

# An Evaluation of *Homo naledi* and “Early” *Homo* from a Young-Age Creationist Perspective

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## Abstract

Fossils of “early” *Homo* have become some of the most challenging to interpret in the fossil record. Creationists have generally argued that “early” *Homo* do not represent the remains of human beings, but previous statistical baraminology studies indicate otherwise. Using the recent publications of *Homo naledi* and a supermatrix of characters covering all named hominins except *Homo naledi*, human baraminology is here re-examined. Results continue to support inclusion of “early” *Homo* in the human holobaramin, and the newly discovered *Homo naledi* can also be placed with confidence in the human holobaramin. Additionally, both the small Dmanisi hominins and the robust D4500 specimen can also be classified as human. The newly-expanded human holobaramin implies a much greater diversity of human forms than previously recognized. More importantly, the earliest humans encountered in the fossil record exhibit the greatest diversity, implying that human diversification had already begun while humans were resident in Babel.

Editor: M. McLain

Received January 8, 2016; Accepted January 22, 2016; Published May 9, 2016

## Introduction

In 1992, creationist anthropologist Marvin Lubenow published *Bones of Contention*, a seminal work of young-age creationist anthropology. At the time, known fossil hominins included the gracile australopiths, *Australopithecus africanus* and *Au. afarensis*, the robust australopiths, now classified as *Paranthropus*, and a few forms referred to our own genus *Homo*. Lubenow emphasized the general ape-like skulls of australopiths and classified them as non-human, even though their ability to walk bipedally was unlike any extant ape. In the genus *Homo*, Lubenow focused on three main types: modern humans, Neandertals, and the various fossils referred to *Homo erectus*, all of which he considered to be genuinely human. Two other taxa were tentatively placed in Lubenow’s system. Lubenow argued that some material attributed to *Homo habilis* was human but other specimens should be referred to the non-human genus *Australopithecus*. Lubenow judged skull KNM ER-1470, sometimes designated *Homo*

*rudolfensis*, to be human.

Lubenow’s classification was very attractive. Even non-specialists could appreciate the skeletal similarity between modern humans and the most famous *H. erectus* specimen, the Turkana (or Nariokotome) boy. Furthermore, the stone tools associated with *H. erectus* also indicated a level of technology beyond that of mere animals. Classifying *H. erectus* as human seemed sensible. Likewise, the Lucy skeleton (*Au. afarensis*) exhibited a number of significant differences from modern humans, both in the skull and full skeleton, which made Lubenow’s classification as non-human quite reasonable.

**New Discoveries.** In more than twenty years since *Bones of Contention*, new discoveries have significantly expanded the hominin fossil record (Table 1). Additional evidence of *Australopithecus* has come to light, including new specimens from central Africa and central Asia. Some of these new fossils have been classified as new species (*Au. garhi*, *Au. bahrelghazali*, *Au. anamensis*, *Au. deyiremeda*, and *Au. sediba*). In Ethiopia,

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**Citation:** Wood. 2016. An Evaluation of *Homo naledi* and “Early” *Homo* from a Young-Age Creationist Perspective. *Journal of Creation Theology and Science Series B: Life Sciences* 6:14-30.

**Table 1.** Significant fossil discoveries since the publication of Lubenow's *Bones of Contention* in 1992.**Newly Named Fossils**

<b>Name</b>	<b>Significance</b>	<b>Citations</b>
<i>Ardipithecus ramidus</i>	Small-brained hominin with opposable hallux. Reported in 1994 from Middle Awash, Ethiopia.	White et al. 1994, 1995
<i>Ardipithecus kadabba</i>	Similar to <i>Ar. ramidus</i> , discovered in 1997 in Middle Awash, Ethiopia.	Haile-Selassie and Woldegabriel 2009
<i>Sahelanthropus tchadensis</i>	Discovered in 2001 in northern Chad, these fossils have the oldest radiometric date of any putative hominins.	Brunet et al. 2002
<i>Orrorin tugenensis</i>	Also discovered in 2001 in the Tugen hills of Kenya, conventional dating puts <i>Orrorin</i> older than <i>Ardipithecus</i> but younger than <i>Sahelanthropus</i> .	Senut et al. 2001
<i>Australopithecus garhi</i>	Gracile australopith from Middle Awash, Ethiopia. Discovered in 1996.	Asfaw et al. 1999
<i>Australopithecus anamensis</i>	Extremely fragmentary fossils from East Turkana, Kenya, initially described in 1995. At least 20 individuals are represented.	Leakey et al. 1995
<i>Australopithecus bahrelghazali</i>	The only australopith discovered in central Africa (Chad). Initially described in 1995.	Brunet et al. 1995
<i>Australopithecus deyiremeda</i>	Discovered in 2011 in Afar, Ethiopia, some argue that this taxon may be synonymous with <i>A. afarensis</i> .	Haile-Selassie et al. 2015
<i>Australopithecus sediba</i>	First published in 2010, there are currently two very complete skeletons. Discovered in a cave at "Cradle of Mankind" in South Africa.	Berger et al. 2010
<i>Kenyanthropus platyops</i>	A very fragmentary cranium discovered in 1999 in East Turkana, Kenya. Some have suggested affinities with <i>Homo rudolfensis</i> .	Leakey et al. 2001
<i>Homo floresiensis</i>	A recent skull found in a cave in Indonesia in 2003 sparked an intense debate over its species status. Believed by some to be closely related to <i>H. erectus</i> .	Brown et al. 2004
Dmanisi hominins	Found in Dmanisi, Georgia, this series of skulls have proved difficult to interpret. Some refer them to <i>H. erectus</i> , others to two separate species, still others to new species <i>H. georgicus</i> .	Gabunia et al. 2000, Vekua et al. 2002, Lordkipanidze et al. 2006, Lordkipanidze et al. 2007, Lordkipanidze et al. 2013
<i>Homo naledi</i>	The richest hominin discovery in Africa was found in the Rising Star Cave at the "Cradle of Mankind" in South Africa. <i>H. naledi</i> had extremely small brains but limbs resembling modern humans.	Berger et al. 2015

Red Deer Cave people	Discovered in southwest China, these fossils have a flat face with flaring cheeks. Radiometric dating suggests these were contemporary with <i>Homo floresiensis</i> .	Curnoe et al. 2012
<i>Homo antecessor</i>	Fragmentary facial bones from Spain, published in 1997. Conventionally dated as the oldest <i>Homo</i> fossils in Europe.	Bermúdez de Castro et al. 1997

### Important New Fossil Specimens

Specimen	Significance	Citations
Additional <i>Homo rudolfensis</i>	New fossils appear to confirm specific status of <i>Homo rudolfensis</i>	Leakey et al. 2012
Dikika juvenile	Skeleton of <i>Australopithecus afarensis</i> believed to be about 3 years old at time of death. Published in 2006, and discovered in Ethiopia.	Alemseged et al. 2006
Kadanuumuu (“Big Man”)	Discovered in Afar, Ethiopia, this skeleton is referred to <i>Australopithecus afarensis</i> .	Haile-Selassie et al. 2010
Mandible LD 350-1	Published in 2015 and discovered in Afar, Ethiopia, this jaw fragment is believed to be the oldest representative of genus <i>Homo</i> , with a conventional date of 2.8 Ma.	Villmoare et al. 2015a
<i>Pan</i> teeth	The first chimpanzee fossils were reported from Kenya with a conventional date of 500,000 years.	McBrearty and Jablonski 2005

two significant skeletons of *Au. afarensis* have been recovered, providing important new insights into that species.

While the textbooks and public continue to think of these fossils by the taxonomic names initially given to them, professional anthropologists have found considerable room to disagree over the identity of many of the fossils, particularly those of “early” *Homo* (Antón 2012). The “early” *Homo* label is generally given to fossils recovered from the upper Pliocene and lower Pleistocene, although there is no definite limit to what may be considered “early” *Homo* (any more than there is a definition of what constitutes *Homo* – see B.A. Wood 2009, Collard and Wood 2015). The uncertain interpretation of these fossils arises from a combination of low taxonomic sample size and the fragmentary nature of the fossils (Ackermann and Smith 2007).

