

COMPARISONS BETWEEN *AUSTRALOPITHECUS SEDIBA* (MH1) AND OTHER HOMININ TAXA, IN THE CONTEXT OF PROBABILITIES OF CONSPECIFICITY

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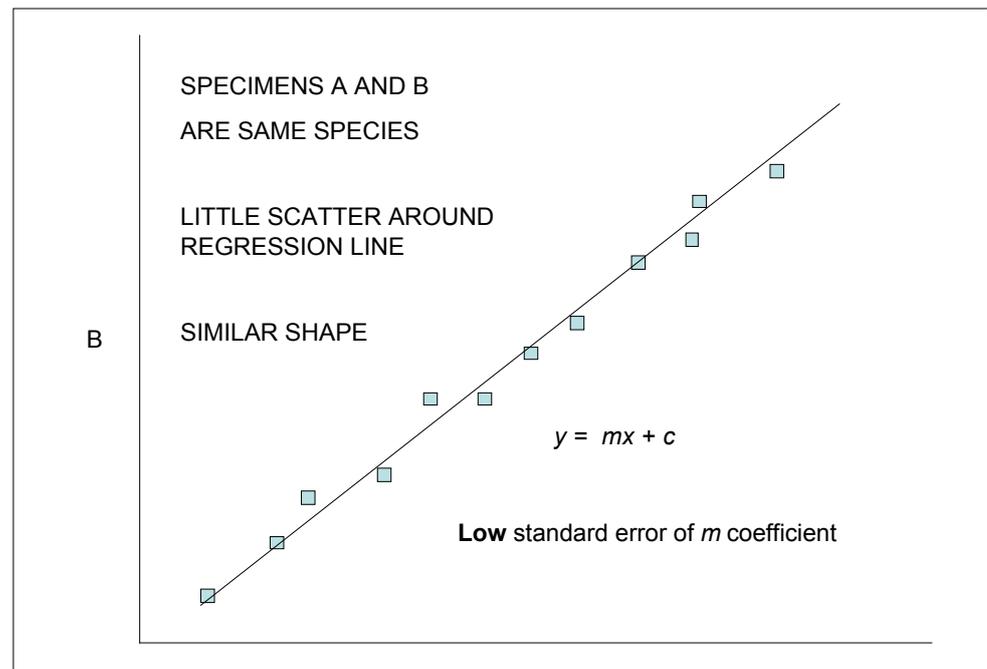
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Berger et al.¹ report the remarkable discovery of two hominin specimens (MH1 and MH2) attributed to a new species, *Australopithecus sediba*, dated to almost 2 million years ago, from the Malapa site in South Africa. They present cranial data for MH1 that can be compared with corresponding measurements for other Plio-Pleistocene hominin taxa using least-squares regression analysis, as illustrated in Figure 1. In the study discussed here, results are presented to show degrees of similarity between MH1 and other hominin species.



When two specimens of the same species are compared, limited scatter is expected, associated with a relatively low standard error of the m -coefficient (SEM).

FIGURE 1

Generalised relationship between measurements of a reference specimen, such as *Australopithecus sediba* (MH1), and those of another specimen, expressed in terms of a general equation of the form $y = mx + c$, where m is the slope and c is the intercept

In pairwise comparisons of linear dimensions, using MH1 as the reference specimen, the slope m in the least-squares linear regression equation $y = mx + c$ is associated with variability in size (measurements for MH1 being associated with the x -axis). However, the log-transformed value of the standard error of the m co-efficient (log SEM) is a measure of the degree of scatter around the regression line and relates to variability in shape, as compared to a reference specimen. Limited scatter around the regression line occurs when two specimens belong to the same species. Under such circumstances, the log SEM values are relatively low. By contrast, a higher degree of scatter around the regression line (and relatively high log SEM values) generally occur when two specimens representing different species (with different shapes) are compared.

The log SEM statistic can be used to assess probabilities of conspecificity relative to data obtained from cranial comparisons for modern pairs of specimens belonging to the same vertebrate species.² As shown in Figure 2, log SEM values approximating $-1.610 (\pm 0.23)$ are associated with a high probability of two specimens belonging to the same species and have been used as the basis for a statistical definition of a species expressed in terms of probabilities.³

Results of comparisons between MH1 and other taxa are presented in Table 1. High probabilities of conspecificity are obtained when MH1 is compared not only to *Australopithecus africanus* (log SEM = -1.425) but also to *Homo habilis* (log SEM = -1.520). Furthermore, on the basis of cranial data presented by Berger et al.¹ for *A. africanus* and *H. habilis*, the log SEM value of -1.606 , obtained from the comparison between these two taxa, is almost identical to the mean log SEM value of -1.610 obtained from the comparison of conspecific pairs of vertebrate taxa.³

The question arises as to whether certain specimens attributed to *A. africanus* (including Sts 5 from Sterkfontein, dated to 2.15 million years ago) and other (younger) specimens attributed to *H. habilis* (including OH 24 from Olduvai Gorge dated to 1.8 million years ago), as well as MH1 and MH2 from Malapa (dated between 1.8 and 1.95 million years ago), are part of a spectrum of variability in geographical

