Likely Discontinuity Between Humans and Non-Human Hominins Based on Endocranial Volume and Body Mass With a Special Focus on *Homo naledi*—A Short Analysis

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Abstract

Encephalization is the perceived process of brain size increase during evolution. However, this process is oversimplified. Previous results from the analysis of the encephalization residual show that significant ER exists only for all members of the genus Homo, except for Homo naledi, but also for Australopithecus sediba and Australopithecus africanus. Analyzing the same data set, plotting mean endocranial volume as a function of mean body weight and applying Ward hierarchical clustering shows that six species of Homo segregate from two species of Homo, three species of Australopithecus, two species of Paranthropus, and Ardipithecus ramidus. These two species of Homo include Homo naledi and Homo habilis. This serves as further evidence supporting the idea that H. naledi should be classified as an ape and is non-human.

Keywords: Homo naledi, Australopithecus, endocranial volume, body mass, encephalization, baramin

Introduction

According to the popular concept of hominin evolution, endocranial volume (ECV) increases from more primitive species to more developed ones according to evolutionary time. This process is known as encephalization, and evolutionists claim that measurements for primate species is a proof of evolution (Matzke 2006). This concept however, is oversimplified, as in the case of the Neanderthals which have a larger ECV than *Homo sapiens* (Bruner, Manzi, and Arsuaga 2003). Furthermore, it has been shown that ECV also scales with body mass (Martin 1981).

Recently Wood (2016) analyzed ECV and body mass data for primates from data sets compiled by Isler et al. (2008), Schoenemann (2013) and De Miguel and Henneberg (2001). Here we must note that measurements of cranial capacity can be influenced by bias, and that the body mass measurements in these studies are also estimates, thus the results in this paper are tentative, contingent upon the accuracy of these estimates and measurements. In Figure 2 of his paper, Wood depicted the relationship between the log(ECV [cc]) value as a function of the log(body mass [g]) value based on a linear model (Wood 2016). Furthermore, it was found that the endocranial residual (ER) value, calculated as the difference between the expected and observed log(ECV) values followed a normal distribution, with a mean value of -8.3.10⁻¹⁸ and a standard deviation of 0.1194. Based on this normal distribution, different species could be shown to have a significant ER value if their value was either less than -0.234 or greater than 0.234 at the 2.5% level.

Homo naledi showed a non-significant ER value of 0.201, with a p-value of 0.046, due to a moderate body mass but an unusually small cranium. Also, Australopithecus africanus has a significant ER value of 0.201 (p=0.0079). The value of the analysis is that it shows that although there may be a smooth transition in ECV from Ardipithecus ramidus to Homo sapiens, ER increases much more abruptly than ECV, from A. africanus to H. sapiens, and then another abrupt increase before Homo sapiens/ neanderthalensis/heidelbergensis.

Results and Discussion

The mean ECV (cc) was plotted for 14 taxa taken from Wood's analysis (Wood 2016) as a function of mean body mass (kg). The results can be seen in Fig. 1. Clustering was performed using Ward's hierarchical clustering. As we can see, two or three clusters are visible, depending on how deep the cutoff is for the clustering. With two clusters, the first main cluster is made up of Homo sapiens, Homo neanderthalensis. Homo heidelbergensis+Homo rudolfensis, Homo erectus, and Homo ergaster. The second cluster is made up of Homo habilis, Homo naledi, Australopithecus sediba, Australopithecus africanus, Australopithecus afarensis, Paranthropus boisei, Paranthropus aethiopicus, and Ardipithecus ramidus. Using a Student's t-test, the p-value for the ECV values for the two clusters is 0.0023, which is highly significant even at the 1% level.

As to whether the first cluster can be split into two subclusters or not, the fact still remains that eight species, including *H. habilis*, *H. naledi*, and *A. sediba* both belong to the same cluster, at least

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Fig. 1. Mean endocranial volume of the 14 hominin species according to mean body mass from Table 1.

based on ECV and body mass. Therefore, baraminic discontinuity exists between these three species and humans in this aspect.

Despite the majority view of *H. naledi* being at the base of the genus Homo and possibly being a transition species between the genus Australopithecus and Homo, other views dissent. Jeffrey Schwartz, professor of anthropology at the University of Pittsburgh thinks that the fossil remains of H. naledi are a mixture of multiple species, based on differences in skull shape in three of the specimens (Callaway 2015). Also, a recent set of analyses based on Principal Component Analysis of 8-12 species of the original data set of Berger et al. (2015) by Neves, Bernardo, and Pantaleoni (2017) showed that H. habilis, H. naledi, and A. sediba belong to the same clade. In both studies, principal component 1 of 2 was influenced by cranial capacity, among other factors. It has been the majority creationist view that H. habilis was not human. For example, Lubenow refers to the remains of *H. habilis* being a mix of human and nonhuman fossils (Lubenow 2004). Interestingly, Young classified *H. habilis* as an australopithecine based on its encephalization (Young 2006). Thus, since *H. naledi* groups with *H. habilis*, then transitively, *H. naledi* is not human, if indeed *H. habilis* can be assumed to be an australopithecine.

There is the possibility that the fossil remains of H. naledi were pathological, although what kind of disease these H. naledi specimens may have been suffering from goes unnamed. However, all 15 remains of H. naledi found in the Dinaledi chamber showed the same set of unusual hominin features. Thus, it would be unlikely that all of the H. naledi individuals had the same malformities in the same bones.

Thus, based on results from previous analyses of *H.* naledi (O'Micks 2016, 2017a, 2017b), and also the fact that *H. naledi* clusters together with species from the genera Australopithecus and Paranthropus based on encephalization tendencies dependent on body mass give further support to the idea that *H. naledi* is not a member of the human holobaramin, but is rather a species of ape, most likely an australopithecine. While it is true that just because a hominin species has a small cranial capacity does not automatically mean that it is an ape or less intelligent, the converse is also true, namely that it cannot be assumed that if **Table 1.** Endocranial volume and mean body mass listed for several hominid species, columns 1–3 taken from Table 1 of Wood, 2016. The mean endocranial volume of *H. naledi* was updated to 545cc with the addition of the LES1 skull's ECV value of 610cc (Hawks et al. 2017).

Species	Mean Endocranial Volume (cc)	Mean Body Mass (kg)	Cluster No.
Aridipithecus ramidus	300	50	2
Australopithecus afarensis	419.5	30.4	2
Paranthropus aethiopicus	410	37.7	2
Paranthropus boisei	503.3	53.1	2
Australopithecus africanus	441.7	27.2	2
Australopithecus sediba	420	25.8	2
Homo naledi	545	42.8	2
Homo habilis	609.3	32.6	2
Homo rudolfensis	788.5	45.6	1b
Homo ergaster	800.7	58.3	1b
Homo erectus	960.1	63.4	1b
Homo heidelbergensis	1231.6	98.9	1a
Homo neanderthalensis	1391.4	84.5	1a
Homo sapiens	1463.8	64.7	1a

a species has a small cranial capacity, then it is not an ape. Baraminology is based on additive evidence (Wood and Murray 2003), meaning that we can add species to a core set of species only if we show continuity between the new species and the already existing set of species. As opposed to this, the present analysis shows *discontinuity* between *H. naledi* and human species based *not just* on endocranial volume but also on body weight, assuming that the measured values in the data set for brain size and body mass are accurate.

Materials and Methods

Mean ECV (cc) and mean body mass (kg) were taken from Table 1 of Wood (2016) for 14 hominin taxa. Euclidean distances were calculated for the data and clustering was performed using the hclust function using the Ward hierarchical clustering method. Calculations were done in R version 3.4.1.

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