Preliminary Baraminological Analysis of *Homo naledi* and its Place within the Human Baramin

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Abstract

Homo naledi is a sensational fossil find. To estimate its relationship to other human species from a creation perspective, two statistical baraminological analyses of craniodental characteristics were conducted using data from a published evolutionary study. In the first analysis, four *Australopithecus* and seven *Homo* species were included, resulted in weak separation into three clusters and two isolated species. In the second analysis, three *Paranthropus* species were added, but lack of matching data required removal of one species of *Australpithecus* and two of *Homo*; results were less resolved than in the first analysis. Neither data set was sufficient to demonstrate discontinuity among clusters conclusively. However, in both analyses *Homo naledi* appears continuous with and fits well within the cluster of *Homo* species, despite some *Australopithecus*-like characteristics. Comparison of postcranial traits further supports the results, as 8 out of 15 characteristics show exclusive similarity to humans compared with only three characteristics shared exclusively with australopithecines. Placement of *H. naledi* in the human baramin is supported. Since this is one of the first morphological dataset available for *H. naledi* and it includes only craniodental characteristics, further baraminological analysis is warranted.

Introduction

A find of about 1,500 fossils from 15 individuals of a human-like creature coming from the Rising Star cave system in South Africa has made news all over the world (Stringer 2015). The fossils have been given the name *Homo naledi*, after the Dinaledi Chamber of the cave system in which they were found. These fossils display both "derived" and "primitive" traits making them similar in some ways to humans but in other ways to australopithecines (Berger et al. 2015). The evolutionary status of early (pre-*erectus*) *Homo* has always been controversial (Antón et al. 2014), and researchers have made several attempts to find the root for this genus. With the discovery of a great wealth of *H. naledi* material, evolutionary biologists are hopeful that hominid relationships will become clearer.

Paleoanthropologists classify *H. naledi* within the genus *Homo*. This is because even though it has some *Australopithecus*-like ("primitive") characteristics, it also has a larger number of human-like characteristics as well as a number of unique morphological characteristics. The cranial volume of *H. naledi* is estimated to range from 465 cc to 560 cc. While this overlaps with the range of australopithecines, we must remember that *H. naledi* is thought of as a small-sized member of the genus *Homo*. Furthermore, these cranial values overlap (or possibly overlap) with a value measured for a *H. erectus* individual (Line 2013; Berger et al. 2015), which is considered to be a member of the human baramin (T.C. Wood 2010). Here it must also be stressed that due to lack of soft brain tissue and cultural evidence one cannot make any far-reaching inferences about the intelligence level of *H. naledi* (since only the actual inside brain structures and cells and the connections between them can give us more information on intelligence). Skull volume can also vary between 1,100 and 1,500 cc within humans (Taylor 1984), so this is not a very good measure of intelligence.

H. naledi does not count as the only example of a small-sized member of the genus *Homo*. More than a decade ago researchers found fossil remains of what seemed to be a small-sized hominin

on the island of Flores in Indonesia (outside the geographical range of the African australopithecines), called *Homo floresiensis* (Brown et al. 2004). *H. floresiensis* lacked the prognathic face and large postcanine tooth size typical of australopithecines (Line 2006). Tools for hunting, such as blades, were also found next to the original *H. floresiensis* remains, which are signs of intelligence (Morwood et al. 2004). Baab et al. (2013) believe that *H. floresiensis* is derived from *H. erectus*.

According to Berger et al. (2015), *H. naledi* is considered to be a small-sized human with human-like hands, feet, body mass and body stature. It is missing the well-developed sagittal crest characteristic of robust australopithecines, such as *A. garhi* and *Paranthropus*, but has a small supraorbital torus, small cranial capacity (characteristic of australopithecines) and sagittal keeling, which makes it unique compared to other species from the genus *Homo*. It also has smaller teeth, and a gracile mandible. Also unique to *H. naledi* is its relatively long thumb. Its upper limbs are shorter, which is characteristic of *Homo*, and its vertebrae resemble those of humans, but its shoulder configuration resembles that of australopithecines, with a distally wide rib cage. The maximum tibia length overlaps with the lower range of humans and the upper range of australopithecines.

A conventional date has yet to be determined for *H. naledi*. These fossils were only partially mineralized and hardly needed to be excavated (Dirks et al. 2015) which may suggest that the fossils are not that old.

