

# Pitfalls reconstructing the last common ancestor of chimpanzees and humans

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The morphological nature of the last common ancestor (LCA) of chimpanzees/bonobos and humans is a fascinating topic in human evolution. Available evidence suggests that both lineages share a LCA that lived in Africa ~8–6 Myr. However, the hominoid fossil record of this time period is inadequate, prompting the use of novel methodological approaches to reconstruct the anatomy of this key ancestor. In a recent example, Young et al. (1) claim that “fossil hominin shoulders support an African ape-like last common ancestor of humans and chimpanzees.” Although I applaud these authors for implementing novel comparative methods to paleoanthropology, fundamental aspects of the experimental design were disregarded, leading to biased conclusions. Herein I provide constructive criticisms on that study, also addressing recurrent pitfalls in the field, to help redirect future research on human paleobiology.

First, the biological meaning of the shape data in the Young et al. (1) analysis is unclear. Procrustes superimposition allows one to elegantly size-adjust data to analyze pure shape. However, Young et al. use allometric residuals as their input data without demonstrating the existence of a common allometric trend in the sample, predicting a significant amount of scapular shape variation. This can fail to correctly identify individuals of the same shape at different size, producing misleading results (2). Later, Young et al. (1) argue that scapular differences between *Pan* and *Gorilla* are associated with body size, undermining the assumption about their “allometrically adjusted” data. Second, Young et al. favor a *Pan*-like LCA even though their results show that *Pan* and *Homo* evolved in opposite directions along the major axis of shape variation (PC1; figure 2 E and F in ref. 1). Third, the linear

evolutionary model from *Pan* into humans relies solely on the intermediate position (in PC1) of a “simulated” *Australopithecus afarensis* adult, based on the “Dikika baby” (~3-y-old at death). However, one of these authors has previously shown that an actual *A. afarensis* adult falls within the human and orangutan variation (figure 2B in ref. 3). Furthermore, this simulated Dikika adult is—like humans—more similar to *Nasalis* than to African apes (figure 2D and table S1 in ref. 1; incongruent with figure S5 in ref. 1). Fourth, Young et al. do not actually test alternative models of evolution (see a formal test including convergence in ref. 4). Instead, they only compare the morphometric lengths of two phylogenetic trees on morphospace. Fifth, all branches in their trees were unfoundedly assumed to have equal length, forcing a punctuated model of evolution (change being independent of time, contrary to their own conclusions), and disregarding the molecularly established branch lengths of most species in their sample (Fig. 1). Some of these pitfalls are also noted by Melillo (5), who further highlighted functional aspects preserved in the scapula of “Kadanuumuu,” an adult specimen of *A. afarensis*.

Perhaps the most relevant message of the study was overlooked: *Homo* and *Pan* share ~99% of their genes, even given their remarkable phenotypic differences (resulting from gene regulation), demonstrating that phylogenetic proximity does not predict phenotypic evolution. Thus, if indeed the LCA exhibited a *Pan*-like scapula, given the mosaic nature of ape and human evolution and that other anatomical regions reveal alternative stories (4, 6), this study (1) highlights even more the complexity of reconstructing the LCA's mosaic anatomy.

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