Creation Research Society Quarterly 2016. 52:249–255.

Human Genetic Data Affirms Biblical History on Many Levels and Is an Excellent Resource for Creation-based Research

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Abstract

Some have claimed that modern genetic data is at odds with biblical history. Yet closer examination reveals that the opposite is true. In terms of the origin of humanity, genetic data support the fact that all humans alive today can trace their ancestry back to a single male and a single female. When evolutionary assumptions are discarded and actual observable mutation rates are used, the molecular clock indicates that those individuals lived within a biblical time frame. Analysis of the human mitochondrial data reveals three major mitochondrial lineages, which appear to point to the three daughters-in-law of Noah. The Y chromosome distribution pattern supports a single paternally based dispersion as expected by the Babel event. Yet many questions remain, even as genetic data accumulate and computers make modeling more accessible to those outside the traditional university setting. The time is ripe for productive creationist research to answer important questions about the genetic history of humans using the wealth of data and tools now at our disposal.

Introduction

The history presented in Genesis makes it clear than humans were created in God's image, separately from all other animals (Genesis 1:20–27). Adam was created directly from the ground, and Eve was made from his side (Genesis 2:7, 21–22). As humans reproduced and filled the earth, the earth became filled with evil, so God chose to send a Flood to destroy the inhabitants (Genesis 6:5–7). Noah, his wife, his three sons, and their wives were the only humans that survived the global cataclysm (Genesis 6:18; 7:7, 13; 8:16; 1 Peter 3:20). All humans alive today have descended from them. Biblical data (Genesis 5, 11) and secular history enable us to estimate the time of Creation around 6,200 years ago and the Flood around 4,600 years ago (Hardy and Carter, 2014).

If this record is correct, it should be consistent with observations we can make today. Over the past several decades, an enormous amount of genomic data has been generated. This includes large-scale projects such as the HapMap

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Accepted for publication February 10, 2016

project and the 1000 Genomes Project (International HapMap 3 Consortium, 2010; 1000 Genomes Project, 2015). While it is recognized that some errors are present in the data (Tomkins, 2011; Merchant et al., 2014; Carter, 2007), there should still be good agreement between the genomic data and the predictions one can make based on biblical history. Indeed, this has been affirmed in creationist journals (e.g., Carter, 2009; Jeanson, 2015), in Protestant theological journals (e.g., Sanford and Carter, 2014), and in a two-part article designed to reach out to Catholics (Sanford and Carter, 2015a, 2015b).

A major point of controversy involves the question of whether the currently observed human genetic variation is compatible with all humans descending from a single couple around 6,000 years ago. Dr. Francis Collins (a prominent evangelical Christian in the world of science, the former director of the Human Genome Project, and the current director of NIH) has gone on record as stating, "There is no way you can develop this level of variation between us from one or two ancestors" (Adkisson, 2011).

Similarly, Dennis Venema, Collins's fellow at the theistic-evolution promoting organization *Biologos*, has said:

> You would have to postulate that there's been this absolutely astronomical mutation rate that has produced all these new variants in an incredibly short period of time. Those types of mutation rates are just not possible. It would mutate us out of existence. (Haggerty, 2011)

Are these claims correct? How would we know and what, exactly, does the Bible predict about human genetics? This paper discusses some initial considerations essential to consistently interpreting the genetic data within a biblical framework. It will also lay some groundwork on what has been done, and what needs to be done, to model human genetic history from a biblical perspective. Such a model can help us understand our past (e.g., human migrations) and potentially may provide insights about human diversity as it relates to adaptation and disease.

Designed Diversity

All people on earth today have come about through the normal process of sexual reproduction. Gamete production in the mother and father created haploid versions of the parental genome through the process of meiosis. During this process, the complimentary copies of the parental autosomes recombined in large sections, gene conversion occurred, and mutations were introduced. Unlike everyone alive today, however, the genomes of Adam and Eve did not come about through natural processes. This is an incredibly important consideration for us and one that our opponents have rarely acknowledged. If Adam and Eve were specially created, we have multiple starting possibilities:

- Adam and Eve had unique genomes, with two original copies of each autosome (this is a good starting assumption); or
- Eve was a near clone of Adam, with the exception that she had no Y chromosome; or
- Eve was a haploid clone of Adam, essentially a product of meiosis, but with doubled chromosomes; or
- Adam and/or Eve were created with multiple genomes, possibly a different haploid set of chromosomes in each of their reproductive cells, essentially limiting future human genetic diversity only by the number of children they could potentially have.

