

Baraminology, the Image of God, and *Australopithecus sediba*

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Abstract

Previous research in hominid baraminology has been sharply criticized by other creationists, especially concerning the proposal to include *A. sediba* in the human holobaramin. These criticisms can be summarized as concerns over methodology, theological objections, and rejection of speciation among human lineages. Methodological concerns, though reasonable, can be recognized and at least partially overcome. Theological objections regarding the image of God or the doctrine of salvation simply fail as valid reasons to reject human baraminology. Concerns over human speciation similarly are not adequate refutations of human baraminology. To advance creationist understanding of baraminology, a new way of explaining the research program of statistical baraminology is introduced: testing the discontinuity hypothesis, the idea that God created organisms in discrete, recognizable groups.

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Introduction

The recent baraminological analysis of fossil hominids (Wood 2010a) elicited strong responses, some by personal communication and others in published form (Line 2010; Menton 2010; Habermehl 2010; DeWitt 2010). In the original study, statistical baraminology methods were used to analyze sets of characteristics of fossil and extant hominids compiled by conventional paleoanthropologists for cladistic analysis. The results of this study revealed evidence of discontinuity between members of the genus *Homo* and members of other genera (*Australopithecus*, *Paranthropus*, *Pan*, etc.). Surprisingly, the newly-described *Australopithecus sediba* (Berger *et al.* 2010) grouped not with other australopiths but with members of *Homo*. Since this clustering was robust and was influenced neither by bootstrap sampling nor by inclusion or exclusion of taxa, I concluded based on the limited data available that *A. sediba* was a member of the human holobaramin and therefore descended from Adam and Eve.

Regarding my hominid baraminology study, the inclusion of *A. sediba* in the human holobaramin has been the primary focus of other creationists' objections (Line 2010; Menton 2010; Habermehl 2010; DeWitt 2010). A recurring theme in many

criticisms is the implication that somehow baraminology is itself faulty or illegitimate. After studying the written and verbal responses to the hominid baraminology study, I can summarize the various objections in three basic concerns: (1) speculation that the data are biased or inadequate; (2) the very idea that humans could have existed as multiple species in the past is objectionable in some way; and (3) that the inclusion of *A. sediba* in the human holobaramin is theologically offensive or problematic for the biblical concept of the "image of God." All three of these issues warrant further commentary and clarification, which I hope to provide here.

The doubts raised about baraminology itself seem to reveal an underlying misunderstanding of the research program of baraminology and its relationship to the methodology of statistical baraminology. Since I have become a well-known advocate of baraminology, I bear at least partial responsibility for not clearly explaining these issues. Consequently, in the final section of this paper, I will attempt to correct this confusion by introducing a new way of thinking about baraminology research that focuses on what I will call the "discontinuity hypothesis." I emphasize that this is not a new baraminology or a new type of baraminology but rather a new way of thinking about baraminology as it is already practiced.

Table 1. Characters summarized from Berger *et al.*'s (2010) published list

Characters shared between *Australopithecus sediba* and *Homo erectus*

1. Weak A-M incursion of temporal lines on frontal bone
2. Wide position of temporal lines on parietal bones
3. Compound temporal nuchal crest in males absent
4. Slight postorbital constriction
5. Reduced pneumatization of temporal squama
6. Low facial hafting
7. Frontal trigon absent
8. Narrow supraglenoid gutter
9. Short horizontal distance between TMJ and M2/M3
10. Parietal transverse expansion present
11. Supraorbital expression torus
12. Supraorbital contour arched
13. Lateral half of infraorbital margin not blunt and protruding
14. Zygomatic arch level with inferior orbital margin
15. Infraorbital region convex
16. Nasal bone projection not above frontomaxillary suture
17. Wide inferior projecting nasal bone
18. High infraorbital foramin
19. Blunt interolateral nasal aperture margin
20. Slight eversion of superior nasal aperture margin
21. Nasoalveolar triangular frame
22. Stepped nasal cavity entrance
23. Straight nasoalveolar clivus contour in coronal plane
24. Weak subnasal projection
25. Maxillary fossula absent
26. Incisor vertical
27. Medial expansion of frontal zygomatic process
28. Curved angular indentation of lateral orbital margin
29. Slight zygomatic prominence
30. Slight lateral flaring of zygomatic arches
31. Outline of superior facial mask squared
32. Infraorbital plate at right angle to alveolar plane
33. Zygomaticomaxillary steps and fossae absent
34. Malar thin
35. Projection of zygomatics posterior to nasal bones
36. Masseteric posterior to sellion
37. Straight lateral anterior facial contour
38. Incisors protrude beyond bi-canine line
39. Parabolic dental arcade
40. Maxillary 12/C diastema absent
41. Mandibular symphysis vertical
42. Slight bony chin
43. Lateral mental foramen opening
44. Post-incisive planum weak
45. Small mandibular corpus cross-sectional area at M1
46. Canine-to-postcanine ratio large
47. No maxillary premolar molarization
48. Weak buccal grooves on maxillary premolars
49. Weak median lingual ridge of mandibular canine
50. Protoconid more mesial cusp than metaconid (molars)
51. Thick enamel

