael Anderson (Museum Preparator, Peabody Museum of Natural History, Yale) critically surveys the two most commonly used methods of reconstruction -- the "skin-depth" method and the "anatomical" method -- and recounts his own experience employing both methods. Despite its apparent objectivity, the skin-depth method, Anderson argues, is seriously flawed:

On first examination, the skin-depth procedure is most appealing because it applies averaged data to the skull using standardized formulas and procedures to reconstruct the face. This standardization of the procedure seems to insure that any bias on the part of the sculptor will be controlled. Therefore, it appears more objective than "freely" sculpting the muscles and facial structures on the skull.

Later, my confidence in this method was shaken on several counts. While learning the procedure in a program of Medical Illustration at the University of Illinois at Chicago, I saw a photograph of what six students had produced, after each had reconstructed identical casts of the same human skull. All six used the same data and standardized formulas and procedures leading one to expect very similar reconstructions. The results, however, were quite dissimilar, a situation that raised questions about the objectivity of the method. The quality of the reconstruction

appeared to be based more on the sculptural ability of the person making the reconstruction than on the objectivity of the procedure. (p. 13)

A second problem with the skin-depth method stems from the skin-depth data themselves: "I could not duplicate my measurements on the same face on second measurement" (p. 13). These and other shortcomings with the skin-depth method have led Anderson to prefer the anatomical method:

By carefully following muscle origin and insertion lines and assessing the physical qualities and functional necessities of each skull, I believe an accurate reconstruction can be accomplished. (p. 14)

"The critical assessment of these methods," concludes Anderson (p. 14) "is possible only through direct application of the procedures and subsequent comparison and evaluation of the results." As Anderson suggests, if one finds a significant disparity in the appearance of reconstructions attempted by preparators working independently, but employing the same method, that disparity should count as evidence against the objectivity of the method.

Now *there's* an experiment we'd like to see: give the same skull to several preparators, tell them to use the anatomical method, and see what the results look like. Interested, Michael Anderson?

REFERENCES

Lewin, Roger. 1987. *Bones of Contention*. New York: Simon & Schuster.

Pilbeam, David. 1978. Book Review. *American Scientist* 66: 378-379.

MORE PROBLEMS WITH THE MOLECULAR CLOCK

Michael J. Behe, "Histone deletion mutants challenge the molecular clock hypothesis," *Trends in Biochemical Science* 15: 374-376, October 1990.

Early in the development of the molecular clock hypothesis, it was discovered that not all proteins "ticked" at the same rate. When compared across a range of species, the fibrinopeptides, for instance, were much "faster clocks" (i.e., having a higher rate of amino acid

substitution) than the very conservative, "slowly ticking" histones. These differences, writes Michael Behe (Chemistry, Lehigh University),

required a modification to the clock hypothesis: the postulate of functional constraints. Thus, for example, histone H4 would diverge less rapidly than fibrinopeptides if a larger percentage of H4 amino acid residues were critical for the function of the molecule. (p. 374)

The problem with the notion of functional constraint, Behe argues, is an absence of experimental support:

Although plausible, it has long been realized that no direct experimental evidence has been obtained 'showing rigorously that histone function is especially sensitive to amino acid substitution or that fibrinopeptide function is especially insensitive to amino acid substitution.' (p. 374)

"Recent experiments," writes Behe, "now indicate that the key assumption of functional constraints may not be valid."

Since the histones are so highly conserved -- "the H4 sequence of the green pea differs from that of mammals by only two conservative substitutions in 102 residues" -- one might expect that "few, if any, substitutions could be tolerated in the H4 sequence" (p. 374). However, experiments (reported in detail by Behe) have shown that large parts of the histone molecule may be deleted without significantly affecting the viability of the organism (in this instance, yeast) -- results which, Behe argues, should trouble defenders of the molecular clock hypothesis:

[The experimental] results pose a profound dilemma for the molecular clock hypothesis: although the theory needs the postulate of functional constraints to explain the different degrees of divergence in different protein classes, how can one speak of 'functional constraints' in histones when large portions of H2A, H2B and H4 are dispensable for yeast viability? And if functional constraints do not govern the accumulation of mutations in histones, how can they be invoked with any confidence for other proteins? (p. 375)

The resolution of the dilemma, Behe contends, must "as far as possible be grounded in quantitative, reproducible experiments, rather than in simple correlations with time that are its current basis" (p. 375). Otherwise, he concludes:

[T]he time-sequence correlation may end up as a curiosity, like the tracking of stock market prices with headline heights, where correlation does not imply a causal relationship.