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Adam and Eve Report

Video Overview: This 4-minute slide presentation video was created after the initial publication of the Adam and Eve Report in 2007. The report has been updated several times since then with support from additional research, but this video is still a good place to learn about the research that originally inspired tracking the parallels between genetics research a*nd The Urantia Book*.

Summary: The Summary gives a brief description of the Adam and Eve Report.

Overview: The length and complexity of this report encouraged us to provide an Overview for those who would like to become familiar with the topic through an efficient presentation of the main points.

Review: The Review walks you through the key elements of this topic.

Post Publication Support: New discoveries and scientific advances increasingly lend support to existing reports. This section provides brief descriptions of the links that offer additional support.

Deeper and Broader: This section provides guidance for those who want to do a deeper and broader study of the topic.

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Prepared by Halbert Katzen J.D.
[Updated 10/3/09]

Adam and Eve Summary

[Updated 10/3/09]

For the most part, *The Urantia Book*'s story about Adam and Eve differs considerably from the one found in the Old Testament. However, both accounts have three things in common: 1) a specific couple, living a long time ago in the Mesopotamia region, had a significant impact on humanity, 2) this couple behaved in a way that caused a big problem, and 3) the behavior problem precipitated the need to leave their original location.

According to *The Urantia Book*, which was published in 1955, the first human beings (roughly corresponding to *Homo* erectus) evolved about 1,000,000 years ago. It also recounts that almost

38,000 years ago Adam and Eve introduced some genetic upgrades into our gene pool, which enhanced brain function and resistance to disease (roughly corresponding with *Homo* sapiens sapiens). The authors extensively recount the development of the civilization that Adam and Eve started and how their descendants migrated around the world and mixed with other races. *The Urantia Book* provides specific information regarding time periods, places, degree of admixture with other races, and the impact on language and other aspects of culture.

Starting in 2004 numerous reports started to be published relating to portions of the Y chromosome and the Microcephalin gene. The Microcephalin gene play a critical role in the growth of the brain. The research results closely correlate with what *The Urantia Book* says about the spread of the genetic and cultural contributions of Adam and Eve. The research into Microcephalin indicates that new genetic material was introduced into the Microcephalin gene about 37,000 years ago and that the rest of the Microcephalin gene was approximately 990,000 years old. None of the obvious explanations for how new material might have been introduced fit well with the results of the research. It then spread into most of the human population quite rapidly, excepting sub-Saharan Africa. Similarly, Y chromosome related studies also document how some types of mutations or other changes occurred around 40,000 years ago, originating in the Mesopotamia region, and spreading quickly into most of humanity, excepting sub-Saharan Africa.

Follow up research comparing the spread of the introduction of new addition to the Microcephalin gene with the use of nontonal languages also showed a strong positive correlation. These correlations also track well with the migrations of Adam and Eve's descendants. Bruce Lahn, from the Howard Hughes Medical Institute at the University of Chicago and the lead researcher responsible for the studies on the Microcephalin gene, is no longer working in this area, having become discouraged because the research results and their interpretation further enflamed what is already such a controversial issue. See *Eugenics, Race, and The Urantia Book* for a comprehensive review of *The Urantia Book*'s statements on this subject. Support for *The Urantia Book*'s story about Adam and Eve is also documented in the Garden of Eden Report and the Gobekli Tepe Report.

Adam and Eve Overview

Statements in *The Urantia Book* supported by the research

The Urantia Book provides specific years for the dawn of humanity and for the couple that sparked the religious traditions about Adam and Eve. "From the year A.D. 1934 back to the birth of the first two human beings is just 993,419 years." "Adam and Eve arrived on Urantia [Earth], from the year A.D. 1934, 37,848 years ago." And it provides details regarding the location of Adam and Eve's second residence. "The two rivers themselves were a good natural defense in those days, and a short way north of the second garden the Euphrates and Tigris came close together so that a defense wall extending fifty-six miles could be built for the protection of the territory to the south and between the rivers."

The Urantia Book indicates that Adam and Eve had a plan for the genetic and cultural uplift of humanity and that they intended for their descendants to share this genetic upgrade throughout the world. The authors speak to the genetic and cultural impact that Adam and Eve and their descendants had on humanity. Examples of these statements include: "Adam and Eve introduced no art of civilization foreign to the progress of human society, but the Adamic blood did augment the inherent ability of the races and did accelerate the pace of economic development and industrial progression. Adam's bestowal improved the brain power of the races, thereby greatly hastening the processes of natural evolution." "The result of the gift of the Adamic life plasm to the mortal races is an immediate upstepping of intellectual capacity and an acceleration of spiritual progress." "You would be far more disease resistant if your races carried more of the Adamic life."

The migrations of Adam and Eve descendants to South America and Africa run parallel to the genetics research. "One hundred and thirty-two of . . . [Adam and Eve descendants] embarking in a fleet of small boats from Japan, eventually reached South America and by intermarriage with the natives of the Andes established the ancestry of the later rulers of the Incas." "They [descendants of Adam and Eve] contributed considerably to the northern groups of the Saharan . . . peoples. But only a few teachers and traders ever penetrated farther south in Africa than the headwaters of the Nile."

Additionally, there is a correlation between the migration of Adam and Eve descendants and the development of nontonal languages. Nontonal languages, like English and other European languages, do not require a word to be given a specific inflective emphasis in order to be imbued with the intended meaning.. “Many modern languages are derived from this early speech of these central Asian tribes [descendants of Adam and Eve] who conquered Europe, India, and the upper stretches of the Mesopotamian plains.”

Microcephalin haplogroup D research

The gene Microcephalin (MCPH1) regulates brain size. It has evolved under "strong positive selection" in the human evolutionary lineage. This means that, once introduced, the microcephalin gene (and changes to it like that one that occurred 37,000 years ago) spread rapidly, which generally indicates some specific survival advantage or strong preference. Research indicates that positive selection with respect to the Microcephalin gene has occurred throughout the history of evolution leading up to human beings. A new segment of genetic material, haplogroup D, was introduced to the Microcephalin gene in humans from a “single progenitor” “about 37,000” years ago. It has reached 70% of the human population but is in significantly lower percentages in sub-Saharan Africa. There is some indication that it might have originated in the general area of Mesopotamia. Both South and Central Native Americans have haplogroup D in high percentages, but the percentage is a little higher in South America.

A follow up study determined that there is a strong positive correlation between the spread of Microcephalin haplogroup D and the use of nontonal languages. Research in this area indicates that genetics do play some role in the use of nontonal languages, but researchers are reluctant, notwithstanding the geographic nature of the variations, to suggest that nontonal languages are superior.

The Stanford study

A study done at Stanford University focused on “a data set of DNA sequence variation at three Y chromosome genes . . . in a worldwide sample of human Y chromosomes. . .” “Mutation 1 defines a clade, separate from the deep African lineages. Within this clade, a younger clade, consisting of 21 lineages of which only one is African, is defined by mutation 2. . .” “The age of mutation 2, at around 40,000 years ago, represents an estimate of the time of the beginning of global expansion.” In speculating about results that were challenging to interpret, the report states, “One solution to this apparent discrepancy is the possibility that the Y chromosome is subject to fairly strong selection . . . The possible role of selection seems quite plausible . . .”

Y haplogroup F

One report on haplogroup F of the Y chromosome states,

The founder of Haplogroup F lived . . . in modern day Middle East and his descendents became the founders of Haplogroups G through to R. Descendents of Haplogroups G to R represent more than 90% of the world's current population.

Today, the original undifferentiated ancient Haplogroup F line is localized mainly to the Middle East. Descendents of Haplogroup F are almost absent in Sub-Saharan Africa, further supporting the theory that Haplogroup F formed shortly after its ancestors migrated out of Africa.

A more recent study, published in 2008 and touting its more advanced dating techniques, puts the origination date at 48,000 (38,700–55,700).

The Controversy

Not surprisingly, research documenting the rapid spread of genetic material effecting brain growth that shows up in high percentages everywhere except sub-Saharan Africa is going to give rise to interpretations that stand a good chance of being controversial and/or subservient to the dictates of “political correctness.” In this case, a lengthy article was published in the Wall Street Journal on the subject, pointing out that “Web sites and magazines promoting white "racialism" quickly seized on Dr. Lahn's suggestive scientific snapshot. One magazine that blames black and Hispanic people for social ills hailed his discovery as ‘the moment the antiracists and egalitarians have dreaded.’”

The article reveals that the lead geneticist involved in doing the Microcephalin research, Bruce Lahn, is no longer interested in continuing with the research. “Dr. Lahn, who left China after participating in prodemocracy protests, says intellectual "police" in the U.S. make such questions difficult to pursue.” “The university's patent office is also having second thoughts. Its director, Alan Thomas, says his office is dropping a patent application filed last year that would cover using Dr. Lahn's work as a DNA-based intelligence test. “We really don't want to end up on the front page...for doing eugenics,” Mr. Thomas says.”

The authors of *The Urantia Book* are direct in asserting that 1) notwithstanding the preeminent importance of our spiritual equality and the moral requirements that go with this, we are physiologically and intellectually diverse in ways that are reasonably categorized as “superior” and “inferior” and 2) to a certain extent, these differences are related to an introduction by Adam and Eve of superior genetics. This aspect of *The Urantia Book*, however well aligned with science it may be, touches on sensitive subject matter in a manner that some people consider “politically incorrect.” Fortunately, *The Urantia Book* also offers new and upgraded explanations and insights to go along with this controversial (and increasingly corroborated) material.

Naturally, those of us working to develop the UBtheNEWS project anticipate that additional genetics studies will be forth coming which further verify *The Urantia Book*’s story about Adam and Eve. Without a comprehensive understanding of *The Urantia Book*’s position on eugenics and race, there is a high probability that the statements it makes will be taken out of context and misinterpreted. This, in turn, discourages appreciating the unique quality of credibility that is emerging with *The Urantia Book*, especially because of advances in the field of genetics. In an effort to minimize such misunderstandings, a comprehensive review of *The Urantia Book*’s statements about eugenics and race has been prepared. See: *Eugenics, Race, and The Urantia Book*. The Garden of Eden Report and the Gobekli Tepe Report document additional support for *The Urantia Book*’s story about Adam and Eve.

Adam and Eve Review

Prepared by Halbert Katzen, JD with special thanks to Fred Harris and Donna Whelan
[Updated 8/21/09]

(The Report presumes familiarity with the Summary and Overview. Please start with the Summary at the top of this page.)

Preface

At nearly 12,000 words, this is one of the longest UBtheNEWS reports. It is written for people whose next step in understanding this material would be to go directly to the research reports and articles on which this report relies. This report is designed not only to provide an organized presentation of the research results, conclusions, and commentary of the researchers, but also to encourage readers to reflect more deeply on some of the challenges associated with learning and conversing about this type of material.

Because new discoveries in genetics research are being made continually, readers are also asked to bear in mind that the report itself is not being prepared as a final statement on the subject. Quite to the contrary, this is only the first major update to the original report, which was prepared during the first half of 2007. The process of researching the advances in genetics that lend support to *The Urantia Book* is still at an early stage of development.

