



S. Joshua Swamidass

The Overlooked Science of Genealogical Ancestry

S. Joshua Swamidass

Do we all descend from a single couple? Most are convinced that the genetic and archeological sciences answer with an unequivocal “no.” It appears that our ancestors share common ancestors with the great apes and arise as a large population, never dipping in size to a single couple. Without contradicting the findings of genetic science, genealogical science gives a different answer to the question. It is likely that there have been many individuals, and potentially couples, across the globe who are each individually genealogical ancestors of all those alive when recorded history began. These ancestors stretch from our distant past to very recently in our history. Consistent with the genetic and archeological evidence, therefore, it is possible that God could have chosen, or specially created, one of these couples for a special role. No argument is offered here that such a historical couple is what the text of Genesis teaches; however, if the text intends a particular couple in the recent past, such a couple could be among the ancestors from whom all those alive today descend.

It seems such a simple question, but it carries a great deal of subtlety and complexity: Do all humans descend from a single couple?

Genetic science appears to answer with a “no.” From genetic data, the population size of our ancestors at different times is estimated. It appears that population sizes never dipped to a single couple in the last several hundred thousand years, during the time in which *Homo sapiens* arises.¹ This conclusion is robust, based on several independent signals: our ancestors arose as a large population, not as a single couple.

It is a subtle and consequential error, however, to think that these findings demonstrate that there are no individual couples from whom we all descend. For the “no” to be correct, we must have inserted into the original question a genetic notion of ancestry. This insertion of “genetic” into the question neglects a key scientific fact: genealogical ancestry is *not* genetic ancestry. Genealogical ancestry traces the reproductive origins of individuals, while genetic ancestry

traces the origin of stretches of DNA. A question about “descent” can be a question about genealogies, and genealogical questions should be answered with genealogical science.

Furthermore, the term “human” is imprecise when referring to those in the distant past. Certainly, all members of the species *Homo sapiens* alive right now are human. In the ancient past, however, the term is ambiguous in both science and theology. For example, there are parallel intracamp debates amongst scientists, theistic evolutionists, and young earth creationists about whether Neanderthals and *Homo erectus* are “human.” Genetically, different species of the *Homo* genus might be less different from one another than subspecies of chimpanzees. There is also

S. Joshua Swamidass (MD, PhD) is a physician, scientist, and Assistant Professor of Laboratory and Genomic Medicine at Washington University in Saint Louis. He leads a computational biology group that studies information at the intersection of biology, chemistry, and medicine (<http://swami.wustl.edu/>). He also is a speaker for InterVarsity Christian Fellowship and Veritas Forums. Recently, he served as a Science Advisor for AAAS Science for Seminaries, and now blogs at Peaceful Science (<http://peacefulscience.org/>).

Article

The Overlooked Science of Genealogical Ancestry

evidence of interbreeding between Neanderthals and *Homo sapiens*. For these reasons, “human” is a term without scientific precision in the past. In view of this ambiguity, several models of human origins do not even consider all *Homo sapiens* in the distant past as “human.”²

With these subtleties in mind, we find a different answer if we mean ancestry and descent in a genealogical sense. Instead of genetics alone, we should look to genealogical science. Could a single couple be among the ancestors of all humans? The answer from genealogical science is a definitive “yes.” There are *many* universal genealogical ancestors (UGAs) in our past, each *individually* from whom we *all* descend. These *genealogical adams and genealogical eves*³ are likely to appear just thousands of years ago, and continue back until ancient times. Two of them could be a particular couple, named Adam and Eve in scripture, from whom we all descend.

Whether this belief is theologically warranted or hermeneutically founded is beside the point of this article: such a belief is not contradicted by the scientific evidence. If Adam and Eve are a particular historical couple in our past, the evidence tells us only that their offspring mixed with a large population of biologically compatible beings. Far from a grand innovation, this history is already put forward in ancient readings of Genesis and suggested by textual analysis of scripture (Gen. 3:1; 4:14,17; 6:1–4; Rom. 5:12–14).⁴ The cited authors can defend these hermeneutical claims for themselves, but our focus is on clarifying what science does and does not say.

There is an ongoing debate about Adam. Is Paul really teaching that we all descend from Adam? Is descent from Adam required to construct a coherent theological system? Does scripture teach that Adam and Eve were specially created? As important as is this debate, the focus here is on the scientific question, seeking to truthfully articulate what science does and does not say. Whether a genealogical Adam is required by theology, or not, the genealogical science here still stands.

Is it scientifically possible that we all descend genealogically from one and only one UGA couple? From a scientific point of view, this is an interesting question that deserves proper treatment. In this article, I neither disclose, defend, nor assert my personal beliefs.

As it should be, my personal position is irrelevant to the question at hand. Instead, this article’s focus is on what science does and does not say. Undoubtedly, this discussion will raise theological and hermeneutical questions of many sorts, but our focus here is on the science.

Genetics Is Not Genealogy

It cannot be overemphasized that genetic ancestry is not genealogical ancestry (fig. 1). Genealogical ancestry traces the reproductive origin of people, matching the common use of “ancestor,” “descendant,” “parent,” and “child.” In contrast, genetic ancestry has a much more exotic meaning, tracing the origin of stretches of DNA. Two assertions begin to clarify the distinction.

- 1. Genealogical ancestry does not imply genetic ancestry.** Consider a child’s father and grandfather. They both are fully the child’s genealogical ancestors. However, they are only partially the child’s genetic ancestors, approximately 1/2 and 1/4, respectively. The same is true of the child’s mother and grandmother. Genetic ancestry continues to dilute each generation: 1/8, 1/16, 1/32 ... to a number so small that it is unlikely a descendant has any genetic material from a specific ancestor.⁵ The many genealogical ancestors that pass to us no genetic material are not our genetic ancestors.
- 2. Genetic ancestry does not imply genealogical ancestry.** About 45% of the human genome is composed of a specific type of DNA, transposable elements. Transposable elements arose initially from viruses that inserted their genetic material into the genomes of our distant ancestors.⁶ These viruses themselves are our genetic ancestors and contributed to our genetic inheritance. They are not, however, our genealogical ancestors.

Genetic ancestry, therefore, is not genealogical ancestry. Which type of ancestry is most relevant to our central question: could all humans “descend” from any individual couple? In nontechnical discussion, questions about “descent” are questions about genealogical ancestry. DNA is a recent discovery, and genetic ancestry is a very new way of looking at the world. In the genomic age, our tendency is to start with genetic ancestry, but we must look to genealogical science to answer genealogical questions.

The scientific literature, in contrast, is predominantly focused on genetic ancestry. References to *most recent common ancestor* (MRCA) refer almost exclusively to the genetic ancestry of a defined stretch of DNA. For example, *mitochondrial eve* (m-MRCA) and *Y-chromosomal adam* (y-MRCA) are genetic MRCAs of the DNA inherited exclusively by one parent, mothers and fathers, respectively. As we will see, these genetic ancestries work entirely differently than does genealogical ancestry.⁷ To answer genealogi-

cal questions, we must instead look to the science of genealogical ancestry.

Four Surprises in Genealogical Ancestry

Genealogical ancestry is surprising. The common meaning of ancestry is genealogical. However, constant exposure to genetic ancestry in science calibrates our intuition around genetics instead.

