The Overlooked Science of Genealogical Ancestry

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Do we all descend from a single couple? Most are convinced that genetic and archeological science answer with an unequivocal 'no.' Genealogical science, however, gives a different answer: there are many couples, pairs of universal genealogical ancestors, each from whom we all descend. These ancestors stretch from our distant past to very recently in our history. Surprisingly, a Middle Eastern farmer from 10,000 years ago is expected to be the ancestor of all those in recorded history. All the findings of evolutionary and genetic science still stand; it appears Homo sapiens (1) share common ancestors with the great apes and (2) arise as a large population. Nonetheless, this finding revises the scientific analysis of several proposals of our origins, creating flexibility in how we understand them. In light of these findings, increased precision in our language is required to accurately explain what evolutionary science does and does not say about our origins. Delimiting the scientific account gives freedom to science-engaged theology. New theological accounts of our origins are possible, and they are entirely consistent with the scientific consensus. There may be a theological or hermeneutical case against a historical Adam. Nothing in science, however, unsettles the confession that we all descend from him.

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

Genetic science seems to answer with a 'no.' From genetic data, the population size of our ancestors at different times is estimated. It appears that populations sizes never dipped down to a single couple in the last several hundred thousand years, during the time during which *Homo sapiens* arise (*1*–*7*). This conclusion is robust, based on several independent signals. *Homo sapiens* arose from a larger population, not a single couple.

However, this reasoning neglects a key scientific fact: genealogical ancestry is *not* genetic ancestry. Genealogical ancestry traces the reproductive origins of individuals, but genetic ancestry traces the origin of stretches of DNA. A question about "descent" is 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 *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 intra-camp debates amongst scientists, theistic evolutionists, and young earth creationists about whether Neanderthals and *Homo erectus* are "human." Likewise, several models of human origins do not count all *Homo sapiens* in the distant past as "human" (*8–10*).

With these subtleties in mind, we find a different answer in genealogical science. Could a single couple be the ancestor 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*[1] are likely to appear just thousands of years ago, and continue back till ancient times. Of course, two of them could be the Adam and Eve of Scripture from whom we all descend.

Depending on how theological "humans" are defined, two of these *genealogical adams* could have been the "first and only humans on earth." Eve could be the "mother of all the living," Adam could be the "one man" from whom God made all nations, and together they could be the "sole-progenitors" of the entire "human race." Perhaps they were specially created by God, "without parents."

Whether or not these doctrines are theologically warranted or hermeneutically founded is beside the point; the scientific evidence does not unsettle them. The evidence only tells us that, if Adam and Eve are real, 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 (Genesis 3:1; 4:14,17; 6:1-4, Romans 5:12-14) (*9–12*).

Certainly, there is an ongoing debate about Adam. Is Paul really teaching we all descend from Adam? Is descent from Adam required to construct a coherent theological system? Does Scripture teach they were special 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.

It is scientifically possible we all descend from the same couple?

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[1] The term is pluralized to emphasize that this is a large group of individuals. The term also includes both men and woman, could just as well be named *genealogical eves*. The term is lowercase, to emphasize that they are not "Adam."

Genetics is not Genealogy

It cannot be overemphasized that genetic ancestry is not genealogical ancestry (Figure 1). Genealogical ancestry traces the reproductive origin of people, matching the common use of "ancestor," "descendent," "parent," and "child." In contrast, genetic ancestry has a much more exotic meaning, tracing the origin of stretches of DNA. Three examples 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 grandmothers. Genetic ancestry continues to dilute each generation: 1/8, 1/16, 1/32…to a number so small it is unlikely a descendent has any genetic material from a specific ancestor. The many genealogical ancestors that pass 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 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 (*13*). These viruses themselves are our genetic ancestors. They are not, however, our genealogical ancestors.

3. **Genetic ancestry follows one parent each generation, but genealogical ancestry follows both parents**. Each piece of DNA is inherited from a single parent. For this reason, as we go back in time, genetic lineages shrink and "coalesce" into a single individual, but genealogical lineages quickly expand to include all people; they "collapse" into a single, gigantic family.

Genetic ancestry, therefore, is not genealogical ancestry. Which type of ancestry is most relevant to our central question, could all humans "descend" from a single couple? 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, or tendency is to start with genetic ancestry, but we must look to genealogic science to answer genealogical questions.

