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Media Review

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Book review: *Who Was Adam? A Creation Model Approach to the Origin of Humanity*

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Fazale Rana and Hugh Ross. 2015. *Who Was Adam? A Creation Model Approach to the Origin of Humanity*. Revised Edition. RTB Press, ISBN 978-1886653115, 469 pp., $25.

Editor: J.W. Francis
Received January 8, 2016; Accepted April 2, 2016; Published May 9, 2016

Reasons to Believe (RTB) is the leading progressive creationist organization in the world, and they actively promote the concept of "creation as science," wherein they propose predictive models that they believe are consistent with the teachings of Scripture and the scientific evidence. As progressive creationists, they believe that Genesis teaches an ancient universe and an old earth, the history of which was punctuated by creative acts of God. For living organisms, these creative acts are presumably at or near the level of individual species. For biblical and scientific reasons, RTB specifically rejects evolution as a mechanism to account for the origin of organismal diversity, especially for the origin of humanity.

In the new edition of RTB's book *Who Was Adam? A Creation Model Approach to the Origin of Humanity*, RTB scholars Fazale Rana and Hugh Ross present an update of their human origins model presented in the first edition of the book published in 2005. The original model proposed that the special creation of humans took place between 10,000 and 100,000 years ago and consisted of a variety of claims derived from their reading of Genesis and other Bible passages. Among them:

- God created Adam and Eve through direct intervention.
- Adam and Eve are the sole ancestors of all humans, living and dead.
- The female human lineage (as inferred from mitochondrial DNA) should be older than the male human lineage (as inferred from the Y chromosome), because the male lineage experienced a more recent genetic bottleneck at the Flood.
- God created humans at a special moment in history.
- God created humans with similarities to animals.
- Because humans are made in the image of God, they will display characteristics not found in any animals.
- Early humans experienced extreme longevity, which decreased after the Flood.
- There was a "universal" Flood (universal to humanity, but not geographically global), after which humanity globally dispersed from a location in the Middle East.

Not surprisingly, the original edition of the book concluded that the biblical and scientific evidence was most consistent with the "RTB model." The new edition of the book approaches the update with a very unique style. Instead of just revising the entire book, they present the original edition essentially unaltered, followed by thirteen short chapters of new material that create a surprisingly frank and sometimes frustrating assessment and update of the original book. Most surprising about this new material is their frequent admission, "We were wrong." Admitting mistakes is difficult under the best circumstances, and it seems especially uncommon among public personalities. Without question, Rana and Ross should be commended for their willingness to admit mistakes.

The book also offers perspectives and thoughts about human origins that are unfortunately uncommon among young-age creationists. For example, Ross and Rana attempt to account for extreme human longevity, as recorded in the genealogies of Genesis 5 and 11. Their discussion of life history research can be helpful to creationists of any variety. Likewise, they tackle the fascinating question of the origin of human disease, a subject which also has bearing on young-age creationist understandings. Many young-age creationists will also find interesting material in their discussion of "junk DNA" and genome functionality.

Despite these significant benefits of the new book, *Who Was Adam?* displays a number of shortcomings, beyond just the authors' preference for an ancient universe. These objections can be summarized briefly below and elaborated with further examples from the text.

- The RTB model in places seems superficial and nonspecific. For example, it predicts both similarity and difference between humans and animals, but it does not specify what type or degree of similarity or difference we should expect. As a result,

Citation: Wood. 2016. Book review: *Who Was Adam? A Creation Model Approach to the Origin of Humanity*. *Journal of Creation Theology and Science Series B: Life Sciences* 6:50-58.

whether discussing similarity or difference, the authors always depict the model as explaining the data, even though it is never clear why.

- The authors seem to exaggerate the status of the science. A single research article disputing a claim is characterized as a decisive refutation. After describing one or two minority opinions among human evolution researchers, the authors describe it as a consensus. Given the material cited in the endnotes, some of these descriptions can only be characterized as rhetorical flourishes designed to portray the RTB model in the best light.
- When confronted with some evidences that seem to contradict their model, the authors resort to special pleading far too often. Instead of merely admitting that the model fits certain data poorly and leaving a matter unresolved, the authors frequently attempt to cast aspersion on research that fits poorly with their model.
- Even in the updated material, there remain significant misunderstandings of the data and the evolutionary interpretations. These problems are most apparent when discussing the problems with the evolutionary explanation. At times, the authors even seem to contradict themselves.
- Finally, the astute reader will notice a lack of original research. This book is a review and interpretation of other peoples' research. Even in cases where they make proposals about molecular relationships or demographic models that could easily be tested, the reader gets no sense that the authors have any intention or interest in actually conducting their own research. They seem content to remain passive observers.