Before discussing these criticisms, we should recall that any creationist analysis of fossil hominids is inherently difficult. Important hominid fossils are extremely fragmentary, and key taxa (such as *A. sediba*) are known from only a few individuals. In addition, the specimens are not available for direct study by amateurs. Despite numerous creationist articles and books on the subject, very few creationists have any training or experience in paleoanthropology. The Bible offers little guidance on this issue either. Other than the occasional mention of giants (e.g., Num. 13:33, II Sam. 21:20), there is no biblical record of the presence or absence of significant physical variations among humans. The

Characters shared between *Australopithecus sediba* and *Australopithecus africanus*

1. Small cranial capacity
2. Compound temporal nuchal crest in males absent
3. Low facial hafting
4. Frontal trigon absent
5. Narrow supraglenoid gutter
6. Lateral half of infraorbital margin not blunt and protruding
7. Zygomatic arch level with inferior orbital margin
8. Infraorbital region convex
9. Nasoalveolar triangular frame
10. Stepped nasal cavity entrance
11. Straight nasoalveolar clivus contour in coronal plane
12. Canine fossa present
13. Maxillary fossula absent
14. Incisor vertical
15. Anterior nasal spine anterior to nasal aperture
16. Straight zygomaticoalveolar crest/malar notch
17. Zygomaticomaxillary steps and fossae absent
18. Masseter origin high
19. Malar thin
20. Masseteric posterior to sellion
21. Incisors protrude beyond bi-canine line
22. Anterior palatal deep
23. Maxillary 12/C diastema absent
24. Slight bony chin
25. Moderate torus marginalis and marginal tubercles
26. Small mandibular corpus cross-sectional area at M1
27. Moderate incisor-to-postcanine ratio
28. Canine-to-postcanine ratio large
29. Maxillary I1:MMR moderate development, lingual face
30. Two mandibular P3 roots
31. Peak of enamel forms between roots of molars
32. Thick enamel
33. Apices of lingual cusp slightly buccal, buccal cusp moderately lingual on premolars and molars relative to occlusal margin

existence of human-like apes is also not mentioned in the Bible. In short, definitive diagnosis of fossil remains as human or ape may not be as easy as some would like – or indeed, even possible for certain poorly-represented taxa. Any conclusions about fossil hominids, especially those on poorly-known taxa, can only be considered tentative.

Biased Data

The first major concern raised by critics of my study is that I relied on biased data generated by evolutionists, thus

nullifying my results. To be sure, the possibility of bias should be considered, but it is not sufficient to simply cast aspersions on someone's work because the person is an evolutionist. We must identify actual evidence of specific bias. In reading the original description of *A. sediba* (Berger *et al.* 2010), there does appear to be a bias against including *A. sediba* in the genus *Homo*, as evidenced by the following observations: First, the craniodental characteristics listed in their table 1 show far more character states in common between *A. sediba* and members of *Homo* than between *A. sediba* and australopiths. For example, *A. sediba* and *H. erectus* share 51 character states out of the 69 listed, while *A. sediba* and *A. africanus* share only 33 character states (Table 1). Why place *A. sediba* in the genus *Australopithecus*? Berger *et al.* (2010) state that nine characters ought to be weighted as more significant in determining the generic classification of *A. sediba*, although they do not explain or justify their emphasis of these nine characteristics.

Second, in Berger *et al.*'s (2010) figure 2, the partial remains of the two *A. sediba* skeletons MH1 and MH2 are shown superimposed on a silhouette of an idealized *A. africanus* skeleton. A close examination of the figure reveals that the limb bones of *A. sediba* fit the *A. africanus* silhouette poorly. In particular, the tibia of MH1 extends well below the ankle of the *A. africanus* skeleton, and the distal ends of the radius and ulna of MH2 do not extend as far as the corresponding bones in *A. africanus*. It would appear that the choice of the *A. africanus* silhouette gives an exaggerated visual impression that the MH1 and MH2 skeletons are more australopith-like than they actually are.

Third, the cladogram included in Berger *et al.*'s (2010) supplementary material as figure S3 indicates that *sediba* occupies a position at the stem of the *Homo* clade. The taxon STW 53, which at the time was not formally named, occupies a position at the stem of the *A. sediba*/*Homo* clade (Figure 1). Since Curnoe's (2010) description of STW 53 places it in the genus *Homo*, *sediba*'s position in Berger *et al.*'s cladogram would support either placing *A. sediba* in *Homo* or reclassifying *H. gautengensis* (the name for STW 53) as *Australopithecus*. Otherwise, *Homo* is rendered polyphyletic. These phylogenetic results certainly call for a significant revision of genus *Homo*, and it seems likely that some secular paleoanthropologists will propose including *A. sediba* in an enlarged genus *Homo*.