The scientific literature, in contrast, is predominantly focused on genetic ancestry. References to *most recent common ancestor* (MRCA) are almost exclusively to the genetic ancestry of a defined stretches 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 genealogical ancestry (*14*, *15*). To answer genealogical questions, we must look to the science of genealogical ancestry instead.

Four Surprises in Genealogical Ancestry

Genealogical ancestry is surprising. Constant exposure to genetic ancestry in science calibrates our intuition around genetics. Nonetheless, the natural understanding of ancestry is genealogical. As surprising as this may be, *genealogical adams*, or 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.

They are Numerous

Many individuals are *each* individually ancestors of "all the living" (Figure 1). All humans alive descend from each of these universal ancestors. The same can be said for all alive in 1AD, 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,[2] 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] This 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 when our species arises. To keep the math simple for illustrative purposes, we might assert 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: $10K\,(320K - 20K)\,/\,30$.

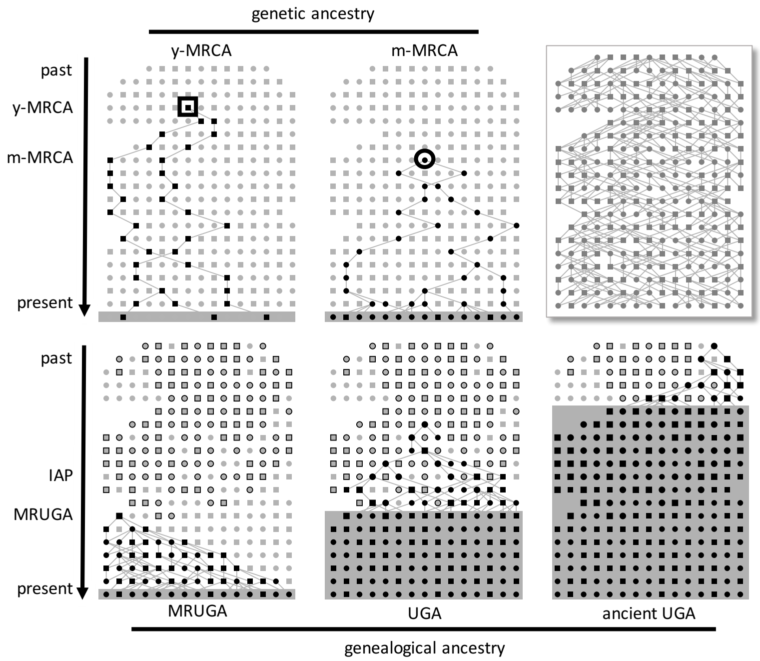

Figure 1. Genetic ancestry is not genealogical ancestry. *Universal genealogical ancestors* (UGAs) are individuals in our past, *each* from whom we all descend. UGAs arises quickly in a large crowd. To illustrate the difference, each panel gives a different view of the same pedigree (top right inset), where ancestral relationships are displayed as lines, men as squares, and women as circles. The grey rectangles highlight the era where 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. Genealogical ancestry (bottom), on the other hand, arise in logarithmic time with the *most recent universal genealogical ancestor* (MRUGA), and quickly become 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.

They are Recent

The *most recent universal genealogical ancestor* (MRUGA) of all living humans might have been situated as recently as 3,000 years ago (*16*). 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.[3] How is this

[3] For example, there are approximately 160 generations between 10,000 and 5,000 years ago. Naïvely assuming 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 (*41*); we arrive at about 2 x 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 that give rise to UGAs in less than 700 years.

possible? Very quickly, all our genealogies begin to "collapse" by sharing more and more ancestors (*17*). 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 (like y-MRCA) appear proportionally to n generations, where n is the population size. But universal genealogical ancestors appear in merely $\log_2 n$ generations (*17*).[4] Moreover, the variability of when UGAs arise is much lower than the variability of when genetic ancestry arises.

They 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 only linearly depends on the size of graph (*18*). 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*, *16*). Likewise, increasing inbreeding increases time to UGA by a small, constant factor (*14*).

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 time. But the wave of genealogical ancestry propagates at a constant speed t, without dissipating (*19*). Genealogically 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 (Figure 2), taking into account the effect of geographical constraints, migration, local barriers to mixing, and population growth (*16*). Surprising even experts (*20*), these barriers do not substantially increase the time to universal ancestry. With low levels of migration, universal ancestors can arise in as few as 3,000 years.