Authors such as Collins and Venema are assuming there was no designed human diversity in Eden. According to that assumption, the four sets of chromosomes in Eden (two sets in Adam and two sets in Eve), would have all been identical. The only exception to this would have been the sex chromosomes (otherwise Adam and Eve would have necessarily both been female). This assumption is both unjustified and unreasonable. There is no reason to think any two chromosomes in Eden would have been identical. Even as Eden must have had designed sexual diversity (male and female), every chromosome could have carried unique alleles. Thus, the antediluvian population could have had much more genetic diversity than is seen among people today. Even if Eve was a near clone of Adam, Adam could have himself been heterozygous at tens of millions of nucleotide positions. Therefore, Venema's statement above is couched in error. He assumes he is starting from a blank slate, essentially a couple containing zero genetic diversity.

The available data can help us make estimates of created diversity in Adam and Eve. Theoretically, one of four nucleotide "letters" must appear at any position in the genome (A, C, G, or T). But when examining any specific location, one person might have a different letter in that position than another. Most variation is biallelic (in other words, only two letters are found at that location among all the people on earth), and there are millions of variable positions of this nature in the human genome (International HapMap 3 Consortium). Thus, any two people will have millions of single-letter differences among them. Yet, these variable locations are largely shared among all people groups, implying that this variation was established in the very early human population. From a biblical perspective, that means these variations had to predate the Babel dispersion, when the human population became fragmented linguistically and geographically (Genesis 11:1–9). Most reasonably, the majority of this genetic diversity would have been present in Adam and Eve at Creation, which could easily mean 10–100 million or more positions were created heterozygous (Carter, 2011).

During meiosis, homologous recombination shuffles the alleles (variants) between chromosomes. This occurs via crossing over and gene conversion. Since there are usually only one or two crossovers that occur per chromosome arm, large sections of DNA remain together on a chromosome as it is passed on. These regions are known as *haplotype blocks* and are recognized by a particular combination of alleles. Over many generations these regions should become more scrambled, shuffling the alleles, and resulting in haplotype blocks that are considerably smaller. Gabriel et al. (2002) estimate that most of the genome is contained in haplotype blocks of substantial size. The specific haplotypes and their boundaries were frequently shared across different populations of humans. All this is consistent with the population bottleneck at the Flood followed by a dispersion following the Babel incident several thousand years ago.

Mutation

The sequence of the genome can be changed by mutation. This could be a single nucleotide change, such as a transition from C to T. Alternatively, mutations may result in structural changes such as the duplication or deletion of a region, producing what is known as *copy number variants* (CNVs). It is now recognized that CNVs are very common sources of variation between humans. While some have no known effect, others are associated with adaptation or disease (Zarrei et al., 2015). Other structural rearrangements, such as inversions, can occur as well (Sudmant et al., 2015).

While there are even more alleles present in the human population that are attributable to mutation, most are not as widespread. Any individual human carries mostly common variants, which are likely created diversity, and fewer population-specific or even "private" alleles, which should largely be attributable to mutation (but see caveat under "The Effects of the Flood Bottleneck"). Detailed analysis of patterns in these alleles is important for understanding human genetic history as well as factors influencing adaptation and disease. Genetic variants that are widespread must have arisen early in human history; genetic variants that are very rare are much more likely to be "young" mutations. Interestingly, recent analyses by evolutionists have revealed that most protein-coding variants appear to be of very recent origin (Tennessen et al., 2012; Fu et al., 2013). Again, even though evolutionary assumptions were used in the estimates, the findings are consistent with the biblical historical parameters.

Historic Population Sizes

Speaking of the acceptable ranges of biblical parameters, historic population sizes are also important for us to consider. The size of a population dictates how much diversity it can hold, for small populations are subject to genetic drift: random sampling of the gene pool each generation can lead to significant changes in allele frequency in small populations. Genetic drift slows to a crawl in populations numbering in the thousands, and is essentially nonexistent in large populations.

