

Humans as second orangutans: sense or nonsense?

A reminder of what the molecular data indicate, and why they can't be ignored or dismissed

Extraordinary claims require extraordinary evidence – or so I was taught as a student. But it sometimes appears as if papers making sensational claims can get published with rather less than compelling evidence, especially if said claims are likely to result in attention from the popular press. An apparent example comes from the *Journal of Biogeography*, with the recent publication of a paper making the astonishing claim that humans are actually more closely related to orangutans than, as (nearly) universally accepted, to chimpanzees.⁽¹⁾

The authors of this study carried out phylogenetic analyses of selected morphological and fossil characters and found a closer relationship of humans with orangutans, rather than with chimpanzees. I do not feel qualified to comment on the adequacy of their analyses, except to note that previous analyses of fossil characters have followed the genetic evidence in grouping humans with chimpanzees,^(2,3) so presumably this new result will be a bone of contention amongst paleoanthropologists. But how do the authors reconcile this result with molecular genetic evidence, going back 40 years now, that unequivocally indicate that African apes (specifically, chimpanzees) are our nearest living relatives?

The authors identify what they consider to be four problematic aspects of the molecular genetic evidence. First, they claim that homoplasy (i.e., parallel changes in independent lineages, or reversal within a lineage) and alignment problems (in particular, how to account for insertions and deletions necessary to align sequences of different lengths) can render phylogenetic analyses of DNA sequence data inaccurate. But no specific examples are given as to how homoplasy and/or alignment problems could possibly have resulted in an erroneous conclusion of a human-chimpanzee relationship. Moreover, neither homoplasy nor alignment issues are expected to have any impact over the time scales in question; in particular, there is no ambiguity in aligning coding sequences among the species in question, and phylogenetic analyses of both mtDNA and nuclear DNA coding sequences unequivocally support the human-chimpanzee relationship.^(4,5) So, this is a red herring.

Second, the authors criticize molecular genetic analyses of human-chimpanzee relationships for having “extremely limited” outgroup sampling. In fact, the studies cited by the authors would be regarded by most as having more than

adequate outgroup sampling, and again the authors cannot point to any molecular genetic study which has suggested anything other than a human-African ape relationship, regardless of which species were included as outgroups. Moreover, one can frame this question as a four-taxon problem, without any outgroup. There are three possible unrooted trees for the four species in question (Fig. 1A–C); which is supported by the data?

The answer, of course, is unequivocally the tree that has an internal branch separating orangutans and gorillas from humans and chimpanzees (Fig. 1C). And, note that no matter how one roots this tree, one will not get an orangutan-human relationship out of it (Fig. 1D). So this is another red herring.

Third, the authors chastise molecular genetic studies as uninformative regarding a human-chimpanzee *versus* human-orangutan relationship if they either fail to include the orangutan, or only include it as an outgroup to study African ape-human relationships. No argument here – except to note that the failure of most recent molecular genetic studies to address a human-orangutan alternative to the accepted human-chimpanzee relationship indicates that this question is considered fully answered and hence not worthy of further attention.

Fourth, the authors claim that inconsistencies between molecular and morphological phylogenies should not necessarily be rejected in favor of molecules, and that “. . . molecular similarities between humans and chimpanzees . . . must represent to some (large) extent unidentified primitive retentions. . .” What sort of mechanism might possibly lead to such “unidentified primitive retentions,” and why this phenomenon should only affect human and chimpanzee DNA, is left unspecified.

Even more egregious than the above vague claims made about DNA sequence data is the complete failure of the authors to realize that there is another class of molecular markers that is particularly informative for investigating phylogenetic relationships. These are Short INterspersed



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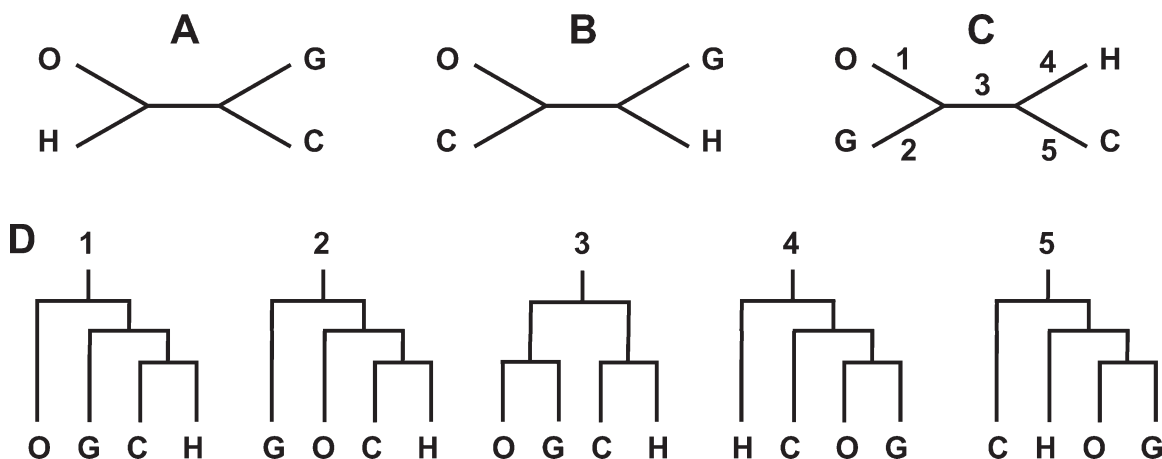