The view of humans in creationist baraminology has changed substantially over the past decades. The circle of hominid species has increased to 28 (Wood 2013), so the question of what counts as human, and where to draw the line between human and non-human has become much more relevant. For example, *H. floresiensis* and Denisovans have been considered to be part of the human baramin (Wise 2005; Savanne 2014). One major work in this area by T.C. Wood (2010) analyzed eight data sets of other research groups, including dozens of species and specimens. Wood came to the conclusion that three controversial taxa, namely *H. habilis*, *H. rudolfensis*, and *A. sediba* are part of the human baramin. This was based on his analysis of a data set from Berger et al. (2010) showing a cluster of *Homo* species along with *A. sediba* in the MDS results. Members of this group (*Homo* + *A. sediba*) also are connected by significant, positive BDC results, and negative BDC results between *A. sediba* and species from the genus *Paranthropus*. The newly discovered species, *H. naledi* has also been placed within the human baramin along with other "early *Homo*" species, such as *H. habilis* and *A. sediba* according to Wood (2016).

However, other creationists objected to the placement of these three species into the human baramin. After all, the Wood study did not examine postcranial characteristics, whereas Berger et al. (2010) did, who actually described *A. sediba*, describing it as an australopithecine. Others (Line 2010; Menton et al. 2010) point out the fact that *A. sediba* has ape-like characteristics, such as its long forearms and fingers, small cranial capacity, and feet similar to australopithecines. However, as Wood (2011) pointed out, it is not clear as to why these characteristics that were chosen to distinguish *A. sediba* from *Homo* are the most relevant. Also, the classification of *H. habilis* and *H. rudolfensis* is also not so clear-cut; some evolutionists classify them as autralopithecines

(B. Wood 2014; B. Wood and Collard 1999; B. Wood and Baker 2011).

In a follow-up baraminological study, Wood (2013) analyzed five data sets containing postcranial characteristics of *A. sediba* and several other *Homo* and australopithecine species, such as hand characteristics. In all of the results, *A. sediba* was neither positively, nor negatively correlated with any other taxon, though in most of them, few species were used. Therefore his original result of placing *A. sediba* within the human baramin was not refuted decisively.

By analyzing multiple characteristics between *H. naledi* and other hominin species, my goal is to determine its place within the human baramin. Also can *H. naledi* possibly bridge the gap between human and non-human species? Furthermore, I examine whether continuous variables from craniodental measurements are consistent with previous results from hominin baraminology.

Methods

A set of 57 craniodental characteristics were retrieved from a paper describing the morphology of this new species in detail (Tables 1 and 2 from Berger et al. 2015) along with the following species: *Paranthropus aethiopicus*, *P. boisei*, *P. robustus*, *Australopithecus anamensis*, *A. afarensis*, *A. africanus*, *A. sediba*, *H. habilis*, *H. rudolfensis*, *H. erectus*, *H. sapiens*, *H. neanderthalensis*, and *H. heidelbergensis* making 14 species in total. A more detailed description of the characteristics that were coded in the Berger study can be found in B. Wood (1991). The three *Paranthropus* species were excluded from the first analysis because they possessed no characters that overlapped with *A. anamensis*, *H. neanderthalensis*, and *H. heidelbergensis*, which gave an error in the BDIST software which was used to do the analysis. However, in order to gain any possible extra insight about the relationship between the eleven species, the *Paranthropus* species were included in a second analysis, whereas the latter three were excluded.

The characters "closest approach of temporal lines" and "root of zygomatic process origin" from Berger et al. (2015) were coded as a "?" since they were either mixed discrete or integer values (former) or had range values (latter).

Since the measurement values in this data set were continuous, the data values were transformed to discrete values (where applicable) by modifying the standard feature-scaling equation in the following way:

$$x'_{i,j} = int\left(\frac{3.999\left(x_{i,j} - min_{j=1..n}\, x_{i,j}\right)}{\left(max_{j=1..n}\, x_{i,j} - min_{j=1..n}\, x_{i,j}\right)}\right) + 1$$

Here the data value $x_{i,j}$ was normalized and then multiplied by a factor of 3.999 in order to map it to a value between 0 and 3; a pseudocount of 1 maps the data value to a discrete value between 1 and 4. The transformed dataset is given in the appendix.