Carter and Hardy (2015) used computer simulations to estimate the population sizes before the Flood, between the Flood and Babel, and within the nation of Israel during their sojourn in Egypt. The latter has been a frequent target of attack by skeptics who claim it is impossible for the Israelites to have attained the population size suggested in the Bible (Exodus 12:37–38; Numbers 1:46). On the contrary, simulations with some parameters indicate that attaining a population size of 2.7 million was possible within 215 years. If the Israelites were in Egypt longer, as many believe the Bible teaches, reaching such a population size was a trivial matter.

In contrast to the Exodus event, we do not have any biblical data that would allow us to estimate the population size at the Flood or at Babel. However, large population sizes at these events, and rapid reestablishment of large populations after each event, would have been relatively easy, given realistic population growth parameters. So, like the designed diversity example above, when we consider the relevant biblical parameters, there is no difficulty establishing appropriate population sizes in the given time. We are not limited to any particular population size, and thus the biblical model can handle data that demand either large or small historic population sizes. In other words, we have far more flexibility than many of our antagonists appear to assume.

The Effects of the Flood Bottleneck

Carter and Powell (2016) showed that the biblical claim that the entire human population was reduced to three reproducing couples is not problematic. There are multiple scenarios (assuming rapid population growth) in which almost no created diversity would be lost due to genetic drift. There are other scenarios (those with very slow growth, or if Noah's family were a small sample of the antediluvian population) where genetic drift would have been extreme. In high-drift scenarios, initial allele frequencies can rapidly change from 50:50 (the distribution they assumed in Adam and Eve) to extremely high/low allele frequencies. In these cases, a great deal of allelic fixation/extinction can occur, resulting in extensive loss of the initial allelic diversity. Intermediate levels of drift would result in partial loss of allelic diversity and a limited number of low frequency alleles (that are not derived by mutation).

When Carter and Powell (2016) compared their models to the real-world genetic diversity found among multiple

world populations, they concluded that modern humanity has experienced a large amount of genetic drift. This does not contradict the information in the paragraph above, but it does mean that of all the *possible* genetic history models, those with a strong bottleneck effect are more likely to reflect biblical human history. But when comparing Europeans to East Asians to Africans, they also saw that the allele frequency in one population was a strong predictor of the allele frequency in the other populations. In other words, the allele frequency spectrum was set up *prior* to Babel. Genetic drift must have occurred between Adam and Noah.

Mitochondrial DNA and Y chromosomes

Interestingly, it was the evolutionists who uncovered genetic evidence of a single woman (Mitochondrial Eve) and a single man (Y chromosome Adam) founding the human race. They also uncovered evidence of a severe population bottleneck, from which they construct their out-of-Africa model (Carter, 2010). These genetic situations are more consistent with a creation model than with evolution.

Mitochondria are organelles found in the cytoplasm of cells. They have some of their own DNA, which is separate from nuclear DNA yet considered part of the genome (all DNA of an organism). Mitochondrial DNA is passed down from mother to child, apparently with no contribution from the father. Based on differences in the sequence between people, it is clear we all could have come from one individual female, often called "Mitochondrial Eve."

Evolutionists place a time frame of when "Mitochondrial Eve" lived by assuming common ancestry between humans and chimps and the evolutionary timescale. However, when measured mutation rates in mitochondrial DNA were used, "Eve" was calculated to have lived around 6,000 years ago. Of course the evolutionists do not accept this time frame, so they have sought ways around the implications (Gibbons, 1998; Jazin et al., 1998). More recent in-depth analysis of mitochondrial DNA has upheld this biblical time frame for humans and found the same pattern in other organisms as well (Jeanson, 2014, 2015).

The out-of-Africa model was proposed by evolutionists to address the fact that patterns of genetic variability suggest a bottleneck occurred in the human lineage, and patterns of mitochondrial DNA variability across various populations suggested it may have originated from Africa (Cann et al., 1987). While various studies occasionally produce conflicting results, this is still the most popular evolutionary model of human history, partially because there is so much genetic diversity among Africans. The time frame and area from which humans dispersed differ from the Bible, but there are three major mitochondrial lineages that have been recognized (Witas and Zawicki, 2004; also see Figure 1). Carter (2009) has pointed out that there are other possible reasons for high genetic diversity in Africans, and (2010) that there is a more plausible ancestral sequence than the one proposed by evolutionists (Figure 2).