Considering all three of these evidences, it seems that Berger *et al.* (2010) do show a mild bias against including *A. sediba* within the genus *Homo*. This is in contrast to the usual creationist opinion regarding fossil hominids: that their ape-like attributes are minimized or ignored in favor of emphasizing their less significant human-like characteristics. Berger *et al.* (2010) seem to be doing the opposite. They emphasize the few ape-like characteristics while minimizing the many more characteristics in common with *Homo*. Since my baraminological analysis unequivocally places *A. sediba* within *Homo*, I suggest that my study has overcome this apparent bias of Berger *et al.* Thus, bias in the data seems to be a diagnosable and negligible problem.

Multiple Human Species

Recognition of multiple species in the human holobaramin would superficially appear innocuous and inconsequential, given

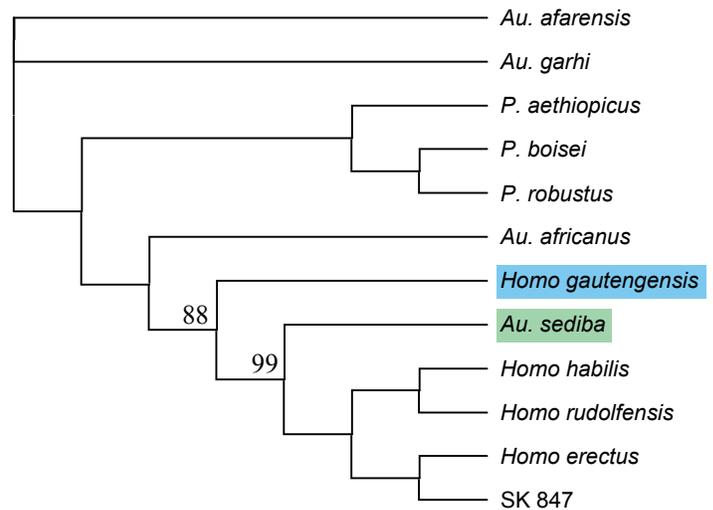


Figure 1. The single most parsimonious tree from Berger *et al.* (2010) with the positions of *Australopithecus sediba* and *Homo gautengensis* (STW 53) highlighted in green and blue respectively. Bootstrap percentages shown are based on 10,000 replicates, as reported by Berger *et al.* (2010). Note: SK (Swartkrans) 847 is a partial cranium referred to *H. erectus* or *H. habilis* (Grine *et al.* 1993).

wide acceptance among creationists of multi-species holobaramins of animals and plants. Something about multiple *human* species, however, repeatedly elicits negative responses (*e.g.*, Menton 2010). Perhaps at the root of this anxiety is an inappropriate view of species, which might be rooted in lingering notions of species fixity. Alternatively, critics might be responding negatively to nineteenth century attempts to classify living humans into separate species for racist purposes.

When I speak of multiple species of human, I use the term *species* strictly in a biological sense. Having said that, I recognize that biologists have proposed many different species concepts over the years (see Wilkins 2009). Some species concepts emphasize genetic or hereditary characteristics, such as reproductive isolation, while others emphasize morphological differences that can be recognized. The diversity of species concepts has been a source of consternation to numerous creationists (*e.g.*, Marsh 1947; Tinkle 1967). In essence, early creationists were concerned that the newer species concepts gave a false impression of evolution by labeling mere varieties as true species.

With disagreements about the precise nature of species, how can anyone be certain that there are multiple species of humans? The problem is not as hopeless as it might seem. As de Queiroz (2007) has argued, the varying species concepts have a certain underlying conceptual unity to them, and this unity can provide a way through the disagreements. Though he expresses his ideas in evolutionary terms, de Queiroz's approach is readily adaptable to a creationist discussion of species. His key insight is the recognition that all species concepts emphasize biologically important criteria, but no single criterion is sufficient to recognize all species. In other words, he advocates a pluralistic approach to the criteria by which we recognize species.

To illustrate this pluralistic approach to species, we can consider some uncontroversial examples from the animal kingdom. The

lion and tiger are easily recognized as different species by any species concepts that emphasize morphological differences. Yet lions and tigers are interfertile and can produce fertile, hybrid offspring, so they are not strictly reproductively isolated, which is a characteristic emphasized by the biological species concept. In the case of cryptic species, however, the opposite is true; cryptic species cannot be distinguished by appearance but they are reproductively isolated.

In the case of fossil hominids, well-known taxa like Neandertals and the *H. erectus* complex are known from numerous individuals (see MacLachy *et al.* 2010) and are well-documented as different from modern humans. Neandertals in particular have good evidence of being a separate species from modern *Homo sapiens*. Neandertals differ from modern humans in their morphology and their development (*e.g.*, Ponce de León and Zollikofer 2001; Smith *et al.* 2010). The recently reported Neandertal genome also revealed genetic differences from modern humans (Green *et al.* 2010). The Neandertal genome also revealed evidence of hybridization with Europeans and Asians, but the levels were so low (<5%) that one may conclude that Neandertals in general did not hybridize with contemporaneous *Homo sapiens*. Though there is no genetic evidence from *H. erectus*, its morphology is even more different from modern *Homo sapiens* than Neandertals, thus supporting classification as separate species.