[4] The *identical ancestor point* arises in about 1.77 $\log_2 N$ generations.

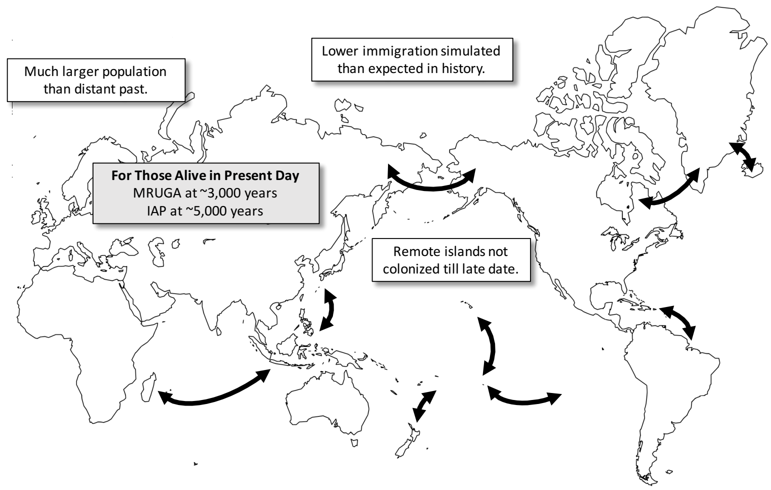

Figure 2. Simulating recent common ancestry. Universal common ancestry has been studied both analytically (*14*, *17*, *19*) and with simulations (*16*, *18*). A 2004 study in *Nature* simulated world geography, migration, and local population structure. Small amounts of migration were enough for MRUGA 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.

They are Unobservable

UGAs are unobservable in genetic data. Detectable ancestors must (1) leave DNA to their ancestors that live till today, and (2) this DNA be must 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*, *21*). As one study explains, many of our ancestors are *genetic super-ghosts* "who are simultaneously (i) genealogical ancestors of *each* of the individuals at the present, and (ii) genetic ancestors to *none* of the individuals at the present" (*15*, *21*). Commonly, UGAs are genetic ghosts who leave DNA to only some of their ancestors, not all. Genetic ghosts are more likely with populations bottleneck and small populations, which both increase the rate at which DNA is lost. This is a critically important point. Since most our ancestors leave us no identifiable DNA, genealogical relationships are "essentially unobservable" in genetic data past about 15 generations (*19*, *22*).

The low level of ancient migration required for recent genealogical ancestry is undetectable in genetic data too (*23*, *24*). 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 *Homo sapiens* (1) share ancestry with the great apes and (2) arose from a larger population that never dipped in size to a single couple (*1*–*7*). Nothing in genealogical science undermines these two conclusions. If Adam existed, the notorious problem in the biblical record regarding intermarriage of his descendants is avoided; their descendants mixed with a larger population of biologically-compatible beings. However, we all count Adam and Eve as genealogical ancestors. They would be two people from whom we all descend, with theological or historical significance.

If Adam was real, what happened to the population "outside the garden?"[5] Their history is rightfully and carefully studied with genetics and archaeology. They provide strong evidence for large-scale population movements in our ancient history. Our ancestors arose in Africa and spread across the globe. We should not, however, regard this as the complete story. The details of migration patterns are not observable in genetics. Often individuals or groups backtracked in the opposite direction as the larger populations (*25*, *26*). The full story of human evolution is that of populations across the globe linked into a common evolutionary fate by pervasive interbreeding everywhere (*27*).

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 descendent of Adam. Interbreeding across the globe links us both genetically and genealogically together (*27*). Both lines of reasoning teach monogenesis of the human race.

Genealogical Isolation

[5] This is a turn of a phrase that does not require that Adam exists or that there was a garden. Instead it refers to those outside a UGA's line.

The most important scientific objection arises from the observation or inference of isolated populations (*20*). Three types of isolation are important here: genetic, geographic, and genealogical isolation. The critical question is whether or not genealogical isolation can persist for several thousand years. As a consequence of the limitations of science, genealogical isolation is not directly observable. Consequently, this question is only answerable 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 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 one hand, it is nearly impossible to rule out the isolation of every population. On the other hand, however, it is nearly impossible rule out low levels of migration in order to demonstrate 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 only seek to show that it is scientifically plausible to presume low levels of migration that prevent populations from being genealogically isolation. Just a single immigrant per generation is all that is required for UGAs to reliably arise in the recent past.