Most well-known of these disagreements are the questions about the classification of *Homo habilis* based on material from Olduvai Gorge in Tanzania. Leakey et al. (1964) defined the species based on six hominin specimens. The type specimen OH 7 was a mandible with dentition, an upper molar, and parietal and hand bones from a juvenile individual. The paratypes consisted largely of dental fragments and a few hand and foot bones. *H. habilis* as originally defined had a substantially larger cranial capacity and smaller molars and premolars than those of *Australopithecus*. Despite these distinguishing characteristics, anthropologists resisted recognizing the taxon for many years after Leakey et al.’s (1964) description. Some attributed the fossils to a subspecies of *Homo erectus*, and others claimed they were the remains of some kind of australopith (see Tobias 2009). Even though many anthropologists today recognize the legitimacy of the species *H.*

*habilis*, there remain some who argue that the species is actually a member of *Australopithecus* (Wood and Collard 1999, B.A. Wood 2009, Collard and Wood 2015).

Closely related to the debate over *Homo habilis* is the classification of KNM ER-1470, a fragmentary cranium consisting of a calvarium with facial and maxilla bones. It has a large cranial capacity relative to australopiths and very little prognathism. In the initial description, Leakey (1973) placed the cranium, with associated femora and fragments of a tibia and fibula, in the genus *Homo* but did not specify a species. Subsequent researchers assumed that it belonged in *Homo habilis* (Cela-Conde and Ayala 2007, p. 173), but in 1986, Alexeev proposed the new species *Homo rudolfensis* for both KNM ER-1470 and KNM ER-1813 (see B.A. Wood 1999). Additional research supported the recognition of two different species (Lieberman et al. 1988; B.A. Wood 1985, 1992), but Lee and Wolpoff (2005) concluded that the variation observed between KNM-ER 1470 and 1813 is not greater than that observed in samples of conspecific individuals from South African fossil sites, thus implying that both types are members of the same species. With the discovery of *Kenyanthropus*, Leakey et al. (2001) suggested that KNM ER-1470 could be transferred to *Kenyanthropus*. After the discovery of additional fossils similar to KNM ER-1470, however, Leakey et al. (2012) retained the species in *Homo*.

From South Africa, some fossil specimens have been referred to “early” *Homo*, but these also remain difficult to classify. For example, StW 53 from Sterkfontein consists of pieces of the calvarium and maxilla. Originally excavated in 1976, the skull was tentatively referred to *Homo habilis* (Hughes and

Tobias 1977). Others have argued that StW 53 was actually an australopith (Ferguson 1989, Kuman and Clarke 2000). Curnoe and Tobias (2006) developed a new reconstruction of StW 53 and proposed retaining it in *Homo habilis*, but in 2010, Curnoe named the skull a type specimen for the new species *Homo gautengensis*. Clarke (2013) expressed his confidence that StW 53 was a male specimen of *Australopithecus africanus*, but Berger et al. (2015) include StW 53 in *Homo habilis*. Blumenshine et al. (2003), reflecting Clarke's diagnosis of StW 53 as *Au. africanus*, also suggested that some of the east African *H. habilis* specimens (namely OH 13, OH 24, OH 62, and KNM ER-1813) may also be a form of australopith.

Perhaps most surprisingly, the numerous skulls discovered at a fossil site conventionally dated at 1.8 Ma near the village of Dmanisi in the republic of Georgia demonstrate an enormous range of forms (Gabunia et al. 2000, Vekua et al. 2002, Lordkipanidze et al. 2006, Lordkipanidze et al. 2007, Lordkipanidze et al. 2013). Some of the crania recovered from the site exhibit traits consistent with *Homo erectus*, while one, D4500, has a number of traits more consistent with australopiths than *Homo*. Partly because these specimens come from a single deposit, Lordkipanidze et al. (2013) and Van Arsdale and Wolpoff (2012) argue that the Dmanisi skulls and consequently all "early" *Homo* specimens are probably referable to a single, highly variable species, *Homo erectus*. Other paleoanthropologists continue to argue that the Dmanisi hominins represent at least two different species (e.g., Bermúdez de Castro et al. 2014, Hublin 2014, Dembo et al. 2015).

Disagreement over the interpretation of Dmanisi fossils differs markedly from the debates over African "early" *Homo*. The uncertainty over African "early" *Homo* is widely acknowledged to be the result of the low sample size and fragmentary nature of the fossil material (e.g., Antón 2012). In contrast, the Dmanisi fossils are far more complete than most fossils attributed to *Homo habilis sensu lato*. The interpretations of the Dmanisi fossils depend on much larger questions of understanding intrataxon variation in hominins, the value of character-based approaches to hominin classification, and the relevance of ecological concerns such as competitive exclusion vs. adaptive specialization.

The recently-announced *Homo naledi* also resembles "early" *Homo*, even though no radiometric dating has been published as of this writing (Berger et al. 2015; see also Thackeray 2015). The species was described based on more than 1500 fossils found in the Rising Star Cave during excavations in November 2013 and March 2014 (Berger et al. 2015). Skeletal remains were taken from floor sediments in a single chamber of the cave, in which only hominin remains (and a few bird bones) are present (Dirks et al. 2015). The skeletal sample is morphologically homogeneous indicating that a single species is present. The bones lack indications of carnivore activity, and the cave contains no evidence of previous occupation by these hominins as of this writing (Dirks et al. 2015). There are at least 15 individuals present, including elderly individuals and several deciduous teeth representing very young children. Dirks et al. (2015) argue that the assemblage of monospecific bones in this cave indicates intentional burial, a cultural behavior previously known only from *Homo sapiens* and Neandertals.

*Homo naledi* also presents a unique mix of character traits. Berger et al. (2015) estimated their stature around 1.5 m, which

is within the range of known *Homo erectus* but slightly taller than australopiths, including *Au. sediba* (Berger et al. 2010). The legs and feet strongly resemble modern humans (Harcourt-Smith et al. 2015), implying a fully bipedal locomotion, but the pelvis more closely resembles australopiths. The hands resemble human hands, except for the marked curvature of the metacarpals and phalanges (Kivell et al. 2015). The arms and shoulders are most similar to arboreal ape species. The thorax is pyramidal, which more closely resembles the thorax of *Au. sediba* than modern *Homo sapiens*. The endocranial capacity is substantially smaller than modern *Homo sapiens*, Neandertals, and *H. erectus*, but larger than *Au. sediba* and *H. floresiensis*. The endocranial capacity most closely resembles classic australopiths.

**What Does It All Mean?** It goes without saying that evolutionary biologists interpret these new findings as evidence of human evolution from nonhuman ancestors. More specifically, fossils classified as "early" *Homo* are supposed to reveal the origin of our own genus from australopith ancestors (Antón 2012, Antón et al. 2014). As new fossils are discovered that expand our evidence of "early" *Homo*, some experts in human evolution emphasize the "bushiness" of evolution rather than the ladder-like progression popularized by the "march" cartoon (Pievani 2012). Antón et al. (2014) recommend a more careful approach and recognize three "groups," which they do not associate directly with the traditional *Homo* species names. Similarly, others (Lee and Wolpoff 2005, Ackermann and Smith 2007, Henneberg 2009, White 2013) resist the multiplication of new species names and argue that the present fossil record of "early" *Homo* cannot distinguish between the various taxonomic hypotheses imposed upon it.

Creationists seemingly have a simpler job than settling which fossils belong to which species. In the young-age creationist perspective, hominin fossils are either human or nonhuman. Following Lubenow's model, modern creationists have classified most of the new discoveries reviewed here as nonhumans (e.g., Sarfati 2001; Line 2010a, 2010b, 2013), although substantial disagreement remains on certain taxa (see T.C. Wood 2010 for a review). Ironically, "early" *Homo* has been a source of disagreement among creationists as it has among conventional anthropologists, although the majority of creationists view *Homo habilis* as nonhuman (e.g., Hummer 1979, Lubenow 1992, Young 2006). T.C. Wood (2010) attributed the creationist disagreements to the same problems that plague conventional anthropology: fragmentary specimens and small sample sizes.