For species known from only a few specimens, however, their status as a true species is certainly open to question. In such cases, I am less interested in whether this or that fossil is a different species and more interested in the baraminic membership of the fossil itself. I refer to these lesser known fossils by their species designations (*Homo rudolfensis*, *Homo habilis*, *Australopithecus sediba*) with the understanding that these names refer to particular small sets of skeletal remains and that the species designations are subject to change. Given their morphological difference from all other fossil hominids, however, it is unlikely that they could be reduced to varieties of previously-known species.

Remember, though, that these are species strictly in the biological sense and not unique creations, separate from the descendants of Adam and Eve. The present situation is quite different from the anthropological polygenism/monogenism controversies of the nineteenth century, where some individuals attempted to argue that modern humans should be divided into separate species (for excellent overviews of these controversies, see Desmond and Moore 2009 and Livingstone 2008). We now recognize that these arguments were driven by racism of white Europeans against Africans, rather than by legitimate scientific issues.

With such ugly misuse of human species classification in the recent past, why risk any association with racist ideology by asserting that there used to be more than one species of human? I am emphatically not arguing that there are different species of *modern* humans. There is no basis for separating modern humans into separate species. Furthermore, classification of extinct humans as separate species is unlikely to be subverted for racist purposes since the non-*sapiens* species are all extinct. There is no opportunity for unethical individuals to use my work as an excuse to mistreat or abuse people who are already dead.

One final point in relation to human species ought to be made. It is possible that some individuals might associate the term

“species” with zoology and therefore react against applying an animal concept to humans (who are not animals). Though some might argue that we should be sensitive to the public’s misconceptions and adjust our use of terminology accordingly, I believe that we ought not pander to public ignorance. We have an excellent opportunity here to educate the public about the reality of biological species, namely that species are nothing special. The term *species* is just a convenient way to describe the genetics, appearance, and mating habits of certain populations of organisms. Though humans can be discussed in a strictly biological sense (just as a doctor might do when discussing disease or injury), this should not be misconstrued as debasing or degrading to humans.

Theological Implications of “*Homo sediba*”

Both in personal discussions about *A. sediba* and in formal written responses, theological questions are raised, particularly about the image of God and the doctrine of salvation, and these questions warrant further discussion than was possible in the original paper. Two questions are pertinent: First, what are the theological consequences if I am wrong about including *A. sediba* in the human holobaramin? Second, what are the theological consequences if *A. sediba* really is human?

If I am wrong about *A. sediba*, then I have made a simple mistake. Like Scheuchzer (1726) who famously mistook a giant salamander fossil for an antediluvian human, I might suffer some public embarrassment (see especially White 1922, p. 228), which can hardly be called “suffering.” A more significant problem would be misleading the public, especially when some members of the public might be critically evaluating creationism or even Christianity itself by my actions. In this regard, it is helpful to recall the history of the Paluxy tracks.

A 1950 article by creationist Clifford Burdick in the Seventh-day Adventist publication *Signs of the Times* brought the Paluxy tracks to public prominence (though they had been mentioned a decade earlier by Allen 1939a, 1939b). After three decades of promotion by creationists as decisive evidence that humans and dinosaurs lived together, research by Kuban (1986) indicated that the alleged human tracks were partially-infilled, plantigrade dinosaur footprints. Additional research raised serious doubts about the authenticity of the tracks (Cole and Godfrey 1985), and John Morris (1986a) summarized the controversy and warned, “it would now be improper for creationists to continue to use the Paluxy data as evidence against evolution.” As a result of this incident, ICR endured criticism from supporters (in Morris 1986b) and from critics (Hastings 1988)

The Paluxy incident differs in important ways from the present issue of *A. sediba*’s proposed humanity. First, Paluxy was from the beginning promoted as definitive evidence that evolution was wrong and creationism was correct (Burdick 1950). In contrast, my own article on *A. sediba* includes a critique of my own findings, which I have extended here and elsewhere (Wood 2010b). Second, the claims about Paluxy were targeted for the most part at the general public in magazines (Burdick 1950) and newsletters (Taylor 1971) prior to any serious technical examination (*e.g.*, Neufeld 1975). In contrast, my hominid baraminology work appears in the technical *Answers Research*

Journal, and it is not written for the comprehension of the general public. Finally, the claims about Paluxy did their damage primarily because people believed or wanted to believe them. Judging by the reaction to the hominid baraminology paper, it appears that very few creationists believe me. As a result, creationists will likely feel vindicated rather than disillusioned if I am shown to be wrong about *A. sediba*.

It would seem then that I run little risk of misleading anyone if I am wrong about *A. sediba*, which brings us to the far more interesting question: What if *A. sediba* really is human? Menton (2010) poses a number of questions about salvation and redemption of putative human species other than *Homo sapiens*, and others have raised the more ontological question of how *A. sediba* would relate to the image of God.