Genetic Isolation is not Genealogical

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 (*28*–*30*). 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 (*20*). However, genetic data cannot detect low levels of migration in the distant past (*14*, *15*).

Genetic isolation, therefore, does not demonstrate genealogic isolation. The most likely consequence of rare interbreeding is genetically isolated populations that are not genealogically isolated. Remember, genealogic 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 (*15*, *21*). 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.

Genetics can, in contrast, uncover evidence against isolation, which would support recent UGAs. Most genetics studies only consider small portions of the genome (*28*). Whole genome sequencing could reveal mixing in the past, even in populations thought to be isolated. Likewise, ancient genomes have revealed ancient migrations undetected by extant sequences (*25*).

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 (*31*, *32*). Colonization in paleo-history time might have been in boats, often along coasts and rivers, enabling rapid dispersal over long distances (*31*, *33*). This dual problem of costal 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 be still intact for thousands of years. During this time, Australia, Tasmania, and America 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 costal route and the Aleutian islands (*31*). Even if immigration ebbed at times, genealogical isolation would require zero successful migrants to the Americas for centuries and millenniums. 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 (*10*). 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 (*10*).

The initial colonization of Australia adds important information. Land-bridges never extended all the way to Australia. Crossing the last stretch required crossing a 50- to 100-kilometer wide body of water. Until the arrival of *Homo sapiens* in the area

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 colonize the Australia (*33*). Similar seafaring feats enabled *Homo sapiens* migration to unexpected places for at least 100,000 years (*34*). This is evidence that ancient *Homo sapiens* were capable of crossing large bodies of water. The geographic isolation of Australia does not demonstrate it was genealogically isolation.

Isolation of Tasmania

Tasmania was connected to Australia by a large land-bridge, until it was submerged by rising seas 8,000 years ago. From this time forward, crossing from to Australia was impossible without seafaring capability. Nonetheless, there remains 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 if the barriers prevented *all* mixing. Even if mixing was limited to rare events, universal ancestors 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—like 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 (*16*). However, these islands are colonized just within the last few millennia (*35*, *36*). They are not, therefore, relevant to UGAs later than about 6,000 years ago.

Caught Between Two Negatives

For any multi-millennium period in our distant past, were any populations genealogically isolated? This question cannot be answered with science. Answering either "yes" or "no" requires making one of two absolute negative claims, each of which is difficult to substantiate.

On one hand, answering "yes, there was genealogically isolated populations" requires asserting 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 like existed.

Absolute negatives of either sort are impossible to confidently know 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.

Estimating Universal Ancestors

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 several generations. Genetic and geographic isolation are still expected, but low levels of migration prevented genealogical isolation.

"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. In many ways, we see smooth transitions of forms from our distant ancestors to the present day. Some point to *Homo erectus* as the first human, noting their mastery of fire, complex language, and impressive tool industry. Commonly in scientific communication, "human" is *anatomically modern* humans, or equivalently *Homo sapiens*.

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 mankind too? Which milestones are theologically significant? The clearest theological definitions typically describe our condition now, often excluding Adam himself in his pre-Fallen state and other boundary cases. Consider two grounded definitions that could plausibly be derived from Scripture. Presuming Adam exists, we can adopt "descendants of Adam" as a self-evidently true description of "humans", even if it is tautological. "God-imaged and fallen" might be a useful theological shorthand. Neither of these definitions map to a scientifically definable group. There, ultimately, is no scientific way of detecting the "breath of God" or His image in us.

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 (*8*, *37*). Dennis Lamoureux identifies theological humans about 50,000 to 40,000 years ago with *behaviorally modern* humans (*38*). Hugh Ross, Fuz Rana, and Greg Davidson identify humans with *Homo sapiens*, y-MRCA and m-MRCA about 100,000 years ago (*39*, *40*). Without providing specific dates, C. John Collins suggests milestones like language and knowledge of moral law (*10*). Adding to this list, we might consider those alive at critical milestones in history, like the rise of civilization about 6,000 years ago and 2,000 years ago. While refinement of the relevant questions may be possible, consensus regarding the answers seems unlikely.