After introducing the human origins debate and their RTB model in the first three chapters, Rana and Ross survey a variety of evidences over the next eleven chapters. The initial chapter of this section, "It's all in the genes," presents an overview of mitochondrial "Eve" and Y-chromosome "Adam," longstanding models in molecular anthropology that trace the ancestors of human mitochondrial genomes and Y chromosomes to single sequence types that lived tens of thousands of years ago. The RTB model claims that these ancestors were Noah and Eve. Since the RTB model predicts that Adam and Eve lived 10,000 to 100,000 years ago, the authors conclude that estimates that put mitochondrial Eve at 150,000 to 200,000 years ago are "likely too high" (p. 69). In the first of many instances of special pleading, Rana and Ross claim that "current methodology lacks the means to correct for the various complicating factors. However, when the complicating factors are qualitatively considered, it seems reasonable to conclude that the date for humanity's origin may come in under 100,000 years." The irony of this statement becomes very apparent in the new chapter 17, "Better dates for humanity's genesis," where they admit that they were wrong and claim that humanity originated between 100,000 and 200,000 years ago. It is unclear why the consensus date for mitochondrial Eve in 2005 was "likely too high," while the exact same consensus in 2015 is now acceptable. It appears that Rana and Ross just changed their minds.

In chapter five, "Bones and stones," the authors introduce their discussion of the fossil record, specifically focusing on the emergence of behaviors and artifacts that the authors consider evidence of the Image of God. Here appears one of the more nagging over-generalizations: Rana and Ross claim that true human artifacts will "differ fundamentally" from the stone tools of non-human hominins (in their model, "non-human" is anything other than *Homo sapiens sapiens*). In the context of the chapter, this seems to mean that non-humans do not make the *variety* of tools, implements, and artifacts associated with anatomically modern humans. Nevertheless, there are still tribes alive today that make stone tools like Neandertals and other hominins. Thus, when appropriate comparisons are made to equivalent modern human technologies, hominin technologies do not appear to be so crude. In contrast, the authors seem to be content declaring their generalizations of "fundamental differences" consistent with the RTB model.

Chapter six, "The Best Possible Time" seems especially odd and ill-suited to the argument being developed. This chapter, presumably authored by Ross, constructs an argument from the history of the universe and the Milky Way galaxy to argue that God created humanity at "just the right" time. The argument greatly resembles general arguments for fine-tuning of the universe, but with an added historical dimension. While most young-age creationists would appreciate structural arguments for fine-tuning (e.g., the earth is just the right distance from the sun to make the surface temperatures tolerable to life), they are unlikely to find agreement here. For example, we are repeatedly assured that human life and civilization could not have begun any earlier in galactic history, but this seems to seriously limit the ability of the Creator. For example, the authors assert, "human civilization could not have arrived, survived, and thrived on Earth any earlier than it did" (p. 102). Really? Is our God incapable of providing a suitable human habitat at any time and in any place He desires? What happened to the God who protected Shadrach, Meshach, and Abednego in the fiery furnace, or the Lord who walked on the stormy sea, or the God who prepared a great fish to save Jonah's life?

Even if one accepted the arguments of chapter six, the reader is still left with a strange discontinuity: Why should we affirm that God used the uninterrupted laws of physics to create the planet while still insisting that God intervened to create humans in a special, miraculous way? Why not merely accept God's activity through uninterrupted natural law to create the planet and us, or just affirm that God can create in any miraculous way He wants? Instead, the reader is left with an apologetic for the timing of human creation that appears to be built on very dubious theological claims. Since the authors do not offer an update of this chapter, the reader can only assume that they still stand by this argument.

Chapter seven, "How the fountain of youth ran dry," provides a very good but abbreviated discussion of longevity research. The authors correctly recognize that senescence is influenced by genetics, and they review the phenotypes of several longevity gene mutations discovered in various animal models. While these genes are undoubtedly important in developing a creationist perspective on extreme longevity, they only hint at what might be possible. The mutants they review extend lifespan by only 50%. Even if today's longest-lived humans could extend their lifespan by 50%, they would still die at about 120-150 years old. While this could explain the longevity of the Israelite patriarchs like Abraham, Isaac, and Jacob, 150 years is still less than 20% of

the pre-Flood patriarchs' reported lifespans.

Furthermore, senescence is not merely dying; it also consists of the general decrease in quality of life due to the decay of body parts that are not maintained or replaced. Teeth fall out, joints wear out, eyes no longer focus, and a myriad other difficulties accompany aging. These difficulties represent another serious challenge to extreme human longevity, but these are not mentioned by the authors in the original book nor in the updated material. While helpfully focusing creationists' attention on this subject, there is much work still to be done on the subject.

The following chapter, "People on the Move," continues their narrative of the global dispersal of humans. It should be noted at the outset that conventional models of global dispersal already favor creationist interpretations. All conventional models accept the origin of humans in the old world, with dispersal from Africa into Europe, across Asia, into Australia and Oceania, and then into the Americas, in that order. Young-age creationists will dispute the dates of these dispersals, but the general pattern and order is consistent with creationist understanding of a geographic origin near the Middle East. Rana and Ross are pleased to highlight this consistency, and they emphasize that most settlements occurred after 40,000 years before present. Dates that conflict with this preferred dispersal narrative are labeled as "controversial" (p. 132), leaving the reader to wonder whether they are truly controversial or merely inconvenient for the RTB model.

The remaining chapters address the plausibility of human evolution. Unfortunately, the quality of the text takes a significant downturn at this point, and the problems listed above become more numerous. The first of these chapters is simply titled "Is human evolution a fact?" It begins by setting up an impossible standard for deciding if human evolution is a "fact:"

> To uphold the theory, the hominid fossil record should be rooted in a single knuckle-walking apelike primate that existed between 6 and 5 million years ago. Over time a variety of hominids should appear in a branching, treelike pattern from this ancestral form, and a clear evolutionary pathway from this supposed ancestor to modern human should be evident. Hominid fossils should also document the gradual emergence of the anatomical and behavioral traits that define humanity, such as large brain size, advanced culture, and the ability to walk erect. Furthermore, transitional forms that connect australopithecines to primitive *Homo* specimens, and then connect these to modern humans, should be readily discerned in the fossil record…. If these broad requirements cannot be met, then human evolution cannot be declared a fact. (pp. 145-146).