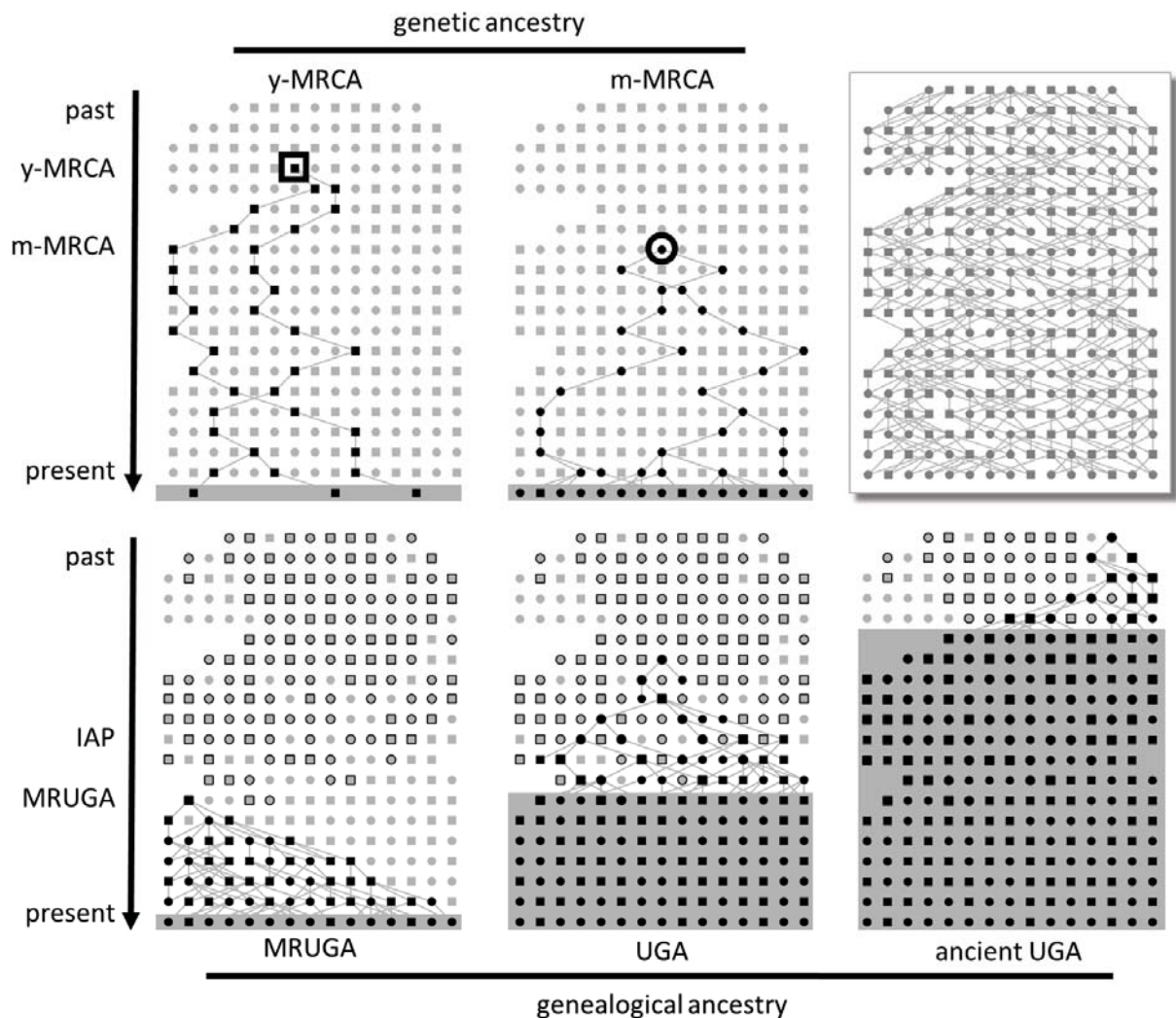


Figure 1. Genetic ancestry is not genealogical ancestry. *Universal genealogical ancestors* (UGAs) are individuals in our past, each from whom we all descend. UGAs arise quickly in a large crowd. To illustrate the difference, each panel gives a different view of the same pedigree (top right inset), in which ancestral relationships are displayed as lines, men as squares, and women as circles. The grey rectangles highlight the era in which the specified ancestor is a universal ancestor, a parent of all those in the region. Y-chromosomal adam (y-MRCA, top left) and mitochondrial eve (m-MRCA, top middle) are types of genetic ancestry (top), all of which take linear time to arise. Autosomal alleles take about twice as long to converge, and are excluded from the figure because they are more difficult to display on a pedigree like this. Genealogical ancestry (bottom), on the other hand, arises in logarithmic time with the *most recent universal genealogical ancestor* (MRUGA), and quickly becomes a cloud of many ancestors. At the *identical ancestor point* (IAP), everyone farther back in the past is either a UGA (black outline) or leaves no descendants. The descendants of three UGAs are marked (bottom), and similar pedigrees are possible for any UGA.

Article

The Overlooked Science of Genealogical Ancestry

As surprising as this may be, *genealogical adams* and *genealogical eves* (UGAs) are numerous, recent, robust, and unobservable. None of these surprises about UGAs undermine the findings of genetic science. The error, rather, is in using genetic ancestry to answer genealogical questions.

1. UGAs Are Numerous

Many individuals are *each* individually ancestors of “all the living” (fig. 1). All humans alive descend from each of these universal ancestors. The same can be said for all alive in AD 1, or all alive when recorded history begins. Intuition can be built by considering a group of grandchildren that share the same grandfather. The grandfather is their common genealogical ancestor, but so also is every ancestor of the grandfather. Considering the distant ancestors shared by their parents, we find even more genealogical ancestors. Unlike genetic ancestors (e.g., y-MRCA and m-MRCA), genealogical ancestors are very numerous. In one scenario,⁸ we expect more than 100 million individuals to be genealogical ancestors of everyone; *all* of us descend from *each* of them. They arise in a sudden cloud of individuals that quickly grows as we look back in time. All our different lineages quickly “collapse” into one family.

2. UGAs Are Recent

The *most recent universal genealogical ancestor* (MRUGA) of all living humans might have been situated as recently as 3,000 years ago.⁹ We can build intuition about this by counting back generations while simultaneously tracking the total population and the number of ancestors we expect from a naïve calculation. First, we have two parents, then four grandparents, then eight great-grandparents. The number of ancestors appears to increase *exponentially* as we go back; however, the number of people in past generations either stays comparatively *constant* in much of paleo-history or *decreases exponentially* over the last 10,000 years.¹⁰ How is this possible? Very quickly, all our genealogies begin to “collapse” by sharing more and more ancestors.¹¹ The first universal genealogical ancestor appears quickly, in just a few thousand years in realistic simulations.

Intuition calibrated by genetics misguides us regarding genealogies. The math illuminates the difference. In a random mating model, universal genetic ancestors, such as y-MRCA, appear proportionally to n generations, where n is the population size. But universal genealogical ancestors appear in merely $\log_2 n$

generations.¹² Moreover, the variability of when UGAs arise is much lower than the variability of when universal genetic ancestry arises.

3. UGAs Are Robust

The theoretical results are not substantially increased as more complexity is modeled; the time to UGA remains logarithmic. When migration is restricted to the idealized geography of a graph, the time to UGA is increased by a constant factor that linearly depends only on the size of graph.¹³ Moreover, time to UGA does not depend on high migration rates between nodes in the graph; less than a single migrant per generation in the distant past robustly yields recent UGAs.¹⁴ Likewise, increasing inbreeding increases time to UGA by a small, constant factor.¹⁵

Moreover, genealogical ancestry propagates more rapidly and reliably than genetic ancestry across a two-dimensional map. Genetic ancestry propagates in a dissipating wave that slows proportionally with \sqrt{t} , where t is the number of generations. But the wave of genealogical ancestry propagates at a constant speed t , without dissipating.¹⁶ Genealogical ancestry, therefore, spreads much more rapidly and reliably than genetic ancestry, even without taking realistic migration into account.

How do these mathematical models extrapolate to more realistic simulations of human history? A study published in *Nature* simulated the ancestry of present-day humans across the globe (fig. 2), taking into account the effect of geographical constraints, migration, local barriers to mixing, and population growth.¹⁷ Surprising even experts, these barriers do not substantially increase the time to universal ancestry.¹⁸ With low levels of migration, universal ancestors can arise in as few as 3,000 years.

4. UGAs Are Unobservable

UGAs are unobservable in genetic data. Detectable ancestors must (1) leave DNA to their descendants, and (2) this DNA must be identifiable as coming from them.

Genealogical ancestors in the distant past, however, are only rarely genetic ancestors; they usually leave their descendants no DNA.¹⁹ As one study explains, commonly, UGAs are *genetic ghosts* who leave DNA to only some of their ancestors, not all.²⁰ Many of our ancestors are *genetic super-ghosts* “who are simul-

taneously (1) genealogical ancestors of *each* of the individuals at the present, and (2) genetic ancestors to *none* of the individuals at the present.”²¹ Genetic ghosts are more likely with populations’ bottlenecks and small populations, both of which increase the rate at which DNA is lost. This is a critically important point. Since most of our ancestors leave us no identifiable DNA, genealogical relationships are “essentially unobservable” in genetic data past about fifteen generations.²²

The low level of ancient migration required for recent genealogical ancestry is undetectable in genetic data too.²³ A *single* migrant per generation to an isolated population is enough to reliably give rise to recent genealogical ancestors. Even when migrants do leave DNA, it is not usually identifiable as from a different population. The most likely migrants are those from the founding population, with DNA very similar to the isolated population.

The evidence of individual ancestors in our genomes degrades exponentially. UGAs themselves, and the ancient migration that makes them possible, are unobservable in genetic data.

Genetic Science Still Stands

None of these surprises in genealogies contradict genetic science in any way. The problem is not genetic science itself, but the error of using genetic ancestry to answer a distinctly genealogical question. Genetic ancestry is not genealogy.

Nonetheless, it still appears that *Homo sapiens* (1) shares ancestry with the great apes and (2) arose from a larger population that never dipped in size to a single couple.²⁴ Nothing in genealogical science undermines these two conclusions. If Adam as an individual existed, the notorious problem of intermarriage of his descendants with one another is avoided; instead, their descendants mixed with a larger population of biologically compatible beings. However, we would also count a particular couple called Adam and Eve as among our genealogical ancestors. They would be two people among those from whom we all descend, with theological or historical significance.

If Adam was a particular individual in our past, what happened to the population “outside the garden”?²⁵ Their history is rightfully and carefully

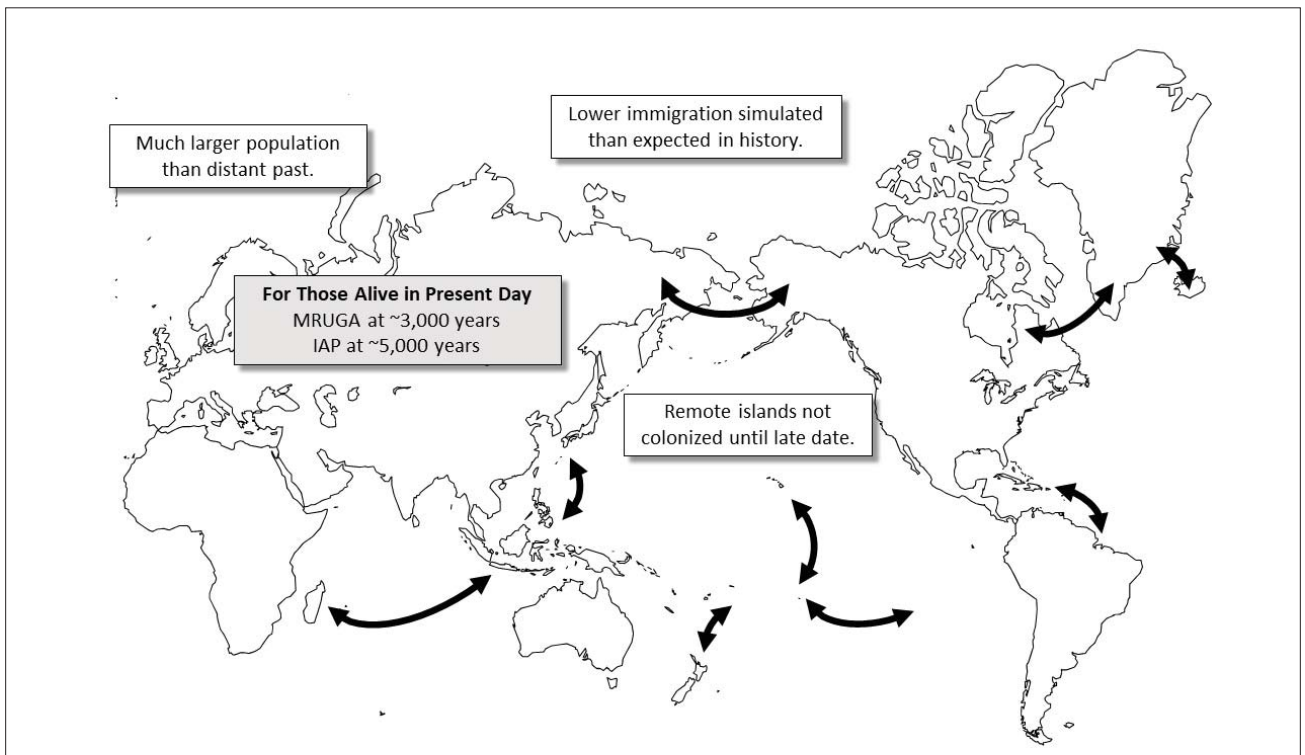


Figure 2. Simulating recent common ancestry. Universal common ancestry has been studied both analytically²⁶ and with simulations.²⁷ A 2004 study in *Nature* simulated world geography, migration, and local population structure.²⁸ Small amounts of migration were enough for MRUGA to arise in about 3,000 years, and to reach the IAP point in about 5,000 years. The arrows show some of the migration routes used in the simulation, and the insets identify three reasons why a simulation like this might overestimate the true wait times in the ancient past.