Universal Ancestors of Descendants

With these subtleties in mind, we can make the first estimate. We define *genealogical adams* as the people who each individually are UGAs of an entire group of *required descendants*; by definition, all "universal" ancestors must ancestor of all the people in this group. After defining the *required descendants*, we can estimate a range, which will stretch from the very distant past to a more recent date. Perhaps we insist Adam 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 point, the date of the MRUGA is the first point. Here, a single UGA appears somewhere in the globe. The most ancient point, the data of the IAP is the third point. Here, each and every one that leaves ancestors is also a UGA. The only people at point this who are not UGA are those who, for example, do not have any children. Between these two points is the nearly IAP, where *nearly* everyone alive (e.g. 95%, 98% or 99%) who leaves ancestors is also a UGA.[6] The "nearly" qualifier applies only to the number of UGAs, and does not diminish the universality.

Peer-reviewed estimates of these dates for all *required descendants* are not available in the scientific literature. Estimates are nevertheless possible. Currently, only one

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[6] In the simulations, these last 2 to 5% were people in Australia and the Americas (*18*). 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 leave ancestors are UGAs.

study models migration, geographic barriers, and population structure to estimate dates for all humans alive today (*16*). The same first author also released an unpublished and un-reviewed report with expanded results using a variety of parameters and these two studies represent the most realistic simulations of UGA (*18*). Building confidence in the estimates, simulations 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 entirely (*17*) or assume only a few kilometers of migration (*19*).

In the best simulations (*16*, *18*), the MRUGA is estimated to arise 3,000 years earlier than the *required descendants*. The IAP is estimated to 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.[7] For reference, this is approximately three times longer, than analytic results assuming random mating.[8] The simulation increases estimates over the theoretical results, but not by much.

Though cautious, these estimates lead to surprising conclusions. For example, consider choosing all those alive in AD 1 (about 2000 years ago) as the *required descendants*. An estimate of the IAP is about 7,000 years ago with a most MRUGA at 5,000 years ago (*16*). Therefore, all farmers in Mesopotamia 6,000 years ago who left any ancestors would each be universal ancestors of everyone alive in AD 1 (Figure 1). This is a cautious estimate. By AD 1, the most remote islands are not yet settled, the population was smaller than present day, and simulation assumes very low levels of migration.

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[7] As the simulation author notes, "the [nearly IAP] and the [IAP] are separated by perhaps 1000 years" (*18*).

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

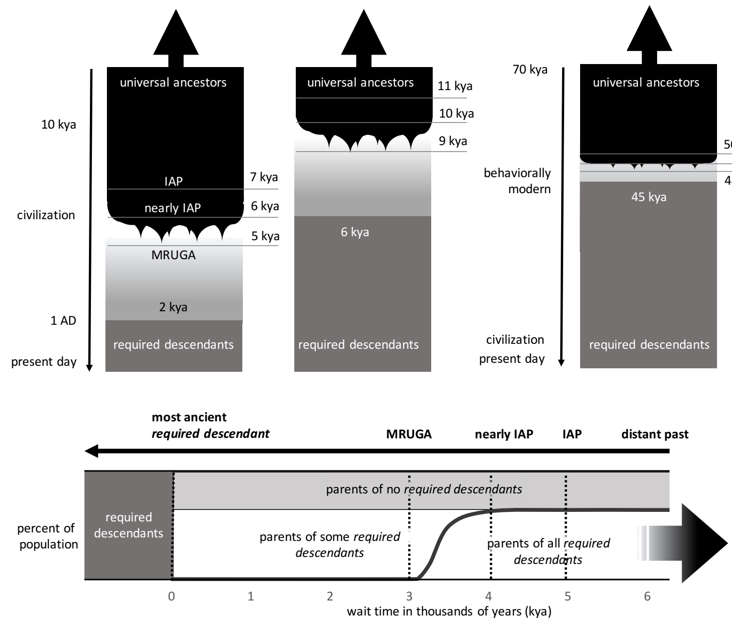


Figure 3. Estimating when universal ancestors arise. Universal genealogical ancestors first arise in about 3,000 years before the *required descendants* and extend back into the distant past. The estimated UGAs of all those alive at AD 1, 6 kya, and 45 kya are displayed in cartooned pedigrees (top). 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).

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?

With the same caveats, 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 (Figure 2). The quickest time, 3,000 years, corresponds the time to the MRUGA and applies to very few, lucky and ideally located individuals. The longest time, 5,000 years, corresponds to the time to the IAP and applies to very few, unlucky, and poorly located individuals, like those in the Americas or Australia. More likely, especially for those in central locations, the wait time is between 4,000 and 3,000 years, the range during which most become UGAs (Figure 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 (Figure 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.