Wood also noted that creationists historically lacked a methodology for assessing similarity and identifying discontinuity. As a remedy for this problem, Wood (2010) applied statistical baraminology to several hominin character sets in order to provide a robust and statistically supported circumscription of the human holobaramin (i.e., the putative descendants of Adam and Eve). Wood's original analysis found a lack of continuity between *Homo* and most members of *Australopithecus*, *Paranthropus*, and extant apes, which is consistent with the separate creation of *Homo* and nonhuman apes.

Wood consequently interpreted the human holobaramin to constitute at least eight different taxa (*H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, *H. ergaster*, *H. habilis*, *H. rudolfensis*, and *Au. sediba*) and possibly three more (*H.*



*floresiensis*, *H. antecessor*, and the Dmanisi hominins). Further efforts to clarify the position of *Australopithecus sediba* were not successful (T.C. Wood 2013). In Wood's perspective, these human taxa represented descendants of Noah as they repopulated the earth after the tower of Babel, although classifying *H. rudolfensis*, *H. habilis*, and *Au. sediba* as human went far beyond what other creationists, including Lubenow, had done in the past.

Not surprisingly, creationist commentators responded negatively to Wood's studies, insisting that *Australopithecus sediba* was not human (Menton et al. 2010). Wood (2011) responded with an essay that clarified the objectives of statistical baraminology and the theological deficiencies of the critics' arguments. Nevertheless, Wood offered no further supporting evidence that *Australopithecus sediba* was a human descendant of Adam and Eve. With the recent publication of *Homo naledi* (Berger et al. 2015) and additional information about the Dmanisi fossils (Dembo et al. 2015), it is now possible to revisit the circumscription of the human holobaramin with significant new fossil material.

Wood's (2011) concept of the "discontinuity hypothesis" provides the basis for this additional study. Based on empirical observations, historical creationist claims, and biblical inferences, Wood's discontinuity hypothesis proposes that "organisms were created in discrete, discontinuous groups that are recognizably different from all other organisms" (Wood 2011). Applied to humans, we should observe a discrete group of organisms, to which humans belong, that is separate and distinct from creatures that are obviously not human (such as chimpanzees). Falsifying the discontinuity hypothesis would involve the converse: showing that humans and nonhumans cluster together in a single group with no evidence of discontinuity. Newly-discovered fossil material of "early" *Homo* provides new opportunities to test the discontinuity hypothesis: Will the new, purported intermediates connect the human cluster to a cluster of nonhumans, or will there still be discrete clusters separating human from animal?

**The Bigger Picture.** Given the current state of evangelical debate over the historical Adam, developing a coherent and consistent creation model of human origins should be a priority for young-age creationists. Despite two millennia of near unanimity among Christian thinkers (VanDoodewaard 2015), some evangelical scholars have recently argued that humanity could not have descended from a single couple named Adam and Eve and even more importantly that belief in the historicity of Adam is not a necessary component of Christian theology (Harlow 2010, Schneider 2010, Enns 2012, Walton 2015). These claims have been resisted by some theologians (e.g., Caneday 2011, Collins 2011, Mahony 2011, Madueme and Reeves 2014, Chou 2016) and creationists (e.g., Anderson 2013, Turpin 2013, Ham 2015), who align with the majority voices in Christianity through the ages: Adam and Eve are historical individuals that introduced sin into the world.

The broader evangelical response generally focuses on the theological requirements for a historical Adam with little attention to developing a model that explains the scientific and scriptural data together. Typical in this regard is Collins (2011), who emphasizes the need only for a covenantal representative in the historical person Adam while still allowing for the possibility that Adam was an evolved, tribal leader. Collins does not believe that

Adam and Eve need be the sole ancestors of all humans or created from dust. His position has been criticized as insufficiently biblical by others who insist that the historical detail contained in Genesis 1-3 is far greater than allowed by Collins's view (T.C. Wood 2012a, McKitterick 2012, Lloyd 2012, Doran and McRoberts 2012, VanDoodewaard 2015).

To provide satisfactory answers to the scientific challenges posed by advocates of a nonhistorical Adam, Christian scholars need a model of human origins that synthesizes information from genomics, paleogenomics, paleoanthropology, cultural anthropology, comparative linguistics, and geology. Toward that end, two recently-published character matrices will be examined using statistical baraminology (T.C. Wood 2005, 2008, 2010). The results of these studies can then be evaluated using the discontinuity hypothesis.

Placing the results of this present study into the context of post-Flood and post-Babel dispersal will allow the refinement of the young-age creation model of human origins. Further refinement of the model will be necessary to better explain the results of comparative genomics and paleogenomics, but genomic theories will depend in part on a robust and defensible model of the fossil record. As a positive interpretation of the hominin fossil record that does not invoke human evolution from nonhuman ancestors, these results will provide further illumination of the existence of the historical Adam.

## Methods

Because the term hominin refers to subfamily Homininae, a clade consisting of the human/chimpanzee last common ancestor and all its descendants (Goodman et al. 1990), the term is incompatible with a creationist perspective, in which there is no evolutionary relationship between humans and chimpanzees. In this work, as in Hartwig-Scherer (1998), Simpson's (1945) mammal classification will be preferred as a formal classification separating extant apes into family Pongidae and extant humans into family Hominidae. Here, hominin should be understood as an informal term for humans and all fossil forms more similar to humans than to extant apes, without any distinction between human and nonhuman. Hence, there can be human and nonhuman hominins, and the goal of this research is distinguishing the two.

For examining the Dmanisi hominins, the supermatrix compiled by Dembo et al. (2015) was obtained from Dryad (<http://datadryad.org/resource/doi:10.5061/dryad.5025v>). The supermatrix consisted of 24 hominin taxa and 380 craniomandibular characters compiled from previously published character matrices, including the matrices used by T.C. Wood (2010) in his first statistical baraminology study of hominins. In the taxon list, the Dmanisi hominins were separated into "small-bodied Dmanisi" and "D4500." The matrix included *Au. sediba* but not *H. naledi*.

To examine *Homo naledi*, eighty-seven craniomandibular characters scored for 15 taxa were obtained from Supplementary Table 2 in Berger et al. (2015). The taxa included two extant apes (*Gorilla gorilla* and *Pan troglodytes*), three *Paranthropus* taxa (*P. aethiopicus*, *P. boisei*, and *P. robustus*), three australopiths (*Au. afarensis*, *Au. africanus*, and *Au. sediba*), and seven members of genus *Homo* (*H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, *H. rudolfensis*, *H. habilis*, and *H. naledi*). Characters

sampled included 73 cranial characters and 14 mandibular characters.

Maximum parsimony analysis was conducted using PAUP4 with 5000 replicates and tree bisection and reconnection branch swapping. Gorilla was treated as an outgroup for parsimony analysis. BDC and MDS for both character sets were calculated using BDISTMDS (<http://www.coresci.org/bdist.html>) with a character relevance cutoff of 0.75 and a taxon relevance cutoff of 0.4, as in previous analyses of fossil hominins (T.C. Wood 2010). BDC was calculated for 100 bootstrap replicates.