Article

The Overlooked Science of Genealogical Ancestry

studied with genetics and archeology. They provide strong evidence for large-scale population movements and intermixing in our ancient history. It was once thought that our ancestors arose in Africa and spread across the globe, leaving some populations isolated for long periods of time. It is now clear that our ancestors arose from multiple regions at once, with a complex history of intermixing across the globe. Often individuals or groups migrated in the opposite direction of the larger populations.²⁹ The full story of human evolution is that of populations across the globe linked in a common evolutionary fate by pervasive interbreeding everywhere.³⁰

What does genealogical science add to this account? Very quickly, in just thousands of years, those “outside the garden” mix with Adam’s lineage. At the present time, therefore, everyone alive is a descendant of Adam, as well as of others. Interbreeding across the globe links us both genetically and genealogically together.³¹ This statement of *monophylogeny* is how modern science counters polygenesis, a false theory of origins often marshaled in support of racism.³² Both genetic and genealogical science affirm *monophylogeny*.

One Plausible Assumption

We can estimate when universal genealogical ancestors arise with one scientifically plausible assertion: at minimum, low levels of migration and intermixing prevent any population from becoming genealogically isolated for more than a few generations. Genetic and geographic isolation are still expected, but low levels of migration prevented genealogical isolation.

The most important scientific objection arises from the observation or inference of isolated populations.³³ Three types of isolation are important here: genetic, geographic, and genealogical isolation. The critical question is whether genealogical isolation can persist for several thousand years. Due to the limits of genetic data, genealogical isolation is not directly observable. Consequently, this question is answerable only if genetic or geographic isolation can reliably identify genealogical isolation.

As we will see, genealogical isolation does not correspond with genetic or geographic isolation. Instead, the question of genealogical isolation poses a dilemma of complementary universal negatives.

A *single* genealogically isolated population will prevent a universal ancestor from arising. However, a *single* migrant or mixing event will break genealogical isolation. On the one hand, it is nearly impossible to rule out the isolation of every population. On the other hand, however, it is nearly impossible to rule out low levels of migration in order to demonstrate that a population was genealogically isolated for long periods of time. Science, therefore, cannot determine whether genealogically isolated populations have existed in our past or not.

Consequently, rather than trying to prove that genealogical isolation does not exist, we seek only to show that it is scientifically plausible to presume low levels of migration that prevent populations from being genealogically isolated. Undetectably low levels of migration are all that is required for UGAs to arise in the recent past.

Genetic Isolation Is Not Genealogical

It is possible that some populations have been genetically isolated for long periods of time. For example, portions of DNA from the Khoisan people of southern Africa and the Aborigines of Australia appear to be genetically isolated for tens of thousands of years.³⁴ This evidence is consistent with substantial cultural and geographic barriers that made mixing and migration difficult and uncommon. Initially, there was hope that genetics might determine if and when populations were genealogically isolated in the distant past.³⁵ However, genetic data cannot detect low levels of migration in the distant past.³⁶

Genetic isolation, therefore, does not demonstrate genealogical isolation. The most likely consequence of rare interbreeding is genetically isolated populations that are not genealogically isolated. Remember, genealogical isolation is broken with a *single* successful dispersal event. Consequently, to demonstrate genealogical isolation, one has to prove that absolutely zero successful immigration has taken place over hundreds or thousands of years. Most genealogical ancestors, however, do not leave any genetic evidence in their descendants.³⁷ Most ancient ancestors leave no identifiable DNA, and are, therefore, unobservable in genetic data. This is not a low-probability loophole. Genetic data is unable to determine genealogical relationships in the distant past.

Genetic evidence can falsify genetic isolation. In this way, genetics has produced strong evidence

against genealogical isolation, which supports the hypothesis of recent UGAs. Most genetics studies consider only small portions of the genome.³⁸ Whole genome sequencing could reveal mixing in the past. Similarly, ancient genomes provide additional evidence for ancient migrations,³⁹ even though human populations are fragmented and might be genetically isolated at times.

The Rising Seas

Rising seas limit our view of migration in the distant past. From about 12,000 to 8,000 years ago, seas rose about 120 meters, submerging very large coastal areas across the globe. As the seas rose, they erased much of the archeological evidence for migration and early settlements.⁴⁰ Colonization in paleo-history time might have been in boats, often along coasts and rivers, enabling rapid dispersal over long distances.⁴¹ This dual problem of coastal dispersion and submerged evidence limits our understanding of the most geographically isolated areas. For this reason, lack of positive evidence for migration is *not* evidence of isolation.

Moreover, for UGAs 10,000 years or earlier, most of the land bridges would still be passable for thousands of years. During this time, Australia, Tasmania, and the Americas would all be easier to access.

Isolation of the Americas

At first glance, the geographic isolation of the Americas seems insurmountable. It was thought that migration to the Americas was contingent on an intermittently open land bridge in Beringia or seafaring technology to cross the Pacific Ocean. Evidence, however, suggests continuous immigration in boats along a coastal route and the Aleutian islands.⁴² Even if immigration ebbed at times, genealogical isolation would require zero successful migrants to the Americas for centuries and millennia. Though we might expect genetically isolated populations in the Americas, it does not follow that the Americas were genealogically isolated too.

Isolation of Australia

Australia is often offered as definitive evidence against recent common ancestors.⁴³ Rising seas submerged land bridges across the world, making it more difficult to cross from South East Asia to Australia and separating Tasmania from Australia.

For this reason, we might expect Australia to be genealogically isolated.⁴⁴

The initial colonization of Australia adds important information. Land bridges never extended all the way to Australia. The last stretch required crossing a 50- to 100-kilometer-wide body of water. Until the arrival of *Homo sapiens* about 60,000 years ago, this final gap was not crossed. It is thought that boats or rafts might have been a unique capability of *Homo sapiens*, at least in this region, and were used to cross the strait in order to colonize Australia.⁴⁵ Similar seafaring feats enabled *Homo sapiens* migration to unexpected places for at least 100,000 years.⁴⁶ This is evidence that ancient *Homo sapiens* were capable of crossing large bodies of water. The geographic isolation of Australia does not demonstrate that it was genealogically isolated.

Isolation of Tasmania

Tasmania was connected to Australia by a large land bridge that was submerged by rising seas 8,000 years ago. From this time forward, crossing to and from Australia was impossible without seafaring capability. Nonetheless, there remain several habitable islands between Tasmania and Australia. Using these islands as a broken bridge, the crossing is possible with the same boats or rafts that enabled colonization of Australia in the first place. Before seas had fully risen 8,000 years ago, the crossing might have been much easier, with large portions of the land bridge still intact.

It was certainly difficult to reach Tasmania after 8,000 years ago. The real question is whether the barriers prevented *all* mixing. Even if mixing was limited to rare events, universal ancestors would arise. For this reason, we cannot know for sure if and when small amounts of migration took place to Australia and Tasmania. It seems reasonable to expect that at least a few boats every century still crossed.

Isolation of Remote Islands

The most remote islands—such as Hawaii, Easter Island, and the most eastern end of Polynesia—are very difficult and dangerous to find without modern technology. For this reason, these islands are key bottlenecks that push back estimates of the most recent ancestor of all present-day humans.⁴⁷ However, these islands were colonized just within

Article

The Overlooked Science of Genealogical Ancestry

the last few millennia.⁴⁸ They are not, therefore, relevant to UGAs later than about 6,000 years ago.

Caught between Two Negatives

For any multimillennium period in our distant past, were any populations genealogically isolated? Answering either “yes” or “no” requires making one of two absolute negative claims, each of which is difficult to substantiate.

On the one hand, answering “yes, there were genealogically isolated populations” requires asserting that there was zero successful migration or intermixing for thousands of years. This negative is not possible to demonstrate with evidence from either genetic or archeological data. Those skeptical of the “yes” answer can posit at least a tiny amount of migration and intermixing, which would undetectably break genealogical isolation.

On the other hand, answering “no, there were no genealogically isolated populations” requires asserting that there were zero populations that were isolated for thousands of years. This negative requires comprehensive knowledge of all populations in our distant past. Those skeptical of the “no” can posit that somewhere, somehow, an isolated population existed.

Absolute negatives of either sort are impossible to know confidently about the distant past. Reasonable scientists will legitimately disagree which absolute negative is most likely. However, it is scientifically plausible to assert the levels of migration and mixing required for universal ancestors to arise. Reaching the limits of science, there is flexibility in the scientific account.

“Humans” in Theology and Science

To estimate when UGAs arise, we must first define who is required to descend from them. We cannot just define this group as the “human race.” In both science and theology, the terms “human” and “humanity,” and their variants, are ambiguous in our distant past. They can mean a wide range of things. This ambiguity arises for deep and intractable reasons.

In science, there is a range of opinions and, at times, a raging debate. We see smooth transitions of forms from our distant ancestors to the present day. Historically, in communication with the public,

“human” is *anatomically modern* humans, or equivalently *Homo sapiens*. Some point to *Homo erectus* as the first human, noting their mastery of fire, complex language, and impressive tool industry. Most recently, the entire *Homo* genus is being called “human,” in recognition of their high similarity to one another and pervasive interbreeding. *Homo sapiens* is different from *Homo erectus*, but a dividing point defined by biology alone appears arbitrary. Consequently, using the term “human” in statements of scientific findings is imprecise and can artificially constrain theology when this imprecision is not clarified.