The data matrixes were then entered into the BDIST program at http://www.coresci.org/bdist.html (Robinson and Cavanaugh 1998; T.C. Wood 2005; T.C. Wood 2008) to obtain baraminic distance correlations, correlation graphs, probabilities, and bootstrap values. A relevance cutoff of 0.75 was selected for both
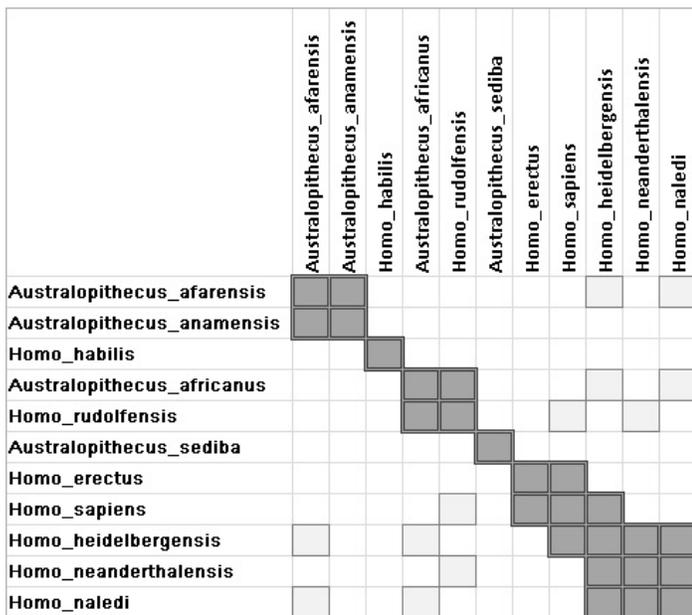
Figure 1. Baraminic distance correlation matrix for four *Australopithecus* species and seven *Homo* species. Dark gray boxes show that two species are significantly correlated. Light gray boxes show that two species are significantly negatively correlated.
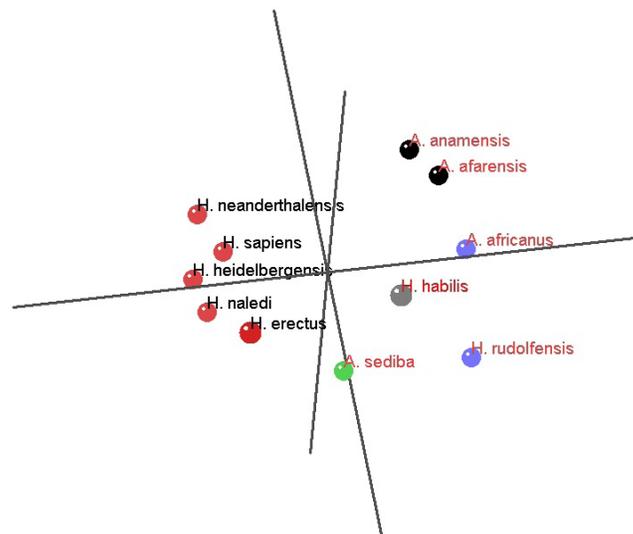

Figure 2. 3D MDS coordinates for the *Australopithecus* and *Homo* species. The coloring of the dots represents the different groups determined by the BDC results. Red: *H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, *H. naledi*. Green: *A. sediba*, Gray: *H. habilis*, Blue: *A. africanus*, *H. rudolfensis*, Black: *A. anamensis*, *A. afarensis*.

analyses. Thirty-two of the 57 characteristics were retained in the first analysis and 23 in the second (with the *Paranthropus* species). The data points were calculated in three-dimensional character space using multidimensional scaling (MDS), also available in the online program package by Wood (2008), and visualized using Kinemage software (available at http://kinemage.biochem. duke.edu/software/mage.php).

Results

First Analysis. Figure 1 depicts the baraminic distance correlation results. Three main groups are evident in the baraminic distance correlation graph along with two uncorrelated species: 1) *Australopithecus afarensis* and *A. anamensis*, 2) *Homo habilis*, 3) *A. africanus* and *H. rudolfensis*, 4) *A. sediba*, and 5) *H. sapiens*, *H. heidelbergensis*, *H. neanderthalensis*, *H. erectus*, and the species of focal interest, *H. naledi*.