The human Y chromosome is remarkably similar among all humans, and the mutation rate is so slow it is difficult to detect (Jobling and Tyler-Smith, 2003). This is consistent with the biblical account, where Noah would have passed his Y chromosome on to his three sons less than 5,000 years ago. Yet, the chimpanzee Y chromosome is radically different from the human Y, which is a challenge for evolutionists to explain even in their extended time frame (Hughes et al., 2010). If humans and chimps had a common ancestor several million years ago, evolutionists are forced to propose that the Y chromosome mutated incredibly fast. But if all human males have very similar Y chromosomes (and they do), Y-chromosome Adam must have lived a very short time ago. Either way this is not consistent with evolutionary predictions. In contrast, this fits well with the biblical history of humans being created separately from all other animals.

Interestingly, global patterns in the Y chromosome suggest a less complex migration pattern than for mitochondrial DNA. It has been suggested that men generally have their families closer to their place of birth, and women leave their families to follow the men (Jobling and Tyler-Smith, 2003). This pattern is also consistent with the Babel dispersion, where families were spread according to identity of the fathers (Genesis 10:1–11:6), and so we would expect the mothers to be spread among the men.

Summary

The human genetic data is remarkably consistent with the biblical history. There is evidence that all humans trace their ancestry back to a single male and female, Adam and Eve. Genetic evidence points to a severe bottleneck, a dramatic decrease in population size, as we would expect from the Flood. Outside of Africa, there are three major lineages of mitochondrial DNA that would correspond to Noah's three daughters-in-law; yet there is a single worldwide lineage of Y chromosome that came from Noah through his three sons. Inside of Africa, the rarest sequences are also the most deviant. In other words, the out-of-Africa theory is based on statistical outliers! There is evidence of a single dispersion by families according to paternity, which corresponds well to the Babel event. When evolutionary assumptions are dropped and actual mutation rates are used, these events are within the biblical time frame.

Yet there is much information the Bible does not directly tells us, even while it does set limits for possible biblical models of human genetic history. For example, in Carter and Powell's