There are similar ambiguities in theology. At which point did “humans” become the “mankind” of scripture? How and when did we receive God’s image and then fall? Are Neanderthals and other hominids part of humankind too? Which milestones are theologically significant?

There are many theological definitions of “human,” but none of them clearly map to science. Consequently, there is a wide range of options explored in the literature. Denis Alexander and John Stott identify Adam about 10,000 years ago in the Middle East to preserve the agrarian details of the Genesis narrative and timeline.⁴⁹ Denis Lamoureux identifies theological humans of about 50,000 to 40,000 years ago with *behaviorally modern* humans.⁵⁰ Hugh Ross, Fazale Rana, and Greg Davidson identify humans with *Homo sapiens* and y-MRCA and m-MRCA at about 100,000 years ago.⁵¹ Without providing specific dates, C. John Collins suggests milestones such as language and knowledge of moral law.⁵²

Adding additional options, John Walton proposed that humankind is first created in the image of God, but then at a later time Adam is identified, perhaps specially created, and then subsequently falls.⁵³ Of note, this portion of his argument is purely textual and does not rely on Ancient Near Eastern literature. Moreover, Adam and Eve are the *first* and *only* theological “humans,” both inside and outside the garden, when they are created.⁵⁴ Walton himself does not specify his model more precisely, but one might look for markers of the Fall to identify when Adam or Eve might have lived. An attractive feature of this model is its affirmation that, at any specific time in the past, all our ancestors equally bear the image of God. This supports important theology of race and lays a foundation for universal rights.⁵⁵ Though

outside the scientific scope of this study, Walton's model merits more consideration.

Keeping in mind that Adam's line would exist alongside others for a time, we might consider those alive at other critical milestones in history, such as at the rise of civilization about 6,000 years ago, and 2,000 years ago when Paul writes Romans, referencing Adam in his theology. As we will see, even this late date could be consistent with identifying everyone mentioned in scripture after Genesis 11 as a descendant of Adam. Once again, the theological status of those outside Adam's line is a question outside the realm of science. It is possible that Walton's model may be helpful in making sense of these options.

Universal Ancestors of Descendants

With these subtleties in mind, we can make the first estimate. We define *genealogical adams* and *genealogical eves* as the people who each individually are UGAs of an entire group of *required descendants*; by definition, all "universal" ancestors must be genealogical ancestors of all the people in this group. After specifying the *required descendants*, we can estimate a range, which will stretch from the very distant past to a more recent date. Perhaps we can insist that Adam was a *Homo sapiens*, or in the *Homo* genus, or lived in a specific era in the past.

The recent end of the range is defined by three critical dates: (1) the *most recent universal genealogical ancestor* (MRUGA), (2) the *nearly identical ancestor point* (nearly IAP), and (3) the *identical ancestor point* (IAP). The most recent date is that of the MRUGA, the first point. Here, a single UGA appears somewhere in the globe. The most ancient date is that of the IAP, the third point. Here, each and every one that leaves ancestors is also a UGA. The only people at this point who are not UGA are those who, for example, do not have any children. Between these two dates is the nearly IAP, where *nearly* everyone alive (e.g., 95%, 98% or 99%) who leaves ancestors is also a UGA.⁵⁶ The "nearly" qualifier applies only to the number of UGAs, and does not diminish the universality.

Peer-reviewed estimates of these dates are available only in the scientific literature, when *required descendants* are chosen to be "those alive in the present day." Other estimates are nevertheless possible. Currently, only one study models migration,

geographic barriers, and population structure to estimate dates for all humans alive today.⁵⁷ The same first author also released an unpublished and unreviewed report with expanded results using a variety of parameters. These two studies represent the most realistic simulations of UGA.⁵⁸ Building confidence in the estimates, simulation results were reasonably consistent, even though all models used very low migration levels. The outliers with the longest estimates use unrealistically low migration across the entire map. The "high" immigration rate models still use very low immigration rates, but a MRUGA can arise in as little as 2,000 years. Other simulations are less relevant because they neglect geographic constraints entirely⁵⁹ or assume only a few kilometers of migration.⁶⁰

In the best simulations,⁶¹ the MRUGA is estimated to arise 3,000 years earlier than the *required descendants*. The IAP is estimated at about 5,000 years earlier than the *required descendants*. The nearly IAP for Mesopotamia is likely closer to the MRUGA data than the IAP; a conservative number is 4,000 years.⁶² For reference, this is approximately three times longer than analytic results assuming random mating.⁶³ The simulation increases estimates over the theoretical results, but not by much.

These estimates lead to surprising conclusions. For example, consider choosing all those alive in AD 1 (about 2,000 years ago) as the *required descendants*. An estimate of the IAP is about 7,000 years ago with a MRUGA at 5,000 years ago.⁶⁴ Therefore, all farmers in Mesopotamia 6,000 years ago who left any ancestors would each be universal ancestors of everyone alive in AD 1 (fig. 3). The reference to 6,000 years, to be clear, is merely a consequence of the math ($4 + 2 = 6$ kya) and should not be interpreted as a specific endorsement of somehow locating Adam here.

Moreover, these are cautious estimates. By AD 1, the most remote islands are not yet settled,⁶⁵ the population was smaller than present day,⁶⁶ and the simulation assumes very low levels of migration.

Descendants of Universal Ancestors

The central question can be asked the other way around. Consider a UGA in the distant past. How long is the "wait time" for this ancestor to become a universal ancestor of all those alive? How quickly does this individual's ancestry spread?

Article

The Overlooked Science of Genealogical Ancestry

The estimates of the prior section guide us to the answer. It will take between 3,000 and 5,000 years for a specific ancestor to become a UGA (fig. 2). The quickest time, 3,000 years, corresponds to the time of the MRUGA and applies to very few, lucky, and ideally located individuals. The longest time, 5,000 years, corresponds to the time of the IAP and applies to very few, unlucky, and poorly located individuals, such as those in the Americas or Australia. More likely, especially for those in central locations such as the Middle East, the wait time is between 4,000 and 3,000 years (fig. 3). A cautious estimate, therefore, of the wait time for typical individuals is 4,000 years, even though a more accurate estimate might be 3,500 years (fig. 4).

The key point, however, is that UGAs do not arise by pure luck or miraculous intervention. They are

not restricted to single lineages or rare individuals or a single location. Instead, UGAs arise everywhere. Typical locations accumulate many UGAs quickly, well before the nearly IAP date at 4,000 years.

Improving Estimates

How confident can we be that UGAs exist? With plausible scientific assumptions, we can be very confident. To make an analogy, we have no way of identifying or observing all my distant ancestors, but this does not reduce our confidence that they existed. Even though they are unobservable, we are entirely certain that they existed. With plausible assumptions, we can estimate approximately when my great-great-great grandparents lived. In the same way, we confidently infer the existence of universal ancestors and estimate when they arise.

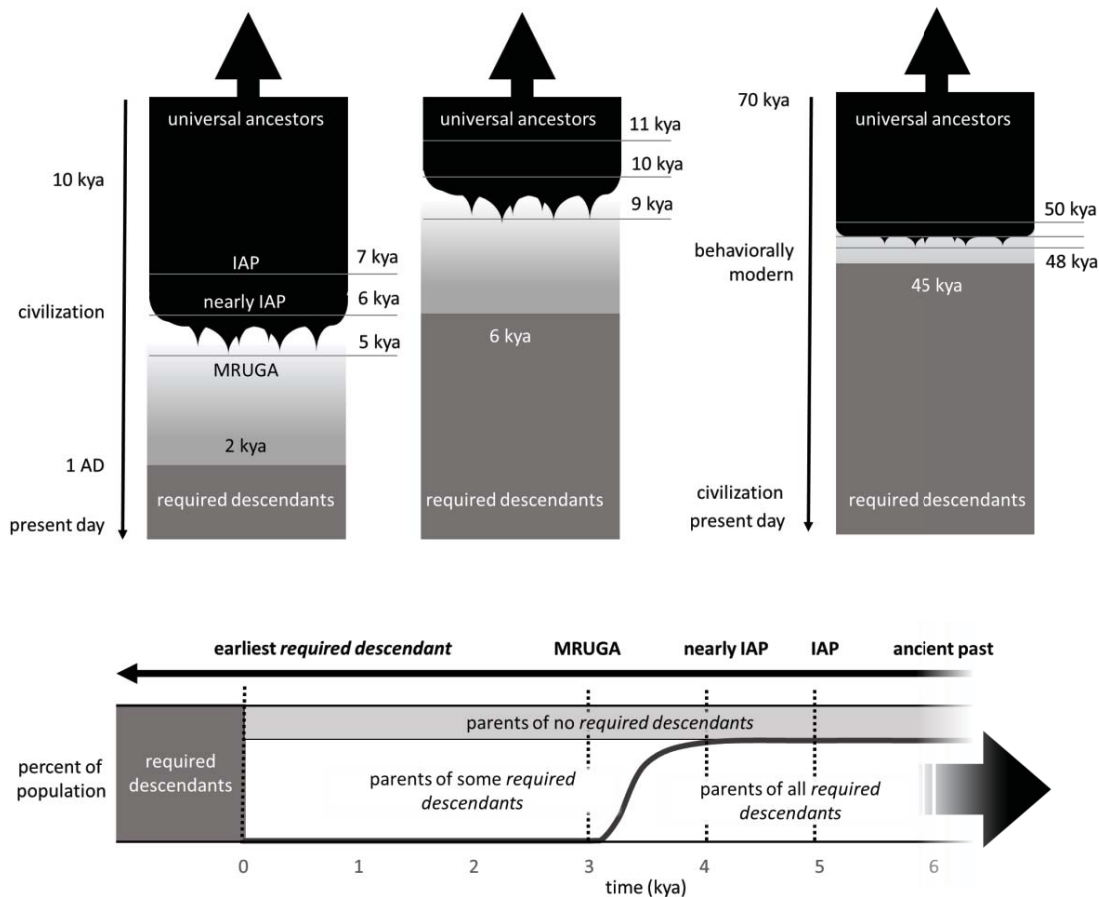


Figure 3. Estimating when universal ancestors arise. Universal genealogical ancestors (UGA) first arise in about 3,000 years before the *required descendants* and extend back into the distant past. The estimated UGAs of all those alive at AD 1, 6 kya, and 45 kya are displayed in cartooned pedigrees (top). The time axes are drawn approximately to scale but width does not correlate with population size. Three dates define the recent end of the range (bottom): (1) the *most recent universal genealogical ancestor* (MRUGA) date, (2) *nearly identical ancestor point* (nearly IAP), and (3) the *identical ancestor point* (IAP).