The original report was only concerned with how the research into Microcephalin haplogroup D provides numerous parallels to *The Urantia Book*. Correlations with Y chromosome research had not been made yet and the tonal language research was still in process. Because the original report only focused on the Microcephalin issue, it was organized in a way that introduced the research first and then brought in correlating aspects of *The Urantia Book*. Further updates to this report, no doubt, will start by presenting the relevant material from *The Urantia Book* first and then showing how various studies are corroborating the information to varying degrees.

At this stage, the Microcephlin research remains the primary producer of intriguing correlations to *The Urantia Book* and this first update is organized largely around the Microcephalin material. It starts with some foundational material from *The Urantia Book* for appreciating its basic assertions.

Then it provides a general review of the Microcephalin research and the Y chromosome research. This will be followed by a cataloguing of all the various correlations that recent research has to *The Urantia Book*'s story about Adam and Eve. Lastly, the tonal language issue will be presented.

The Urantia Book's fundamental assertions

A full understanding of *The Urantia Book*'s description of who Adam and Eve were and the nature of their genetic contribution is not going to be covered in this paper. To do so would require getting into theological and cosmological aspects of the book that would significantly add to the length of the report without providing material which makes the correlations between *The Urantia Book* and recent research any more or less valid. The theological and cosmological aspects of *The Urantia Book* are intertwined with its historical account about the civilization started by Adam and Eve. This presents certain challenges when it comes to providing and contextualizing quotes from *The Urantia Book*. Statements in this report that seem to allude to other issues or that seem needlessly vague or ambiguous are likely being crafted that way to avoid getting into the theological and cosmological aspects of this topic. Of course, the footnotes will lead you directly to the chapter in *The Urantia Book* that has this information, if you are interested.

In discussing the genetic and cultural contribution introduced by Adam and Eve, *The Urantia Book* states:

> Biologic evolution and cultural civilization are not necessarily correlated; organic evolution in any age may proceed unhindered in the very midst of cultural decadence. But when lengthy periods of human history are surveyed, it will be observed that eventually evolution and culture become related as cause and effect. Evolution may advance in the absence of culture, but cultural civilization does not flourish without an adequate background of antecedent racial progression. Adam and Eve introduced no art of civilization foreign to the progress of human society, but the Adamic blood did augment the inherent ability of the races and did accelerate the pace of economic development and industrial progression. Adam's bestowal improved the brain power of the races, thereby greatly hastening the processes of natural evolution.(1)

The descendants of Adam and Eve are referred to as "Adamites" or the "violet race." The mix of Adamites and "Nodites" are referred to as "Andites." (While an understanding of who the Nodites were is not pertinent to this report, those familiar with the Biblical account of Adam and Eve may recall that Cain left Eden and went to the "land of Nod.") *The Urantia Book* asserts:

> The purer strains of the violet race had retained the Adamic tradition of peace-seeking, which explains why the earlier race movements had been more in the nature of peaceful migrations. But as the Adamites united with the Nodite stocks, who were by this time a belligerent race, their Andite descendants became, for their day and age, the most skillful and sagacious militarists ever to live on Urantia. Thenceforth the movements of the Mesopotamians grew increasingly military in character and became more akin to actual conquests.

These Andites were adventurous; they had roving dispositions. . . [T]heir later descendants never stopped until they had circumnavigated the globe and discovered the last remote continent.(2)

Regarding the issue of general health and thus reproductive advantage, it is worth noting that *The Urantia Book* does comment on how the introduction of Adam and Eve's genetics improved health.

The authors comment on "the reversion of certain primitive plant life to the prechlorophyll levels of parasitic bacteria on . . . an extensive . . . scale." This is said to have led to "many distressful diseases in the higher mammals, particularly in the more vulnerable human species." The authors assert that Adam and Eve's genetic contribution ideally could have "so reinforce[d] the resisting powers" of the human body "as to make it practically immune to all diseases produced by the vegetable type of organism."(3) "You would be far more disease resistant if your races carried more of the Adamic life."(4)

The Urantia Book is explicit in stating that both brain power and health were improved by the introduction of Adam and Eve's genetics, which were "equal to each other, differing only in reproductive nature and in certain chemical endowments."(5)

Overview of the Microcephalin and Y chromosome research

A September 2005 article published by the Howard Hughes Medical Institute provides a good summary, and thus an excellent starting point, for appreciating some of what has recently been discovered about the Microcephalin gene.

> Howard Hughes Medical Institute researchers, who have analyzed sequence variations in two genes that regulate brain size in human populations, have found evidence that the human brain is still evolving.
>
> They speculate that if the human species continues to survive, the human brain may continue to evolve, driven by the pressures of natural selection. Their data suggest that major variants in these genes arose at roughly the same times as the origin of culture in human populations as well as the advent of agriculture and written language.
>
> The research team, which was led by Bruce T. Lahn, a Howard Hughes Medical Institute investigator at the University of Chicago, published its findings in two articles in the September 9, 2005 issue of the journal Science.
>
> Their analyses focused on detecting sequence changes in two genes—Microcephalin and "abnormal spindle-like microcephaly associated" (ASPM)—across different human populations. In humans, mutations in either of these genes can render the gene nonfunctional and cause microcephaly—a clinical syndrome in which the brain develops to a much smaller size than normal.
>
> In earlier studies of non-human primates and humans, Lahn and his colleagues determined that both Microcephalin and ASPM showed significant changes under the pressure of natural selection during the making of the human species. "Our earlier studies showed that Microcephalin showed evidence of accelerated evolution along the entire primate lineage leading to humans, for the entire thirty to thirty-five million years that we sampled," he said. "However, it seemed to have evolved slightly slower later on. By contrast, ASPM has evolved most rapidly in the last six million years of hominid evolution, after the divergence of humans and chimpanzees."
>
> In order to identify sequence changes that occurred in Microcephalin and ASPM in the evolutionary lineage leading to humans, Lahn and his colleagues took the following approach: They determined the DNA sequences of the two genes among a large number of primate species and searched for sequence differences between humans and nonhuman primates. By doing statistical analysis on these sequence differences, they could demonstrate that the differences were due to natural selection that drove significant sequence changes in the lineage leading to humans. These changes accumulated presumably because they conferred some competitive advantage.
>
> The evidence that Microcephalin and ASPM were evolving under strong natural selection in the lineage leading to humans led Lahn and his colleagues to consider exploring whether these two genes are still evolving under selection in modern human populations. "In the earlier studies, we looked at differences that had already been set in the human genome," he said. "The next logical question was to ask whether the same process is still going on today, given that these genes have been under such strong selective pressure, leading to the accumulation of advantageous changes in the human lineage. If that is the case, we reasoned we might be able to see variants within the human population that are rising in frequency due to positive selection, but haven't gone to completion yet."
>
> The researchers first sequenced the two genes in an ethnically diverse selection of about 90 individuals. The researchers also sequenced the genes in the chimpanzee, to determine the "ancestral" state of polymorphisms in the genes and to assess the extent of human-chimpanzee divergence.
>
> In each gene, the researchers found distinctive sets of polymorphisms, which are sequence differences between different individuals. Blocks of linked polymorphisms are called haplotypes, whereby each haplotype is, in essence, a distinct genetic variant of the gene. They found that they could further break the haplotypes down into related

variants called haplogroups. Their analysis indicated that for each of the two genes, one haplogroup occurs at a frequency far higher than that expected by chance, indicating that natural selection has driven up the frequency of the haplogroup. They referred to the high-frequency haplogroup as haplogroup D.

When the researchers compared the ethnic groups in their sample for haplogroup D of ASPM , they found that it occurs more frequently in European and related populations, including Iberians, Basques, Russians, North Africans, Middle Easterners and South Asians. That haplogroup was found at a lower incidence in East Asians, sub-Saharan Africans and New World Indians. For Microcephalin, the researchers found that haplogroup D is more abundant in populations outside of Africa than in populations from sub-Saharan Africa.

To produce more informative statistical data on the frequency of haplotype D among population groups, the researchers applied their methods to a larger population sample of more than one thousand people. That analysis also showed the same distribution of haplogroups.

Their statistical analysis indicated that the Microcephalin haplogroup D appeared about 37,000 years ago, and the ASPM haplogroup D appeared about 5,800 years ago - both well after the emergence of modern humans about 200,000 years ago. “In the case of Microcephalin, the origin of the new variant coincides with the emergence of culturally modern humans,” said Lahn. “And the ASPM new variant originated at a time that coincides with the spread of agriculture, settled cities, and the first record of written language. So, a major question is whether the coincidence between the genetic evolution that we see and the cultural evolution of humans was causative, or did they synergize with each other?”

Lahn said that the geographic origin and circumstances surrounding the spread of the haplogroups can only be surmised at this point. “One can make guesses, but our study doesn't reveal how these positively selected variants arrived," he said. "They may have arisen in Europe or the Middle East and spread more readily east and west due to human migrations, as opposed to south to Africa because of geographic barriers. Or, they could have arisen in Africa, and increased in frequency once early humans migrated out of Africa.”

While the roles of Microcephalin and ASPM in regulating brain size suggest that the selective pressure on the new variants may relate to cognition, Lahn emphasized that this possibility remains speculative. “What we can say is that our findings provide evidence that the human brain, the most important organ that distinguishes our species, is evolutionarily plastic,” he said. Finding evidence of selection in two such genes is mutually reinforcing, he pointed out. “Finding this effect in one gene could be anecdotal, but finding it in two genes would make it a trend. Here we have two microcephaly genes that show evidence of selection in the evolutionary history of the human species and that also show evidence of ongoing selection in humans.”

Lahn emphasized that it would not be correct to interpret the findings as indicating that one ethnic group is more “evolved” than another. Any differences among groups would be minor compared to the large differences in such traits as intelligence within those groups, he said. “We're talking about the average impact of such variants,” he said. “We still have to treat each individual as an individual. Just because you have one gene that makes you more likely to be a little taller, doesn't mean you will be tall, given the complex effect of all your other genes and of environment.” Lahn also said that a multitude of other genes likely exist that influence brain size and development, and further research could reveal far more complex effects of natural selection on such genes.

Lahn speculated that the new findings suggest that the human brain will continue to evolve under the pressure of natural selection. “Our studies indicate that the trend that is the defining characteristic of human evolution - the growth of brain size and complexity - is likely still going on. If our species survives for another million years or so, I would imagine that the brain by then would show significant structural differences from the human brain of today.”

> For both Microcephalin and ASPM , Lahn and his colleagues are trying to find out the precise traits that are under natural selection. They are also performing more detailed studies of the two genes in human populations to better understand their evolutionary history. And they are searching for other brain-related genes that have changed under the pressure of natural selection. “We want to know how broad a trend these two genes represent,” said Lahn. “Did we get really lucky and hit on two rare examples of such genes? Or, are they representative of many other such genes throughout the genome. I would bet, though, that we will find evidence of selection in a lot more genes.”
>
> Lahn and his colleagues are now working to understand how subtle changes in the sequences of these two genes can alter their function in such a way that would result in favorable selection. While there is some evidence from earlier studies that Microcephalin and ASPM code for proteins that regulate the proliferation of brain cells from immature neural stem cells, their function has not yet been determined, said Lahn.(6)

Two Y chromosome studies provide support for the story about Adam and Eve found in *The Urantia Book*. The first study we will review was reported out of the Stanford University School of Medicine in 2000 (the “Stanford study”).