Gentry (2008) briefly surveyed interpretations of the image of God in Christian theology. Following a similar survey by Westermann (1994), Gentry noted five ways of understanding the image of God and advocated a sixth. The first view, commonly attributed to Irenaeus (but see Purves 1996), distinguishes the image of God from the “likeness” also mentioned in Gen. 1: 26. Irenaeus interpreted the image as natural qualities that make humans like God and the likeness as supernatural qualities that we share with our Creator. The second view, that the image refers to mental or spiritual qualities that make us like God and set us apart from the animals, is easily the most popular view among contemporary Christian commentators (e.g., Orr 1948). The third view locates the image in a physical likeness to God, and the fourth view sees humans as God’s ruling representatives. The fifth view identifies the image as our ability to have a relationship with God. In contrast to these Gentry argued that the image of God is neither a quality we possess nor a relationship we have. Instead, the image of God is a position we occupy as servant kings, with a covenant relationship to God (as His children) and to creation (as God’s designated rulers).

For five of these views, the image of God is not equated to any physical quality. Indeed, most modern theologians would argue that the physical form of a human does not alter a person’s status as the image of God. A multiple amputee possesses just as much of the image of God as a person with Down Syndrome or an undeveloped embryo or a person of “normal” adult development. Similarly, *A. sediba*’s humanity would pose no theological problem insofar as *A. sediba* is just a physically different form of human. The only interpretation of the image of God that could possibly be threatened by *A. sediba*’s humanity would be equating the image with a physical resemblance, a position somewhat common among critical exegetes (see discussions in Clines 1968; Miller 1972; Westermann 1994, pp. 149-150) and rabbinic theologians (see Gottstein 1994). I suspect that most evangelical theologians would view God as a spirit, with no body to resemble the body of humans. Thus, we may dispense with this unusual view of the image of God.

Viewing *A. sediba* as human therefore offers no challenge or threat to the image of God. What then would including *A. sediba* in the human holobaramin do to the doctrine of salvation? Menton (2010) asked, “... is man one of a kind, or can humans be taxonomically classified into various species like animals? ... May we assume that the first Adam and the last Adam (the incarnate Christ) are the same species? Is this important for

Christ’s substitutionary atonement?” To answer his first question, multiple species of humans does not threaten our uniqueness in creation. As I have just argued, humans remain the image of God no matter their form. Whether or not Adam and Christ were the same species is equally irrelevant. Christ died for all humans, regardless of their appearance.

In conclusion, then, I see no legitimate theological objection to including *A. sediba* in the human holobaramin or to recognizing that there were once multiple human species. The number of human species is not taught in the Bible (since *species* is a modern concept foreign to the concerns of scripture), and biblical theology easily accommodates multiple human species. Consequently, this is a matter to be decided on the biological evidence alone.

Baraminology and the Discontinuity Hypothesis

Running through most of the critiques of hominid baraminology is a skepticism of statistical baraminology as a research program. Statistical baraminology relies on the refined baramin concept (Wood *et al.* 2003) for its philosophical justification, but it is important to remember that though reasonable, the refined baramin concept is at its core a hypothetical description of creation. The refined baramin concept is based in part on the description of creation in Genesis 1 and in part on the hypothesis of what we might call recognizable discontinuity.

For a biblical justification of baramins, we can rely only on the general description of creation in Genesis 1. Creationists commonly link the idea of baramin directly to the Hebrew term *mîn* or “kind” (especially since the etymology of *baramin* is from the Hebrew words for “create” and “kind”), but a careful examination of *mîn* cannot sustain its use as a technical term of classification (Wood *et al.* 2003). Particularly in the kosher food lists of Deuteronomy 14 and Leviticus 11, we find *mîn* applied to groups at different levels of our modern taxonomy. Furthermore, the common assertion that Genesis 1 teaches that baramins are limited to reproducing “after their kind” is also unbiblical. In Genesis 1 *mîn* is not used in context with reproduction (instead, “after its kind” describes the *creation* of organisms), and the commands to reproduce in Genesis 1:22 and 1:28 make no mention of *mîn*.

Despite the imprecise term *mîn*, the general description of the creation of animal and plant life allows room for hypothesizing something like “created kinds” or baramins (I am here using baramin in a technical, biological sense). The terminology used to describe creation is neither taxonomically exact (to the level of mentioning particular species) nor vague (mentioning only “animals” or “plants”). Genesis gives enough description (e.g., “fruit trees,” “flying things,” “creeping things”) to rule out universal common ancestry and the evolution of humans from animals, but not enough description to say precisely what species of animals and plants were originally created.

Biologically, it is clear from a wide array of evidences that species are not fixed. This has also been the opinion of all manner of creationists even before Darwin (Wood 2008a; Garner 2009). At the same time, there appear to be marked differences between organisms that make classification possible. We do not find the form of organisms insensibly grading into other organisms. Instead, we find classes that are recognizably different from

other classes. These differences led creationist pioneer Frank L. Marsh to claim that morphological discontinuity marked the limits of the created kinds (e.g., Marsh 1947, pp. 100-101, 116-117, 133-135, 163, 165). It should be noted that Marsh believed that morphology alone was an unreliable guide to classifying organisms in baramins (1947, p. 164), but with fossil organisms, morphology is often all the evidence we have available to us.