Given the spotty and fragmentary hominin fossil record, expecting any clarity *for any model* is unrealistic. Even if human evolution were true and the fossil record preserved wonderful and numerous fossils of every descendant of the hypothetical human/chimpanzee last common ancestor, there is no guarantee that we would be able to recognize any "clear" lineage from non-human to human. These criteria seem to be designed to set up an impossible straw man, against which the "reasonable" RTB model can be compared.

The chapter then shifts focus to a review of the current debate over the number of species present in the hominin fossil record. Some anthropologists see a few, highly variable species, while others emphasize differences and have no reservations about recognizing numerous species. Incredibly, the authors conclude that this discussion "undermines confidence in the evolutionary scenarios advanced to explain human origins" (p. 150), even though they opened the book with a quote from Darwin, "In a series of forms graduating insensibly from some apelike creature to man as he now exists, it would be impossible to fix on any definite point when the term 'man' ought to be used" (quoted on p. 25). The debate over the number of hominin species seems like a beautiful illustration of exactly what Darwin meant: if human evolution were true, it would be impossible to draw a sharp distinction between one species and another. Rana and Ross appear to be unaware of this.

Even more ironic, the inability to agree on species boundaries seems more problematic to the RTB model, which emphasizes species as the unique creations of God. Rana and Ross write, "… these animals should show little if any evolutionary change, and the fossil record should show evidence of such stasis" (p. 147). How is stasis exemplified in a fossil record so variable that experts cannot agree on the basic question of which fossils belong to which species? How can Rana and Ross credibly conclude that, "The pattern of the hominid fossil records can … be readily explained within the framework of RTB's human origins model" (p. 158)? Again, they seem entirely unaware that the rhetorical strategy they have employed seems to contradict their own position.

The chapter concludes with a review of phylogenetic controversies among paleoanthropologists, in which the authors predictably conclude that the controversies invalidate the "fact" of human evolution. Instead of looking for areas of agreement in phylogenies, Rana and Ross only highlight a handful of disagreements, some of which undoubtedly have more to do with paleoanthropologists' egos than the data. Despite nomenclatural disagreements, the majority of phylogenies are consistent with the broad strokes of proposed scenarios of human evolution. For example, the most recent phylogeny by Dembo et al. (2015) was generated from a supermatrix of 380 characters compiled from previously published studies. Their tree shows *Sahelanthropus* and *Ardipithecus* as the most basal members of the clade, followed by the various australopiths and then a clade of *Homo*. *Paranthropus* is a sister clade to *Homo*, and *Homo sapiens* is the sister taxon to a clade of Neandertals and *Homo heidelbergensis*. All of these relationships are consistent with the notion that australopiths are the nearest evolutionary relatives to *Homo* and Neandertals are the nearest evolutionary relatives to *Homo sapiens*. Even though computer-aided hominin phylogenies were only just beginning when the first edition of *Who Was Adam?* was being written, we still should expect more from Rana and Ross, since the broad strokes mentioned above were well accepted at the time. Confessing this reality is certainly inconvenient for creationists, but ignoring it is even worse. Creationists must deal with reality as it is not as we would like it to be.

Chapter ten focuses on bipedalism and brain size and contains a very controversial graph. Their Figure 10.2 depicts radiometric ages for hominin fossils and their encephalization quotient (EQ). The average EQ for four taxa are shown: *Australopithecus*, *Homo habilis*, *Homo erectus*, and *Homo sapiens sapiens*. Rana and Ross highlight the gap between *H. erectus* and *H. sapiens sapiens* as evidence of a non-gradual change that sets *H. sapiens sapiens*