> We consider a data set of DNA sequence variation at three Y chromosome genes (SMCY, DBY, and DFFRY) in a worldwide sample of human Y chromosomes. . . In particular, we focused on estimating the expected time to the most recent common ancestor and the expected ages of certain mutations with interesting geographic distributions. . . [A]lthough previous studies have noted that Y chromosome variation shows extreme geographic structure, we estimate that the spread of Y chromosomes out of Africa is much more recent than previously was thought. We also show that our data indicate substantial population growth in the effective number of human Y chromosomes.(7)
>
> Mutation 1 defines a clade, separate from the deep African lineages. Within this clade, a younger clade, consisting of 21 lineages of which only one is African, is defined by mutation 2. . .
>
> It is of interest to estimate the expected age of mutation 1, which presumably preceded any movement out of Africa, and of 2, which would have been present in any hypothetical bottleneck before the global expansion.(8)
>
> These results indicate that male movement out of Africa first occurred around 47,000 years ago. The age of mutation 2, at around 40,000 years ago, represents an estimate of the time of the beginning of global expansion.(9)
>
> In view of the fact that for much of the last 50,000 years humans have been widely dispersed around the globe, with rapid population growth for a significant fraction of that time, it is striking that the estimated time to the MRCA [most recent common ancestor] is so short. From the Y chromosome, one would conclude that the ancestral population size 50,000 years ago was very small indeed. Yet this view is at odds with the results from other loci such as b-globin, which have very ancient MRCA times.
>
> One solution to this apparent discrepancy is the possibility that the Y chromosome is subject to fairly strong selection, either in the form of positive selection for advantageous mutations (hitchhiking) or negative selection against mildly deleterious mutations (background selection). The possible role of selection seems quite plausible . . .(10)

The other study we will consider is concerned with haplogroup F on the Y chromosome (“Y haplogroup F”). The part of the Y chromosome that is the subject of the Stanford study is distinct from Y haplogroup F. Microbiologist Johnathan Storlie, PhD summarizes the research on Y haplogroup F as follows:

> Descendents of the Haplogroup F branch are distinguished by markers in their Y-DNA called M89 and M213. The presence of the M89 and M213 markers are unique to all individuals who descended from this line and can be confirmed with SNP testing.

> Haplogroup F is an important ancient haplogroup whose descendents are responsible for forming the majority of the civilizations in the world today. The founder of Haplogroup F lived 40,000 to 60,000 years ago in modern day Middle East and his descendents became the founders of Haplogroups G through to R. Descendents of Haplogroups G to R represent more than 90% of the world's current population.
>
> Today, the original undifferentiated ancient Haplogroup F line is localized mainly to the Middle East. Descendents of Haplogroup F are almost absent in Sub-Saharan Africa, further supporting the theory that Haplogroup F formed shortly after its ancestors migrated out of Africa.(11)

Regarding the age of Y haplogroup F, however, a 2008 study specifically compares itself to the test results published in a 2002 study and asserts a better methodology for calculating the MRCA. The 2002 study put the origination date for Y haplogroup F at 50,300 (±6500); the 2008 study puts the origination date at 48,000 (38,700–55,700).(12)

It is important to note that the methodology used to calculate the MRCA, while providing an indication of when something originated, does not give an indication of whether there was a single progenitor. In wikipedia's discussion of MRCA it states, "The existence of an MRCA does therefore not imply the existence of a population bottleneck or first couple."

Age of Microcephalin and Y chromosome related changes

Advances in the field of genetics are equipping geneticists with the tools to make increasingly accurate and specific speculations about when and how genetic changes occurred in the past. Some methodologies only yield results for when something occurred, while others can also give indications of how such an event occurred. The Microcephalin research provides information about when and how but the Y chromosome studies only addressed when.

By isolating locations on chromosomes that are responsible for specific traits and then cross referencing the frequency of these traits in a given population with a baseline genetic ancestor, in this case a chimpanzee, researchers are able to calculate when a trait first appeared in the human gene pool. The chimpanzee provides a reference point, an "outgroup," from which all the human genetic samples are considered sufficiently distant.(13)

The Microcephalin research results indicate:

> The age of [Microcephalin] haplogroup D was found to be ~37,000 years, with a 95% confidence interval of 14,000 to 60,000 years.(14)
>
> [T]he D chromosomes coalesce to its most recent common ancestor (MRCA) at 37,000 years before present, whereas the non-D chromosomes coalesce at a far older 990,000 years before present.(15)

The Stanford study states, "The age of mutation 2, at around 40,000 years ago, represents an estimate of the time of the beginning of global expansion."(16) Similarly, the 2008 study on Y haplogroup F puts the origination date at 48,000 (38,700–55,700) years ago.

The Urantia Book states, "Adam and Eve arrived on Urantia [Earth], from the year A.D. 1934, 37,848 years ago."(17) Regarding the first human beings, it says, "From the year A.D. 1934 back to the birth of the first two human beings is just 993,419 years,"(18) and it also notes, "This wonderful pair, the actual parents of all mankind, were in every way superior to many of their immediate descendants, and they were radically different from all of their ancestors, both immediate and remote."(19)

In *The Urantia Book*'s version of human history, the two most significant genetic developments are the mutation that started humanity and the genetic upgrade contributed by Adam and Eve. It was published decades before advances in the study of genes made it possible to do this type of research. The subjective appreciation for how closely the research results align with *The Urantia Book*'s dates are for the reader to evaluate.

The single progenitor of Microcephalin haplogroup D

The Urantia Book's claim that the genetic change occurring about 37,000 years ago came from a pair of individuals is supported by the Microcephalin research, which indicates that haplogroup D came from a single progenitor. Interestingly, in a section discussing Adam and Eve's physiology it specifically states that they were "equal to each other, differing only in reproductive nature and in certain chemical endowments."(20)

The specific nature of the research and analysis that led to the conclusion that haplogroup D originated from a single progenitor also gets into issues related to where haplogroup D came from and whether this should be considered an "upgrade" or "improvement" to human genetics. The presentation of the Microcephalin research immediately stirred up a controversy and this will be addressed later in the report. For now, more truncated quotes are offered to document that "single progenitor" is, in fact, the conclusion that was reached.

> The estimate that all modern copies of the D alleles descended from a single progenitor copy about 37,000 years ago is based on the measurement of sequence difference between different copies of the D alleles.(21)
>
> Within modern humans, a group of closely related haplotypes at this locus [Microcephalin], known as haplogroup D, rose from a single copy ≈37,000 years ago. . .(22)

Eurasians

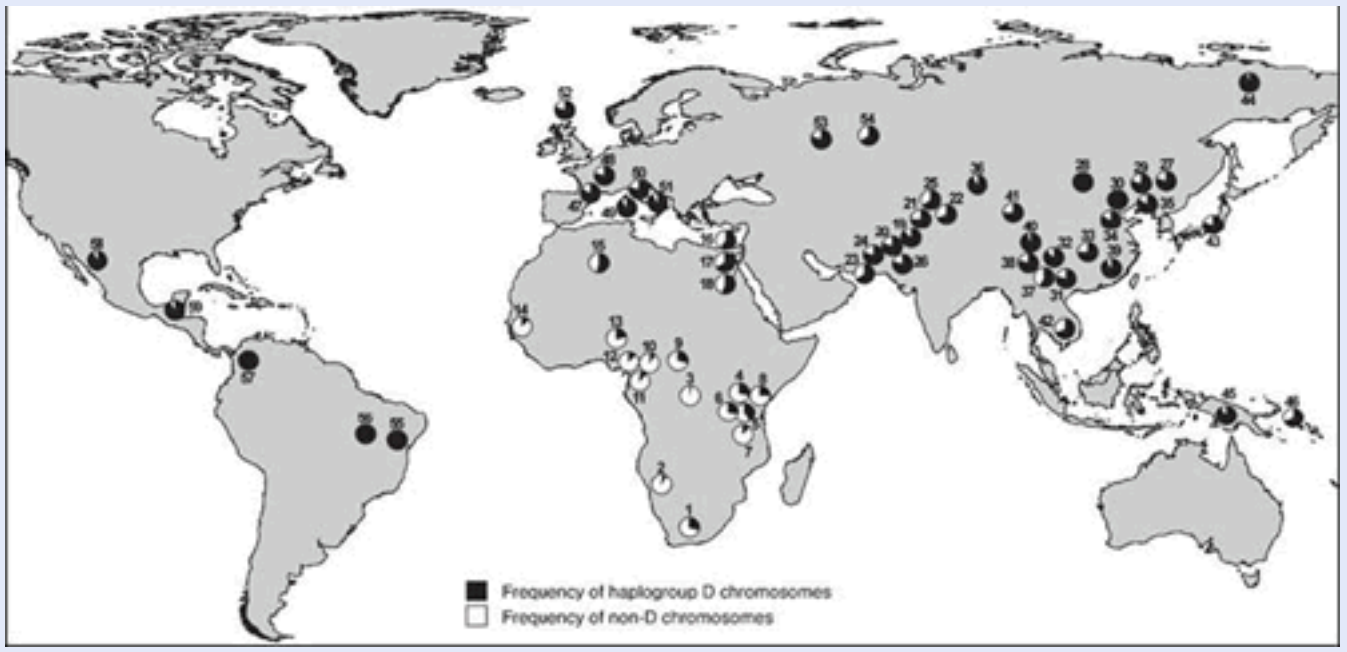


Figure 1

Microcephalin haplogroup D is generally found in high percentages in Eurasia. See Figure 1. This supports the assertions made in *The Urantia Book* regarding the migration of Adam and Eve's descendants. The authors of the book recount:

> Some of the Adamites early journeyed westward to the valley of the Nile; others penetrated eastward into Asia, but these were a minority. The mass movement of the later days was extensively northward and thence westward. It was, in the main, a gradual but unremitting northward push, the greater number making their way north and then circling westward around the Caspian Sea into Europe.
>
> About twenty-five thousand years ago many of the purer elements of the Adamites were well on their northern trek. And as they penetrated northward, they became less and less Adamic until, by the times of their occupation of Turkestan, they had become thoroughly admixed with the other races. . . Very few of the pure-line [Adamites] ever penetrated far into Europe or Asia.(23)
>
> As the period of the early Adamic migrations ended, about 15,000 B.C., there were already more descendants of Adam in Europe and central Asia than anywhere else in the world, even than in Mesopotamia. . . The lands now called Russia and Turkestan were occupied throughout their southern stretches by a great reservoir of the Adamites

> mixed with. . . [the] red and yellow [races].(24)
>
> [T]he Adamites were a real nation around 19,000 B.C., numbering four and a half million, and already they had poured forth millions of their progeny into the surrounding peoples.(25)

Native Americans

The results of research on Microcephalin haplogroup D and ASPM, while revealing similarities that provide general support for the importance of Microcephalin in the evolution of the human brain, also revealed distinctions that make the comparison to *The Urantia Book* all the more distinguished.

