

Approximation of a biological species constant?

Sir, — Morphological variability is a characteristic of biological species, in both extant and extinct taxa. As a working hypothesis, I propose that quantification of such variability through morphometric analyses, based on least-squares regression analysis of measurements of conspecific pairs of specimens, can be used to approximate a biological species constant.

As demonstrated by Thackeray *et al.*,¹ the degree of variability between any two specimens of the same species can be expressed by comparing measurements of specimen A (*x*-axis) and conspecific specimen B (*y*-axis). Variables can include cranial dimensions of the kind used previously.¹ In such comparisons, there is usually little scatter around the regression line associated with the equation of the form $y = mx + c$, where m is the slope of the regression line. The limited scatter is directly associated with similarity in shape of the two specimens. The degree of scatter around the regression line is quantified by the standard error of the m -coefficient ($s.e._m$). The $s.e._m$ value for pairs of conspecific specimens is relatively low. By contrast, when measurements of two specimens (C and D) representing different species are compared, there is a greater degree of scatter around the regression line, and the $s.e._m$ value is relatively high.² The high degree of scatter

around the regression line is a direct reflection of differences in the morphology of specimens C and D. The slope is a function of variability in size.³

Of special interest is the distribution of $s.e._m$ values obtained from pairwise comparisons of extant conspecific pairs of specimens. Thackeray *et al.*¹ showed that there is a lognormal distribution of $s.e._m$ values when pairwise comparisons are made between conspecific specimens of extant vertebrates including mammals (such as rodents, ungulates and primates), birds (such as hornbills and eagles), and reptiles (such as lizards) as well as extant invertebrates (e.g. coleoptera and lepidoptera). In an extended study (using a larger sample including *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus* in addition to *Homo sapiens*), $\log s.e._m$ values tend to be centrally distributed around a mean $\log_{10} s.e._m$ value of -1.61 , with a standard deviation of 0.23 ($n = 1424$ specimens, including both vertebrates and invertebrates).

For vertebrates alone, the mean $\log s.e._m$ value is -1.61 ± 0.23 ($n = 1252$ specimens), not significantly different from the mean value of -1.66 ± 0.20 calculated for invertebrates ($n = 172$ specimens).

I propose as a working hypothesis that when comparisons are made between any two specimens of the same species, $\log s.e._m$ approximates a 'biological species constant' ($T = -1.61$) across evolutionary time and geographical space. The value 1.61 is an approximation of the so-called 'Golden Ratio', which is expressed in many ways in nature, as recognized by, for example, the Pythagoreans, Euclid and Leonardo da Vinci.⁴

The advantage of the approach out-

lined here is that the mean $\log s.e._m$ value of -1.61 ± 0.23 essentially provides a definition of a species based on morphometric analyses. It facilitates the assessment of probabilities of conspecificity between any two fossils, including hominids of the kind from both South and East Africa,⁵ recognising that there is morphological variability in both time and space, and recognising also that there are not necessarily clear boundaries between species in space or time.^{6,7}

I thank R. Catchpole, P. Knox-Shaw and H. Thackeray for comments on an earlier draft of the manuscript. Funding has been provided from the National Research Foundation and the Embassy of France in South Africa.

1. Thackeray J.F. *et al.* (1997). Probabilities of conspecificity: application of a morphometric technique to modern taxa and fossil specimens attributed to *Australopithecus* and *Homo*. *S. Afr. J. Sci.* **93**, 195–196.
2. Aiello L.C., Collard M., Thackeray J.F. and Wood B.W. (2000). Assessing exact randomization-based methods for determining the taxonomic significance of variability in the human fossil record. *S. Afr. J. Sci.* **96**, 179–183.
3. Thackeray J.F., Helbig J. and Moss S. (1995). Quantifying morphological variability within extant mammalian species. *Palaeont. afr.* **32**, 23–25.
4. Livio M. (2002). *The Golden Ratio: The Story of Phi, The World's Most Astonishing Number*. Broadway Books, New York.
5. Thackeray J.F. (1997). Probabilities of conspecificity. *Nature* **390**, 30–31.
6. Thackeray J.F. (2006). Reconceptualization of African hominins dated between 1.5 and 2.5 mya. *Ann. Transv. Mus.* **43**, 116–117.
7. Thackeray J.F. (2006). Darwin, South Africa and the emergence of the genus *Homo*. *Trans. R. Soc. S. Afr.* **61**, 127–130.

J.F. Thackeray

Human Origins and Past Environments programme, Transvaal Museum, P.O. Box 413, Pretoria 0001, South Africa. E-mail: mrspl@global.co.za