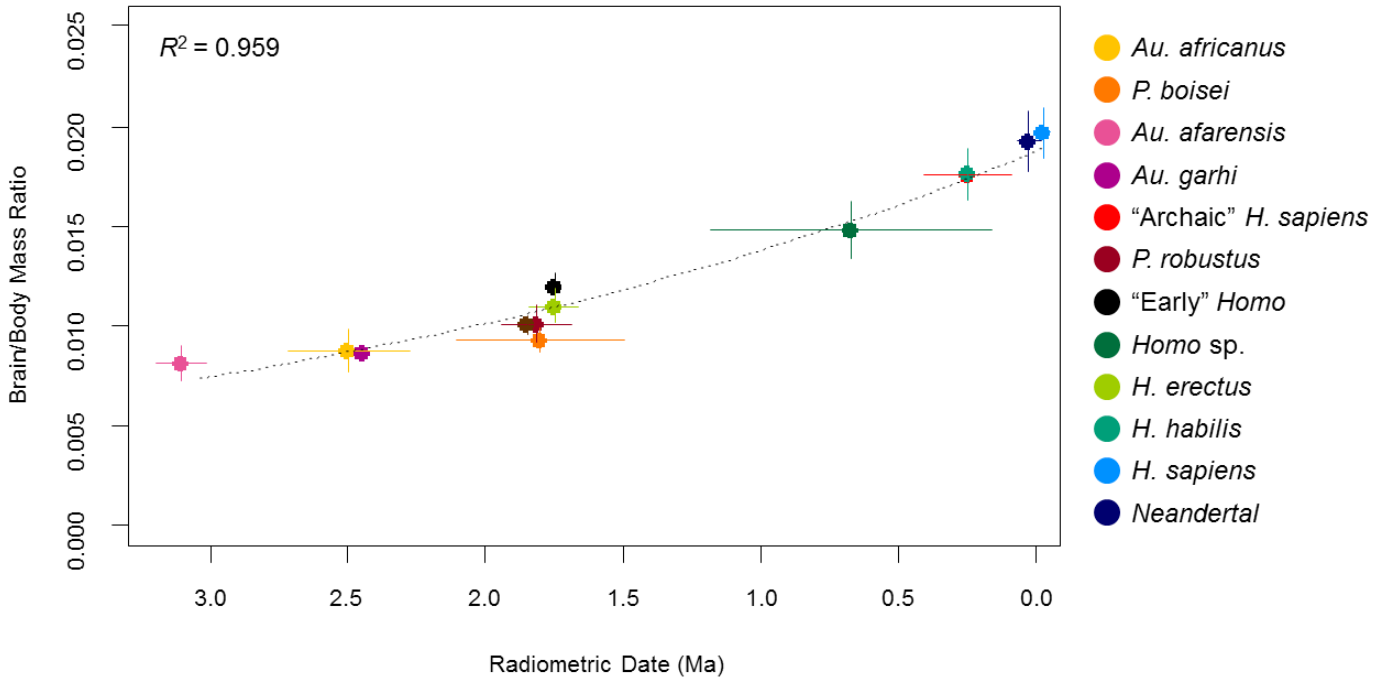

Figure 1. Ratio of brain mass to body mass of 215 hominin specimens as a function of average radiometric date for twelve taxa using data compiled by Matzke (http://phylo.wikidot.com/fun-with-hominin-cranial-capacity-through-time). Bars represent ±one standard deviation for specimen dates and brain/body mass ratios. The best fit line is represented as a dotted line with R^2 indicated on the graph.

apart from other hominins.

The problems with the depiction are numerous. First and most glaring, they have selected only certain taxa and omitted others, most obviously Neandertals. Second, since only averages are shown, we have no sense of the range of values, and hence the separation of *H. sapiens sapiens* from the other taxa is artificially inflated.

To the authors' credit, they admit some of these mistakes in the updated material on pp. 356-358. They acknowledge that they should have shown at least Neandertals, but they insist that if the graph were fixed, there would be a distinct gap between *Homo sapiens sapiens* and all other hominins. Glaringly absent is the corrected graph, even though the data for such a graph are readily available. Matzke digitized the data in 2006, and it is freely available from his website (http://phylo.wikidot.com/fun-with-hominin-cranial-capacity-through-time). A graph of 215 hominin specimens, averaged by taxon, is shown in Figure 1. The gap they insist would be present is not evident, and the averages form a smooth curve with an R^2 of 0.959. This willingness to describe hypothetical research without actually doing it exemplifies the authors' resistance to engaging in first-hand, original research.

The next two chapters cover *Homo erectus* and Neandertals, respectively. In both, the authors emphasize that these fossils are not the remains of anything we could describe as "advanced." Everything about them is significantly different from the advanced culture and symbolic thinking of modern humans. Of course, much of this relies on absence of evidence, which, as the saying goes, is not evidence of absence. The best we could conclude is that Neandertals and erectines do not exhibit evidence of the "advanced" behaviors associated with modern humans. Instead, the authors want to be more emphatic and insist that the apparent differences between modern humans and Neandertals/erectines are expected based on their model. Again, though, the reader is left to wonder just what similarities would or would not be consistent with the RTB model. How much similarity is too much? How much is too little? We have only the authors' qualitative—and biased—judgment on the matter.

In chapter 13, the authors address the question of comparative studies of human and chimpanzee genomes. After opening the chapter with an admirable review of the history of comparative studies between the human and chimpanzee genomes, the authors then turn to questioning the similarities. Rana and Ross claim, "Studies that reveal a 99 percent genetic similarity between humans and chimpanzees have stacked the deck in a way that guarantees a high degree of likeness" (p. 216). A careful examination of their argument reveals several errors by Rana and Ross.

First, they note a comparative clone mapping study by Fujiyama et al. (2002), which they describe as, "…the project team found that about 15,000 of the 65,000 DNA fragments did not align with any sequence in the Human Genome Database" (p. 216). The sequences they refer to were Bacterial Artificial Chromosome (BAC) end sequences, a notoriously messy means of mapping

large-insert clones. Fujiyama et al. attempted to sequence *both* ends of 64,116 BACs, resulting in 114,421 BAC end sequences. Only 14,901 (13%) of those did not match any sequence in the human genome, a considerably smaller fraction than reported by Rana and Ross.

Second, they cite a study by Ebersberger et al. (2002) that examined another random sample of sequences from the chimpanzee genome. According to Rana and Ross, "Only two-thirds of the sequences from the chimp genome aligned with the sequences in the human genome…. one-third found no matches" (p. 216). This claim is directly contradicted by Ebersberger et al., who report that 28% of their sequences were excluded from their study because they matched more than one repeat sequence in the human genome. Only 7% of their sequences found no matches in the human genome.