Lahn comments on the significance of the similarities between the Microcephalin and ASPM genes:

> Finding evidence of selection in two such genes is mutually reinforcing, he pointed out. “Finding this effect in one gene could be anecdotal, but finding it in two genes would make it a trend. Here we have two microcephaly genes that show evidence of selection in the evolutionary history of the human species and that also show evidence of ongoing selection in humans.”(26)

However, the sudden spread of ASPM haplogroup D did not follow the same pattern as the spread of Microcephalin haplogroup D.

> When the researchers compared the ethnic groups in their sample for haplogroup D of ASPM , they found that it occurs more frequently in European and related populations, including Iberians, Basques, Russians, North Africans, Middle Easterners and South Asians. That haplogroup was found at a lower incidence in East Asians, sub-Saharan Africans and New World Indians. For Microcephalin, the researchers found that haplogroup D is more abundant in populations outside of Africa than in populations from sub-Saharan Africa.(27)

The tests done on South and Central American populations showed an especially high occurrence of Microcephalin haplogroup D, with the Central American populations having slightly less than the South American populations. This distinction between the South and Central American populations is consistent with *The Urantia Book*. In a section covering the time period from 12,000 B.C. to 8,000 B.C., it recounts that a number of Adam and Eve’s descendants made it by boat to South America from Asia. (28)

> One hundred and thirty-two of this race [Andites], embarking in a fleet of small boats from Japan, eventually reached South America and by intermarriage with the natives of the Andes established the ancestry of the later rulers of the Incas.(29)

The transoceanic spread of Microcephalin haplogroup D, in contrast with the more regional spread of ASPM haplogroup D, all the more highlights the specific parallels with *The Urantia Book*’s depiction of the spread of Adam and Eve’s descendants to South America.

Sub-Saharans

Figure 2

The Urantia Book's account of the migrations of Adam and Eve's descendants is consistent with the research results that show Microcephalin haplogroup D to be present in significantly lower percentages in sub-Saharan populations.(30)

> Isolated in Africa, the indigo peoples . . . received little or none of the race elevation which would have been derived from the infusion of the Adamic stock.(31)
>
> The Andites not only migrated to Europe but to northern China and India, while many groups penetrated to the ends of the earth as missionaries, teachers, and traders. They contributed considerably to the northern groups of the Saharan . . . peoples. But only a few teachers and traders ever penetrated farther south in Africa than the headwaters of the Nile. Later on, mixed Andites and Egyptians followed down both the east and west coasts of Africa well below the equator, but they did not reach Madagascar.
>
> The migratory conquests of the Andites continued on down to their final dispersions, from 8000 to 6000 B.C. As they poured out of Mesopotamia, they continuously depleted the biologic reserves of their homelands while markedly strengthening the surrounding peoples. And to every nation to which they journeyed, they contributed humor, art, adventure, music, and manufacture. They were skillful domesticators of animals and expert agriculturists. For the time being, at least, their presence usually improved the religious beliefs and moral practices of the older races. And so the culture of Mesopotamia quietly spread out over Europe, India, China, northern Africa, and the Pacific Islands.(32)

The minimal migration of Adam and Eve's descendants to sub-Saharan Africa is also supported by the Y chromosome research. The Stanford study found, "Mutation 1 defines a clade, separate from the deep African lineages. Within this clade, a younger clade, consisting of 21 lineages of which only one is African, is defined by mutation 2. . ."(33) With respect to Y haplogroup F, "Descendents of Haplogroup F are almost absent in Sub-Saharan Africa, further supporting the theory that Haplogroup F formed shortly after its ancestors migrated out of Africa."(34)

Though the presence of Microcephalin haplogroup D is considerably lower in sub-Saharan Africa than the rest of the world, it is somewhat more abundant in the region of the headwaters of the Nile River, which, of course, specifically supports of *The Urantia Book*'s statement that "only a few teachers and traders ever penetrated farther south in Africa than the headwaters of the Nile." See Figure 2.

The comment that "to every nation to which they journeyed, they contributed humor, art, adventure, music, and manufacture" begs to be analyzed and scrutinized. However, the standard for UBtheNEWS reports is to stay focused on the more "hard science" aspects of corroborating information in *The Urantia Book*. For this reason, readers are left to their own evaluation of this

commentary by the authors of *The Urantia Book*.

Original Location

One of the similarities between the Biblical account of Adam and Eve and *The Urantia Book*'s account is that they both assert that Adam and Eve had some problems at their original location, which precipitated their departure. Just as these depictions of Adam and Eve place them in Mesopotamia, the results of research on Y haplogroup F also indicate an origin in this region.

> The founder of Haplogroup F lived . . . in modern day Middle East and his descendents became the founders of Haplogroups G through to R. . .
>
> Today, the original undifferentiated ancient Haplogroup F line is localized mainly to the Middle East. Descendents of Haplogroup F are almost absent in Sub-Saharan Africa, further supporting the theory that Haplogroup F formed shortly after its ancestors migrated out of Africa.(35)

The Urantia Book's account provides the following statements:

> It required almost a full year for the caravan of Adam to reach the Euphrates River. Finding it in flood tide, they remained camped on the plains west of the stream almost six weeks before they made their way across to the land between the rivers which was to become the second garden.
>
> . . . The two rivers themselves were a good natural defense in those days, and a short way north of the second garden the Euphrates and Tigris came close together so that a defense wall extending fifty-six miles could be built for the protection of the territory to the south and between the rivers.(36)
>
> The second Eden was the cradle of civilization for almost thirty thousand years. Here in Mesopotamia the Adamic peoples held forth, sending out their progeny to the ends of the earth. . .(37)
>
> "The secondary or northern . . . headquarters [was] situated east of the southern shore of the Caspian Sea near the Kopet mountains. From these two centers there went forth to the surrounding lands the culture and life plasm which so immediately quickened all the races."(38)

It is important to remember that *The Urantia Book*'s account of the history of humanity is at odds with the "out of Africa" *theory* of human evolution. It says humans evolved a million years ago in Mesopotamia.(39) Current scholarly opinion, for the most part, embraces a bias in favor of the out of Africa theory. At least tacitly, the team led by Bruce Lahn accepts this theory because they state in their reports:

> Fossil records indicate that anatomically modern humans first emerged ≈200,000 years ago in Africa and since then spread throughout the world.(40)
>
> The emergence of anatomically modern humans has been estimated to be 200,000 years before present. Haplogroup D is obviously much younger, which indicates that positive selection was at work in a period considerably postdating the emergence of anatomically modern humans in Africa.(41)

What exactly it means to be a "modern human" and where modern humans originated from are controversial enough subjects by themselves, both scientifically and socially. Lahn's team overlays these subjects with research that indicates a gene involving the growth of the brain has spread rapidly through most of the population but is in much lower percentages in the sub-Saharan population. Naturally, these types of studies and the interpretation of the data need to be handled delicately by the professionals involved with them, as can be seen in the following statements from a Howard Hughes Medical Institute online publication:

> Lahn emphasized that it would not be correct to interpret the findings as indicating that one ethnic group is more "evolved" than another. Any differences among groups would be minor compared to the large differences in such traits as intelligence within those groups, he said. "We're talking about the average impact of such variants," he

said. “We still have to treat each individual as an individual. . .”(42)

Interestingly, the very next paragraph of this same article goes on to say:

> Lahn speculated that the new findings suggest that the human brain will continue to evolve under the pressure of natural selection. “Our studies indicate that the trend that is the defining characteristic of human evolution—the growth of brain size and complexity—is likely still going on. . .”(43)

When the methodology of the research—the statistical sampling of racial groups—supports making the previous statement, but cannot be “correctly” used as an “indication” that “one ethnic group is more “evolved” than another,” one has to wonder what the definition of “correctly” is and whether it has anything to do with being “politically correct.” Pointing this out is not intended as an implied criticism regarding the different ways the subject is addressed in these two or other reports and articles. Rather the point is to highlight the double standard that researchers face regarding their choice of study, reporting results, and drawing conclusions; be unbiased in your work but do not offend the current version of political correctness.

The caution, associated with interpreting the data in a manner that is inconsistent with the predominantly held theory, is reflected in the subtle distinctions between statements from two different publications that came out during the second half of 2006.

> Lahn said that the geographic origin and circumstances surrounding the spread of the haplogroups can only be surmised at this point. “One can make guesses, but our study doesn't reveal how these positively selected variants arrived,” he said. “They may have arisen in Europe or the Middle East and spread more readily east and west due to human migrations, as opposed to south to Africa because of geographic barriers. Or, they could have arisen in Africa, and increased in frequency once early humans migrated out of Africa.”(44)

> Furthermore, the worldwide frequency distribution of the D allele, exceptionally high outside of Africa but low in sub-Saharan Africa, suggests, but does not necessitate, admixture with an archaic Eurasian population.(45)

It is interesting to note that the first quote comes from an article published on the Howard Hughes Medical Institutes website that is written for “general consumption.” It summarizes and contextualizes the research. The second quote is from the Discussion section scholarly, peer reviewed report published by the Proceedings of the National Academy of Sciences. In the general consumption article “one can only make guesses.” In contrast, the scholarly interpretation of data justifies a “suggests, but does not necessitate” statement regarding a Eurasian origin—Mesopotamia, of course, occupies the central region of Eurasia.

While *The Urantia* Book—in stating that a genetic upgrade occurred about 38,000 years ago involving an enhancement to brain function that did not migrate much into sub-Saharan Africa—admittedly, is not aligned well with today’s version of what it means to be politically correct, it is aligned well with the results of research into Microcephalin.

Culture progress and Microcephalin haplogroup D

Going into an analysis of the relative qualities of the various cultures established by different races is not within the scope of this report. However, noting direct correlations between *The Urantia Book* and comments in reports and articles about Microcephalin research regarding major shifts in human development are within the scope of this report. Examples of such comments include the following:

> “In the case of Microcephalin, the origin of the new variant coincides with the emergence of culturally modern humans,” said Lahn. “. . . So, a major question is whether the coincidence between the genetic evolution that we see and the cultural evolution of humans was causative, or did they synergize with each other?”(46)

> They [Lahn’s research team] speculate that if the human species continues to survive, the human brain may continue to evolve, driven by the pressures of natural selection. Their data suggest that major variants in these genes arose at roughly the same times as the origin of culture in human populations as well as the advent of agriculture and

written language.(47)

The distinction between the “origin of culture” and the “advent of agriculture and written language” is intended to parallel the “single progenitor” changes that occurred with Microcephalin hapolgroup D and ASPM, approximately 37,000 and 5,800 years ago, respectively.