Australopithecus anamensis and *A. afarensis* are significantly positively correlated with a correlation value of 0.782, a baraminic distance of 0.387, and bootstrap value of 94%. While the correlation between *A. africanus* and *A. afarensis* is 0.558, that is still too low to be considered significant. For *H. neanderthalensis* and *H. heidelbergensis*, the baraminic distance is 0.118, correlation value is 0.949, and bootstrap value is 100%. Also, the average baraminic distance value among all species pairs is 0.764, which is relatively high compared to other baraminology studies. This could be the case due to the reduced nature of the data set. The median bootstrap value for species pairs is 90%, which is moderate.

Homo sapiens, *H. heidelbergensis*, *H. neanderthalensis*, *H.*
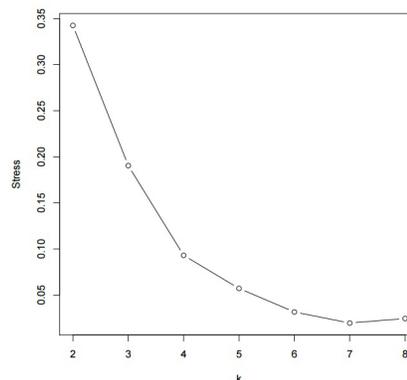
Figure 3. Stress graph showing stress values at different dimensions for the MDS analysis in Figure 2. The minimum stress value is at seven dimensions, suggesting there is distortion in this 3D depiction of the data.

erectus, and *H. naledi* form the largest group of the five species based on the correlation matrix. There are two subgroups, each coalesced by significant positive correlation: 1) *H. sapiens* with *H. erectus* and 2) *H. heidelbergensis*, *H. neanderthalensis*, and *H. naledi*. The two subgroups are held together only by significant positive correlation between *H. sapiens* and *H. heidelbergensis*. Positive correlations between the remaining pairs is weak. Excluding the relationship between *H. neanderthalensis* and *H. heidelbergensis*, bootstrap values are low.
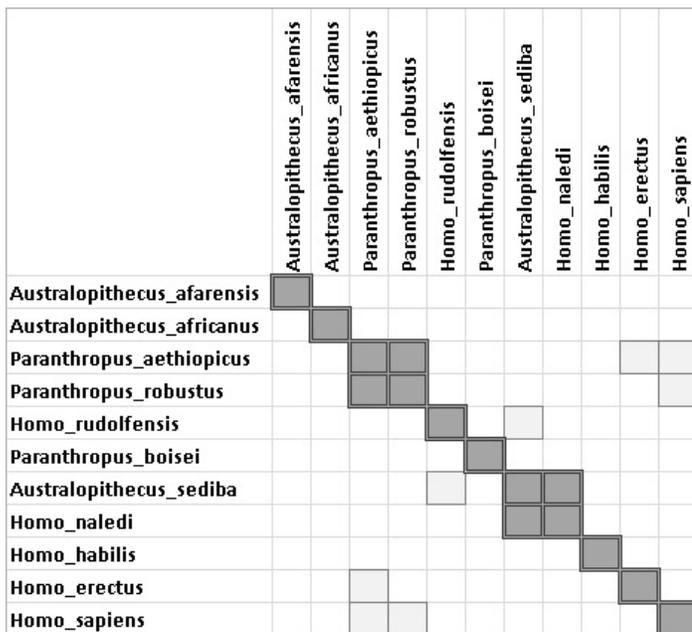
Figure 4. Baraminic distance correlation matrix for three *Australopithecus* species, three *Paranthropus* species, and four *Homo* species. Dark gray boxes show that two species pairs are significantly correlated. Light gray boxes show that two species are significantly negatively correlated.

Homo rudolfensis and *A. africanus* have a baraminic distance of 0.481, and a correlation value of 0.678. However, the bootstrap value of only 58% is low. *Homo rudolfensis* and *H. erectus* are rather far away from each other, with a baraminic distance of 0.926, and a bootstrap value of 96%, and a moderate negative correlation vale of -0.454.

Homo habilis shows no significant positive or negative correlation with any other species; it is closest to *A. afarensis*, with a baraminic distance of 0.562. The bootstrap value is only 68%, and also the baraminic correlation value is only 0.454, which only represents a moderate correlation. *Australopithecus sediba* lacks significant correlation. The closest species to it are *H. naledi* and *H. habilis*, each with a distance of 0.667. Of the remaining australopithecines, it is closest to *A. afarensis* at a distance of 0.767 and a nonsignificant correlation of -0.12.