## Results

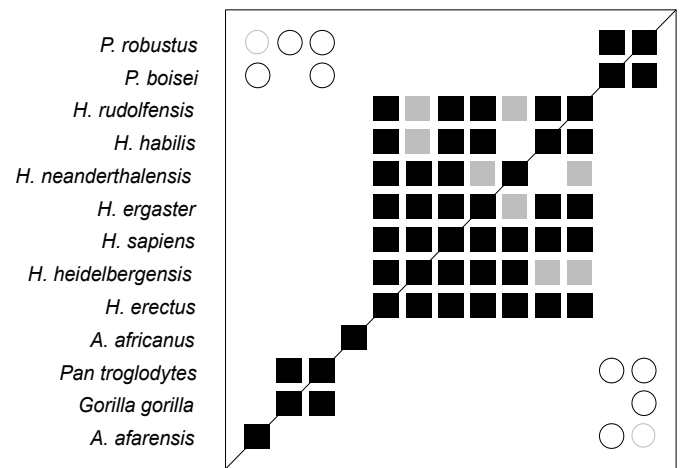
**Dmanisi hominins.** At a taxic relevance cutoff at 0.4, eleven taxa were eliminated from the character matrix, including the two Dmanisi hominins, which had taxic relevance scores of 0.345 for the small-bodied Dmanisi and 0.174 for D4500. Consequently, BDC and MDS were calculated for two subsets of Dembo et al.'s character set. The first subset consisted only of thirteen taxa that met the taxic relevance cutoff: *H. sapiens*, *H. ergaster*, *H. habilis*, *H. erectus*, *H. rudolfensis*, *H. heidelbergensis*, *H. neanderthalensis*, *Au. africanus*, *Au. afarensis*, *P. boisei*, *P. robustus*, and the extant chimpanzee and gorilla. In the second set, the two Dmanisi taxa were added to the first subset for a total of fifteen taxa.

For the first subset excluding the Dmanisi hominins, character relevance filtering resulted in only 197 characters with relevance >0.75 and subsequently used for calculating baraminic distances. Baraminic distance correlation (BDC) results are shown in Figure 1, and three clusters are apparent. The first consists of the two *Paranthropus* taxa. The second contains all species of *Homo*, and the third cluster contains the extant apes. The australopiths *A. africanus* and *A. afarensis* are not positively correlated with any other taxa. Significant, negative BDC is limited to comparisons involving members of *Paranthropus*, and no significant, negative BDC is observed involving any member of *Homo*.

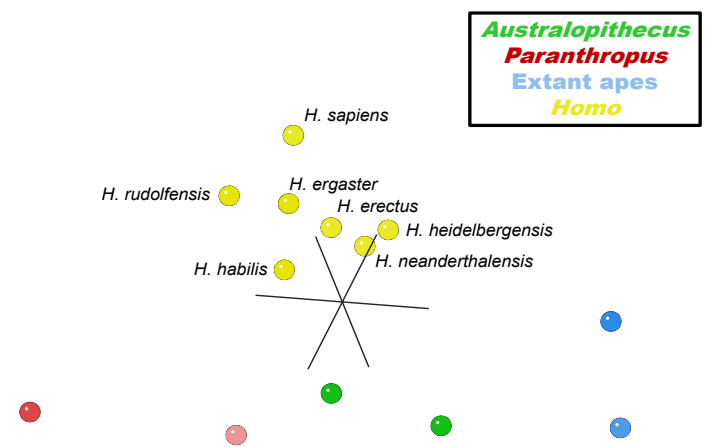
Bootstrapping values for the BDC of the first subset are quite high. Bootstrap values <90% are only observed for four of the twenty positive baraminic distance correlations between members of *Homo*. A bootstrap value of 87% is also observed for the significant, negative BDC between *A. afarensis* and *P. robustus*. All remaining positive and negative BDC that were statistically significant had bootstrap values  $\geq 90\%$ . The median bootstrap value was 100%.

The 3D multidimensional scaling (MDS) results support the findings of the BDC (Figure 2). The 3D stress for the MDS is 0.12, with a minimal stress of 0.08 observed at five dimensions. *Homo* taxa form a tight cluster with other taxa separate from it.

For the subset including the Dmanisi hominins, the results differed notably. First, the number of characters that met the character relevance cutoff was reduced to only 77. Second, the BDC results had considerably lower bootstrap values, with a median of only 90%. The BDC results reveal three clusters similar to those seen in the first subset (Figure 3). When Dmanisi hominins are included, the australopiths become part of the cluster of extant apes. Most importantly, both Dmanisi hominins are included in the *Homo* cluster. The small-bodied Dmanisi hominin shares significant, positive BDC with all *Homo* taxa except *H.*



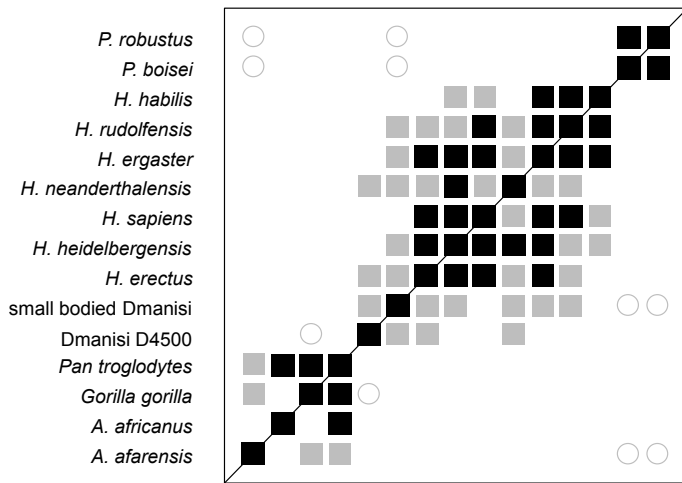
**Figure 1.** BDC results for the dataset of Dembo et al. (2015). Squares indicate taxa with significant, positive BDC; circles indicate taxa with significant, negative BDC. Black symbols have bootstrap values (100 replicates) >90%; gray symbols have bootstrap values  $\leq 90\%$ .



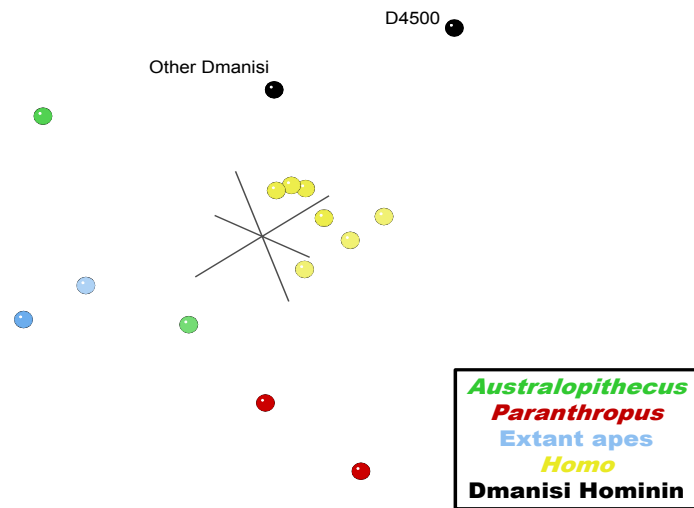
**Figure 2.** Three-dimensional MDS results for the dataset of Dembo et al. (2015). Taxa of genus *Homo* are shown in yellow, *Paranthropus* in red, gorilla and chimpanzee in blue, and *Australopithecus* in green.

*habilis* and *H. sapiens*. Dmanisi skull D4500 shares significant, positive BDC with *Homo erectus* and *H. neanderthalensis*. Both Dmanisi taxa also share significant, positive BDC with each other. All significant, positive correlations involving Dmanisi taxa had bootstrap values <90%. Significant, negative BDC occurred only between five taxon pairs. Both *Paranthropus* taxa were negatively correlated with the small-bodied Dmanisi and *Au. afarensis*, and D4500 was negative correlated with gorilla. All significant, negative correlations had bootstrap values <90%.

The 3D MDS results also differed strikingly from those obtained without the Dmanisi hominins (Figure 4). The 3D stress

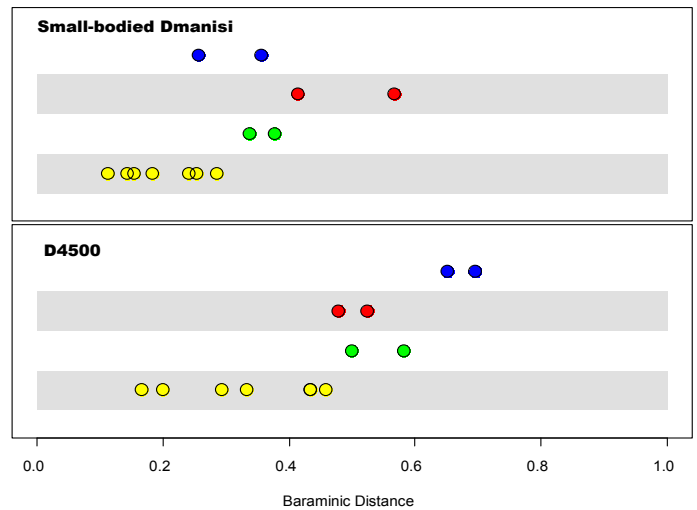


**Figure 3.** BDC results for the dataset of Dembo et al. (2015) including the two Dmanisi taxa. Squares indicate taxa with significant, positive BDC; circles indicate taxa with significant, negative BDC. Black symbols have bootstrap values (100 replicates) >90%; gray symbols have bootstrap values ≤90%.