Regarding Adam and Eve’s contribution to culture, *The Urantia Book* states:

> Evolution may advance in the absence of culture, but cultural civilization does not flourish without an adequate background of antecedent racial progression. Adam and Eve introduced no art of civilization *foreign to the progress of human society*, but the Adamic blood did *augment the inherent ability of the races* and did accelerate the pace of economic development and industrial progression. Adam's bestowal improved the brain power of the races, *thereby greatly hastening the processes of natural evolution*. [emphasis added](48)
>
> When all is summed up, Adam and Eve made a mighty contribution to the speedy civilization and accelerated biologic progress of the human race. They left a great culture on earth, but it was not possible for such an advanced civilization to survive in the face of the early dilution and the eventual submergence of the Adamic inheritance. It is the people who make a civilization; civilization does not make the people.(49)

(These statements about a superior civilization getting started in Mesopotamia, but then experiencing an “early dilution” and “eventual submergence,” not only are supported by archaeological discoveries that continue to be made at the Gobekli Tepe site in Turkey, but also explain an aspect of the site that is otherwise very mysterious—the structures date back at least twelve thousand years but were intentionally buried eight thousand years ago. See the Gobekli Tepe Report.)

Speed

The speed at which Microcephalin haplogroup D, mutation 2, and Y haplogroup F have spread is harmonious with the descriptions in *The Urantia Book* about Adam and Eve’s intentions and the degree to which their descendants followed through. The comments in the previous section about cultural development are also complemented, of course, by the research results related to the rapid rate at which the genetic changes spread.

When a new genetic development spreads quickly into a population, geneticists, naturally, are inclined to believe there is a reason, to theorize about it, and then try to test for it. What the researchers say about the spread of these genetic shifts will be reviewed after looking at the explanation provided in *The Urantia Book*.

In describing the intentions and wisdom that guided Adam in establishing a new civilization, the authors relate that he originally intended:

> . . . not to initiate the program of racial uplift and blending until his own family had numbered one-half million. It was never intended that the Garden should be the permanent home of the Adamites. They were to become emissaries of a new life to all the world; they were to mobilize for unselfish bestowal upon the needy races of earth.
>
> . . . [H]e was to establish racial, continental, and divisional headquarters to be in the charge of his immediate sons and daughters, while he and Eve were to divide their time among these various world capitals as advisers and co-ordinators of the world-wide ministry of biologic uplift, intellectual advancement, and moral rehabilitation. (50)

The problems associated with the need to find a new location also necessitated a new plan.

> After becoming established in the second garden on the Euphrates, Adam elected to leave behind as much of his life plasm as possible to benefit the world after his death. . . . [B]efore Adam died. . . 1,682. . . women were impregnated with the Adamic life plasm [through artificial insemination]. Their children all grew up to maturity except 112, so that the world, in this way, was benefited by the addition of 1,570 superior men and

women. . .(51)

The location and impact of the cultural centers that took root with the genetic contribution of Adam and Eve is summarized as follows:

> *The violet race—Adamites and Adamsonites*. The chief center of Adamite culture was in the second garden, located in the triangle of the Tigris and Euphrates rivers; this was indeed the cradle of Occidental and Indian civilizations. The secondary or northern center of the violet race was the Adamsonite headquarters, situated east of the southern shore of the Caspian Sea near the Kopet mountains. From these two centers there went forth to the surrounding lands the culture and life plasm which so immediately quickened all the races.(52)

The blending and cultural implications of these developments are also specifically addressed:

> For twenty thousand years the culture of the second garden persisted, but it experienced a steady decline until about 15,000 B.C., when the regeneration of the Sethite priesthood and the leadership of Amosad inaugurated a brilliant era. The massive waves of civilization which later spread over Eurasia immediately followed the great renaissance of the Garden consequent upon the extensive union of the Adamites with the surrounding mixed Nodites to form the Andites.
>
> These Andites inaugurated new advances throughout Eurasia and North Africa. From Mesopotamia through Sinkiang the Andite culture was dominant, and the steady migration toward Europe was continuously offset by new arrivals from Mesopotamia. But it is hardly correct to speak of the Andites as a race in Mesopotamia proper until near the beginning of the terminal migrations of the mixed descendants of Adam. By this time even the races in the second garden had become so blended that they could no longer be considered Adamites.
>
> The civilization of Turkestan was constantly being revived and refreshed by the newcomers from Mesopotamia, especially by the later Andite cavalrymen. . . [Their language] was a blend of the Andonic dialect of that region with the language of the Adamsonites and later Andites. Many modern languages are derived from this early speech of these central Asian tribes who conquered Europe, India, and the upper stretches of the Mesopotamian plains.(53)

There are three chapters, or “Papers” as they are referred to in *The Urantia Book*, that extensively cover the migration of Adam and Eve’s descendants. Readers wanting additional details can review Papers 78 through 80. The statements above about their general impact, genetically and culturally, are part of an extended recounting of the migrations of their descendants and interactions with the people they encountered. All of which is, of course, harmonious with the genetic evidence indicating that, however it occurred, there was an especially rapid spread of some new genetics, probably originating near Mesopotamia around the time *The Urantia Book* says Adam and Eve lived—“from the year A.D. 1934, 37,848 years ago.”

In genetics the terms positive selection, negative selection, and drift are used, respectively, to describe circumstances that indicate a propensity to spread, an obstacle to spreading, or a neutral/random spread. Naturally, strong positive selection—rapid spread—begs for an explanation. Here is some of the commentary related to Microcephalin haplogroup D:

> The gene microcephalin (MCPH1) regulates brain size during development and has experienced positive selection in the lineage leading to Homo sapiens. Within modern humans, a group of closely related haplotypes at this locus, known as haplogroup D, rose from a single copy ≈37,000 years ago and swept to exceptionally high frequency (≈70% worldwide today) because of positive selection. . . Furthermore, it buttresses the important notion that, through such admixture, our species has benefited evolutionarily by gaining new advantageous alleles.(54)
>
> The much younger coalescence age of the D chromosomes, despite their much higher frequency, is consistent with the action of positive selection on the D allele as reported previously.(55)
>
> This rapid rise in frequency indicates that the D alleles underwent positive selection in the recent history of humans. This means that these alleles conferred a fitness

> advantage on those who possessed one of them such that these people had slightly higher reproductive success than people who didn't possess the alleles, said Lahn.(56)

Reflections on the spread of mutation 2 are found in the following statements from the Stanford study:

> [A]lthough previous studies have noted that Y chromosome variation shows extreme geographic structure, we estimate that the spread of Y chromosomes out of Africa is much more recent than previously was thought. We also show that our data indicate substantial population growth in the effective number of human Y chromosomes.(57)

> The age of mutation 2, at around 40,000 years ago, represents an estimate of the time of the beginning of global expansion.(58)

In view of the fact that for much of the last 50,000 years humans have been widely dispersed around the globe, with rapid population growth for a significant fraction of that time, it is striking that the estimated time to the MRCA is so short. From the Y chromosome, one would conclude that the ancestral population size 50,000 years ago was very small indeed. Yet this view is at odds with the results from other loci such as b-globin, which have very ancient MRCA times.

> One solution to this apparent discrepancy is the possibility that the Y chromosome is subject to fairly strong selection, either in the form of positive selection for advantageous mutations (hitchhiking) or negative selection against mildly deleterious mutations (background selection). The possible role of selection seems quite plausible . . .(59)

Considerations on the spread of Y haplogroup F are reflected in these statements:

> Haplogroup F is an important ancient haplogroup whose descendents are responsible for forming the majority of the civilizations in the world today. . . Descendents of Haplogroups G to R represent more than 90% of the world's current population.
>
> . . . Descendents of Haplogroup F are almost absent in Sub-Saharan Africa, further supporting the theory that Haplogroup F formed shortly after its ancestors migrated out of Africa.(60)

Microcephalin haplogroup D, mutation 2, and Y haplogroup F each spread rapidly throughout most of humanity. The rapid spread over the related time period is altogether harmonious with *The Urantia Book*'s depiction of the spread of Adam and Eve's descendants.

Where did the quickly spreading changes from about 40,000 years ago come from?

The research into Microcephalin haplogroup D and mutation 2 in the Stanford study both yield results that are difficult to explain. Because the research done on Microcephalin haplogroup D indicates a single progenitor, the difficulty in interpreting the results is a bit more intriguing and is given more attention. Only a few comments on the issue make it into the Stanford study. "One solution to this apparent discrepancy is the possibility that the Y chromosome is subject to fairly strong selection. . . The possible role of selection seems quite plausible . . ."(61)

When a genetic introduction apparently comes from "out of nowhere" and spreads quickly into the human gene pool, scientists appropriately stay within the material world when speculating about such things. It's a mutation or a crossbreeding which took place, perhaps between *Homo* sapiens and *Homo* neanderthalenis. While a "complete" understanding of *The Urantia Book* perspective on Adam and Eve would require venturing into cosmological and theological areas, such details are not at all necessary for appreciating how these new discoveries in genetics are lending support to what the book says about Adam and Eve. Understanding that Adam and Eve are said to have come from "out of nowhere" is sufficient The particulars of the theological and cosmological explanation in *The Urantia Book* do not add anything substantial to the general intrigue deriving from having made these assertions before this type of research was possible.

Because of their complexity and sudden appearance, geneticists are inclined to think that Microcephalin haplogroup D had to come from somewhere, as compared to being a mutation. This inclination is evidenced by the conspicuous absence of speculations about whether a mutation

occurred. The problem is that the evidence regarding the appearance of Microcephalin haplogroup D supports an "out of nowhere" or mutation theory, but the complexity of haplogroup D demands a different explanation. So an unusual interbreeding becomes the more intriguing possibility for the researchers.

> In this study, we investigate the origin of the microcephalin D allele in modern humans. We show that the D allele is unlikely to have arisen within a panmictic population. [A panmictic population is one where all individuals are potential partners. This assumes that there are no mating restrictions, neither genetic or behavioural, upon the population, and that therefore all recombination is possible. (62)] Instead, our data are consistent with a model of population subdivision followed by introgression to account for the origin of the D allele. . . These two alleles are differentiated by a large number of sequence differences accumulated during the prolonged isolation of the two populations. At or sometime before ≈37,000 years ago, a (possibly rare) interbreeding event occurred between the two lineages, bringing a copy of the D allele into anatomically modern humans. Whereas the original D-bearing *Homo* population had since gone extinct, this introgressed copy of the D allele in humans had subsequently spread to exceptionally high frequency throughout much of world because of positive selection.
>
> . . .
>
> Speculation about the identity of the archaic *Homo* population from which the microcephalin D allele introgressed into the modern human gene pool points to the Neanderthal lineage as a potential (although by no means only) candidate. . .
>
> Our results not only provide genetic evidence in support of the possibility of admixture between modern humans and an archaic *Homo* lineage but also support the notion that the biological evolution of modern humans might have benefited from the contribution of adaptive alleles from our archaic relatives. In the case of microcephalin, it is all the more intriguing given the fact that the adaptive allele is associated with an important brain development gene.(63)
>
> Under this scenario, just as in the first scenario, two subdivided populations were reproductively isolated from each other for a prolonged period, such that one population was fixed for the D allele, whereas the other population was fixed for the non-D allele. Unlike the first scenario, however, the two populations did not admix completely. Rather, a rare interbreeding event occurred between the two populations ≈37,000 years ago, which resulted in the introgression of a copy of the D allele from the D-bearing into the non-D population. The D-bearing population subsequently went extinct, but the introgressed D allele spread to exceptionally high frequency in the remaining population because of positive selection. Because this scenario invokes positive selection specifically at the microcephalin locus, it is not expected to have a genome-wide effect. Other regions of the genome brought over by the interbreeding event are expected to be lost by genetic drift unless they also confer a selective advantage. As discussed below, the lopsided and deeply divided genealogy observed at the microcephalin locus is highly atypical of the genome, which is consistent with this introgression scenario.(64)

The research supports a single progenitor. This essentially requires the interbreeding to be a rare occurrence. And because they cannot find haplogroup D anywhere else, whatever it came from is apparently now extinct. Naturally, it does not make a lot of sense to suggest that *Homo* neanderthalensis, which is considered an inferior species compared to Homo sapiens, would contribute a superior haplogroup to the Microcephalin gene, as is suggested by the rapid spread into 70% of the population of *Homo* sapiens. But for the "pure scientist" there are not a lot of alternatives about which to speculate.