Overall, significant negative correlations are sparse and their bootstrap values are low. Only *Homo heidelbergensis* and *H. naledi* were significantly negatively correlated with *A. afarensis* and *A. africanus*. Only *H. sapiens* and *H. neanderthalensis* were significantly negatively correlated with *H. rudolfensis*, which forms the small cluster with *A. africanus*.

Figure 2 is a spatial depiction of the baraminic relationships between the 11 species based on the 3D MDS coordinates calculated by the BDIST program. Figure 3 represents a stress graph, with a minimum stress value at seven dimensions, although the stress value is 0.19 at three dimensions. What can be seen fairly well is that the five most similar species of *Homo* form a cloud of taxa. Not surprisingly, *A. afarensis* and *A. anamensis* cluster close to each other on the MDS graph, but also far from the *Homo*
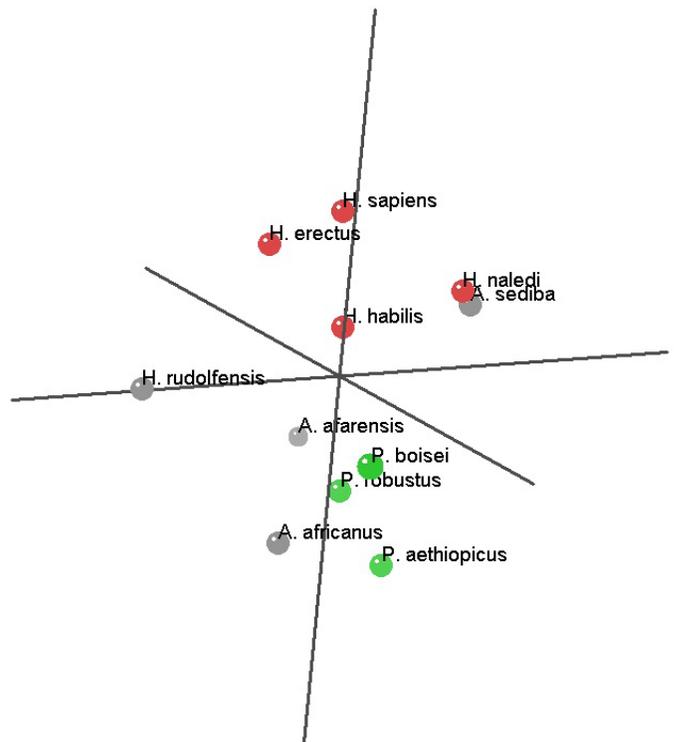

Figure 5. 3D MDS coordinates for the taxa from Figure 4. The coloring of the dots represents the different groups determined by the BDC results for the analysis including the three Paranthropus species. Red: *Homo*, Gray: *Australopithecus*, Green: *Paranthropus*.
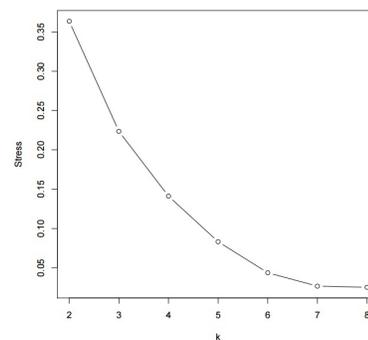

Figure 6. Stress graph showing stress values at different dimensions for the analysis involving the three *Paranthropus* species. There is minimum stress at eight dimensions, suggesting there is distortion in this 3-D depiction of the data.

cluster and the other three species. The four other species from the three correlation groups (*A. sediba*, *H. habilis*, *A. africanus*, and *H. rudolfensis*) all appear more or less equidistant from each other. Thus, while there appears to be a distinct gap between the *A. afarensis* and *A. anamensis* cluster and the *Homo* cluster, it is not clear whether the remaining species form an arching bridge between the two clusters or whether all or some should be considered to form additional separate clusters. Because the

stress is so high, the scatter plot may not accurately represent the information in the baraminic distance analysis.

Second Analysis. The analysis with the three *Paranthropus* species used a partially different subset of the original data from that used in the first analysis; baraminic distance analysis was noticeably different (Figure 4). Only two groups of two species each appeared in which the members were significantly positively correlated: 1) *P. aethiopicus* and *P. robustus*, and 2) *A. sediba* and *H. naledi*. All other species were neither significantly positively nor negatively correlated: *A. afarensis*, *A. africanus*, *H. rudolfensis*, *P. boisei*, *H. habilis*, *H. erectus*, and *H. sapiens*.

