

Comparisons of Frogs, Humans, and Chimpanzees

Lorraine M. Cherry, Susan M. Case, Joseph G. Kunkel and Allan C. Wilson
(*Science* 204:434-435.)

Evolutionary biology is in need of a yardstick or metric with which to measure morphological evolution in creatures as diverse as frogs and mammals. Two types of metric have been suggested to measure morphological distance, one based on quantal traits and the other on quantitative traits. Quantal traits are those whose state varies and is scored as 0 or 1 (presence or absence of a tongue). Quantitative traits are those whose state varies continuously (length of leg) and in this case the degree of difference between states is measured quantitatively.

Findley (1) recommends that quantal traits be used for comparing the magnitude of the morphological difference between humans and chimpanzees with that between frogs. He chooses six quantal traits such that the state in *Xenopus* differs from that in *Rana*, whereas the state in humans is identical to that in chimpanzees (1). We present a counter list of six quantal traits, for which the opposite result is obtained. For these traits, chimpanzees and humans differ, whereas *Xenopus* and *Rana* are the same. Table I records the results of comparing additional pairs of species with respect to the 12 traits. Frogs belonging to different species, genera or families are identical for all 12 of the traits, confirming the hypothesis that phenotypically chimpanzees differ more from humans than one frog family differs from another.

Most numerical taxonomists, however, would argue that 12 quantal traits are too few for an adequate test. As chimpanzees and humans are reported to differ by at least 312 quantal traits (2), it occurred to us to invite Findley to try to come up with a similar number of quantal traits by which *Xenopus* and *Rana* could be distinguished. An exercise like this could be entertaining, but it might not have scientific value. We are not convinced that it is valid to use quantal traits for estimating overall degree of morphological difference between species. Our skepticism stems chiefly from considering the problem of how to avoid bias in the picking of quantal traits. This problem is illustrated by the contrasting results obtained in the above example. Depending on which of the two sets of six traits one picks, the chimpanzee human

difference seems either small or evolution (6) large relative to the *Xenopus Rana* difference.

We feel that quantitative traits may be more appropriate than quantal traits for obtaining reliable estimates of morphological distance. It is well known from studies of quantitative genetics that such linear traits usually exhibit continuous variation in genetic tests. Furthermore, in our own morphological work with hundreds of species (3, 4), every quantitative trait examined varies in length both within and among species. Variability within a particular taxonomic group is therefore not a criterion for choosing among quantitative traits.

Cherry *et al.* (1) have developed a morphological distance metric based on quantitative traits from all major parts of the body. The metric is monotonically related to traditional zoological estimates of phenotypic distance among frogs (3). Findley (1) seems to have overlooked the significance of this empirical demonstration of the utility of the metric based on quantitative traits.

Regardless of the approach preferred, it seems from the information already available that, relative to differences among frog families the morphological difference between humans and chimpanzees is large. However, at the protein sequence level, the chimpanzee-human difference is very small by frog standards. As pointed out before, species within a genus of frogs usually differ far more from each other in their protein sequences than do humans from chimpanzees (3, 5). Thus morphological evolution and protein sequence evolution can proceed at contrasting rates. This contrast has important implications for our understanding of the mechanism of

LORRAINE M. CHERRY

Biochemistry Department, University of California, Berkeley 94720, and

Biology Department, San Diego State University, San Diego, California 92182

SUSAN M. CASE

Museum of Comparative Zoology, Harvard University, Cambridge, Massachusetts 02138

JOSEPH G. KUNKEL

Department of Zoology, University of Massachusetts, Amherst 01002

ALLAN C. WILSON

Biochemistry Department, University of California, Berkeley

References and Notes

1. J. S. Findley, *Science* 204, 434 (1979).
2. A. Keith, thesis, University of Aberdeen (1894); *Nature (London)* 85, 508 (1911).
3. L. M. Cherry, S. M. Case, A. C. Wilson, *Science* 200, 209 (1978).
4. L. M. Cherry, S. M. Case, J. G. Kunkel, J. S. Wyles, A. C. Wilson, in preparation.
5. M.-C. King and A. C. Wilson, *Science* 188, 107 (1975).
6. We thank R. L. Cann and V. M. Sarich for discussion.

Table 1. Morphological comparisons for 12 quantal traits. The traits examined include the six listed by Findley (1) and the following six: cranium (ethmoid meets or does not meet parietal); upper jaw (premaxilla fused or unfused to maxilla); lower jaw (simian shelf present or absent); ribs (number of pairs, 13 or less than 13); pelvis (sciatic notch present or absent); and foot (first digit opposable or non-opposable).

Species compared	Number of traits different
<i>Primates</i>	
Human versus chimpanzee	6
<i>Frogs</i>	
Different suborders	
<i>Xenopus</i> versus <i>Rana</i>	6
Different families	
<i>Hyla</i> versus <i>Rana</i>	0
Different genera	
<i>Hyla</i> versus <i>Acris</i>	0
Different species	
<i>Hyla regilla</i> versus <i>eximia</i>	0