The Urantia Book's assertion that Adam and Eve came from out of nowhere and intentionally started a civilization with an agenda of genetically uplifting humanity fits simply and well with the evidence. Additionally, this explains why scientists have trouble finding any evidence of the "archaic *Homo* lineage." And naturally, this is explains why they would have just as much trouble interpreting the data in manner that would fit other strictly scientific theories. *The Urantia Book*'s cosmology may not contribute anything by way of proof, but it does contribute something by way of explanation; it is consistent with the science and deserves credit for advancing an explanation in

advance of the supporting science.

Tonal Languages

In the wake of the Lahn-led Microcephalin research, interest developed to determine whether the spread of Microcephalin haplogroup D tracks with anything else related to brain function. This inquiry led to the documentation of a strong relationship to the use of nontonal languages. An article from May 2007, titled *Speaking in tones? Blame it on your genes*, summarizes the issue this way:

> Genetic differences between human populations may have influenced which languages are spoken around the world today, research has suggested.
>
> People who carry particular variants of two genes involved in brain development tend to speak nontonal languages such as English, while those with a different genetic profile are more likely to speak tonal languages such as Chinese.
>
> In tonal languages, which are most common in South East Asia and sub-Saharan Africa, subtle differences in pitch can change the meaning of vowels, consonants and syllables. Nontonal languages, which prevail in Europe, the Middle East and North Africa, use pitch only as a way of conveying emphasis or emotion.
>
> . . .
>
> All humans have the innate ability to speak either type fluently, but the research indicates that genes may make one class slightly easier to learn. . . .
>
> . . .
>
> "This does not mean that people with one set of genes cannot speak the other type of language, or that you have to be any smarter to learn one of these groups of languages rather than another," Robert Ladd, who led the research, said. "What we have found, though, suggests that these genes might have a very small effect on individuals, and a larger effect on the populations in which they live. As the language is passed on culturally, it would then be more likely to develop along one path than the other."
>
> He cautioned, however, that the research had so far found only an association that appears to be more than chance, and that more work was needed to confirm a causal effect.(65)

The original research report, published in Proceedings of the National Academy of Sciences, gets into the details, of course:

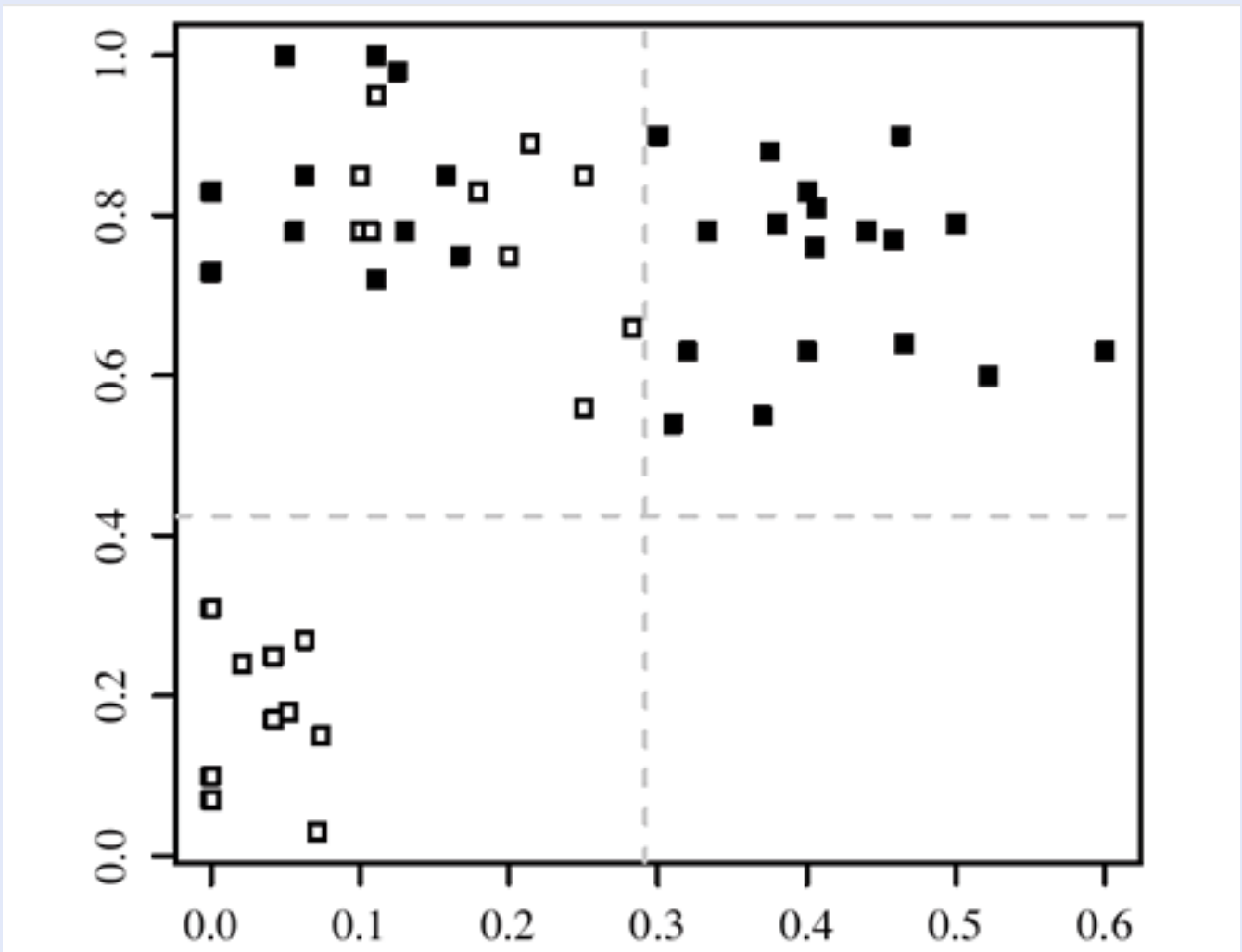
> Here, we consider the relation between allele frequencies and linguistic typological features. Specifically, we focus on the derived haplogroups of the brain growth and development-related genes ASPM and Microcephalin, which show signs of natural selection and a marked geographic structure, and on linguistic tone, the use of voice pitch to convey lexical or grammatical distinctions. We hypothesize that there is a relationship between the population frequency of these two alleles and the presence of linguistic tone and . . . that it is not due to the usual explanatory factors represented by geography and history.(66)
>
> Tone languages are the norm in sub-Saharan Africa and are very common in continental and insular southeast Asia. They are rare in the rest of Eurasia, North Africa, and Australia. They are relatively common in Central America, the Caribbean, and the Amazon basin, and occur sporadically elsewhere among the aboriginal languages of the Americas.(67)
>
> In the present study, we performed statistical tests of this hypothesis on the basis of a large database comprising 983 alleles and 26 linguistic features collected for 49 world populations (see Materials and Methods), controlling for geographical and historical factors. We considered linguistic features rather than linguistic groupings (dialects, languages, linguistic families, or phyla), because our hypothesis concerns specifically the interaction between linguistic typological diversity and population genetic

diversity. We found that, in general, the relationship between these two diversities is fully explained by geographical an[d] historical factors, whereas, in the specific case of tone, ASPM-D, and MCPH-D, there is an important and significant correlation between their distributions even after controlling for geography and history. Therefore, we propose that this relationship is causal; that is, the genetic structure of a population can exert an influence on the language(s) spoken by that population. Further experimental support is required, but these findings suggest a fundamental direction for future research targeted at understanding the complex relationship between genetic factors, cultural evolution, and linguistic phenomena.(68)

[The research shows] that, in general, linguistic features do not correlate with alleles. . . [but that] taken individually, tone and ASPM-D and tone and MCPH-D are highly significantly correlated and the strength of their relationship is >98.5% of all of the 25,558 correlations between linguistic features and alleles in our database.(69)

Interestingly, the authors of *The Urantia Book* specifically mention the interrelationship between the spread of Adam and Eve descendants and the global development of linguistic similarities.

The civilization of Turkestan was constantly being revived and refreshed by the newcomers from Mesopotamia, especially by the later Andite cavalrymen. . . [Their language] was a blend of the Andonic dialect of that region with the language of the Adamsonites and later Andites. Many modern languages are derived from this early speech of these central Asian tribes who conquered Europe, India, and the upper stretches of the Mesopotamian plains.(70)



Linguistic tone versus the population frequency of the adaptive haplogroups of *ASPM* and *Microcephalin*. The horizontal axis represents the frequency of *ASPM-D*, whereas the vertical axis represents the frequency of *MCPH-D*. Filled squares represent nontonal languages and open squares tonal languages. Gray dashed lines correspond to 0.292 *ASPM-D* and 0.425 *MCPH-D*. See last paragraph of *Results* for details.

Figure 3

Before offering a final quote from the report covering the relationship between non tonal languages and Microcephalin haplogroup D and having arrived at the end of the presentation of the recent research that lends support to *The Urantia Book*'s narrative about Adam and Eve, it is important to address the cultural context in which this type of research work is done. It is well in evidence at this

point that *The Urantia Book*'s authors recount an integrated history of new genetic and cultural developments that were intentionally orchestrated.

> The result of the gift of the Adamic life plasm to the mortal races is an immediate upstepping of intellectual capacity and an acceleration of spiritual progress.(71)
>
> Evolution may advance in the absence of culture, but cultural civilization does not flourish without an adequate background of antecedent racial progression. Adam and Eve introduced no art of civilization foreign to the progress of human society, but the Adamic blood did augment the inherent ability of the races and did accelerate the pace of economic development and industrial progression. Adam's bestowal improved the brain power of the races, thereby greatly hastening the processes of natural evolution. (72)

They are direct in asserting that 1) notwithstanding the preeminent importance of our spiritual equality and the moral requirements that go with this, we are physiologically and intellectually diverse and 2) to a certain extent, these differences are related to an introduction by Adam and Eve of superior genetics. This aspect of *The Urantia Book*, however well aligned with science it may be, is making bold statements about a highly controversial and sensitive subject area in a manner that many people would consider "politically incorrect."