Third, they cite a study by Anzai et al. (2003) that looked at the 1.8 Mb major histocompatibility region and found substantial differences between the genomes. Rana and Ross correctly report the 86.7% identity reported by Anzai et al. for this genomic region in chimps and humans, but they imply that this number is representative of the genome as a whole. They write, "The most comprehensive genetic comparisons indicate that humans and chimpanzees share a genetic similarity closer to 85 percent than to 99 percent" (p. 226). Since the MHC region is known to be highly variable even within humans (Horton et al. 2004), this region is unrepresentative of the whole genome. Even if it weren't, a 1.8 Mb segment of one chromosome is only one locus that constitutes 0.05% of the complete genome. It can hardly be called "comprehensive."

The chapter then shifts focus to a different question: What is the source of the anatomical, physiological, and behavioral differences between humans and chimpanzees? Frankly, this is an extremely important and relevant question, but Rana and Ross do not seem to understand the importance of the question. They conclude, "In many instances, it's not the genes present that are important but the way they function. What does it mean to be 98 percent chimpanzee? In terms of evolution, essentially nothing." Here, they have conflated evolutionary with physiological significance. The many phenotypic differences between humans and chimpanzees do indeed reflect important differences in gene expression ("the way they function"), but these differences do not imply that the similarities are meaningless. On the contrary, the genetic similarity becomes all the more peculiar when we recognize that very similar genomes can produce such different organisms. Evolution claims that this similarity is explained by common ancestry.

To account for the similarity itself, Rana and Ross offer a very short explanation on p. 228: "The large number of shared genes found among the genomes of humans, chimpanzees, mice, rats, and other animals reflects elegant design efficiency. The Creator appears to have selected a gene set that could be used to construct a wide range of organisms." While they are correct, their proposal again lacks specificity: Why do humans and chimps share such similar genomes, while the genomes of humans and mice differ so dramatically (see Mouse Genome Sequencing Consortium 2002)? What is the basis of the *pattern* of similarity (Wood 2006)?

It is ironic then that Rana and Ross conclude this chapter by claiming that, "Each new discovery coming from genetic comparisons between humans and chimpanzees seems to weaken the case of evolution" (p. 227). Upon careful examination, their conclusion seems to be based on erroneous interpretations of the technical literature, irrelevant conclusions from physiological studies, and a failure to observe the nature of the similarity problem. In their very brief update chapter (24), they still conclude that "the hoopla surrounding the human-chimp genetic similarities is largely irrelevant" (p. 336). Thus, these problems have not been addressed or acknowledged in the ten years since they first wrote their chapter.

The new chapter also introduces a new erroneous claim. Citing the gorilla genome sequence (Scally et al. 2012), Rana and Ross claim that 22% of gorilla DNA sequences are more similar to human orthologues than chimpanzees. In reality, Scally et al. report their percentages as the frequency that gorilla DNA sequences more closely resemble either chimpanzee or human than chimpanzee and human resemble each other. Rana and Ross then claim that this result was "unanticipated" because it contradicts the accepted phylogeny in which chimpanzees and humans are most closely related and gorillas are more distantly related.

In reality, this observation was anticipated as a result of Incomplete Lineage Sorting (ILS). Researchers studying the phylogeny of living apes and humans expected that ILS should confuse their efforts at phylogenetic inference (e.g., see Rokas and Carroll 2006, Degnan and Rosenberg 2009, Hobolth et al. 2011). Rana and Ross mention ILS but claim that "these explanations raise questions." They allege that the divergence time between gorillas and the chimp/human clade ought to eliminate any trace of ILS, but they offer not even a simple calculation to support this claim. Again, they describe hypothetical research that would support their position, but they do not actually do the proposed study.

Chapter 14 of the original material, "What about 'Junk' DNA?" again focuses on functionality rather than pattern. As in the previous chapter, the authors conflate evolutionary and physiological significance of 'junk' DNA. Rana and Ross conclude, "The scientific community now recognizes that noncoding DNA is functional. This realization greatly weakens one of the mainstays for human evolution and for the shared ancestry of humans and chimpanzees." The updated chapter (25) restates the same arguments with new evidence from the ENCODE project, indicating that the authors have not changed their views on "junk" DNA.

Their arguments fall short of their assertions that "junk" DNA is inconsistent with evolution. Even if it were true that noncoding DNA is "functional" (an undefined quality if ever there was one), it does not follow that the similarity of functional DNA negates common ancestry of humans and chimpanzees. Similarity requires explanation, regardless of whether it's similar genes or similar intergenic DNA. One could even argue that functionality is irrelevant to the evolutionary argument for common descent. Indeed, the classic argument for common ancestry from vertebrate limb homology is based on the underlying similarity of functional elements.

Correctly understood, the argument for "junk" DNA is primarily an argument against a designer or creator, and even then, it is not a compelling argument. The argument might be stated as, "An intelligent creator would not create functionless

junk. If there exists functionless junk, then it was not created by an intelligent creator." Even as stated, though, the existence of truly functionless "junk" DNA would still not be inconsistent with God's creation, since it is now cursed because of sin and contains many things that are the result of degeneration over time. Furthermore, the argument as stated is presumptuous in assuming that we know what "function" is and how to measure it or that we know what the creator would or would not do. Finally, since rudimentary organs were known prior to evolution (e.g., see Darwin's discussion in Origin of Species), there were nonevolutionary, design-based interpretations of "nonfunctional" structures, thereby demonstrating that "nonfunctional" structures do not falsify a model of design.