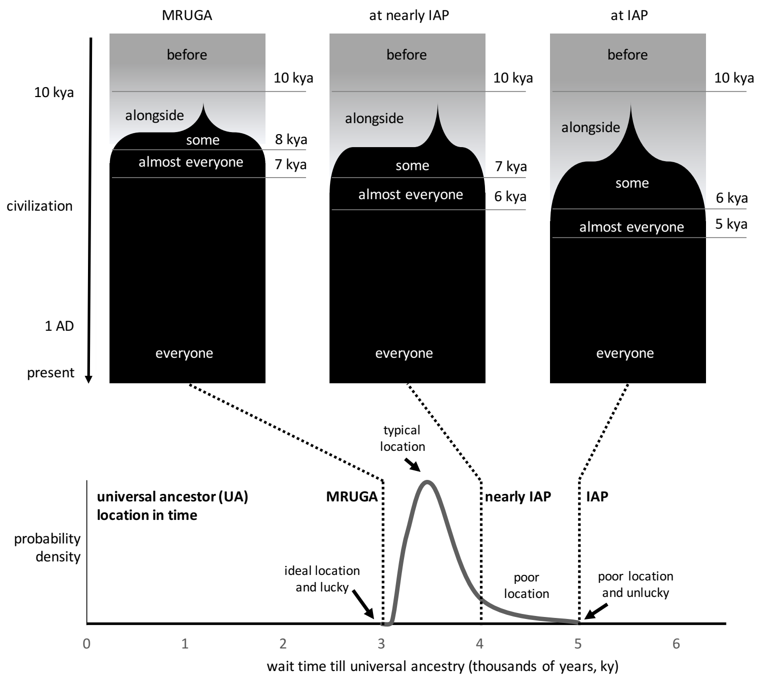


Figure 4. Estimating the descendants of universal ancestors. Cartooned pedigrees show the estimated ancestors at the MRUGA, nearly IAP, and IAP points (top). Universal ancestors usually become universal in less than 4,000 years, before the nearly IAP (bottom). The most likely time that UGAs first arise 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 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.

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 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.

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 at a time in the past, and m is a billion, the approximate population at present day (*17*). For example, at 5,000 years ago, there were about 18 million in the world (*41*), 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. Perhaps increased interest in these results might 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 corresponds 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. This is because our intuition is calibrated by genetic ancestry, which works very differently than genealogies.

A Genealogical View of Origins

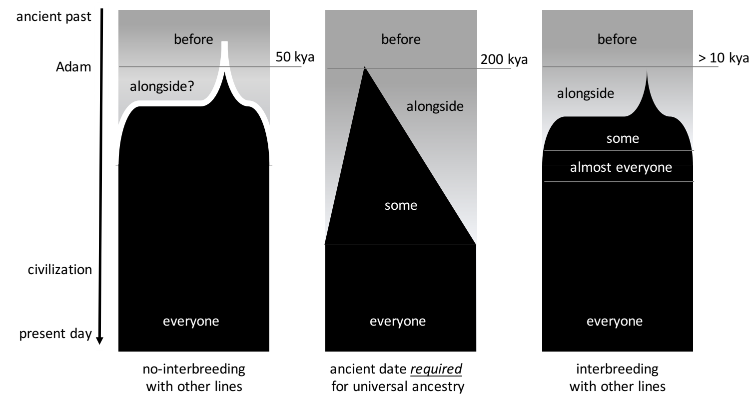
Ancient Adam Models

Several models have been constructed with the goal of preserving genealogical descent from Adam (*9*, *10*, *39*, *40*). Usually, this includes placing Adam as far back as y-MRCA, 200,000 or 100,000 years ago (*39*, *40*). This move requires either abandoning the Genesis setting and narrative, or maintain that agriculture arises tens of thousands of years before it appears in the archeological record.

If the goal is to preserve universal genealogical ancestry, however, choosing an ancient Adam is unnecessary (Figure 5). As we have seen, an Adam situated just 10,000 years ago is expected be the universal ancestor of all those in recorded history. Taking this as far as it can go, an Adam situated just 6,000 years ago is expected to be the universal ancestor of all those alive in AD 1. Of course, this also remains true if Adam is placed in the distant past alongside y-MRCA (*39*).