**Figure 4.** Three-dimensional MDS results for the dataset of Dembo et al. (2015) including the two Dmanisi taxa. Taxa of genus *Homo* are shown in yellow, *Paranthropus* in red, gorilla and chimpanzee in blue, *Australopithecus* in green, and the Dmanisi hominins in black.

was 0.189, and the minimal stress 0.171 was observed at four dimensions. Consequently, the match between the MDS distances and the baraminic distances calculated from the character matrix are poor. As in the subset excluding Dmanisi, *Homo* taxa form a tight cluster separated from other taxa, but the Dmanisi hominins are also notably separated from other *Homo* taxa. This would seem to imply that the Dmanisi hominins are not part of the *Homo*



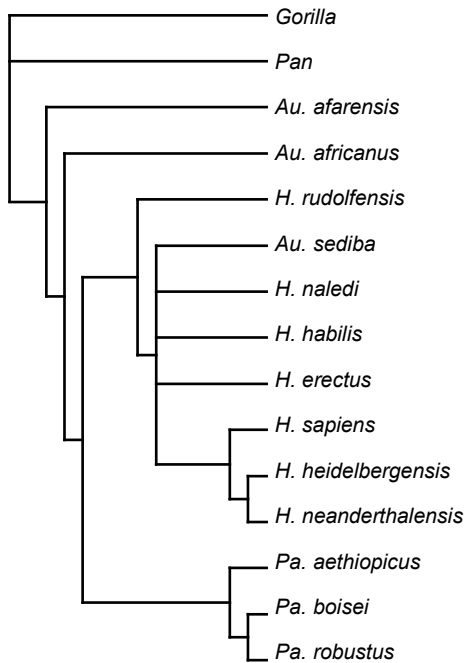
**Figure 5.** Calculated baraminic distances for both Dmanisi taxa. Distances to taxa of genus *Homo* are shown in yellow, *Paranthropus* in red, gorilla and chimpanzee in blue, and *Australopithecus* in green.

cluster, but the original baraminic distances (Figure 5) indicate that the Dmanisi hominins are both most similar to members of *Homo*.

***Homo naledi*.** Maximum parsimony analysis of the full 15 taxa and 87 characters resulted in three equally parsimonious trees of 204 steps each. In all three trees, four basal taxa, *Gorilla*, *Pan*, *Au. afarensis*, and *Au. africanus* appeared in the same branch order, and *Paranthropus* was the sister clade to a clade containing *Homo* and *Au. sediba*. All three trees also placed *H. rudolfensis* as the most basal member of *Homo*. The three trees differed primarily in the arrangement of *Au. sediba*, *H. habilis*, *H. naledi*, and *H. erectus*. The strict consensus of all three trees is shown in Figure 6.

For calculating baraminic distances, all taxa and characters met relevance cutoffs, and the full character matrix was used to calculate baraminic distances. BDC results for the full set of taxa reveal four groups of taxa: (1) the extant apes *Pan troglodytes* and *Gorilla gorilla*, (2) the australopiths *Au. africanus* and *Au. afarensis*, (3) three taxa of the genus *Paranthropus*, and (4) the genus *Homo* plus *Au. sediba* (Figure 7). Within each group, every possible taxon pair shares significant, positive BDC. Between groups, sporadic but significant, negative BDC occurs only between group 4 taxa (*Homo* + *Au. sediba*) and members of each of the other three groups. Specifically, *Au. afarensis* is negatively correlated with four members of group 4; *Gorilla* is also negatively correlated with four members of group 4. All three members of *Paranthropus* are negatively correlated with four different members of group 4. Significant, positive BDC was not observed between any members of different groups.

The bootstrap results indicate high bootstrap values for positive BDC but low bootstrap results for negative BDC. Only one instance of significant, negative BDC had a bootstrap value ≥90%, between *Paranthropus aethiopicus* and *Australopithecus sediba*. Within the *Paranthropus* and extant ape groups, all positive BDC had bootstrap values ≥90%. Within the much larger group 4,



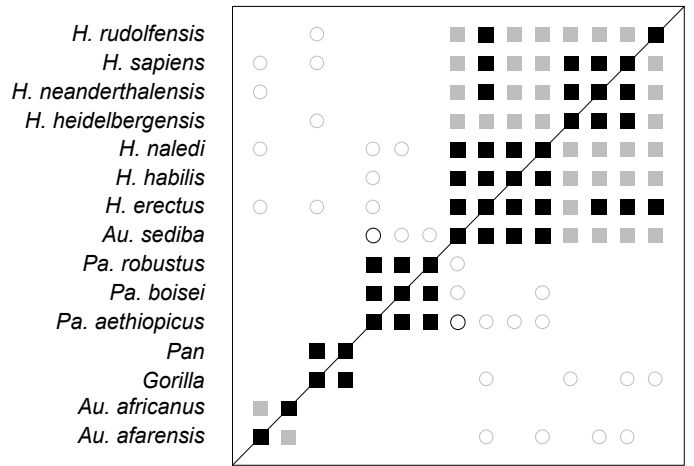
**Figure 6.** Strict consensus of three most parsimonious trees calculated from the character set given in Berger et al.'s (2015) supplemental table 2.

bootstrap values were high for significant, positive BDC between *Homo sapiens*, *H. neanderthalensis*, and *H. heidelbergensis* and between *H. naledi*, *H. habilis*, *H. erectus*, and *Au. sediba*. *H. erectus* also exhibited high bootstrap values for positive BDC with *H. sapiens*, *H. neanderthalensis*, and *H. rudolfensis*. The remaining instances of significant, positive BDC within group 4 had bootstrap values <90%.

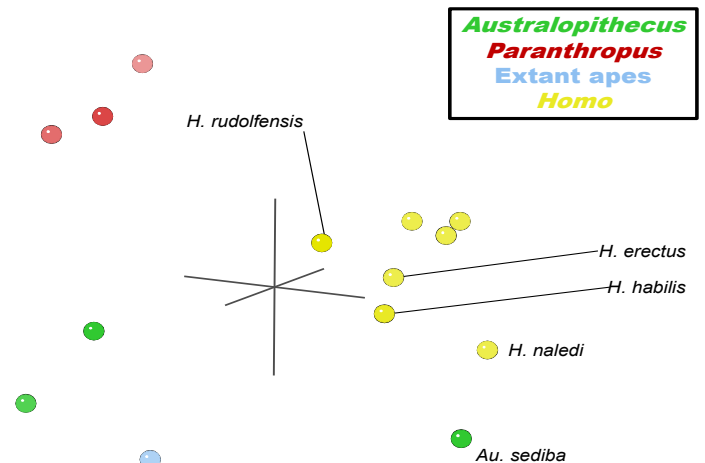
Multidimensional scaling results generally support the BDC findings (Figure 8). The stress at three dimensions was 0.14, and the minimal stress was 0.07 at five dimensions. In the three-dimensional projection, Group 4 appears as a diffuse cloud of taxa distinctly separated from the other three groups. *H. naledi*, *Au. sediba*, and *H. rudolfensis* appear to be outliers from the main cluster of group 4 taxa (*H. sapiens*, *H. neanderthalensis*, *H. erectus*, and *H. habilis*).