When we consider the biblical and biological evidence together, it seems quite reasonable to hypothesize that God created organisms in the categories that we call baramins, within which considerable diversification and speciation can take place but between which there are significant dissimilarities that Marsh called discontinuity. Though these conclusions are reasonable, as I explained above, they are not clearly and irrefutably taught in the Bible and are therefore open to empirical testing, insofar as we can do so. This is the research program of baraminology, to evaluate the claim that organisms were created in discrete, discontinuous groups that are recognizably different from all other organisms. We can call this idea the “discontinuity hypothesis.”

To test the discontinuity hypothesis, statistical baraminology uses tabulations of characteristics to try to estimate morphological “distances” between organisms. Based on these distances, it is possible that significant differences reflecting a discontinuity could be detected. Presently, the dominant method to do this is a simple correlation technique (see Wood 2002 for an explanation of this technique), although other methods could also be proposed and developed. Thus far, research using the correlation technique has been promising, although not decisively in favor of the discontinuity hypothesis. Predictions of discontinuity appear to be accurate in about 60% of the test cases, but this is not statistically significant (Wood 2009). This is one reason why testing statistical baraminology on fossil hominids is so important. Since we know biblically that humans and apes had separate origins (Gen. 2:7), the discontinuity hypothesis would predict that humans will be recognizably different from apes. The significance of hominid baraminology is that members of the genus *Homo* can be readily distinguished from australopithecids and other apes, which confirms the discontinuity hypothesis.

Statistical baraminology does have drawbacks, however, especially in the area of character selection (Williams 2004; Wood 2008b). Put simply, how do we know which characteristics are important in distinguishing baramins? Since the characteristics are used to calculate distances, it would be easy to assemble a set of characteristics that could exaggerate differences (or similarities) between any set of taxa. For example, how do we know that the characteristics listed in Table 1 have anything to do with the baraminic status of *A. sediba*? This sounds like it would render statistical baraminology ultimately arbitrary and meaningless, but there are ways of dealing with the problem of character selection.

First, try to avoid imposing a creationist bias (e.g., for finding discontinuity at a particular taxonomic level) by evaluating character sets compiled by noncreationist experts. It is true that these sets of characters could also be biased, but since they are compiled for cladistic analysis rather than statistical baraminology, I doubt that the bias would be consistently in favor of the discontinuity hypothesis. In practice, this seems to be the case. Though the rank of family is generally where we

find the strongest evidence of discontinuity, there are significant exceptions (Wood 2006). Baraminological analyses of some character sets even yield uninterpretable results, as it did for two character matrices in the hominid baraminology study (Wood 2010a). Since discontinuity is observed as predicted in 60% of cases studied (Wood 2009), I would argue that any “pro-evolutionary” bias does not seem to be adversely affecting statistical baraminology studies.

Second, bootstrap sampling provides a means of evaluating the sensitivity of correlations to the underlying sets of characteristics. By randomly sampling characteristics and recalculating distances and correlations, we can distinguish correlations that are observed regardless of the set of characters chosen from those that depend on a specific combination of characters. Those correlations that appear commonly in bootstrap sampling are robust and presumably more biologically meaningful than those that require a certain set of characteristics. Consequently, though DeWitt (2010) is concerned that *Australopithecus africanus* is positively correlated with members of *Homo* in some analyses, the bootstrap values of those correlations are low. The importance of these correlations are justifiably minimized, since the correlations seem to be highly dependent on a specific combination of characters. The positive correlations observed between *A. sediba* and members of the genus *Homo* differ in that they have very high bootstrap values, implying that the correlations are likely biologically meaningful.

A third method of coping with the problem of character choice is to use multiple character sets compiled for the same taxa, which I did for the fossil hominids. Consistent correlations observed in different datasets would have the same interpretation as high bootstrap values; these correlations are more likely to be biologically significant. The eight character sets of fossil hominids that I examined were by no means independent samples (since most used various subsets of characteristics used by the others), but they were different enough to potentially yield different results. Though two character sets yielded inconclusive results, the remaining datasets implied a consistent discontinuity between *Homo* and other hominids. In this regard, it is important to note that the position of *Australopithecus sediba* in the genus *Homo*, though strongly supported by the data used in my study, is only supported by one character set. It would be preferable to have additional character sets from other specialists to confirm this classification.

Finally, with regard to character selection, DeWitt (2010) is correct that the characters in statistical baraminology are all equally weighted. Though he finds this questionable, he and other critics provide little justification for using the characters they prefer to distinguish *A. sediba* from members of genus *Homo*. DeWitt (2010) emphasizes limb proportions, and Menton (2010) notes the differences in noses between *A. sediba* and *Homo sapiens*. Why these specific characteristics should be diagnostic of the human holobaramin is unclear. In contrast, the equal weighting scheme of statistical baraminology has an advantage, in that it uses “a suite of characters to define ‘human’” rather than reducing “humanness to cranial capacity, limb proportions, ... bipedality,” or any other specific characteristic that might have varied in the past (Wood 2010a).