Smaller population sizes in the past could substantially reduce the wait times to UGAs. Quantitatively, wait time estimates should scale with $\log n / \log m$, where n is the population size at a time in the past, and m is seven billion, the approximate population at present day.⁶⁷ For example, at 5,000 years ago, there were about 18 million people in the world,⁶⁸ the scaling factor is about 0.8, and the corrected MRUGA estimate is about 2,400 years. At 10,000 years ago, there were about 2 million people in the world, the scaling factor is about 0.7, and the corrected MRUGA estimate is about 2,100 years.

A more rigorous approach uses improved simulations. Unfortunately, simulations at the level of detail

in the 2004 *Nature* study are difficult to implement and run, so this hypothesis is not easily verified.⁶⁹ Perhaps increased interest in these results will stimulate scientists to embark on these efforts.

Until then, the estimates presented here are reasonable, and are based on the best simulation of common ancestry available. Building confidence, the simulation results correspond closely with theoretical analysis. Moreover, the results of this simulation have stood uncontested for more than a decade in the literature. Certainly, the results are surprising. The reason is that our intuition is calibrated by genetic ancestry, which works very differently than genealogies.

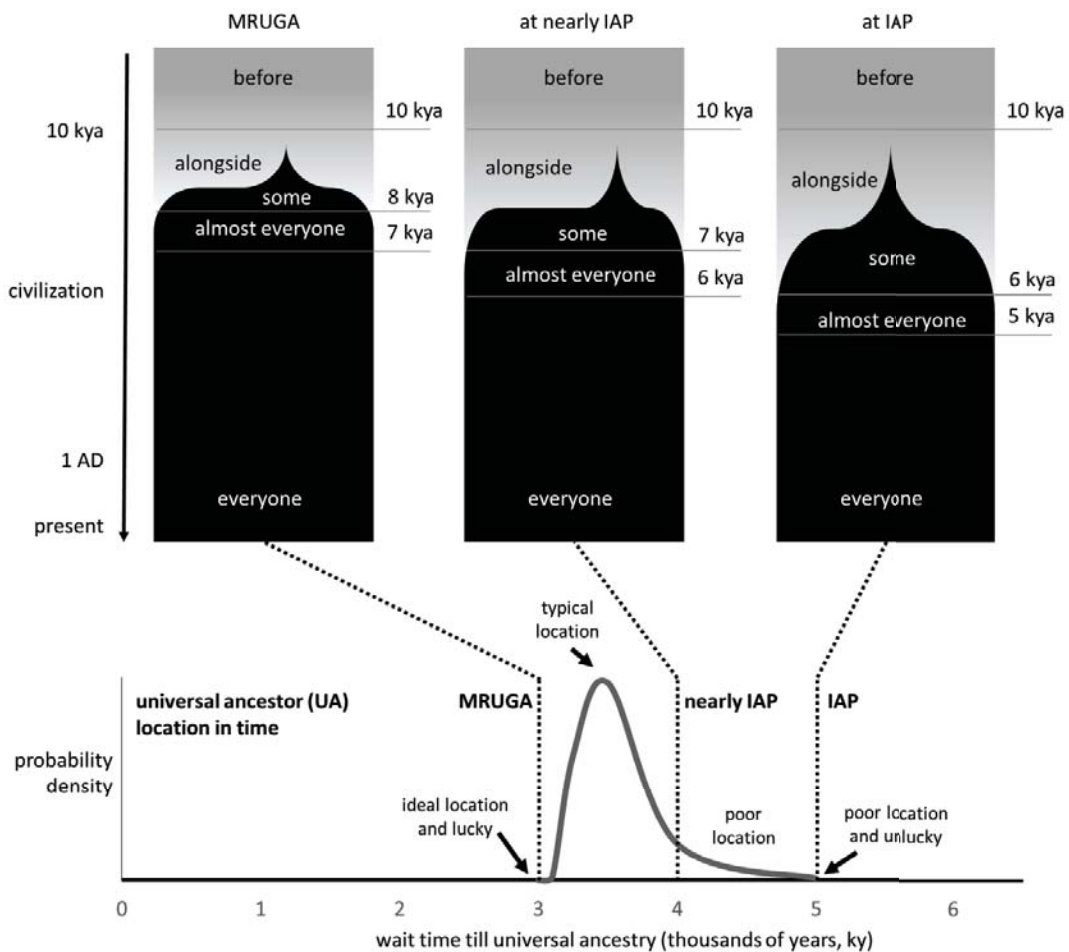


Figure 4. Estimating the descendants of universal ancestors. Cartooned pedigrees show the estimated ancestors at the MRUGA, nearly IAP, and IAP points (top). Universal ancestors usually become universal in less than 4,000 years, before the nearly IAP (bottom). The most likely time that UGAs first arise in a region is well before the nearly IAP, so most of the recent UGAs have pedigrees with dates about halfway between MRUGA (top left) and the nearly IAP (top middle) pedigrees. There are four eras to consider in relation to any specific UGA. In the first era, there are only those *before* the ancestor. In the second era, there are many living *alongside* the descendants of the ancestor. In the third era, *almost everyone* is a descendant of the ancestor. The non-descendants are those in the most isolated populations. In the fourth era, *everyone* alive is a descendant of the ancestor.

Article

The Overlooked Science of Genealogical Ancestry

A Genealogical View of Origins

We now turn to scientifically assessing several models of Adam that have been proposed in the literature by others. In this analysis, citation or explication of a model does not in any way imply endorsement. There will be intractable disagreement about the theological and hermeneutical merit of each model, but that is entirely beside the point. Our intention is merely to clarify what science does and does not say in these cases in the light of science. Those who find these models theologically flawed or hermeneutically unwarranted can and should take up their concerns with the advocates of these models. We, however, are focused exclusively on the relationship of these models to genealogical and genetic science.

Ancient Adam Models

Several models have been constructed with the goal of preserving genealogical descent from a particu-

lar individual named Adam.⁷⁰ Usually, this includes placing such an Adam as far back as y-MRCA, 200,000 or 100,000 years ago.⁷¹ This move requires either abandoning the Genesis setting and narrative, or maintaining that agriculture arises tens of thousands of years before it appears in the archeological record.

However, if the goal is to preserve universal genealogical ancestry, then choosing an ancient Adam is unnecessary (fig. 5). As we have seen, an Adam situated just 10,000 years ago is estimated, based on this analysis, to be the universal ancestor of all those in recorded history. Taking this as far as it can go, a couple, Adam and Eve, situated just 6,000 years ago could be estimated to be the UGAs of all those alive in AD 1, before the ministry of Jesus of Nazareth begins, and before Paul’s writes Romans with reference to Adam. It is possible that this couple might even be UGAs when Genesis was compiled,

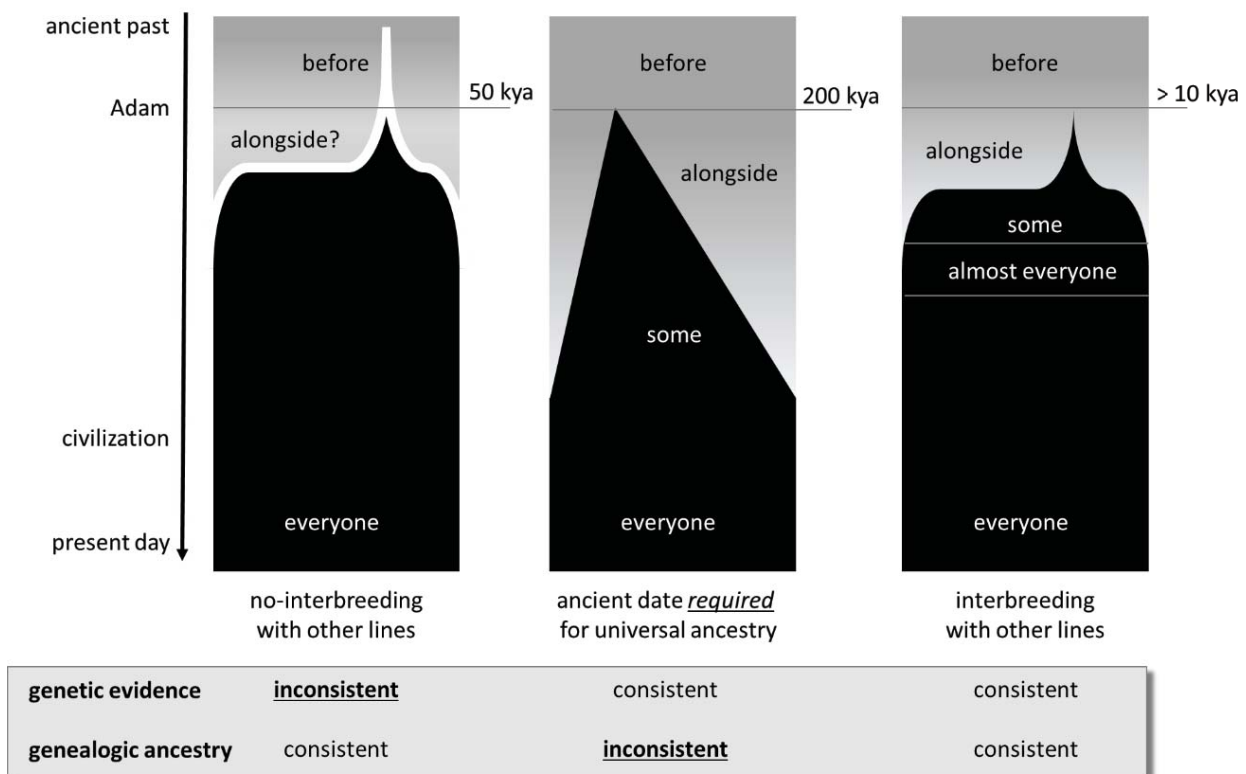


Figure 5: Ancient and recent ancestral models. Some models intend to include Adam as a universal ancestor and achieve this by placing him far back in time. In one model (left), Adam’s descendants do not mix with other lines. In this case, the model is consistent with genealogical ancestry but is contradicted strongly by genetic evidence. Allowing for mixing with other lines fixes this problem. In another model (middle), Adam is placed about 200,000 years in the past to match with y-MRCA. However, it is unnecessary to place Adam so far back (right), because genealogical ancestry converges in just thousands of years.

about 3,000 years ago. Of course, they would also be UGAs if they are located in the distant past alongside y-MRCA.⁷²

Whether or not these moves are warranted is a separate question, but the science itself does not force an *ancient* universal ancestor on those who think a genealogical relationship to Adam is important. All that must be accepted is that Adam’s line did mix with others, and that the findings of population genetics are our most accurate view of those “outside the garden” who become our ancestors too.⁷³ This appears to be the only way that population genetics presses on our understanding of Adam.