## Discussion

These results are consistent with Wood's previous statistical baraminology analysis published in 2010. Wood's 2010 results consistently showed significant, positive BDC shared between members of *Homo*, including *Homo habilis* and *Homo rudolfensis*. The present results show the same correlations, including *Homo habilis* and *Homo rudolfensis*. Wood's 2010 analysis that included *Au. sediba* revealed significant, positive BDC between *Au. sediba* and all other members of *Homo* included in the analysis (*H. sapiens*, *H. rudolfensis*, *H. erectus*, and *H. habilis*). The present results also show significant, positive BDC between *Au. sediba* and all other members of *Homo*.



**Figure 7.** BDC results for the dataset of Berger et al. (2015). Squares indicate taxa with significant, positive BDC; circles indicate taxa with significant, negative BDC. Black symbols have bootstrap values (100 replicates) >90%; gray symbols have bootstrap values ≤90%.



**Figure 8.** Three-dimensional MDS results for the dataset of Berger et al. (2015). Taxa of genus *Homo* are shown in yellow, *Paranthropus* in red, gorilla and chimpanzee in blue, and *Australopithecus* in green.

In three of Wood's 2010 BDC studies, *Au. africanus* was also positively correlated with members of *Homo*. Otherwise, no *Australopithecus* or *Paranthropus* taxa or extant apes shared significant, positive BDC with members of *Homo*. Wood's 2010 MDS results supported the BDC results in that *Homo* formed a single cluster of taxa separated from other non-*Homo* taxa. *Au. sediba* was clearly part of the *Homo* cluster, but even for character matrices where *Au. africanus* shared significant, positive BDC with members of *Homo*, *Au. africanus* did not appear to be part



of the *Homo* cluster.

In the present study, *Au. africanus* is never positively correlated with any members of *Homo*, confirming Wood's 2010 judgment that *Au. africanus* does not belong to the *Homo* cluster. In contrast to the previous study, *Au. sediba* appears to be more of an outlier in this MDS analysis, even though it remains positively correlated with other *Homo* members in the BDC results. In all of the present BDC results, comparisons between members of *Homo* and all other taxa (except *Au. sediba*) resulted in only significant, negative correlation. This confirms Wood's 2010 inference of a discontinuity separating *Homo* (+*Au. sediba*) from all other taxa in the sample.

Furthermore, the inclusion of *Au. sediba* in *Homo* is also supported by the present phylogenetic analysis. Although the precise relationship between *Au. sediba*, *H. habilis*, *H. naledi*, *H. erectus* and the clade including *H. sapiens* cannot be resolved using the present characters, *Homo rudolfensis* is basal to all of these taxa, indicating that the full *Homo* genus includes *Au. sediba*. The alternative would require reclassifying *Homo rudolfensis* as something other than *Homo*. As noted above, some authors suggest that *H. rudolfensis* is actually a member of genus *Kenyanthropus* (Leakey et al. 2001), but the phylogeny of Dembo et al. (2015) does not support a relationship between *H. rudolfensis* and *Kenyanthropus*. Dembo et al.'s best tree also found that *Au. sediba* and *H. habilis* form a clade, and they recommend that *Au. sediba* should be included in *Homo* or that *Au. sediba* and *H. habilis* should be classified in a new genus. Taken together, the present phylogenetic results and those of Dembo et al. (2015) support the inclusion of *Au. sediba* in *Homo*.

The present results also extend Wood's 2010 analysis by including new taxa in the *Homo* cluster. Most clearly, *Homo naledi* is unmistakably part of the *Homo* cluster. *H. naledi* shares significant, positive BDC with all other *Homo* taxa (+ *Au. sediba*) and significant, negative BDC with two *Paranthropus* species and *Au. afarensis*. These correlations support the inclusion of *H. naledi* in the *Homo* cluster.

The position of the Dmanisi hominins is less clear, although the present evidence would support the tentative placement of both forms of Dmanisi in the *Homo* cluster. The BDC results show positive correlation between members of *Homo* and both Dmanisi taxa, and neither Dmanisi forms are positively correlated with any non-*Homo* taxa. The MDS results show that the Dmanisi hominins are far outliers from the *Homo* cluster, but the stress is quite poor (0.189). The actual baraminic distances indicate that the Dmanisi taxa are most similar to other members of *Homo* (Figure 5). Consequently, we may tentatively place the Dmanisi hominins in the *Homo* cluster as well.

In 2010, Wood interpreted the *Homo* cluster as a human holobaramin consisting of *H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, *H. ergaster*, *H. habilis*, *H. rudolfensis*, and *Au. sediba*. In addition, StW 53, which was subsequently referred to *H. gautengensis* by Curnoe (2010), also clustered with the human cluster. The present study supports including *H. naledi* and the Dmanisi hominins in the same holobaramin. Since neither of the present character matrices are true independent samples of taxa and characters, the present results are not independent confirmations of the previous results, but the different samples of characters and taxa in the present matrices do not result in any

significant modifications of the previous results of Wood in 2010.

In support of recognizing Dmanisi hominins as human, we may also note the extensive stone tools of the Oldowan type recovered from the Dmanisi site (Mgeladze et al. 2011) and the survival of an edentulous individual. Dmanisi skull 3444 experienced antemortem tooth loss, and the bone around the tooth sockets has been extensively resorbed (Lordkipanidze et al. 2006). Skull 3444 therefore came from an individual who lived several years after losing almost all its teeth. Does this imply complex social behavior of caring for the disabled among the Dmanisi hominins? Some researchers have assumed so, but extant primate populations are known to have occasional individuals with extensive tooth loss (e.g., Cuzzo and Sauter 2004, Millette et al. 2009), implying that complex social care of the disabled is not necessary to explain the occasional edentulous individual. Nevertheless, the combination of tool manufacture and survival of an edentulous individual *together* could indicate that the Dmanisi hominins may have exhibited social traits common to humans. Together with the baraminic distance results, these cultural evidences further strengthen the inference that the Dmanisi hominins were human.

As a result, the present study even more firmly supports a greater diversity in the human holobaramin than creationists have previously recognized. Whereas other creationists have taken a conservative approach to the human holobaramin and included only *Homo sapiens*, Neandertals, and *Homo erectus* (following Lubenow), Wood's 2010 results and the present study support including much more different forms in the human holobaramin. For example, *Au. sediba* adults are much smaller than adult *Homo sapiens*, and they have significant differences in the pelvis and lower limbs, resulting in less elegant bipedal locomotion than that of *H. sapiens* (DeSilva et al. 2013). *H. naledi* is somewhat shorter than modern *Homo sapiens* and has a much smaller cranium and shorter thorax (Berger et al. 2015). Several features of the *H. naledi* skeleton suggest habitual arboreal or climbing locomotion.

Based on Berger et al.'s (2015) character matrix, both *H. naledi* and *Au. sediba* also share characteristics with *Australopithecus* that are not shared with any other member of *Homo*. *Au. sediba* shares three characteristics with *Australopithecus* that are not observed in members of *Homo*: small cranial capacity (character 1), a marked development of the canine jugum (character 65), and a maxilla-alveolar index that is longer than wide (character 72). *H. naledi* shares two characteristics with *Australopithecus* not observed in members of *Homo*: a lateral entoglenoid process (character 33) and an intermediate petrous orientation (character 38).

Consequently, if the present study is correct in its conclusions, young-age creationists have seriously underestimated the variability of the human holobaramin. While we have successfully recognized some human-like apes as animals, we have not given nearly enough attention to the possibility that some true humans could exhibit more ape-like traits than do modern *Homo sapiens*. As a consequence, creationists who distinguish human from non-human based on similarity only to *modern* humans may be exhibiting dehumanization rather than legitimate baraminological analysis (Wood 2014). Dehumanization is the psychological tendency to view "other" people (dissimilar to one's self) as less human or not human (Haslam 2006).