In my original paper, I listed three cautions about interpreting the results from my original paper (Wood 2010a). In the context

of this discussion of statistical baraminology, I hope the reader can better appreciate them now. First, I argued that the character sets used were not holistic, even though the refined baramin concept requires that baramins be defined using holistic similarities. Besides cranial features, an ideal baraminology study would also use postcranial characters, but these characters are presently unavailable for most hominid taxa. Some important species (*Homo habilis* and *Homo rudolfensis*) have few or no postcranial remains. My second caution was the recognition that many character states were unknown for many taxa. This is another unavoidable drawback for statistical baraminology studies of fossil taxa. Since the key fossils are fragmentary and incomplete, the number of characteristics that can be used in statistical baraminology is limited. Precisely how unknown character states affect baraminology is presently unknown, but they are definitely another detraction from a truly holistic sample of characters. My third caution dealt with the selection of characters, which I explained above.

Considering all of these reasons for skepticism regarding my original results, should we consider my research any better than pure speculation? I think so, for at least three reasons. First, previous creationist treatments of hominids have usually (but not always) focused on a small set of traits to distinguish human from nonhuman. While these traits are useful for distinguishing modern *Homo sapiens* from fossil hominids, it is unknown whether these traits can distinguish the human holobaramin from ape holobaramins. Since a justification for using these traits is usually (but not always) omitted, such qualitative creationist treatments of fossils have an unfortunately arbitrary appearance.

Second, statistical baraminology ought to be a preferred method for creationist evaluation of fossil taxa because we can assign estimates of the significance of the similarities and differences, which qualitative evaluations of individual traits cannot. For example, while DeWitt (2010) lists a number of characteristics that differ between *A. sediba* and “all humans,” we have no way of knowing how important these differences are. With statistical baraminology, the correlation test can be used to estimate the significance of organismal similarity or difference. We can thus begin to distinguish between a random distribution of similarity and biologically significant clustering of taxa.

Third and most importantly, my analysis of fossil hominids did reveal evidence of discontinuity between members of *Homo* and other ape taxa. As I said in my original paper, the accusations against creationists that we cannot distinguish ape from human are now truly false. Not only can we do that, but we can assign statistical probabilities to the differences that divide human from non-human and to the similarities that unite humans with other non-*sapiens* human species. As noted above, this is an important confirmation of the discontinuity hypothesis.

In a sense, *A. sediba* was the first real test case of my analysis of fossil hominids. I originally wrote my hominid paper without the character set that included *A. sediba*. While that first manuscript was undergoing editing and peer review, the *A. sediba* paper appeared, which afforded me the opportunity to evaluate my original conclusions of discontinuity between *Homo* and *Australopithecus*. *A. sediba* made an especially attractive test case, since it was being touted as the most human-like of any australopith. Consequently, I could have found that *A. sediba*

bridged the discontinuity between *Homo*, *Australopithecus*, and *Pan*, uniting humans and chimpanzees into a single holobaramin. Needless to say, that result would have been a spectacular failure of statistical baraminology or a falsification of the discontinuity hypothesis itself. Instead, I found that *A. sediba* grouped with one of the existing groups, and the evidence of discontinuity was confirmed (Figure 2).

In conclusion, though there are definitely good reasons to be wary of statistical baraminology, these reasons are not insurmountable or decisive. Given the benefits of statistical baraminology, it remains an important tool for testing creationist claims about biology. Casual dismissal of baraminology because it gave a result we are personally uncomfortable with would be a serious error. If some creationists are uncomfortable with including *A. sediba* in the human holobaramin (which they certainly are), they ought to do their own statistical analysis to demonstrate discontinuity between *A. sediba* and members of the true human holobaramin (whatever species that might encompass). Selectively quoting experts or qualitatively listing characteristics that differ between *Homo sapiens* and *A. sediba* are inadequate refutations of statistical baraminology. Further evaluations of the baraminic position of *A. sediba* are possible, simply by addressing the drawbacks already detailed in this paper and in the original report (Wood 2010a). For example, if postcranial characteristics could be analyzed, the results could at the very least modify my original conclusions, if not falsify them. At this point, however, preliminary results from an evaluation of postcranial characteristics for *A. sediba* are inconclusive (Wood 2010b).

What should we do with *A. sediba*?

I have here dealt with the major objections to including *A. sediba* in the human holobaramin and found none of them compelling. There is one final consideration that I would like to mention: the veiled suggestion that this baraminology study, or baraminology in general, “concedes” too much to evolution. This was a criticism leveled at Frank Marsh as well (Numbers 2006, pp. 150-151). One of his critics asked, “If we ... allow as much variation in animals as some of our most devout variationists call for ... it is going to be a little hard to talk to evolutionists about what might have happened in a few hundred millions of years” (quoted in Wood 2008a). I find this argument as absurd as Marsh did. Recognizing the reality of speciation (even among humans) concedes nothing to human evolution. If *A. sediba* descended from Adam, then he is human not animal. Likewise, australopiths like *africanus* or *afarensis* are animals. They did not evolve into humans, and they could not evolve the image of God. There is no concession here whatsoever. Instead, what modern creationist research like my study of the hominids is calling us to modify our apologetic arguments in the face of evidence. I agree that theology, especially historically well-established theological principles, ought not yield immediately or automatically to every new scientific development, but apologetics must always be sensitive to the best scientific evidence available. In principle, we must be ready to modify apologetics when new evidence becomes available.