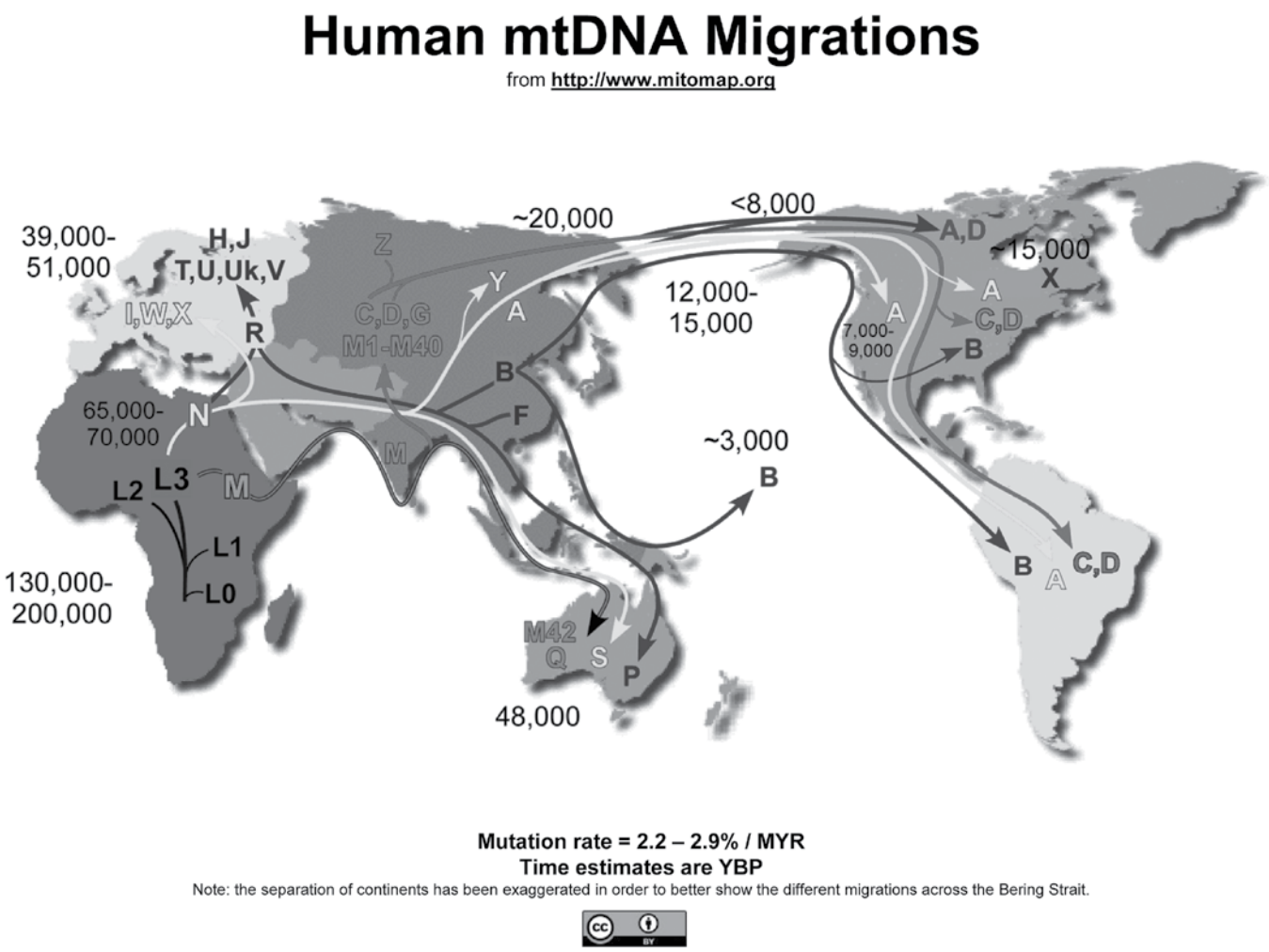

Figure 1. The evolutionary map of world migrations based on mitochondrial DNA has some striking similarities to predictions based on the biblical history. The out-of-Africa theory tells of a single dispersal of people, centered near and travelling through the Middle East, in the recent past. This type of pattern, with the migration originating in the Middle East, is predicted based on the history surrounding the Tower of Babel. Map from mitomap.org (http://www.mitomap.org/pub/MITOMAP/MitomapFigures/WorldMigrations2013.pdf).

model, the data forced them to conclude that either the antediluvian population was small or Noah and his wife and/or daughters-in-law were closely related. Is it unfair of us to appeal to a limited set of explanatory models when trying to fit the data to biblical history? Hardly, for this is exactly how the out-of-Africa theory developed (Carter, 2009), and it is still common practice among evolutionists today (Henn et al., 2016). Not only that, but most students of Creation and the Flood also have assumed the Flood bottleneck would involve a high degree of inbreeding, with possible loss of original diversity. This is especially true since Wieland's provocative 1994 article on the subject (Wieland, 1994). The inbreeding we might expect during the Flood/Babel period would produce exactly the allele frequency spectrum we see among modern people today.

Much of the discussion above could not have been part of any serious analysis of biblical history prior to just several years ago. The main reason for this has been the rise of powerful computers. With the rise of cloud computing, individuals now have inexpensive access to high-level computing resources once reserved for universities and governments. We would like to appeal to others interested in these subjects to build their own computer models. There are many questions remaining, and much refinement to existing conclusions can