Figure 1. The three possible unrooted trees for four species **A–C**; O – orangutan, H – human, C – chimpanzee, G – gorilla. The molecular genetic evidence overwhelmingly favors tree C. There are five possible branches (numbered 1–5) in tree C to which an outgroup can potentially attach, thereby producing a rooted tree. The corresponding five possible rooted trees are shown in **D**; note that none of them produce an orangutan-human grouping.

Elements (SINEs), which evolve by the insertion of copies from a master element into new locations in the genome. Since the probability is negligible that independent insertion events would occur between exactly the same two base pairs, parallel changes involving SINEs should be extremely rare. And, since subsequent deletions of inserted elements hardly ever occur, and if they do they leave behind a signature of the original insertion event (either part of the SINE remains, or some of the flanking sequence is also deleted), reversals involving SINEs should also be extremely rare. Thus, SINEs are expected to behave as perfect phylogenetic characters, and indeed actual data support this expectation,^(6,7) although inconsistencies between SINEs in a phylogeny are occasionally observed, because of interspecies hybridization events or ancestral lineage sorting.⁽⁸⁾ For phylogenetic analyses, then, SINEs are about as good as it gets.

And what do SINEs tell us about human-orangutan *versus* human-chimpanzee relationships? The most comprehensive such study⁽⁹⁾ found 33 SINEs that were shared by gorillas, humans, and chimpanzees (but not orangutans), and 7 SINEs that were shared by humans and chimpanzees (but not gorillas). There were no SINEs shared exclusively by humans and orangutans – all SINEs shared by humans and orangutans were also present in gorillas and chimpanzees, and hence represent insertion events that happened in an ancestor of orangutans, African apes, and humans. To be sure, there was one inconsistency in the phylogeny in that one SINE was shared by humans and gorillas, but not chimpanzees, but this probably reflects sorting of ancestral lineages during the relatively short period encompassing the diver-

gence of gorillas, humans, and chimpanzees.⁽⁹⁾ In sum, analyses of SINEs agree with DNA sequence data by convincingly demonstrating a human-chimpanzee relationship, and providing no evidence whatsoever for the human-orangutan alternative.

So what are we to make of the claims of an orangutan-human relationship based on morphological characters? If such claims are substantiated, for even a few morphological characters, then the obvious answer would be that morphology does not always indicate phylogeny. The extent to which genes, physiology, and environment act and interact to influence these morphological characters is completely unknown – what is classified as the same morphological character in two different species may easily reflect different genetic changes. To take just one example, enamel thickness is cited as a trait linking orangutans with humans (both having thick enamel) and chimpanzees with gorillas (both having thin enamel).⁽¹⁾ However, more detailed three-dimensional studies of molar enamel reveals a far more complicated situation involving variability in the three-dimensional, whole crown distribution of enamel thickness that is not at all captured in a simple thin *versus* thick enamel classification.^(10,11) In sum, there is no reason to expect that morphological characters are necessarily good phylogenetic characters.

It is thus ironic that the authors attempt to discredit the molecular data as reflecting large amounts of homoplasy, when in fact morphological characters are much more likely to reflect homoplasy. But it is a pity that the authors chose to interpret their data as indicating an orangutan-human

phylogenetic relationship, as such an outrageous claim all but guarantees that the paper will be dismissed outright as nonsense by many, when in fact convergence between humans and orangutans for any morphological character may be of some biological interest, precisely because such convergence cannot reflect phylogeny.

Finally, what are we to make of the fact that a paper whose arguments about the relative value of molecular genetic *versus* morphological evidence for phylogenetic analyses can be so readily dismissed gets published in a peer-reviewed, scientific journal? An accompanying editorial⁽¹²⁾ offers the illuminating insight that the paper "... comments on a topic of such keen general interest and therefore may well gain wide attention in the scientific and popular press." That it did, as the journal's website proudly points to coverage of the paper in *The New Scientist*. The editors also admit that although the reviewers were not convinced by the paper, nevertheless it "... was felt to be a contribution worth putting out to the test of further scientific scrutiny," even though "... this perspective might superficially appear to be nonsensical to the majority of molecular anthropologists and systematists..." Yes, sometimes the conventional wisdom is overturned, and alternative views do deserve to be heard – but if publication in a peer-reviewed journal is to have any meaning at all, editors and reviewers have a responsibility to ensure that well-established contributory evidence is not dismissed in a superficial way.

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