After a short chapter summarizing the original book, chapter 16 opens 122 pages of new material giving a ten-year update to the RTB model. Why bother with new material updating the model? Why not just revise the original book? According to the authors, the strategy of adding a new section allows them to critically evaluate what was written in the original book. Most importantly, by highlighting corrections and revisions to the original model, Rana and Ross assert that this shows that the RTB model is "a scientific model" (p. 260). While this strategy of adding new material effectively highlights modifications to the model by Rana and Ross, an important question remains: Is the RTB model *good* science?

The new material begins with the fascinating chapter, "Better Dates for Humanity's Genesis," in which the authors admit, "We were wrong" (p. 268). The new dates are based on additional research on Y-chromosome Adam. According to the authors, newer studies now place the date for the human Y-chromosome's origin at approximately the same time as mitochondrial Eve. Consequently, they retract their claim about the discrepancy between the female and male ancestor (biblical Eve vs. Noah), and they suggest that the RTB model should be revised to a new date for Adam and Eve around 150,000 years ago. They even claim that this new date is "gratifying" because it aligns "with estimates of humanity's origin from the fossil record" (p. 267).

Rana and Ross's reasoning about this new dating raises a host of questions. In the original book, they made it clear that the discrepancy between the dates for the male and female ancestors of modern humans was a *prediction* of their model. They reason that the four women surviving the Flood could have carried four different mitochondrial sequences, while the men could only have carried Noah's Y chromosome. Hence, the Y chromosome ancestor should be younger than the mitochondrial ancestor. In the new material, they repeat this argument, but they treat their original prediction as an interpretation of data rather than an actual prediction. Nonetheless, placing Y-chromosome Adam as a contemporary of mitochondrial Eve leaves their original prediction either falsified or in need of additional research.

Rana and Ross's concession that their new date better accords with the fossil record also leaves important questions unanswered. In chapter five, the authors discuss *Homo sapiens idaltu* and other "archaic" *Homo sapiens* fossils. After reviewing anatomical and behavioral issues, they insist that these fossils come from "animals that walked upright, possessed limited intelligence, and had some type of culture, but animals nonetheless" (p. 87). They seem so certain that they declare, "All the data support this interpretation [that 'archaic' *Homo sapiens* are animals]" (p. 87).

Their new assessment of the concordance between genetic and fossil estimates of the origin of *Homo sapiens* leaves the reader with little guidance on interpreting their earlier assessment of the fossil record. Are we to understand that Rana and Ross now accept that "archaic" *Homo sapiens* fossils from 100,000 to 200,000 years ago are human? What are we to make of their certainty, seemingly born from anatomical and behavioral evidence, that these fossils came from animals? If they were so wrong about their assessment of these fossils, could they be wrong about other fossil forms, like Neandertals?

Chapter eighteen ("When did Modern Human Behavior Begin?") exposes another seeming contradiction. In chapter five, when discussing fossil dating inconsistent with their model, they made great efforts to question the use of luminescence dating as an inaccurate method. Thus, they claimed that it was "possible and likely" that inconsistent dates "represent an overestimate" (p. 99). In the new material, since they accept an earlier date for the creation of Adam and Eve, they are left with the new conundrum of why advanced human culture appears so much later in the fossil record. Without explanation, they conclude that "luminescent dates for the artifacts should be taken seriously." How does this relate to their earlier methodological objections to using luminescence dating? It would seem that they now accept luminescent dates of human artifacts merely because it is more convenient for their model, and their earlier comments on luminescence were rhetoric.

The following chapter updates their discussion of the fossil record, and reviews the substantial fossil discoveries from the past ten years. Rana and Ross repeat their claim that resolving species is a prerequisite to demonstrating the "fact" of evolution. They write, "Without an understanding of the biological variation within a species and the actual number of species, it is impossible to interpret the fossil record from an evolutionary perspective" (p. 285). In the conclusion of the chapter, they demonstrate some sensitivity to the nuances of the fossil record when they acknowledge that the very existence of fossil hominins is consistent with human evolution. Nevertheless, they still conclude that it would be "reasonable to think that greater clarity would emerge" (p. 289) as new fossils are discovered. The chapter ends with the claim that the RTB model "readily accommodates each of these hominid finds" (p. 289) despite the model's reliance on distinguishing species of animals from humans, which should make it difficult to support where species boundaries are uncertain.

The next two chapters introduce the problem of Neandertal genomics and what the authors call the "messy interbreeding problem." As is now well-known, sequencing of the Neandertal genome revealed that the ancestors of modern Eurasians and north Africans carry alleles that originated from interbreeding from Neandertals. This would seem to pose a very serious challenge to the RTB model, which views Neandertals as animals. If humans interbred with animals, what would the spiritual status of the hybrids be? Since Neandertal genes introgressed into the modern human population, the hybrid offspring must have found mates among humans and had children of their own. Even if we concede the possibility of an animal Neandertal raping a human woman, why would her human contemporaries allow her to carry the child to term or even care for it? How could a half-human,

half-animal possess enough cultural awareness to find a mate of its own? Indeed, the problems seem so insurmountable that Rana wrote in 2004, "If Neanderthals interbred with modern humans, then by definition, they must be human."