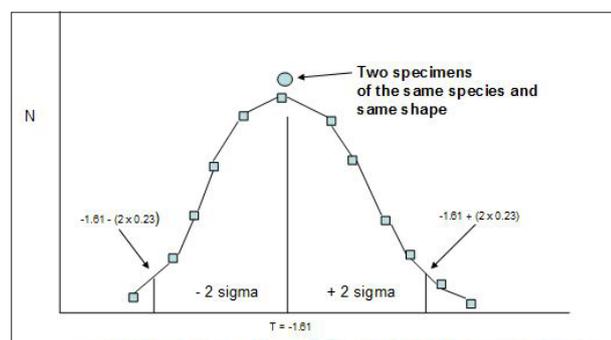
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TABLE 1

Log-transformed values of the standard error of the m -coefficient (log SEM) in least-squares linear regression analyses associated with the equation $y = mx + c$, using *Australopithecus sediba* (MH1) as the reference specimen (x-axis), compared to other Plio-Pleistocene African hominins

Species to which MH1 is compared	Log SEM
<i>Homo habilis</i>	-1.520
<i>Australopithecus africanus</i>	-1.425
<i>African Homo erectus/ergaster</i>	-1.419
<i>Homo rudolfensis</i>	-1.284
<i>Australopithecus robustus</i>	-1.161
<i>Australopithecus boisei</i>	-1.151
<i>Australopithecus afarensis</i>	-0.847

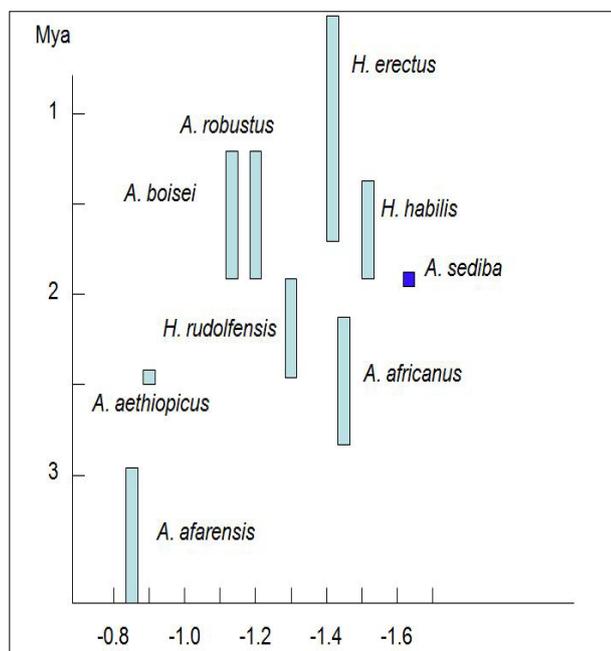
Log SEM values are arranged in ascending order, reflecting increasing degrees of dissimilarity with MH1.



A log normal distribution of SEM values is obtained for pairwise comparison of conspecific vertebrates and invertebrates, based on a study of extant species.²

FIGURE 2

Generalised distribution of log standard error of m (SEM) values obtained when measurements of two specimens of modern taxa are compared against each other using least-squares linear regression analysis



Source: Berger et al.¹

Note: Calculations are author's own.

A value of approximately -1.6 would be assumed for MH1 compared to other specimens of the same species, using modern conspecific vertebrate taxa as a frame of reference.²

T = log SEM, based on pairwise comparisons of conspecific specimens.

FIGURE 3

Log standard error of m (SEM) values for hominin taxa, based on comparisons with MH1 (holotype of *Australopithecus sediba*), plotted relative to the approximate time span of each species

space and time. Relative to MH1, *Homo rudolfensis* groups closely with *Australopithecus robustus* and *Australopithecus boisei*, which have low probabilities of conspecificity when compared to *A. sediba*. *Australopithecus afarensis* and *Australopithecus aethiopicus* cluster together, distinct from *A. sediba*, as expected for taxa that occur earlier in time and that are more distant in geographical space on the African continent.

Log SEM values for hominin taxa, based on comparisons with MH1 (holotype of *A. sediba*) are plotted relative to the approximate time span of each species in Figure 3. A log SEM value of approximately -1.6 is assumed for a comparison between MH1 and other specimens of the same species. In relation to the chronology of hominin species, log SEM values plotted in Figure 3 are not inconsistent with a hypothesis of a time-successive transition from *A. africanus* to early *Homo*, as an ancestor-descendant sequence.

MH1 and MH2, with a mosaic of characters, confirm the view that the transition from *Australopithecus* to *Homo* was part of a continuum of variability. Log SEM values (Table 1) confirm the lack of clear boundaries between Early Pleistocene hominin taxa and provide one way of assessing degrees of similarity and probabilities of conspecificity in the context of a spectrum of variability through geographical space and evolutionary time. Palaeoanthropologists are urged to seek a new paradigm for classifying and assessing variability in Plio-Pleistocene hominins, without relying on binomial nomenclature to classify specimens.

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