

Notes and Comments

A Comment on: The Recognition and Evaluation of Homoplasy in Primate and Human Evolution. (Lockwood, C.A., and J.G. Fleagle, 1999, *Yrbk Phys Anthropol* 42:189–232.)

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In my professional experience, the *Yearbook of Physical Anthropology* has been an extremely useful outlet for publications in biological anthropology and a very handy source of information, especially since the association conceived of its use to publish significant summaries of key topics. However, responding to a Yearbook article is possible only in the journal, and it is for this reason that I note here a troublesome misrepresentation of my work in the 1999 Yearbook.

In it, Lockwood and Fleagle (1999, p. 224) made the following argument, reviewing a series of debates that took place in Fleagle's own journal, *Evolutionary Anthropology*, as part of their discussion about the uses and misuses of homoplasy.

Wolpoff (1994) criticized Tattersall's (1994) view that Neandertals and humans are different species and have distinct evolutionary trajectories because several similarities between Neandertals and humans would be forced to evolve in parallel. Tattersall (1996) retorted with statements that "Neanderthal-like" characters should be expected in some modern human populations, like the early humans from Europe, because Neandertals and humans are closely related, and homoplasy among their populations is likely to be common. Therefore homoplasy is a weak argument against a recent origin of humans, who then replaced Neandertals in Europe. Wolpoff (1997) later reversed his position on homoplasy, deciding that it could be used to support a multiregional argument for human evolution. His view was that homoplasy is so probable in closely related organisms that cladistic definitions of modern humans (tending to exclude Neandertals) cannot be trusted.

I have never "reversed" my position on homoplasy, and it is hard to understand where this assertion about my "reversed" position came from. The higher occurrence of homoplasies between closely related species makes a cladistic approach difficult to apply at this level of phylogenetic resolution, because it relies on the parsimonious assumption that homology is the most probable cause of identity. Nevertheless, multiple homoplasies and parallel patterns of anatomical changes are still improbable, even between closely related species, and the interpretation that such similarities can be explained as homoplasy is even more questionable when there is no compelling reason to believe that the populations being compared were reproductively isolated. This is why I have supported multiregional evolution with the argument that the alternative explanation, of geographic differentiation and different regional continuities involving different distinct human species, is improbable because it requires the interpretation that there were numerous homoplasies and parallel evolutionary trends (Wolpoff and Caspari, 1996). To cite a few examples, why should there be a high incidence of the H-O mandibular foramen form and the combination of both large frontal and maxillary sinuses in European Neandertals and Aurignacian/Pavlovians, but nowhere else in the world? Why should the malar notch and upper central incisor shoveling involving a strong marginal ridge and straight crown face evolve twice in China? Why should a strong lateral frontal trigone appear only in the Ngandong Indonesians and Pleistocene Native Australians? In australopithecine species, the homoplasies are, for the most part, in functional systems, whereas for the

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above-mentioned similarities and many others, the features are nonadaptive. The point is that recognizing that homoplasies are relatively more common among closely related species does not make homoplasy the most persuasive explanation for so many similarities, and there is no way to construe my stance as being that multiregional evolution is supported by the untrustworthiness of cladistic definitions of modern humans that exclude Neandertals.

It is true and Lockwood and Fleagle are absolutely correct to say that I think cladistic definitions of modern humans cannot be trusted, but that is not a reversal of opinion. In fact, it is hardly surprising and would be the case whether or not modern humans are a unique species. I am certainly not the first to note that phylogenetics defines *relationships*, not *species*. Modern humans are not an evolutionary entity of any sort, and they cannot be defined beyond the description that modern humanity means all living people and their immediate ancestors (Wolpoff and Caspari, 1997). But even if they were an evolutionary entity, it remains the case that there can be no cladistic definition of modern humans, or of any other species or subspecies. In any event, long before this debate began, I showed that modern humans cannot be defined without including Neandertals, unless that definition does not include all modern humans, which would make no sense (Wolpoff, 1986). This, however, is a statement about *variation* and not about homoplasy, which is an explanation of *similarity*.

Moreover, one place this alleged "reversal" of my position certainly did *not* come from is the article cited. This article was mostly about the identification of homoplasy and the problems raised by homoplasy in australopithecine phylogenetics, where its debilitating effects are well recognized and continue to create havoc, as expressed in the low consistency indexes for the various phylogenetic schemes. The few comments I made about homoplasy in Pleistocene human evolution are detailed here.

In spite of all of the difficulties that homoplasies have created in establishing the pattern of relationship between closely related hominid species, there are paleoanthropologists who insist on using the same cladistic techniques to *establish the pattern of relationships of populations within one—ours!* But using cladistics within our species is plagued with even more problems than the analysis of closely related species. Many more sources of similarities than homoplasies also do not reflect the pattern of descent, because human populations are not isolated and constantly branching, as are species (Wolpoff, 1997, p.8).

I have left intact the italics and bold-face type I placed in the manuscript as submitted, although these were removed from the publication during the editorial process. Perhaps they would have helped avoid this misinterpretation by emphasizing that this part of the discussion was about variation within a species, which I have long argued cannot be described in terms of homology and homoplasy, a position also reflected in the Lockwood and Fleagle article.

I, for one, think the debates with Tattersall have been quite useful, and I regret other authors stumbling into what Tattersall and I have successfully avoided, the mischaracterization of the positions represented in the ongoing discussion between us. This cannot possibly serve to clarify the issues at stake, but will confuse them, which is an unfortunate accomplishment for an article reviewing the topic.

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