Now faced with overwhelming evidence for Neandertal/human interbreeding, Rana and Ross admit that it happened, but they deny that it threatens the RTB model. In contrast to Rana's 2004 claim, they now write, "Just because humans and Neanderthals interbred, does not mean they must be the same species" (p. 310). They also claim that the Bible's prohibitions against bestiality make it "not surprising" (p. 311) that humans interbred with animals. Despite the enormous theological and biological problems for the RTB model, the reader is assured that human-Neandertal interbreeding does "not invalidate the RTB human origins model" (p. 311). At this point the astute reader might begin wondering what evidence would invalidate the RTB model. If the new dates for Y-chromosome Adam and interbreeding with Neandertals does not falsify the RTB model, what will?

The following chapters address Neandertal and hominin culture, drawing comparisons to behaviors observed in chimpanzees. These chapters spend less time disparaging evolutionary models, and instead provide a positive argument for why evidence of "culture" in hominin taxa other than *Homo sapiens* is consistent with the RTB model. The authors discuss several important studies and provide a plausible interpretation. One wishes that more of the book took this approach of interpreting data rather than disparaging evolutionary models or evidence that is inconsistent with the RTB model.

Chapters 24 and 25 address comparative genomics and "junk" DNA, which have already been addressed in this review. Chapter 26 covers "Criticisms of RTB's Human Origins Model" in which six objections are addressed. The objections are

1. Humanity arose from a population, not an ancestral pair.
2. Humanity arose from multiple locations, not a single place.
3. Human chromosome 2 shows solid evidence for evolution.
4. RTB misrepresents hominin brain sizes (see previous discussion).
5. Agriculture emerged well after humans arrived.
6. There are no 900-year-old human fossils.

Some of these objections are important problems for the RTB model, and some are important problems for creation models in general. The question of humanity arising from more than one location (#2) is an unconventional view not generally accepted in human evolution, except for evidence of ancient interbreeding. Otherwise, the consensus currently points to Africa as the source of *Homo sapiens*. The dispute over brain sizes (#4) was discussed previously in this essay.

The problem of ancestral population size is especially troubling, given the apologetic value it provides to models of theistic evolution (see Venema 2010). Rana and Ross raise some interesting questions about ancestral population size estimates based on instances of known population sizes from conservation biology. What is unclear from their text is whether these examples have direct bearing on the question of ancestral human population size estimates. Do they use the same algorithms or formula? Have corrections been made? There have been multiple studies of ancestral human population sizes, and errors of one methodology may be partially compensated by the different methods used. Unsurprisingly, Rana and Ross conclude "we are not willing to abandon our conviction that mitochondrial Eve and Y-chromosomal Adam correspond to the biblical Eve and Adam" (p. 353). Their faith is admirable, but they provide only suggestive hints at how these estimates may be accommodated in a creation model.

Rana and Ross's discussion of human chromosome 2 is encouraging in that they accept the evidence of chromosomal fusion, even though they dispute that this supports evolution. They claim that it would be very unlikely that a chromosomal fusion could happen, and therefore conclude that the fusion was designed by the Creator. Given the separate creation of humans and apes, it is at least possible that the fusion was not a historical event and that the evidence of fusion was an intentional design of chromosome 2. Unfortunately, the reader is left with the question of why chromosome 2 appears to be a fusion if that fusion never happened, but the authors do not address this question.

With regard to the emergence of agriculture, Rana and Ross admit that the evidence is currently challenging for the RTB model, but they "anticipate that future discoveries will continue to push *back* the date for proto-agricultural practices" (p. 360). Their abbreviated discussion of extreme longevity merely offers the uncertainty of age estimation as an explanation for the absence of skeletal remains from very old humans.

The penultimate chapter "Three New Questions to Address," looks at the origin of races, the origin of human disease, and comparative genomics. The discussion of human ethnic differences is helpful and unsurprisingly consistent with the RTB model. Rana and Ross's discussion of the origin of human diseases is again helpful but brief. An entire book on just this topic would be very welcome. The final question of comparative human and primate genomics is not a "new question" at all (even within the book), but Rana and Ross choose this location to introduce a novel means of thinking about comparative genomics. With a surprisingly deep historical sensitivity, they revive the archetype concept of Sir Richard Owen. Unfortunately, they quickly fall back on straw man arguments. They claim that we should prefer evolutionary interpretations of genomic similarity only if the following claims are true (p. 370):

1. The genomes' shared sequences are nonfunctional.
2. Events that generated shared sequences are rare, random, and nonrepeatable.
3. Vertical gene transfer is the only mechanism that produces shared features.

Since none of these are actual assumptions found in evolutionary literature and one can easily find evolutionary research on each subject, their conclusions about evolution can be easily dismissed.

On what amounts to a single page of text (p. 371-372), they introduce an outline of an "RTB comparative genomics model," which consists of the following claims: Genomes are created, and after creation, genomes have continually experienced mutations. The mutations are subject to the normal forces of population genetics (selection and drift). They therefore claim that similarities result from one of two sources: deliberate design or "the outworking of physical, chemical, or biochemical processes that occur frequently, are nonrandom, and are reproducible" (p. 372). Since these are very basic assumptions common to any creation model of biology, they can hardly be called "the" RTB model.