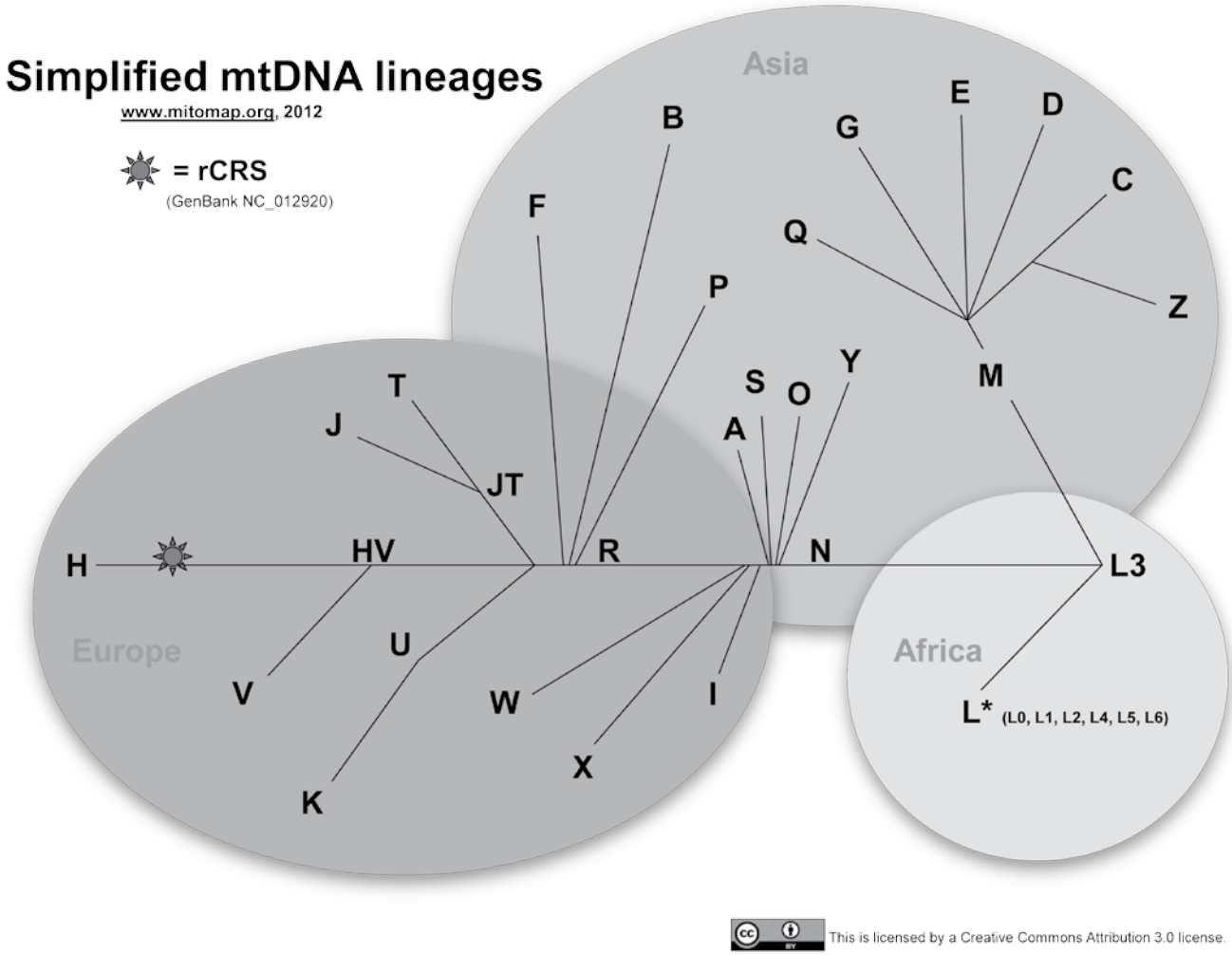

Figure 2. A diagram showing the relationship among major mitochondrial lineages. Evolutionists root the "tree" in Africa, but the sequences from there are statistical outliers. Carter (2007) placed the root at R, based on the most common nucleotides in each position across different human populations, but finding the location of the real root is a matter of statistics and historical uncertainties. Diagram from mitomap.org (http://www.mitomap.org/pub/MITOMAP/MitomapFigures/simple-tree-mitomap-2012.pdf).

be done. For example, if Neanderthals are human, how can we account for the presence of such genetically distinct humans that early in post-Flood history? And if Neanderthals interbred with humans early in modern human history (Kuhlwilm et al., 2016), what does this mean for the out-of-Africa theory since Neanderthals were supposedly not part of the bottleneck that led to the origin of "*Homo sapiens*?" And if sub-Saharan Africans came out of Babel, why do they display higher levels of genetic diversity than the rest of the world put together? These are fascinating questions, and as of right now they seem to be answered only by evolutionists. Creationists need to continue to develop competing robust models.

Robust creation models serve a purpose beyond just satisfying our curiosity about our history. A robust creation model that fits the data well can be used to make predictions, further test between the biblical history and the evolutionary one, and possibly give us valuable insights that relate to questions about adaptation and disease. These models would also help effectively counter challenges frequently leveled at biblical Creation. There is a tremendous opportunity for creation research in this area.

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