Whether or not these moves are warranted is a separate question, but the science itself does not force an ancient Adam on those who think a genealogical relationship to Adam is important. All that must be accepted is that Adam's line mixed with others, and the findings of population genetics as our most accurate view of those "outside the garden" who become our ancestors too (*1*–*7*). This appears to be the only way population genetic presses on our understanding of Adam.

How these adjustments affect theology is a separate question. Scientifically, however, it is not necessary to place Adam into the distant past to preserve universal descent from him.



genetic evidence	**inconsistent**	consistent	consistent
genealogic ancestry	consistent	**inconsistent**	consistent

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.

Recent Adam Models

Some identify Adam as a Paleolithic farmer about 10,000 years ago in Mesopotamia, alongside a larger population of *Homo sapiens* (*8*, *10*, *37*). This model was offered by both a leading old testament scholar and a famous theologian, Derek Kidner and John Stott (*37*, *42*). 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 mankind independent of a genealogical connection to Adam (*9*, *10*). It is asserted that an farmer situated 10,000 years ago could not be a universal ancestor (*9*, *10*). 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 genealogical theology of Adam (Figure 6).

Mesopotamia is a location we might expect universal ancestors to arise quickly. From the birthplace of civilization, his descendants would 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 descend 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 (*32*), 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 a universal ancestor, and genealogical isolation like this is unobservable. Consequently, it is scientifically certain under plausible assumptions that we share a genealogical connection to Adam in this model.

Whether or not this connection is important theologically cannot be answered by science. A recent Adam, however, is compatible with both representational and genealogical theology. The representational model has merit and might be partly or entirely true. However, science does not force a choice on theology here.

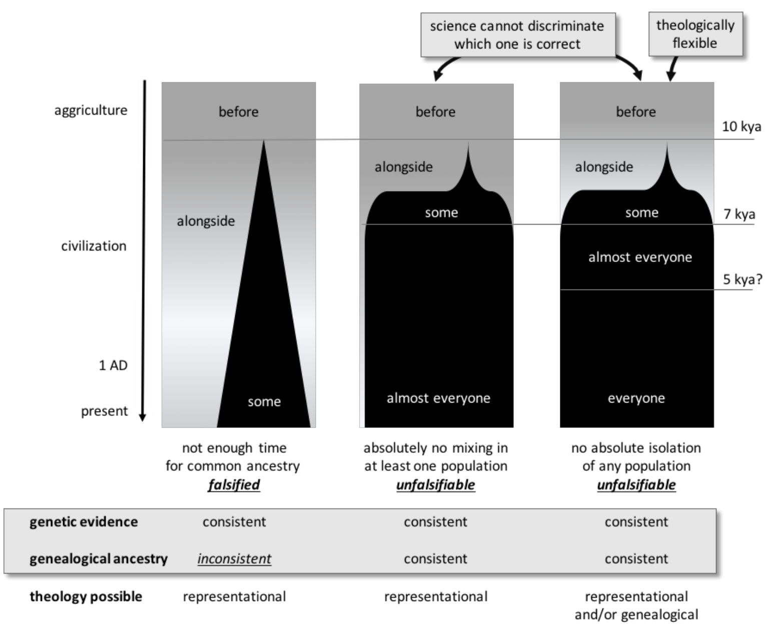


Figure 6. Recent representational models. It is commonly thought that, if Adam lived 10,000 years ago, there was not enough time for him to be a UGA (left). Consequently, a genealogical relationship to Adam seems ruled out by science. Representational theologies circumvent this problem by passing original 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 discriminate between the two models; both depend on absolute negatives, which are very difficult or impossible to prove. There is intrinsic value, however, in delimiting the scientific account by explaining plausible options that increase theological freedom. For this reason,

the scientifically plausibility of a recent UGA should be emphasized, whether or not this genealogical relationship is ultimately deemed important.

Accommodating Diversity

In light of these findings, more care is needed in explaining what science does and does not say. The terms “ancestor” and “human” are too ambiguous. More precision is required, or the findings of science will be overstated or even misrepresented. Consider these common questions.

1. Could all humans “descend” from a single couple?
2. Could Adam and Eve be our “sole-progenitors,” without other “humans” outside the garden?
3. Could Eve have lived 6,000 years ago, and still be the “mother of all the living?”