The shortest baraminic distance is between *A. sediba* and *H. naledi* at 0.35, with a significant correlation of 0.745. However, the bootstrap value is only 82%. The connection between *P. aethiopicus* and *P. robustus* has a baraminic distance of 0.476, with a correlation of 0.625, also significant, but with a bootstrap value of only 45%. *Homo sapiens* and *H. erectus* have a distance of 0.522, a correlation of 0.558, which is too small to be significant, and a bootstrap of 69%. Otherwise, *A. africanus* is moderately positively correlated with *A. afarensis* at 0.572, and *A. sediba* is likewise correlated with *H. habilis* at 0.398, both too low to be significant. There are only four species pairs that are significantly negatively correlated: *Homo sapiens* and *H. erectus* with *P. aethiopicus*; *Homo sapiens* with *P. robustus*; and *A. sediba* with *H. rudolfensis*. *A. africanus* is moderately but not significantly negatively correlated with *H. sapiens* and *H. erectus*. The average baraminic distance is 0.764, and the median bootstrap value is 96%.

Figure 5 gives the 3D MDS results showing the spatial distribution of the 11 species involved in that analysis. Figure 6 shows the stress graph, with a minimum stress value at eight dimensions, ~0.02. The scatter plot forms a diffuse cloud within which three pairs of species are evenly spaced, and thus is not too informative. Of the three species pairs, *A. sediba* and *H. naledi* are the most conspicuous. *P. aethiopicus* and *P. robustus* stand relatively close to each other as well as do *H. sapiens* and *H. erectus*.

Discussion

The results indicate that there is a cluster of five species of *Homo*, including *H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, and *H. naledi*. This result is very consistent with the general consensus of creationists that *H. erectus* and Neanderthals are human. As described in the results, the relationship between *H. neanderthalensis* and *H. heidelbergensis* is one of the two strongly positively correlated relationships discovered in the data set. The inclusion of *H. naledi* in this cluster supports its placement in the human holobaramin as delimited by Wood (2010, 2013, 2016). However, based on the data here the positive correlations between the species in this cluster generally have low bootstrap values, which mean that this cluster might be especially sensitive to character selection and may or may not accurately delimit the human holobaramin. The data suggest there is continuity among the five *Homo* species (and thus a monobaramin), but discontinuity from the remaining taxa is equivocal from these data. Likewise, there is continuity between *Australopithecus anamensis* and *A. afarensis* (a monobaramin) and between *Paranthropus*

aethiopicus and *P. robustus* (a third monobaramin). The second analysis supports continuity between *Homo naledi* and *A. sediba* (as a possible fourth monobaramin). If one combines results of the two analyses, then there is support for inclusion of *A. sediba* in the monobaramin with the five *Homo* species. *Homo rudolfensis* and *A. africanus* may represent a fifth monobaramin, but the MDS results do not support that conclusion. The species lacking significant correlations and/or that appear isolated in the MDS results may represent separate monobaramins because at least one analysis fails to demonstrate continuity with other species. Furthermore, these data do not provide clear-cut discontinuity among monobaramins, but they are suggestive that there may be discontinuities separating the *Homo*, *A. afarensis/anamensis*, and *Paranthropus* monobaramins from each other.

The baraminic distance matrix was calculated using only craniodental characteristics, but Berger et al. (2015) describe postcranial characteristics of *H. naledi* as well. Both craniodental and postcranial morphological characteristics of *H. naledi* and its comparison with australopithecines can be seen in Table 1. Eight out of 15 characteristics show exclusive similarity to humans compared to only three characteristics shared exclusively with australopithecines. This is consistent with the placement of *H. naledi* in the human monobaramin deduced from the baraminological analysis.

H. habilis formed an isolated species, separate from the other monobaramins. Based on his 48-year study of *H. habilis*, B. Wood (2014) argued that it should also be put into its own genus, neither australopithecine nor human. *H. habilis* presents a mosaic of morphological characteristics, and has proven difficult to classify (Schwartz and Tattersall 2015). *Homo rudolfensis* has at times been classified with it as *H. habilis sensu lato*. The limb length measurements of *H. habilis* as well as the shape of the mandible in specimen OH7 resemble australopithecines (Spoor et al. 2015). Also, when a body mass model was used to calculate its encephalization quotient, *H. habilis* was shown to have approximately the same encephalization as australopithecines (Young 2006).