Therefore, before presenting what Ladd's team (not to be confused with Lahn) said in 2007 about the results of the tonal language research as it relates to race, we will first review a portion of the 2,300-word article that appeared June 16, 2006 in the Wall Street Journal about the controversial aspects of Lahn's research into Microcephalin.

> Last September, Bruce Lahn, a professor of human genetics at the University of Chicago, stood before a packed lecture hall and reported the results of a new DNA analysis: He had found signs of recent evolution in the brains of some people, but not of others.
>
> It was a triumphant moment for the young scientist. He was up for tenure and his research was being featured in back-to-back articles in the country's most prestigious science journal. Yet today, Dr. Lahn says he is moving away from the research. "It's getting too controversial," he says.
>
> Dr. Lahn had touched a raw nerve in science: race and intelligence.
>
> What Dr. Lahn told his audience was that genetic changes over the past several thousand years might be linked to brain size and intelligence. He flashed maps that showed the changes had taken hold and spread widely in Europe, Asia and the Americas, but weren't common in sub-Saharan Africa.
>
> Web sites and magazines promoting white "racialism" quickly seized on Dr. Lahn's suggestive scientific snapshot. One magazine that blames black and Hispanic people for social ills hailed his discovery as "the moment the antiracists and egalitarians have dreaded."
>
> Dr. Lahn has drawn sharp fire from other leading genetics researchers. They say the genetic differences he found may not signify any recent evolution -- and even if they do, it is too big a leap to suggest any link to intelligence. "This is not the place you want to report a weak association that might or might not stand up," says Francis Collins, director of the genome program at the National Institutes of Health.
>
> Several scientific groups have set out to disprove or challenge Dr. Lahn's discoveries. His own university now says it is abandoning a patent application it filed to cover a DNA-based intelligence test that drew on his work.
>
> As scientific tools for probing genes become increasingly powerful, research into human differences has exploded. Most of the time, scientists are looking for clues about the causes of disease. But some research is raising tensions as scientists such as Dr. Lahn venture into studies of genetic differences in behavior or intelligence.
>
> . . .

> The 37-year-old Dr. Lahn says his research papers, published in Science last September, offered no view on race and intelligence. He personally believes it is possible that some populations will have more advantageous intelligence genes than others. And he thinks that "society will have to grapple with some very difficult facts" as scientific data accumulate. Yet Dr. Lahn, who left China after participating in prodemocracy protests, says intellectual "police" in the U.S. make such questions difficult to pursue.
>
> The accuracy of Dr. Lahn's work and his views on race came up in his tenure review last fall, says a person familiar with it. After debate, his department voted unanimously in his favor, according to another faculty member. A more senior committee agreed and awarded Dr. Lahn the post of full professor, although it wasn't unanimous, this person says.
>
> Dr. Lahn stands by his work but says that because of the controversy he is moving into other projects. . . .
>
> Dr. Lahn says he isn't as eager as he once was to continue studying brain differences. . . .
>
> The university's patent office is also having second thoughts. Its director, Alan Thomas, says his office is dropping a patent application filed last year that would cover using Dr. Lahn's work as a DNA-based intelligence test. "We really don't want to end up on the front page...for doing eugenics," Mr. Thomas says.
>
> More recently, Dr. Lahn says he was moved when a student asked him whether some knowledge might not be worth having. It is a notion to which he has been warming. Dr. Lahn says he once tried testing himself for which version of the brain genes he has. The experiment's outcome was blurry "but it wasn't looking good," he says. He hasn't tried testing himself again.(73)

This is the real world of attempting to do genetics research on the most important organ in the body. People are concerned about discovering certain types of factual information and how such information will be interpreted. This concern is powerful enough to affect the course of research and the interpretations that are attached to it.

Bearing all this in mind, the report on tonal languages states the following:

> Our findings therefore do not support any racial or deterministic interpretation. Finally, note that this bias could be either for or against tone, but the fact that nontonality is associated with the derived haplogroups [] suggests that tone is phylogenetically older and that the bias favors nontonality. The bias is presumably a selectively neutral byproduct of the two derived haplogroups, not connected to the selective pressures on them, because there is no evidence that tone itself confers any advantage or disadvantage on speakers. We cannot, of course, rule out the scenario whereby the natural selection detected for these haplogroups is partially due to their linguistic effects.(74)

Ironically, the distinct racial differences related to the spread of Microcephalin haplogroup D, which were the part of the intrigue for doing this study in the first place, are an insufficient basis for supporting any conclusions that are race related, even though the correlations between tonal languages, the absence of Microcephalin haplogroup D, and sub-Saharan Africa are obvious and undisputed. Apparently, the authors of this report feel so restricted in their interpretation of the subject, that they are unwilling to even speculate about the relative value of tonal and nontonal languages.

Does one need a PhD in linguistics to be qualified in asserting that the linguistic flexibility associated nontonal languages—to be able to imbue any word with any tonal emphasis or inflection—is superior and advantageous? Is a more restrictive system of combining phonetics and inflection supposed to simply be accepted as being of equal worth with no discussion of the matter whatsoever? Is this what scholarly objectivity looks like?

Normally, editorial commentary such as this would not find its way into a UBtheNEWS report. In this case, however, because the problem is being discussed openly and talked about in terms of how it affects research, researchers, and the interpretation of data, a modicum of editorial commentary

seems warranted.

Commentary

First of all, thank you for taking the time to develop a more in depth appreciation for how recent genetics research has been catching up to *The Urantia Book*'s story about Adam and Eve. For all kinds of reasons, this subject matter is becoming increasingly timely and relevant. Engaging this topic immediately faces us with complexities and challenges on both scientific and social levels. Genetics issues lead to eugenics issues. The blunt statement from the director of the Univeristy of Chicago's patent office simplifies the problem very nicely, "We really don't want to end up on the front page...for doing eugenics." The authors of *The Urantia Book* are equally good at being blunt. "Adam's bestowal improved the brain power of the races, thereby greatly hastening the processes of natural evolution."(75)

Humanity learns and grows and changes over time. New discoveries and scientific advances are increasingly bringing us a more accurate understanding of our world, past and present. *The Urantia Book* does not change over time and it places its credibility on the line by asserting that "the historic facts . . . will stand on the records of the ages to come." When it was published in 1955, the type of research techniques that gave rise to this report was not yet invented.

Fortunately, *The Urantia Book* also offers extensive explanations and insights to support us in learning how to handle the facts and hold a conversation about the facts from a significantly more "evolved" perspective. Please read the *Eugenics, Race, and The Urantia Book* paper for a comprehensive review of this topic. If we are going to stop fearing the discovery of facts and learn how to use them for collective and altruistic purposes, we need to address the concerns that give rise to those fears in a new way. *The Urantia Book* provides a perspective that is not only fresh and timely but also uniquely credible and increasingly so for more than fifty years.

Naturally, those of us participating in the development of the UBtheNEWS project feel confident, based on the overall trend toward corroborations of historical and scientific information in *The Urantia Book*, that we will continue to document discoveries involving other genetic changes that generally correspond to the time period and migration patterns associated with *The Urantia Book*'s story about Adam and Eve and their descendants. This is a field that is developing very quickly; the studies referenced in this report started coming out in 2004. The first time this report was written in 2007, it did not have any of the Y chromosome or tonal language information. Research into whether other studies have produced results with similar parallels to *The Urantia Book* is at an early stage of development.

Look for additional updates to this report in the not too distant future. . .

Footnotes:

(1) Urantia Book 81:5.1
(2) Urantia Book 78:4.5,6
(3) Urantia Book 65:5.2
(4) Urantia Book 76:4.7
(5) Urantia Book 51:1.3
(6) http://www.hhmi.org/news/lahn4.html
(7) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(8) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(9) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(10) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(11) https://sites.google.com/a/luther.edu/johnathan-storlie-phd/john-s-y-dna-haplogroup-history
(12) http://genome.cshlp.org/content/early/2008/04/02/gr.7172008.full.pdf+html
(13) http://www.pnas.org/content/103/48/18178.full
(14) http://hominid.uchicago.edu/publications/2005%20Science-Microcephalin%20evol.pdf
(15) http://www.pnas.org/content/103/48/18178.full
(16) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(17) Urantia Book 74:0.1
(18) Urantia Book 62:5.1
(19) Urantia Book 63:1.1

(20) Urantia Book 51:1.3
(21) From the Howard Hughes Medical Institute's online Research News dated November 6, 2006. http://www.hhmi.org/news/lahn20061006.html
(22) http://www.pnas.org/content/103/48/18178.full
(23) Urantia Book 78:3.2,3
(24) Urantia Book 78:3.5
(25) Urantia Book 78:2.5
(26) http://www.hhmi.org/news/lahn4.html
(27) http://www.hhmi.org/news/lahn4.html
(28) Urantia Book 78:5.4,8
(29) Urantia Book 78:5.7
(30) http://www.hhmi.org/news/lahn4.html
(31) Urantia Book 64:6.26
(32) Urantia Book 78:5.5,8
(33) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(34) https://sites.google.com/a/luther.edu/johnathan-storlie-phd/john-s-y-dna-haplogroup-history
(35) https://sites.google.com/a/luther.edu/johnathan-storlie-phd/john-s-y-dna-haplogroup-history
(36) Urantia Book 76:1.1,3
(37) Urantia Book 78:0.1
(38) Urantia Book 78:1.3
(39) Urantia Book 62:4.3
(40) http://www.pnas.org/content/103/48/18178.full
(41) http://hominid.uchicago.edu/publications/2005%20Science-Microcephalin%20evol.pdf
(42) http://www.hhmi.org/news/lahn4.html
(43) http://www.hhmi.org/news/lahn4.html
(44) http://www.hhmi.org/news/lahn4.html
(45) http://www.pnas.org/content/103/48/18178.full
(46) http://hominid.uchicago.edu/publications/2005%20Science-Microcephalin%20evol.pdf
(47) http://www.hhmi.org/news/lahn4.html
(48) Urantia Book 81:5.1
(49) Urantia Book 76:6.4
(50) Urantia Book 73:7.3,4
(51) Urantia Book 76:4.8
(52) Urantia Book 78:1.3
(53) Urantia Book 78:5.1-3
(54) http://www.pnas.org/content/103/48/18178.full
(55) http://www.pnas.org/content/103/48/18178.full
(56) http://www.hhmi.org/news/lahn20061006.html
(57) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(58) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(59) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(60) https://sites.google.com/a/luther.edu/johnathan-storlie-phd/john-s-y-dna-haplogroup-history
(61) http://pritch.bsd.uchicago.edu/publications/YMRCA.pdf
(62) http://en.wikipedia.org/wiki/Panmictic
(63) http://www.pnas.org/content/103/48/18178.full
(64) http://www.pnas.org/content/103/48/18178.full
(65) http://www.timesonline.co.uk/tol/news/uk/science/article1851794.ece
(66) http://www.pnas.org/content/104/26/10944.full.pdf
(67) http://www.pnas.org/content/104/26/10944.full.pdf
(68) http://www.pnas.org/content/104/26/10944.full.pdf
(69) http://www.pnas.org/content/104/26/10944.full.pdf
(70) Urantia Book 78:5.1-3
(71) Urantia Book 52:3.6
(72) Urantia Book 81:5.1
(73) Wall Street Journal Online
(74) http://www.pnas.org/content/104/26/10944.full.pdf
(75) Urantia Book 81:5.1

Post Publication Support

Research on the Dual Origin of Modern Man and pre-Modern Man

This page presents research on how new discoveries about ancient human history, especial genetics research, lend support to the *The Urantia Book*'s statements about when four major genetic changes occurred in the development of civilization. *The Urantia Book* says that the first two major changes were mutations. The initial mutation evolved man out of the animal level of existence into a pre-civilizable expression of humanity. The second one gave human beings a genetic foundation that was civilizable, but still pre-modern. These occurred approximately 1,000,000 years ago and 500,000 years ago. The second two major changes involved superhuman additions to the gene pool. These occured approximately 200,000 years ago and 38,000 yars ago.