For example, Wood and Murray (2002) wrote, "Some similarity will result simply because of the fidelity of reproduction. Strictly speaking, this would be a kind of evolutionary homology. Other 'homologous' similarities, such as vertebrate limbs, undoubtedly arise as part of the design plan" (pp. 147-148).

The final chapter of the book is supposed to be a "scorecard" to see how the RTB model has fared over the ten years since the first edition of *Who Was Adam?* To the authors' credit, they do not attempt to claim that the RTB model explains all the data. They acknowledge that "challenges" have forced them to modify their model, even though they do not believe that their model has been falsified. One can certainly understand enthusiasm for a favorite model, but their willingness to change their model speaks very highly of Rana and Ross. Too often in the creation-evolution debate, advocates loudly proclaim that their model explains everything and that all other models explain nothing. Finding even the small humility required to admit, "We were wrong" is very worth celebrating.

Still, as a scientific proposal, the RTB model should be evaluated carefully without overindulgent sentiment. How has the RTB model fared? More specifically, can we compare this model to a young-age creationist model and determine which one better explains the evidence? Rana and Ross have no interest in this, declaring that "any stance that regards the universe and Earth as merely 6,000 to 10,000 years old lacks scientific credibility" (p. 45), but since young-age creationism is the dominant belief among evangelicals, it is worth evaluating.

Of the eight components of the RTB model, most would be readily accepted by a young-age creationist. We can all affirm that God created the first humans physically and spiritually through direct intervention, that Adam and Eve are the sole ancestors of all humans, that humans originated in a single location (both pre- and post-Flood), that humans are made in God's image, that early lifespans were significantly longer than they are now, that there was a universal Flood, and that humanity dispersed from somewhere near the Middle East. Young-age creationists might even concede that God created humans at a special point in history (the six days of creation), even if we differ on our chronologies.

When the RTB model more closely approximates the conventional "Out of Africa" model of human evolution, the young-age creation model departs substantially from it. For example, where Rana and Ross would generally accept dates for mitochondrial Eve or fossil hominins, young-age creationists would disagree. Questioning conventional dating may not seem credible to Rana and Ross, but it has some advantages over the RTB model. For example, rather than assuming that Neandertals and other human-like hominins are not human (in part) because they lack the advanced culture of *H. sapiens*, young-age creationists may assert instead that the culture of hominins could merely be the result of the cultural disruption caused by the confusion at Babel. Indeed, most of the arguments about lack of culture in these hominins become less forceful if we admit that these are not individual species persisting for millennia in a primitive lifestyle but a form of human relegated to a disadvantaged existence for just a few generations.

Several of the remaining challenges to the RTB model could find resolution in a young-age creationist model. For example, the RTB model's failure to find significant anatomical differences between *Homo sapiens sapiens* and other hominins (as exemplified by the brain size graph) is resolved by the observation of a persistent statistical discontinuity between members of *Homo* and nonhuman hominins (Wood 2010, 2016). Likewise, the substantial gap between the first "humans" and the advent of advanced culture becomes explicable if it is a gap between the first confused post-Babel populations and the re-establishment of advanced culture several generations later. The location of the creation of humanity becomes less problematic in the young-age creationist model, since a global Flood would have wiped out all evidence of that location anyway. Young-age creationists need merely explain how human populations dispersed from Babel. Furthermore, since young-age creationists universally acknowledge that Neandertals are fully human, the "messy problem" of interbreeding is not a problem at all.

Nonetheless, a young-age creationist approach leaves questions, some of which also challenge the RTB model. Most prominent among them are the questions of comparative primate genomics and ancestral population size estimates. Unique to a young-age creationist model is the aforementioned problem of conventional dating. Beyond the question of how to explain radiometric dating in a young-age creationist context, we should also wonder how to explain genetic divergence of Neandertals and Denisovans in the young-age creationist model. Though anyone can easily critique another model, it is much harder to construct and defend an alternative explanation.

The most startling difference between the RTB and young-age creationist approach is the absence of any original research from RTB. Rana and Ross appear to be content as sideline commentators, even when research or studies they themselves propose could easily be done. Though young-age creationism does not have a stellar track record in original research, many young-age creationists are eager to engage directly with data through original research. Judged by that criterion alone, it would seem that answers to outstanding questions in human origins are more likely to be resolved by young-age creationists than RTB, unless Rana and Ross change their approach and start doing their own original research to resolve the remaining difficulties in the RTB model.

Is the RTB model science? Insofar as it makes specific claims about data, we must conclude that it is. Far more interesting is the question of whether it is *good* science. Unfortunately, in *Who Was Adam?* readers will find a pattern of special pleading and misunderstandings, and a marked resistance to performing original research, as documented above. More importantly, the RTB model currently lacks specificity in its predictions that would allow it to be rigorously tested, and when it is rigorously tested (with the date of Y-chromosome Adam and the interbreeding of Neandertals), the authors of the model abruptly change their view and claim that the results did not falsify their model after all. These features are not hallmarks of good science. The RTB model could be further refined and improved, but at this point, it is unlikely to convince the unconvinced.

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