Homo rudolfensis clusters with *A. africanus*, with a baraminic distance of 0.481 between the two taxa (first analysis only, but well separated in the second). That these two species might cluster with each other is unsurprising, since *Homo rudolfensis* has sometimes been reclassified with the australopithecines (B. Wood and Collard 1999; B. Wood and Baker 2011). Berger et al. (2010) also state that "the closest morphological comparison for *A. sediba* is *A. africanus*." Such taxonomic reassignment is not all that uncommon in hominid taxonomy (Kennedy 1999; B. Wood 1999; Line 2013; Schwartz and Tattersall 2015). *Homo rudolfensis* was thought to belong to the genus *Homo* because of its large and round skull. However, other characteristics suggest this species should be allied with the australopithecines: the occipital flaring, the long, ape-like upper lip, marks of large masseter muscles, large tooth sockets, and a cranio-facial index value of 59, which is well within the range of 51.0-64.5 characteristic of australopithecines (the range for humans is 30.0-45.0) (Mehlert 1999). Although the correlation is only moderate, the negative relationship between *H. rudolfensis* and *H. erectus* does have a high baraminic distance (0.926, within the top 20%) and a high bootstrap value of 96%.

Interestingly, of all the australopithecines included in this data

Table 1. *Homo*-like, *Australopithecus*-like, and unique morphological characteristics of *Homo naledi*.

Character	*Homo*-like	*Australopithecus*-like	Unique
sagittal crest	missing from skull		sagittal keeling
shape of cranium	similar to *Homo*		
cranial volume		within range of australopithecines	
supraorbital torus	present	present	
shape of face	flat		
mandibular dentition	parabolic		
molar size gradient		M1 < M2 < M3	
body mass range	similar to *Homo*		
proportion of digits	similar to *Homo*	extended thumb	
upper limb	shorter than lower limb		
shoulder configuration		similar to australopithecines	
rib cage		distally wide	
vertebrae	similar to *Homo*		
maximum tibia length	overlaps with lower range of humans	overlaps with upper range of humans	
foot morphology	similar to *Homo*		

set, *H. naledi* shows the highest correlation to *A. sediba*, which purportedly shows some *Homo*-like characteristics (Berger et al. 2010; Berger 2012; Irish et al. 2013). Thus, if *H. naledi* is part of the *Homo* holobaramin, then this result would be similar to T.C. Wood's result (2010) including *A. sediba* into the human holobaramin. *A. sediba* is the australopithecine species closest to the human baramin in morphological resemblance. For example, its reduced dental size, incipient nose and pelvis shape make it similar to *Homo*. However, the holotype of *A. sediba* (MH1) was a juvenile, whose characteristics could make it look more primitive, meaning that there can be substantial morphological differences within a given species. This is a common problem in paleontology when it is sometimes difficult to distinguish between plesiomorphic (that is, ancient) and juvenile characteristics as has been discussed for reptilian fossils (Tsuihiji et al. 2011; Aaron 2014). Furthermore, other characteristics of *A. sediba* and other australopithecines contradict the idea of a fluid transition towards humans. For example, the lateral plantar process, which is a part of the heel bone is more ape-like in *A. sediba*, and is more human-like in *A. afarensis*. The talus also lies broadly between the African apes and human (Zipfel et al. 2011). The more primitive foot and ankle characteristics of *A. sediba* are relevant, in that they influence bipedalism, which is a key step in the transition in the evolution of humans.

Australopithecus sediba was once viewed as a stem taxon compared to the genus *Homo* because of its "primitive" characteristics, but is now thought to be too recent for that (Pickering et al. 2011; Berger 2012). On the other hand, it has longer arms and extended thumbs, and according to Irish et al. (2013) it shares some less variable dental and cranial characteristics with *H. rudolfensis*. Furthermore, its cranial volume is well within the

range of australopithecines (420 cc), and it reached a maximum height of 1.3 meters (Balter 2010; Line 2010).