How these adjustments affect theology is a separate question. Scientifically, however, it is not necessary

to place Adam in the distant past to preserve universal genealogical descent from him.

Recent Adam Models

Some scholars identify Adam as a Paleolithic farmer about 10,000 years ago in Mesopotamia, alongside a larger population of *Homo sapiens*.⁷⁴ This model was offered by Derek Kidner and John Stott.⁷⁵ Their motivation for placing Adam here is to preserve the setting and chronology of the Genesis accounts.

This model is often coupled with the “representational” or “headship” model of original sin, in which sin spreads to all humankind independent of a genealogical connection to Adam.⁷⁶ It is asserted that a farmer situated 10,000 years ago could not be

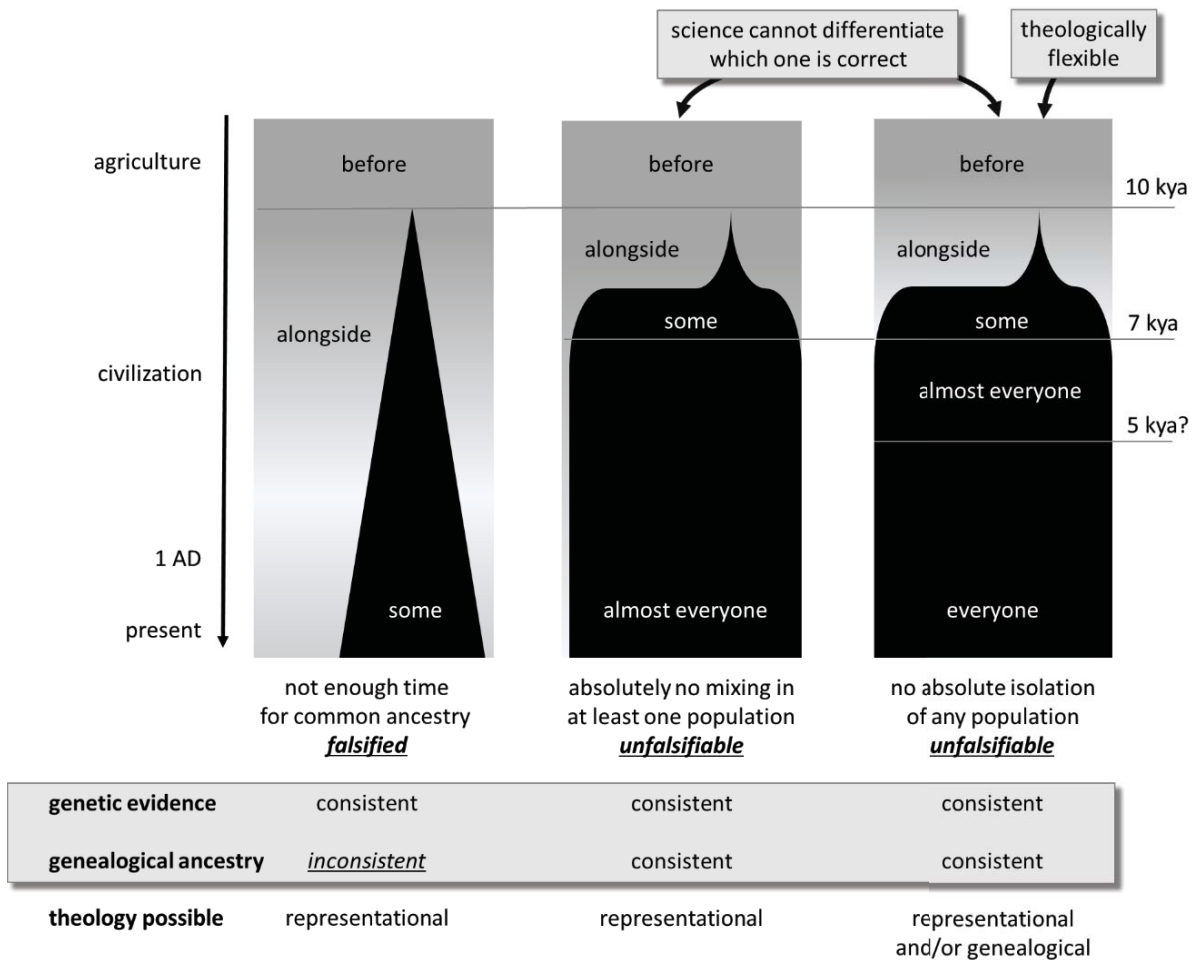


Figure 6. Recent representational models. It is commonly thought that, if a particular person named Adam lived 10,000 years ago, there was not enough time for him to be a UGA (left). Consequently, a genealogical relationship to such an Adam seems ruled out by science. Representational theologies circumvent this problem by passing original sin from Adam to all of us without a genealogical relationship. Whether or not a representational view of Adam is correct, the scientific reasoning is in error. Two alternate models are possible (middle and right); both are consistent with scientific knowledge, both are consistent with representational theology, but one (right) is consistent with genealogical theology. It appears impossible to scientifically differentiate between the two models; both depend on absolute negatives, which are very difficult or impossible to prove.

Article

The Overlooked Science of Genealogical Ancestry

a universal ancestor.⁷⁷ Consequently, theology that includes descent from Adam seems inconsistent with this scenario. A commonly offered solution is a representational model of original sin, which does not depend on descent from Adam. As we have seen, however, it is a scientific error to maintain that recent Adam models are incompatible with a universal genealogical descent from Adam (fig. 6).

Mesopotamia is a location from which we might expect universal ancestors to arise quickly. From the birthplace of civilization, descendants of a particular Adam could have spread, by riding the population boom of the agricultural revolution, to the remote corners of Europe, Asia, Australia, Africa, and the Americas. When recorded history begins about 6,000 years ago, everyone alive might already have descended from him. Moreover, the date of 10,000 years ago is merely an estimate, and could be revised earlier. Adam might be placed in the Gulf Oasis at 12,000 years ago,⁷⁸ while keeping all the essential details of the model fixed. Placing him this far back would make universal ancestry even more certain. Only a population that is genealogically isolated for thousands of years would prevent universal ancestors, and genealogical isolation of this type is unobservable. Consequently, it is likely in this model, under plausible assumptions, that we could all have descended from a particular couple. Of course, whether this possibility is important theologically cannot be answered by science.

Conclusion

This newly found theological freedom in the scientific account is an invitation to science-engaged theology. New evolutionary scenarios are possible.

Those who find theological significance in a genealogical connection to Adam are invited to consider important questions. How should we think of beings “outside the garden,” even if they remain in our distant past? A genealogical Adam affirms *monophylogeny* in the present day, but how theologically coherent is a history with other beings alongside Adam? It is also surprising that genealogical ancestors are not usually genetic ancestors. In what way, then, could genealogical relationships, nonetheless, be theologically meaningful for doctrines such as original sin?

These theological questions aside, more care is needed in stating the findings of science. Our ances-

tors arise as a population, not as a single couple, and they share ancestry with the great apes. However, at the same time, there are also many universal ancestors and potentially ancestral couples, each individually from whom we all descend.

Acknowledgments

This work is a product of the *Inquiry into Common Ground* (<http://peacefulscience.org>), supported by a STEAM grant from Fuller Theological Seminary and funded by the Templeton Foundation. Special thanks to Jeff Hardin, Jeff Schloss, Darrel Falk, Ken Keathley, Gavin Ortlund, Stephen Schaffner, Tom McCall, Loren Haarsma, Jon Garvey, Sy Garte, and Devin Gouvêa for pre-submission feedback on this manuscript, and to Geoffrey Fulkerson, Hans Madume, and Tom McCall for inviting the original submission to their online symposium. Thanks also to Alan Templeton for his technical critique. Jon Garvey and David Opderback are recognized for publishing on the web, as early as 2010, that there might be significance in the 2004 *Nature* study, concerning the conversation between science and theology. An early version of this manuscript was first published as a supplement to an article by *The Creation Project* in June 2017. ★

Notes

¹F. J. Ayala et al., “Molecular Genetics of Speciation and Human Origins,” *Proceedings of the National Academy of Sciences of the USA* 91, no. 15 (1994): 6787-94, <https://doi.org/10.1073/pnas.91.15.6787>; Scott McKnight and D. R. Venema, *Adam and the Genome: Reading Scripture after Genetic Science* (Grand Rapids, MI: Brazos Press, 2017); D. R. Venema, “Genesis and the Genome: Genomics Evidence for Human-Ape Common Ancestry and Ancestral Hominid Population Sizes,” *Perspectives on Science and Christian Faith* 62, no. 3 (2010): 166-78, <http://www.asa3.org/ASA/PSCF/2010/PSCF9-10Venema.pdf>; S. Schiffels and R. Durbin, “Inferring Human Population Size and Separation History from Multiple Genome Sequences,” *Nature Genetics* 46 (2014): 919-25, <https://doi.org/10.1038/ng.3015>; H. Li and R. Durbin, “Inference of Human Population History from Individual Whole-Genome Sequences,” *Nature* 475 (2011): 493-96, <https://www.nature.com/articles/nature10231>; P. Soares et al., “Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock,” *American Journal of Human Genetics* 84, no. 6 (2009): 740-59, <https://doi.org/10.1016/j.ajhg.2009.05.001>; D. L. Wilcox, “Genetic Insights for Human Origins in Africa and for Later Neanderthal Contact,” *Perspectives on Science and Christian Faith* 66, no. 3 (2014): 140-53, <http://www.asa3.org/ASA/PSCF/2014/PSCF9-14Wilcox.pdf>.