The present study also reinforces Wood's inference of

**Table 2.** Hominins other than *Homo sapiens* included in the human holobaramin.

Taxon	Representative	Evidence	Citations
Red Deer Cave people	Longlin 1	Morphological similarity	This study
Neandertal	Feldhofer, La Chapelle-aux-Saints, La Ferrassie	Cultural, statistical baraminology, interbreeding	Lubenow 1992, Wood 2010, Wood 2012a
<i>Homo heidelbergensis</i>	Kabwe (Broken Hill)	Statistical baraminology	Wood 2010
<i>Homo erectus s.l.</i>	KNM-WT 15000	Cultural, statistical baraminology	Lubenow 1992, Wood 2010
<i>Homo habilis</i>	KNM-ER 1813	Statistical baraminology	Wood 2010
<i>Homo rudolfensis</i>	KNM-ER 1470	Statistical baraminology	Lubenow 1992, Wood 2010
South African <i>Homo</i> ( <i>Homo gautengensis</i> )	StW 53	Statistical baraminology	Wood 2010, Wood 2011
<i>Homo naledi</i>	DH1	Cultural, statistical baraminology	Wise 2015
<i>Homo floresiensis</i>	LB 1	Cultural	Wise 2005
<i>Australopithecus sediba</i>	MH 1	Statistical baraminology	Wood 2010
Dmanisi hominins	D2700, D4500	Statistical baraminology	This study
Denisovans		Cultural, interbreeding	Wood 2011

discontinuity between the human holobaramin and non-humans. Whereas BDC analysis of the Dembo et al. (2015) supermatrix revealed few instances of significant, negative BDC between humans and non-humans, there were additional instances of significant, negative correlation in the BDC results of the Berger et al. (2015) character matrix. The occurrence of significant, negative correlation can be caused by the presence of significant, holistic dissimilarity, or discontinuity. Further, in both character matrices, no significant, positive BDC was observed between members of *Homo* (+ *Au. sediba*) and other nonhuman animals. Consequently, we may tentatively conclude that a discontinuity surrounds genus *Homo* (+ *Au. sediba*).

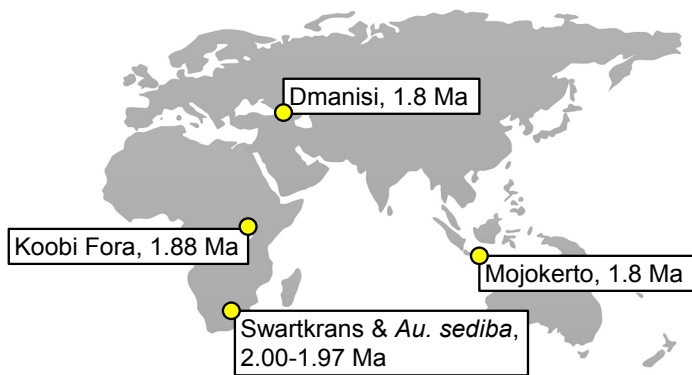
The existence of a robust discontinuity separating human from non-human is reinforced when we recall how much *Homo naledi* and *Au. sediba* differ from other members of *Homo*. In theory, the discontinuity could be eliminated by the discovery of taxa that share characteristics of animals and humans, thus bridging the apparent gap between *Homo* and non-*Homo*. *Homo naledi* and *Au. sediba* would seem to fit those requirements, but the BDC and MDS analysis still support separating hominins into separate clusters even when these intermediate forms are included. As a result, we may be even more confident that the discontinuity between human (the *Homo* cluster) and non-human (other clusters) is real and will withstand future fossil discoveries.

We can also add additional forms to the human holobaramin, even though they were not part of the present or previous analyses. For example, Wise (2005) argued based on usage of stone tools and fire that the Flores fossils referred to *Homo floresiensis* are the remains of true humans. In addition, Wise noted that their location east of Wallace's line implied dispersal by boats, reflecting advanced technology. Thus, although Wood's (2010) baraminological analysis of *H. floresiensis* was inconclusive, we may still include the Flores form in the human holobaramin. In

addition, Curnoe et al.'s (2015) morphometric analysis of the Red Deer Cave people revealed a strong affinity with *Homo sapiens*, thus implying that the Red Deer Cave people are also human. Based on the evidence of interbreeding, Wood (2012a) argued that the Denisovans were also human. To that argument, we may also add the presence of an exquisite chloritite bracelet (Derevianko et al. 2008) in the same deposit as the original Denisovan fossil. The technological skills necessary for manufacture of the bracelet implies an advanced human culture. The full range of human forms based on the current and previous analyses is listed in Table 2.

**Revising the Young-Age Creation Model.** Classifying hominins as human or not human is just the beginning of understanding what these fossils mean. To place hominins in the larger context of our understanding of earth and human history, we need to consider a wide range of data from linguistics, geography, genomics, genetics, and geology, as well as information from the historical records of Genesis. First of all, with the majority of creationist geologists (contra Froede and Akridge [2008]), we can identify all hominin fossils as the remains of post-Flood creatures. All hominins therefore represent the colonizers that refilled the earth after the Flood. We can further infer with Wise (2008), that any hominins classified as truly human must represent post-Babel populations, globally dispersing several centuries after the animals. The lag in human dispersal between the Flood and Babel gives a first-order explanation for the occurrence of human fossils above animal fossils in the fossil record (Wise 2008). Since animals dispersed prior to humans, post-Flood fossils of animals should be found stratigraphically lower than post-Flood fossils of humans.

If the hominins called "early" *Homo* are indeed human, as argued in this study, then the first humans encountered in the fossil record are very unlike living humans. Even more, these first



**Figure 9.** Conventional radiometric dates and locations of the earliest fossils attributed to the human holobaramin in this study.

humans seem to exhibit a greater variability than we presently see in human people groups. This variability is most evident in Dmanisi, where very different hominin skulls have been recovered from the same site and radiometric age, evidently representing a single population (Lordkipanidze et al. 2013). What does this variability mean?

In studies of animal and plant baramins, creationists have argued for a period of rapid diversification after the Flood, corresponding to a high rate of speciation as well as morphological and ecological innovation (Wise 2002, Wood and Murray 2003). The mechanism of this rapid diversification is still a matter of investigation, but the observation of high variability among the earliest post-Flood humans is very consistent with this diversification model. More importantly, it suggests that human diversification began during the construction of Babel, while humans were still a single, small population. Thus, the diversification was sympatric, and diversity preceded dispersal. This is a significant contrast to most evolutionary models, which are generally allopatric models of diversification in which diversity arises only after dispersal, although interest in non-allopatric models is rising (e.g., see Bird et al., 2012, Yukilevich 2014, Papadopulos et al. 2014).

Geographically, we find the earliest hominin fossils already nearly globally distributed (Figure 9) (see Antón and Swisher 2004). The Dmanisi hominins in the republic of Georgia are dated to 1.8 Ma (Garcia et al. 2008). *Australopithecus sediba* in South Africa dates to approximately 1.97 Ma (Pickering et al. 2011). In east Africa, “early” *Homo* fossils from Koobi Fora are older than 1.88 Ma (McDougall 1985). The oldest specimens of South African *Homo gautengensis*, which some refer to *Homo habilis*, date to approximately 2.0 Ma. In east Asia, *Homo* fossils have been dated to 1.81 Ma in Java (Swisher et al. 1994). Stone tools of the Oldowan type from Erk-el-Ahmar have been dated to 1.7-2.0 Ma (Ron and Levi 2001). Additional remains older than 2.0 Ma have been attributed to *Homo*, although these attributions are contested (Antón 2012, Villmoare et al. 2015a, Hawks et al. 2015, Villmoare et al. 2015b). Dates such as these differ by at least 200,000 years in conventional, radiometric time, but when rescaled to a young-age creationist time scale, they are nearly contemporaneous.

The near contemporaneous appearance of a variety of human

forms in southeast and central Asia and southern and eastern Africa raise important geographic questions. First, do we have the correct location of Babel and the mountains of Ararat? That question is quite beyond the scope of this present paper, but we may proceed with the traditional assumption that Ararat (and hence Babel) is located somewhere south of the modern Caucasus Mountains (Crouse 2001). Second, if the Caucasus region is the source of post-Flood human dispersal, why do we not see more evidence of early human fossils from the Caucasus region? Was the global dispersal fast enough that we find little fossil evidence? Third, will we find additional *Homo* fossils prior to 2.0 million radiometric years that show a more restricted geographic range of humans in the past? As noted above, there are a few fossils from >2.0 Ma that are attributed, not without controversy, to *Homo* (Antón 2012, Antón et al. 2014). The newly-discovered Ledi-Geraru mandible is the radiometrically oldest of these, dated to 2.8 Ma (Villmoare et al. 2015a). In addition, clear evidence of animal butchery by stone tools at Gona, Ethiopia has been dated to 2.58-2.1 Ma (Dominguez-Rodrigo et al. 2005). Are these the first of other fossils that will reveal the original dispersal from Babel?