The present analyses can be compared to the ones performed by T.C. Wood (2010), wherein he found significant positive correlations between *H. rudolfensis*, *H. habilis*, *A. sediba*, and members of the *Homo* baramin. Although the present study found tentative evidence for the discontinuity between these species and the five members of the *Homo* baramin, as well a positive correlation between *H. rudolfensis* and *A. africanus*, none of the corresponding bootstrap values were high enough to prove that these relationships are statistically robust. Thus, though these results may not confirm Wood's results, they do not deny them either. According to the second analysis including the three *Paranthropus* species, there is a low distance between *H. naledi* and *A. sediba*, with a high correlation. This would seemingly confirm Wood's results that *A. sediba* should be classified within the human holobaramin, yet the bootstrap value (82%) is not large enough to confirm this.

All these considerations show that while there is some morphological variation within australopithecines and the genus *Homo*, discontinuity is likely between these two monobaramins. Even though these data are insufficient to actively corroborate the previous baraminological analyses by T.C. Wood (2010, 2013, 2016), they are consistent with his results. Species from these two groups at times may show characteristics of species in other monobaramins, but the characters may be examples of modular designs that can be recombined in different baramins. This is why *H. naledi* may also show unique morphological characteristics within the human baramin. Hence, there is no continuity between the (non-sedibine) australopithecines and members of the genus *Homo*. Such continuity is really only an evolutionary construct

that is imposed upon the data. Just as several species such as *A. sediba* and *H. habilis* have been envisioned in the conventional literature to be part of the transition between australopithecines and modern humans (Irish et al. 2013; Schwartz and Tattersall 2015), now *H. naledi* is considered as a possible candidate for that transition. However, the study here suggests that this species should be classified as human and discontinuous from australopithecines.

Schwartz and Tattersall (2015) write rather candidly [my emphasis in bold]:

> The fact that detail has often been overshadowed by generalization in the study of the hominin fossil record is a product of paleoanthropology's unique history. **But tradition alone cannot justify maintaining the status quo. Perhaps it is time to forget parochial habit and to begin approaching hominid systematics as students of other organisms do**, especially in undertaking broader and morphologically more detailed comparisons than have been customary, and in revisiting morphological criteria for species recognition. **If we want to be objective, we shall almost certainly have to scrap the iconic list of names in which hominin fossil specimens have historically been trapped**, and start from the beginning by hypothesizing morphs, building testable theories of relatedness, and rethinking genera and species.

Since this is one of the first morphological dataset available for *H. naledi*, and includes only craniodental characteristics, it is important to stress that these results are only preliminary. Further baraminological analysis is warranted, especially including more postcranial characteristics from more species, which might be difficult for *H. habilis* and *H. rudolfensis*. Genomic analyses should also be used to provide more details and insight, if possible. After all, studying a wide variety of characteristics only strengthens baraminological analyses. For example, the whole genome sequences for Neanderthals (Green et al. 2010) and Denisovans (Reich et al. 2010) have already been determined, and SNPs between Neanderthals and modern humans have been analyzed (Ahmed and Liang 2013). Gunbin et al. (2015) also performed a study of miRNA targeting genes between the genomes of human, Neanderthal, and Denisova. Similarly, it would also be interesting and instructive to compare whole paleogenome sequences obtained from these archaic human and australopithecine species, which could settle a number of questions.

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Appendix. Data Matrix of transformed characters based on and in presentation sequence of characters in Tables 1 and 2 of Berger et al. (2015).

```
P_aethiopicus   11212?11313?4441112433334??????????????????????????????
P_boisei        11112?21413?3333444444443??????????????????????????????
P_robustus      1?2?1?11414?4222323433434??????????????????????????????
A_anamensis     ???????????????????????34?24343241333334444444134333343
A_afarensis     12212?12??2?1221322222234343233233323333341434234 4343344
A_africanus     11111131224?12123322222243412322334344442334442444444444
A_sediba        11?1122113???1113212112132121212133313242?1?2121122323333
H_naledi        12321221131?41241212111111111111111213121211112 1212122
H_habilis       11222132223?32233212112122331222233333333333 32243434343
H_rudolfensis   2333423242???22344232333343??44443344442?1?2?22444444444
H_erectus       23444324434?42234312122132344221212232222223331222332212
H_sapiens       44444444442?3113331111131332121112311112313341223322212
H_neanderthal   ?????????????????????????1444121111121111141413111111 1111
H_heidelberg    ?????????????????????????13431211111111111313121111111111
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