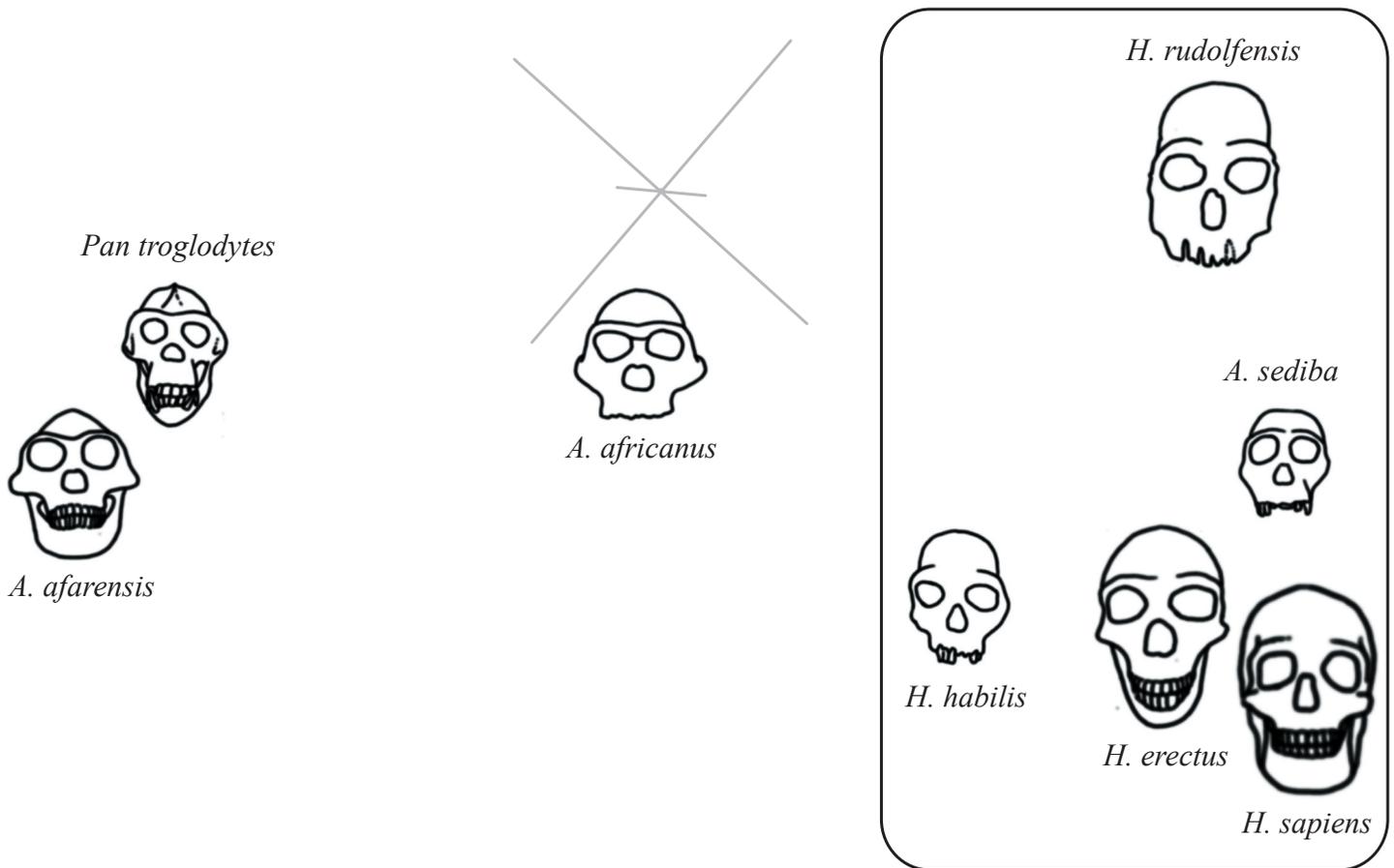


Figure 2. Clustering of hominids based on the multidimensional scaling of Wood (2010a, Figure 13). Although direct comparison of *A. sediba* and *H. sapiens* reveals numerous differences, *A. sediba* definitely belongs to the same cluster as *H. sapiens* (circled) in this analysis of cranial characteristics. Sketches courtesy Roger Sanders.

What then should we tell the public about *A. sediba*? The first thing I would emphasize is the firm commitment of creationists to the truth and authority of God's Word. Based on the creation account of Genesis 1 and 2, we do not accept the animal ancestry of humans. Instead, humans are a unique creation in the image of God. I would next reiterate the areas of general agreement among creationists that Neandertals and the *H. erectus* complex are human and that certain australopiths are not human. Finally, I would explain that many fossils are inherently difficult to classify because they are partial, fragmentary remains and because there are very few of them. Thus, creationists and evolutionary paleoanthropologists disagree over the significance of fossils like *Homo habilis* and *Australopithecus sediba*. My own analysis indicates that the human holobaramin has some surprising members, but that is definitely not the final word. Further studies are already underway to better comprehend these remarkable fossils.

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