²D. Alexander, *Creation or Evolution: Do We Have to Choose?* (Oxford, UK: Monarch Books, 2008); D. B. Haarsma and

- L. D. Haarsma, *Origins: Christian Perspectives on Creation, Evolution, and Intelligent Design* (Grand Rapids, MI: Faith Alive Christian Resources, 2011); and C. J. Collins, *Did Adam and Eve Really Exist? Who They Were and Why You Should Care* (Wheaton, IL: Crossway, 2011).
- ³The terms are pluralized to emphasize that this is a large group of individuals. They are lowercase letters to emphasize that they are not all "Adam" and "Eve."
- ⁴Haarsma and Haarsma, *Origins: Did Adam and Eve Really Exist?*; J. H. Walton, *The Lost World of Adam and Eve: Genesis 2-3 and the Human Origins Debate* (Downers Grove, IL: InterVarsity Press, 2015); and J. B. Lumpkin, *The Books of Enoch: The Angels, the Watchers and the Nephilim* (Blountsville, AL: Fifth Estate Publishers, 2009).
- ⁵C. Wiuf and J. Hein, "On the Number of Ancestors to a DNA Sequence," *Genetics* 147 (1997): 1459-68; and S. Gravel and M. Steel, "The Existence and Abundance of Ghost Ancestors in Biparental Populations," *Theoretical Population Biology* 101 (2015): 47-53, <https://doi.org/10.1016/j.tpb.2015.02.002>.
- ⁶J. K. Pace II and C. Feschotte, "The Evolutionary History of Human DNA Transposons: Evidence for Intense Activity in the Primate Lineage," *Genome Research* 17 (2007): 422-32, <https://doi.org/10.1101/gr.5826307>.
- ⁷J. Lachance, "Inbreeding, Pedigree Size, and the Most Recent Common Ancestor of Humanity," *Journal of Theoretical Biology* 261, no. 2 (2009): 238-47, <https://doi.org/10.1016/j.jtbi.2009.08.006>; and Gravel and Steel, "The Existence and Abundance of Ghost Ancestors in Biparental Populations."
- ⁸This is an estimate of the *minimum* number of UGAs in a class of scenarios. The bias of almost every number chosen drives the estimate downward. Some of the terms here will be unclear at this point, but will be defined in later sections. If we expect Adam to be the common ancestor of all those alive at AD 1, a very ancient estimate of the identical ancestor point might be 20,000 years ago. If we want Adam to be a *Homo sapiens*, there is uncertainty in knowing when our species arises. To keep the math simple for illustrative purposes, we might assert that Adam appears sometime after 320,000 years ago. To produce a cautious estimate, we would use the effective population size of 10,000 individuals per generation and 30 years per generation; simple arithmetic brings us to 100 million UGAs: 10K (320K - 20K) / 30.
- ⁹D. L. T. Rohde, S. Olson, and J. T. Chang, "Modelling the Recent Common Ancestry of All Living Humans," *Nature* 431 (2004): 562-66, <https://doi.org/10.1038/nature02842>; and D. L. T. Rohde, "On the Common Ancestors of All Living Humans" (2003), <https://tedlab.mit.edu/~dr/Papers/Rohde-MRCA-two.pdf>. *Author's note*: This is a non-peer-reviewed web supplement.
- ¹⁰For example, there are approximately 160 generations between 10,000 and 5,000 years ago. Naïvely assuming that all ancestors are unique, we can compute the number of ancestors alive 10,000 years ago from the population at 5,000 years ago, 18 million people (see K. Klein Goldewijk, A. Beusen, and P. Janssen, "Long-Term Dynamic Modeling of Global Population and Built-Up Area in a Spatially Explicit Way: HYDE 3.1," *The Holocene* 20, no. 4 [2010]: 565-73, <https://doi.org/10.1177/0959683609356587>); we arrive at about 2×10^{55} ancestors, more than the number of stars in the universe. However, there were just 2 million people alive 10,000 years ago. The naïve calculation, therefore, double counts
- by a stunning 10^{49} times per ancestor. In a random mating model, this high degree of double counting gives rise to UGAs in less than 700 years.
- ¹¹J. T. Chang, "Recent Common Ancestors of All Present-Day Individuals," *Advances in Applied Probability* 31, no. 4 (1999): 1002-26, <https://doi.org/10.1017/S0001867800009587>.
- ¹²*Ibid.* The identical ancestor point arises in about $1.77 \log_2 N$ generations.
- ¹³Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans"; Rohde, "On the Common Ancestors of All Living Humans."
- ¹⁴Lachance, "Inbreeding, Pedigree Size, and the Most Recent Common Ancestor of Humanity"; and Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans."
- ¹⁵Lachance, "Inbreeding, Pedigree Size, and the Most Recent Common Ancestor of Humanity."
- ¹⁶J. Kelleher et al., "Spread of Pedigree versus Genetic Ancestry in Spatially Distributed Populations," *Theoretical Population Biology* 108 (2016): 1-12, <https://doi.org/10.1016/j.tpb.2015.10.008>.
- ¹⁷Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans."
- ¹⁸J. Hein, "Human Evolution: Pedigrees for All Humanity," *Nature* 431 (2004): 518-19, <https://doi.org/10.1038/431518a>; P. Donnelly et al., "Discussion: Recent Common Ancestors of All Present-Day Individuals," *Advances in Applied Probability* 31 (1999): 1027-35, <https://doi.org/10.1017/S0001867800009599>; and J. T. Chang, "Reply to Discussants: Recent Common Ancestors of All Present-Day Individuals," *Advances in Applied Probability* 31 (1999): 1036-38, <https://doi.org/10.1017/S0001867800009605>.
- ¹⁹Wiuf and Hein, "On the Number of Ancestors to a DNA Sequence"; and Kelleher et al., "Spread of Pedigree versus Genetic Ancestry in Spatially Distributed Populations."
- ²⁰Wiuf and Hein, "On the Number of Ancestors to a DNA Sequence"; and Gravel and Steel, "The Existence and Abundance of Ghost Ancestors in Biparental Populations."
- ²¹Gravel and Steel, "The Existence and Abundance of Ghost Ancestors in Biparental Populations."
- ²²Kelleher et al., "Spread of Pedigree versus Genetic Ancestry in Spatially Distributed Populations"; and C. D. Huff et al., "Maximum-Likelihood Estimation of Recent Shared Ancestry (ERSA)," *Genome Research* 21 (2011): 768-74, <https://doi.org/10.1101/gr.115972.110>.
- ²³M. C. Whitlock and D. E. McCauley, "Indirect Measures of Gene Flow and Migration: $F_{ST} \neq 1/(4Nm+1)$," *Heredity* 82 (1999): 117-25, <https://doi.org/10.1038/sj.hdy.6884960>; and J. Wang and M. C. Whitlock, "Estimating Effective Population Size and Migration Rates from Genetic Samples over Space and Time," *Genetics* 163, no. 1 (2003): 429-46, <http://www.genetics.org/content/163/1/429>.
- ²⁴Ayala et al., "Molecular Genetics of Speciation and Human Origins"; McKnight and Venema, *Adam and the Genome: Reading Scripture after Genetic Science*; Venema, "Genesis and the Genome"; Schiffels and Durbin, "Inferring Human Population Size and Separation History from Multiple Genome Sequences"; Li and Durbin, "Inference of Human Population History from Individual Whole-Genome Sequences"; Soares et al., "Correcting for Purifying Selection"; and Wilcox, "Genetic Insights for Human Origins in Africa and for Later Neanderthal Contact."
- ²⁵This is a turn of phrase that does not require that Adam exist or that there be a garden. Instead, it refers to those outside a UGA's line.