The geography of human fossils provides additional support for the young-age creation model herein developed when we consider location together with variation. The highly variable Dmanisi hominins, dated to 1.8 Ma, are recognized as the most variable hominin population in the world. They also happen to be found in very close proximity to the traditional site of Babel and the mountains of Ararat. Dmanisi is less than 200 miles from the mountains believed to be the mountains of Ararat. If Babel, near Ararat, was the site of a highly variable human population, the extreme variability observed in the geographically proximate Dmanisi hominins can be readily understood.

Culturally, non-*sapiens* humans appear to lack advanced technology and ritualistic practices associated with modern humans. Why is this? Some creationists attempt to argue that Neandertals actually do possess advanced cultural practices similar to our own (e.g., Lubenow 1992, Phillips 2000, Jaronyk 2007); however, the absence of such practices is more pronounced in other human forms, such as *Homo erectus*. Other than the manufacture of stone tools and use of controlled fire (Clark and Kurashina 1979, Kimbel et al. 1996, Goren-Inbar et al. 2004), these *Homo* forms appear to be quite “primitive.”

In answering the question of the missing cultural indicators, we must first recall that in the young-age creationist model these human forms are not existing for hundreds of thousands of years making only stone tools. Instead, most of these forms may represent only a few generations of people who were culturally disadvantaged at the confusion of Babel. Most of the earliest post-Babel groups were still recovering basic technologies lost after the confusion. Within a few generations, however, most people had recovered sufficiently advanced culture to appear “human” again to modern archaeologists.

**Implications and Predictions.** Because it is a work in progress, this young-age creationist model raises almost as many questions as it answers. In order to avoid any appearance (or accusation) of favoritism toward this model, it is appropriate to review some of the more outstanding questions raised.

First, where are the fossils of the people killed in the Flood?



If all hominin fossils are post-Flood, what happened to the pre-Flood people? This question is not unique to this model but is a perennial problem for young-age creationist models of all types.

Second, what could cause such variation to arise in a single population? Numerous hypotheses have been proposed to explain post-Flood diversification (e.g., T.C. Wood 2003, Borger 2009, Lightner 2009), but none of them have convinced a consensus of creationist scholars. For some, this problem represents a significant barrier to recognizing other forms of *Homo* as human (Habermehl 2010).

Third, why is there only one “species” of human alive today? Were there simply *Homo sapiens* in each of the main three lineages descended from Noah’s three sons? If so, why do we not find *Homo sapiens* fossils until the most recent fossil layers?

Fourth, where are the rest of the non-human hominin fossils? In conventional dating, the oldest hominins date to 6-7 Ma, but the Flood/post-Flood boundary would have a radiometric age of much older than that, assuming that the K/T is the Flood/post-Flood boundary (Ross 2012). According to Wise’s (2009) Post-Flood Continuity Criterion (PFCC), we should expect to see a continuous fossil lineage from the end of the Flood for each terrestrial animal baramin. Will we find in the future additional non-human hominin fossils, or do they belong to a larger primate baramin that already exhibits an unbroken fossil record to the end of the Flood?

Fifth, how can we integrate this fossil-based model with the findings of comparative genomics and paleogenomics? What does the evidence of multiple genetic lineages of humans mean (T.C. Wood 2012b)? What does evidence of interbreeding between modern humans and extinct human forms tell us about post-Babel dispersal (T.C. Wood 2012a)? Even more importantly to the larger context of evangelical debates over the historical Adam, what does the similarity of human and nonhuman genomes mean if not common ancestry (T.C. Wood 2006)?

Sixth, what is Babel? Traditionally, Babel is associated with Sumerian ziggurats known from archaeological remains (Seely 2001; Walton 1995). If, however, the Babel dispersal pre-dates 2 Ma in conventional dating, no Babylonian ziggurat can be the tower of Babel. Are the remains of this earliest human culture still to be found?

In addition to these questions, we may also make certain predictions assuming that the model (or portions thereof) are true. First and most obviously, we can predict with some boldness now that fossils truly bridging the gap between human and nonhuman will not be found. If *Au. sediba* and *H. naledi* do not statistically connect humans with nonhumans, it is unlikely that any future taxa will. Future discoveries will continue to cluster with existing groups.

Second, if non-human hominins form their own unique baramin, we may predict based on Wise’s PFCC that additional, bipedal hominins could be found pre-dating the supposed human-chimpanzee “last common ancestor” at 5 Ma. Consequently, at 7Ma, *Sahelanthropus* is not a debatable hominin nor merely a member of a nonhuman ape kind (Murdock 2004) but rather an important confirmation of creationist claims about human baraminology and the fossil record. As a bipedal creature, *Sahelanthropus* fills in the fossil interval between the Flood/post-Flood boundary and the commencement of the nonhuman

hominin fossil record.

Third, future discoveries of “early” *Homo* will not clarify or resolve the species status of any of the proposed species. Instead, we should continue to discover a confusing mosaic of forms representing the morphological diversity of the Babel population. Indeed, one could argue that the term “species” is not appropriate to apply to these earliest human forms. Since they survived only a few generations and exhibited extreme variability in a single population (see Dmanisi), they do not appear to be analogous to modern biological species, which persist for many generations and exhibit substantial morphological uniformity. Consequently, the current debate over the number of hominin species is unlikely to ever be resolved, since the fossils in question are not from what we understand to be “species.”

**What about Adam?** In the context of the larger evangelical debate over the historical Adam, the present study provides several benefits even though it does not identify the actual historical Adam. First, it continues to develop a rigorous model to explain the hominin fossil record. Human evolution is often portrayed as undeniable in part because of the fossil record, leading some evangelical scholars to conclude that theology must be reimagined in the light of evolution. Very little attention is given to the possibility that the fossil record could be “reimagined” in light of the historicity of Genesis. Here, an alternative interpretation of the fossil record is shown to be at least possible.

Second, the expansion of the human holobaramin to include multiple “early” *Homo* forms should rectify the problem of looking for Adam in the wrong place. In modern treatments of the historical Adam, scholars assume that Adam and Eve should have been the parents of modern *Homo sapiens* only (e.g. Venema 2010, Poythress 2013). In light of the present study, such assumptions exclude a number of human forms and thus do not represent the correct genealogical location of Adam and Eve. If looking for Adam and Eve, we must look much farther than just *Homo sapiens*.

Third, discussions of the origin of human uniqueness and the *imago dei* are challenged by the idea of human evolution (e.g., Peterson 2011, Fergusson 2013, Hecce 2015, Moritz 2015). In particular, human cultural indicators such as burial and tool use that traditionally have been identified with the *imago dei* are now known from hominins other than *Homo sapiens*. If we view human as only *Homo sapiens*, then these cultural indicators really do challenge our understanding of human uniqueness. If, however, we broaden our understanding of what is “human” to include other members of genus *Homo*, the problem of human “uniqueness” is largely alleviated. There is no need to propose the evolution of the *imago dei* (Peterson 2011, De Smedt and De Cruz 2014) or the presence of the *imago dei* (or the “likeness” of God) in animals (Putz 2009, Deane-Drummond 2012).

Despite these advantages, the work presented here is unlikely to sway any scholar already convinced of the authority of science and the malleability of theology. Nevertheless, young-age creationists ought not be discouraged. Instead, we ought to persist in developing this model to expand our understanding of the post-Flood dispersal and diversification of humans and ultimately bring glory to God. As the model develops and matures, it will become increasingly powerful and persuasive. Additionally, as we encourage a new generation to bring both science and religion



under the rule of Christ, we can be assured of a bright and exciting future for Christians in science.

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