Depending on precisely how they are phrased and what is meant, the literal answer could be yes or no. The word usage by most people, however, is not technical or fixed. It is misleading to limit to answer these questions with,

> “No, we do not because the y-MRCA and m-MRCA lived at different times, and our ancestral population never reduced in size to a single couple.”

This answer neither clarifies the distinctions between genealogical and genetic ancestry nor the subtlety of “human,” “descent,” and “sole progenitors.” These are all ambiguous terms where there is no clear translation between theology and science. Moreover, it is not scientifically accurate to answer genealogical questions with genetics, and without explaining the large number of universal ancestors we all share.

Depending on how these terms are defined theologically, the evidence does not dispute these claims. For this reason, a responsive answer to the spirit of the questions might be,

> “Yes, all humans in recent history descend from *many* single couples, each of whom are individually ancestors of us all. Of course, Adam and Eve could be one of these couple. Depending on what we mean by these terms, they could be our ‘first parents,’ our ‘sole-progenitors,’ the parents of ‘all the living’ and all ‘humans.’ They could even have been the first theological humans ever, without parents, and without other humans outside the garden. It all depends what we mean by these words in the distant past.”

Clarifications should follow, and the details should be carefully explained. It is a scientific error, however, to answer genealogical questions with genetic ancestry. It is unkind to present science in the manner most incompatible with another's deeply held beliefs. Questions about universal descent are answered by explaining the millions of universal ancestors we all share.

This is not to defend the theological or hermeneutical warrant of such positions. Rather, there is intrinsic value in honest explanations of what science does and does not say.

Accommodating Diversity

The only way science presses on a genealogical understanding of Adam is by suggesting, alongside Scripture, that his descendants refrained from incest by mixed with a larger population of biologically-compatible beings. Adam could be recent. He could have lived Mesopotamia. He could have been the first theological "human," and he could have been specially created from the dust. For this reason, any rethink of a genealogical Adam, if it is warranted, must come on its own, independent of evolution, and without claiming the authority of science.

To this honest account, resistance may be strong from those pressing a theological and hermeneutic case against a historical Adam (*9–11*, *38*). Even if this case has merit, resistance to a honest and accurate account of science is a mistake. Completing relevant science should not be interpreted as endorsing or supporting a specific theology. Instead, this is an opportunity to accurately delimit the scientific account, grant legitimate freedom to theologians, and accommodate the diversity of the Church.

An Invitation to Theology

Genealogical science is surprising and overlooked, but it also solidly within mainstream science and entirely consistent with the genetic evidence. It is not a "creative" reinterpretation of the evidence, nor does it challenge widely agreed upon scientific conclusions. Instead, these findings add material information to the theological conversation, completing the scientific account. Genetically it appears humans arose a population and share common biological ancestry with the great apes. Genealogically it appears that several of our ancestors are universal; all of us is descend from each of them. This new information limits how science presses on theology and that is why this finding is important.

What does this mean for the Church? Nothing in evolutionary science unsettles the confession that we all descend from the same couple. Nothing in the genetic data disputes the Augsburg and Westminster Confessions. Even if these confessions are theologically misguided, hermeneutically unfounded, or in need of revision. Nothing in science unsettles them.

New found theological freedom in the scientific account is an invitation to science-engaged theology. New evolutionary scenarios are possible. Perhaps most importantly, they might be consistent with confessions affirmed in corners of the Church heretofore disaffected by the scientific account. In light of genealogical science, they can coherently affirm (1) the scientific consensus of evolutionary science, (2) universal descent from a historical Adam, and (3) recover most of setting and timeline of Genesis account. For this reason, let us together imagine new ways to accommodate the full diversity of the Church into the scientific world.

Those who find theological significance in a genealogical connection to Adam are invited into important questions. How should we think of beings "outside the garden," even if they remain in our distant past? A genealogical Adam affirms monogenesis in the present day, but how coherent is a history 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 like original sin? Theological questions will arise and we can begin to address them. What lies ahead, however, is more fundamental to the human condition.

At the present time, humans are all God Imaged and Fallen, but what about the distant past? What about our future?

There is mystery here. The details of our origins may always be questions, without definitive answers. Perhaps, they are invitations to wonder again together. To imagine the details of our past around campfires. To ponder great mysteries without fear. To embrace creativity in our theology and imagination in our science. To enter humbly into unknowns. To together ask the grand question of our origins; What does it mean to be human?

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