Article

The Overlooked Science of Genealogical Ancestry

- ²⁶Lachance, "Inbreeding, Pedigree Size, and the Most Recent Common Ancestor of Humanity"; Chang, "Recent Common Ancestors of All Present-Day Individuals"; and Kelleher et al., "Spread of Pedigree versus Genetic Ancestry in Spatially Distributed Populations."
- ²⁷Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans"; and Rohde, "On the Common Ancestors of All Living Humans."
- ²⁸Ibid.
- ²⁹M. G. Llorente et al., "Ancient Ethiopian Genome Reveals Extensive Eurasian Admixture in Eastern Africa," *Science* 350, no. 6262 (2015): 820–22, <http://science.sciencemag.org/content/350/6262/820>; J. A. Hodgson et al., "Early Back-to-Africa Migration into the Horn of Africa," *PLoS Genetics* 10, no. 6 (2014): e1004393, <https://doi.org/10.1371/journal.pgen.1004393>; and Garrett Hellenthal et al., "A Genetic Atlas of Human Admixture History," *Science* 343, no. 6172 (2014): 747–51, <http://science.sciencemag.org/content/343/6172/747>.
- ³⁰A. R. Templeton, "Human Races: A Genetic and Evolutionary Perspective," *American Anthropologist* 100, no. 3 (1998): 632–50, <https://doi.org/10.1525/aa.1998.100.3.632>; P. Ralph and G. Coop, "The Geography of Recent Genetic Ancestry across Europe," *PLoS Biology* 11, no. 5 (2013): e1001555, <https://doi.org/10.1371/journal.pbio.1001555>; and A. R. Templeton, "Biological Races in Humans," *Studies in History and Philosophy of Biological and Biomedical Sciences* 44, no. 3 (2013): 262–71, <https://doi.org/10.1016/j.shpsc.2013.04.010>.
- ³¹Ibid.
- ³²D. N. Livingstone, *Adam's Ancestors: Race, Religion and the Politics of Human Origins* (Baltimore, MD: The Johns Hopkins University Press, 2008).
- ³³Hein, "Human Evolution: Pedigrees for All Humanity."
- ³⁴A. G. Morris, "Isolation and the Origin of the Khoisan: Late Pleistocene and Early Holocene Human Evolution at the Southern End of Africa," *Human Evolution* 17, no. 3–4 (2002): 231–40, <https://doi.org/10.1007/BF02436374>; K. Huoponen et al., "Mitochondrial DNA Variation in an Aboriginal Australian Population: Evidence for Genetic Isolation and Regional Differentiation," *Human Immunology* 62, no. 9 (2001): 954–69, [https://doi.org/10.1016/S0198-8859\(01\)00294-4](https://doi.org/10.1016/S0198-8859(01)00294-4); and D. C. Petersen et al., "Complex Patterns of Genomic Admixture within Southern Africa," *PLoS Genetics* 9, no. 3 (2013): e1003309, <https://doi.org/10.1371/journal.pgen.1003309>.
- ³⁵Hein, "Human Evolution: Pedigrees for All Humanity."
- ³⁶Whitlock and McCauley, "Indirect Measures of Gene Flow and Migration: $F_{ST} \approx 1/(4Nm+1)$ "; Wang and Whitlock, "Estimating Effective Population Size and Migration Rates from Genetic Samples over Space and Time"; and Huff et al., "Maximum-Likelihood Estimation of Recent Shared Ancestry (ERSA)."
- ³⁷Wiuf and Hein, "On the Number of Ancestors to a DNA Sequence"; and Gravel and Steel, "The Existence and Abundance of Ghost Ancestors in Biparental Populations."
- ³⁸Morris, "Isolation and the Origin of the Khoisan."
- ³⁹Llorente et al., "Ancient Ethiopian Genome Reveals Extensive Eurasian Admixture in Eastern Africa."
- ⁴⁰J. I. Rose, "New Light on Human Prehistory in the Arabo-Persian Gulf Oasis," *Current Anthropology* 51, no. 6 (2010): 849–83, <https://doi.org/10.1086/657397>; and M. W. Pedersen et al., "Postglacial Viability and Colonization in North America's Ice-Free Corridor," *Nature* 537 (2016): 45–49, <https://doi.org/10.1038/nature19085>.
- ⁴¹Pedersen et al., "Postglacial Viability and Colonization in North America's Ice-Free Corridor"; and D. Bulbeck, "Where River Meets Sea: A Parsimonious Model for *Homo sapiens* Colonization of the Indian Ocean Rim and Sahul," *Current Anthropology* 48, no. 2 (2007): 315–22, <https://doi.org/10.1086/512988>.
- ⁴²Pedersen et al., "Postglacial Viability and Colonization in North America's Ice-Free Corridor."
- ⁴³Collins, *Did Adam and Eve Really Exist?*
- ⁴⁴Ibid.
- ⁴⁵Bulbeck, "Where River Meets Sea: A Parsimonious Model for *Homo sapiens* Colonization of the Indian Ocean Rim and Sahul."
- ⁴⁶T. F. Strasser et al., "Stone Age Seafaring in the Mediterranean: Evidence from the Plakias Region for Lower Palaeolithic and Mesolithic Habitation of Crete," *Hesperia* 79, no. 2 (2010), 145–90, <https://doi.org/10.2972/hesp.79.2.145>.
- ⁴⁷Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans."
- ⁴⁸J. M. Wilmshurst et al., "High-Precision Radiocarbon Dating Shows Recent and Rapid Initial Human Colonization of East Polynesia," *Proceedings of the National Academy of Sciences of the USA* 108, no. 5 (2011): 1815–20, <https://doi.org/10.1073/pnas.1015876108>; and T. L. Hunt and C. P. Lipo, "Late Colonization of Easter Island," *Science* 311, no. 5767 (2006): 1603–1606, <http://science.sciencemag.org/content/311/5767/1603.full>.
- ⁴⁹Alexander, *Creation or Evolution?*; J. R. W. Stott, *Romans: God's Good News for the World* (Downers Grove, IL: InterVarsity Press, 1994).
- ⁵⁰D. O. Lamoureux, "Beyond Original Sin: Is a Theological Paradigm Shift Inevitable?," *Perspectives on Science and Christian Faith* 67, no. 1 (2015): 35–49, <http://www.asa3.org/ASA/PSCF/2015/PSCF3-15Lamoureux.pdf>.
- ⁵¹G. Davidson, "Genetics, the Nephilim, and the Historicity of Adam," *Perspectives on Science and Christian Faith* 67, no. 1 (2015): 24–34, <http://www.asa3.org/ASA/PSCF/2015/PSCF3-15Davidson.pdf>; and F. Rana and H. N. Ross, *Who Was Adam? A Creation Model Approach to the Origin of Humanity* (Covina, CA: Reasons to Believe, 2015).
- ⁵²Collins, *Did Adam and Eve Really Exist?*
- ⁵³Walton, *The Lost World of Adam and Eve*.
- ⁵⁴Walton refers to Adam as the first "true" human, which we are referring to as "theological human."
- ⁵⁵R. W. Wills, *Martin Luther King Jr. and the Image of God* (New York: Oxford University Press, 2009), <https://doi.org/10.1093/acprof:oso/9780195308990.001.0001>.
- ⁵⁶In the simulations, these last 2 to 5% were people in Australia and the Americas (see Rohde, "On the Common Ancestors of All Living Humans"). At the nearly IAP, central locations like Mesopotamia have reached the IAP. Put another way, at the nearly IAP, essentially all individuals in Mesopotamia that left descendants are UGAs.
- ⁵⁷Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans."
- ⁵⁸Rohde, "On the Common Ancestors of All Living Humans."
- ⁵⁹Chang, "Recent Common Ancestors of All Present-Day Individuals."
- ⁶⁰Kelleher et al., "Spread of Pedigree versus Genetic Ancestry in Spatially Distributed Populations."
- ⁶¹Rohde, Olson, and Chang, "Modelling the Recent Common Ancestry of All Living Humans"; and Rohde, "On the Common Ancestors of All Living Humans."

S. Joshua Swamidass

⁶²As the simulation author notes, “the [nearly IAP] and the [IAP] are separated by perhaps 1000 years” (see Rohde, “On the Common Ancestors of All Living Humans”).

⁶³The logarithm base 2 of 1 billion people computes to 30 generations; this number times 30 years per generation gives us about 900 years up to MRUGA.

⁶⁴Rohde, Olson, and Chang, “Modelling the Recent Common Ancestry of All Living Humans.”

⁶⁵Wilmshurst et al., “High-Precision Radiocarbon Dating Shows Recent and Rapid Initial Human Colonization of East Polynesia”; and Hunt and Lipo, “Late Colonization of Easter Island.”

⁶⁶Klein Goldewijk, Beusen, and Janssen, “Long-Term Dynamic Modeling of Global Population and Built-Up Area in a Spatially Explicit Way: HYDE 3.1.”

⁶⁷Chang, “Recent Common Ancestors of All Present-Day Individuals.”

⁶⁸Klein Goldewijk, Beusen, and Janssen, “Long-Term Dynamic Modeling of Global Population and Built-Up Area in a Spatially Explicit Way: HYDE 3.1.”

⁶⁹Rohde, Olson, and Chang, “Modelling the Recent Common Ancestry of All Living Humans.”

⁷⁰Haarsma and Haarsma, *Origins*; Collins, *Did Adam and Eve Really Exist?*; Davidson, “Genetics, the Nephilim, and the Historicity of Adam”; and Rana and Ross, *Who Was Adam?*

⁷¹Davidson, “Genetics, the Nephilim, and the Historicity of Adam”; and Rana and Ross, *Who Was Adam?*

⁷²Davidson, “Genetics, the Nephilim, and the Historicity of Adam.”

⁷³Ayala et al., “Molecular Genetics of Speciation and Human Origins”; McKnight and Venema, *Adam and the Genome: Reading Scripture after Genetic Science*; Venema, “Genesis and the Genome”; Schiffels and Durbin, “Inferring Human Population Size and Separation History from Multiple Genome Sequences”; Li and Durbin, “Inference of Human Population History from Individual Whole-Genome Sequences”; Soares et al., “Correcting for Purifying Selection”; and Wilcox, “Genetic Insights for Human Origins in Africa and for Later Neanderthal Contact.”

⁷⁴Alexander, *Creation or Evolution*; Collins, *Did Adam and Eve Really Exist?*; and Stott, *Romans*.

⁷⁵D. Kidner, *Genesis: An Introduction and Commentary* (Downers Grove, IL: InterVarsity Press, 2008); and Stott, *Romans*.

⁷⁶Haarsma and Haarsma, *Origins*; and Collins, *Did Adam and Eve Really Exist?*

⁷⁷Ibid.

⁷⁸Rose, “New Light on Human Prehistory in the Arabo-Persian Gulf Oasis.”

ASA Members: Submit comments and questions on this article at www.asa3.org→FORUMS→PSCF DISCUSSION.

Reworking the Science of Adam

A half-day workshop preceding ASA 2018 at Gordon College, Wenham, MA, on Friday afternoon, July 27, 2018, led by S. Joshua Swamidass. For updated info, visit www.asa3.org.

A Paid Advertisement

BIOETHICS & BEING HUMAN
Conference June 21-23, 2018
on the campus of
Trinity International University
Deerfield, IL USA

THE CENTER FOR BIOETHICS & HUMAN DIGNITY
CELEBRATING 25 YEARS!

PLENARY SPEAKERS

- Christina Bieber Lake, PhD**
Wheaton College
- Dennis Hollinger, PhD**
Gordon-Conwell Theological Seminary
- C. Christopher Hook, MD**
Mayo Clinic
- Warren Kinghorn, MD, ThD**
Duke Divinity School
Duke University Medical School
- Paul Scherz, PhD, PhD**
Catholic University of America
- Read Mercer Schuchardt, PhD**
Wheaton College
- Michael Sleasman, PhD**
The Center for Bioethics & Human Dignity
- Pia de Solenni, SThD**
Roman Catholic Diocese of Orange
- Morse Tan, JD**
NIU College of Law
- Stephen Williams, PhD**
Union Theological College

REGISTER FOR EARLY BIRD PRICING BY MARCH 15
www.cbhd.org/conf2018

THE CENTER FOR **BIOETHICS & HUMAN DIGNITY**
TRINITY INTERNATIONAL UNIVERSITY

In Partnership with:
American Association of ProLife OB|GYNs
American College of Pediatricians