Deeper and Broader

Political Issues

The Barossa, South Australia: Strong evidence for Race related IQ gene discovered
The moment the anti-racists and egalitarians have dreaded has now arrived.
In September, University of Chicago geneticists published data in the prestigious journal Science that links two sets of genetic variations (alleles) to brain size, race, and spurts in human evolution. In particular, these genetic variations-arguably responsible for greater intelligence-were relatively common in Europe and Asia, but markedly less common in sub-Saharan Africa. Previously, the same researchers had shown these variations to be much more frequent in man than in other mammals, though our closest relatives, the chimpanzees, showed levels that suggest some evolution in the direction of humans. This excellent new Chicago work has been carried out under the direction of a young Chinese, Dr. Bruce Lahn. His team had studied the prevalence of variants of two genes that are disabled or damaged in human cases of severe microcephaly, in which the brain develops to only 30 percent its normal size. The fact that they are damaged in microcephalics suggests they are necessary for normal brain growth.
http://www.barossa-region.org/Australia/Strong-evidence-for-Race-related-IQ-gene-discovered.html

Royal Society Publishing, april 22, 2007:
No evidence that polymorphisms of brain regulator genes Microcephalin and ASPM are associated with general mental ability, head circumference or altruism
Abstract: We test the hypothesis that polymorphisms of the brain regulator genes MCPH1 and ASPM contribute to variations in human brain size and its correlates. We measured general mental ability, head circumference and social intelligence in 644 Canadian adults (496 Caucasians, 36 Orientals, 84 Mixed Race/Other and 28 Blacks; 257 men and 387 women). The gene polymorphisms were assessed from buccal DNA; mental ability by Wonderlic Personnel Test and Multidimensional Aptitude Battery; head circumference by stretchless tape; and social intelligence by prosocial attitude questionnaires. Although all measures were construct valid and the allele frequencies showed expected population differences, no relationship was found between the genes and any of the criteria. Among Caucasian 18–25 year olds, for example, the two mental ability tests correlated with each other ($r=0.78$, $N=476$, $p<0.001$), with head circumference ($r=0.17$, $N=182$, $p<0.05$) and with prosocial attitudes ($r=0.23$, $N=182$, $p<0.001$).
http://rsbl.royalsocietypublishing.org/content/3/2/157.full

Gene Expression quoting a Wall Street Journal article, June 16, 2006
Coverage of the controversy: "Last September, Bruce Lahn, a professor of human genetics at the University of Chicago, stood before a packed lecture hall and reported the results of a new DNA analysis: He had found signs of recent evolution in the brains of some people, but not of others. It was a triumphant moment for the young scientist. He was up for tenure and his research was being featured in back-to-back articles in the country's most prestigious science journal. Yet today, Dr. Lahn says he is moving away from the research. "It's getting too controversial," he says. Dr. Lahn had touched a raw nerve in science: race and intelligence. What Dr. Lahn told his audience was that genetic changes over the past several thousand years might be linked to brain size and intelligence.
http://www.gnxp.com/blog/2006/06/bruce-lahn-moving-on-to-non-iq.php

Tonal Languages

A Replicated Typo, January 24, 2009: ASPM, Microcephalin and Tone
Disclaimer: I know this post is on a paper released over a year ago; however, I'm still going to write about it for three reasons: 1) I did a presentation about it earlier this week (20/01/08); 2) I think it

relates to a recent buzz around gene-culture co-evolution; and, 3) It's a bloody awesome paper.
http://replicatedtypo.wordpress.com/2009/01/24/aspm-microcephalin-tone/

PLoS Biol, July 2008:
Across the Curious Parallel of Language and Species Evolution
Recently, genetics has joined the list of possible influences on how languages change. Last year, Dan Dediu and Robert Ladd, two linguists working at the University of Edinburgh, published a paper showing that the geographical distribution of variant forms of two genes active during brain development, called ASPM and Microcephalin, correlates with the distribution of tonal languages, where the inflection of a word changes its meaning . In places where the ancestral form of the genes is commonest, such as in Southeast Asia and sub-Saharan Africa, the languages, such as Chinese and Yoruba, tend to be tonal. Where the derived form predominates, such as in Europe, West Asia, and North Africa, the languages, such as Spanish and German, are nontonal. "Cultural change and biological change share the same fundamental properties of variation, selection and inheritance."
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=2475544

PNAS, June 26, 2007: Linguistic tone is related to the population frequency of the adaptive haplogroups of two brain size genes, ASPM and Microcephalin
Abstract: The correlations between interpopulation genetic and linguistic diversities are mostly noncausal (spurious), being due to historical processes and geographical factors that shape them in similar ways. Studies of such correlations usually consider allele frequencies and linguistic groupings (dialects, languages, linguistic families or phyla), sometimes controlling for geographic, topographic, or ecological factors. Here, we consider the relation between allele frequencies and linguistic typological features. Specifically, we focus on the derived haplogroups of the brain growth and development-related genes ASPM and Microcephalin, which show signs of natural selection and a marked geographic structure, and on linguistic tone, the use of voice pitch to convey lexical or grammatical distinctions. We hypothesize that there is a relationship between the population frequency of these two alleles and the presence of linguistic tone and test this hypothesis relative to a large database (983 alleles and 26 linguistic features in 49 populations), showing that it is not due to the usual explanatory factors represented by geography and history. The relationship between genetic and linguistic diversity in this case may be causal: certain alleles can bias language acquisition or processing and thereby influence the trajectory of language change through iterated cultural transmission.
http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pmcentrez&artid=1904158

Anthropology.net, May 29, 2007:
Role of ASPM and Microcephalin on Linguistic Tone
I want to share with you news about some yet to be released research on the role of two genes, ASPM & Microcephalin, in language tone, which has just hit the press releases. ASPM & Microcephalin are known to play a role in brain development of primates. The role of these two genes in language tone has not been investigated until now.
Language tone has direct tangents to both human evolution and linguistic anthropology. Now that I think of it even cultural anthropology has a lot to do with language tone.
http://anthropology.net/2007/05/29/role-of-aspm-and-microcephalin-on-linguistic-tone/

The Telegraph, April 30, 2007:
Learning Chinese languages makes you musical, claim scientists
Learning to speak Mandarin and Vietnamese as a child helps make you more musical, claims a study that suggests being fluent in the languages helps you have perfect pitch.
http://www.telegraph.co.uk/news/newstopics/howaboutthat/5245655/Learning-Chinese-languages-makes-you-musical-claim-scientists.html

Additional Information

Inter*active* Fly: GeneBrief, Microcephalin
A general, but extensive, overview of the microcephalin gene.
http://www.sdbonline.org/fly/genebrief/microcephalin.htm

Pie Charts of Y Haplogroups and Mitocondrial DNA
Note that genetic diversity is highest in the area where *The Urantia Book* says that humanity's major changes occured.
http://www.scs.uiuc.edu/~mcdonald/WorldHaplogroupsMaps.pdf

Wikipedia: Microcephalin
Good source of general information and reference links.
http://en.wikipedia.org/wiki/Microcephalin

Wikipedia: Haplogroup F on the Y chromosome
Wikipedia maintains a database for the devlepment of genetics research. Haplogroup F on the Y chromosome, in particular, plays a key role in the parallels with *The Urantia Book*'s discussion about Adam and Eve.
http://en.wikipedia.org/wiki/Haplogroup_F_(Y-DNA)

Science, July 2006: Response to Comment on "Ongoing Adaptive Evolution of ASPM, a Brain Size Determinant in Homo sapiens" and "Microcephalin, a Gene Regulating Brain Size, Continues to Evolve Adaptively in Humans"
Abstract: Currat et al. present computer simulations to argue that the haplotype structure found at the microcephalin and ASPM genes can be better explained by demographic history rather than by selection. The demographic models they adopt, however, strongly contradict a decade of empirical research on human demographic history and do not account for the critical features of the data on which our argument for selection was based.
http://www.sciencemag.org/cgi/content/full/313/5784/172b

University of Chicago Chronicle, September 22, 2005:
Lahn's analysis of genes indicates human brain continues to evolve
Human evolution—in what has become our most important organ, the brain—is still under way, University researchers report in two related papers published in the Friday, Sept. 9 issue of Science. The studies show two genes linked to brain size are rapidly evolving in humans.
"Our studies indicate that the trend that is the defining characteristic of human evolution—the growth of brain size and complexity—is likely still going on," said lead researcher for both papers Bruce Lahn, Assistant Professor in Human Genetics and an investigator in the Howard Hughes Medical Institute.
http://chronicle.uchicago.edu/050922/brainevolution.shtml

Science News, September 9, 2005:
University Of Chicago Researchers Find Human Brain Still Evolving
Human evolution, University of Chicago researchers report, is still under way in what has become our most important organ: the brain. In two related papers, published in the September 9, 2005, issue of Science, they show that two genes linked to brain size are rapidly evolving in humans.
http://www.sciencedaily.com/releases/2005/09/050909221043.htm

Oxford Journal, February 24, 2004: Reconstructing the evolutionary history of microcephalin, a gene controlling human brain size
Abstract: The defining process in the evolution of primates and particularly humans is the dramatic expansion of the brain. While many types of genes could potentially contribute to this process, genes that specifically regulate brain size during development may be especially relevant. Here, we examine the evolution of the microcephalin gene, whose null mutation in humans causes primary microcephaly, a congenital defect characterized by severe reductions in brain size without other gross abnormalities. We show that the evolution of microcephalin's protein sequence is highly accelerated throughout the lineage from simian ancestors to humans and chimpanzees, with the most pronounced acceleration seen in the early periods of this lineage. We further demonstrate that this accelerated evolution is coupled with signatures of positive selection. Statistical analysis suggests that about 45 advantageous amino acid changes in microcephalin might have fixed during the 25–30 million years of evolution from early simian progenitors to modern humans. These observations support the notion that the molecular evolution of microcephalin may have contributed to brain expansion in the simian lineage leading to humans. We have recently shown that ASPM, another gene linked to primary microcephaly, experienced strong positive selection in the ape lineage leading to humans. We therefore propose that genes regulating brain size during development may have the general propensity to contribute to brain evolution in primates and particularly humans.
http://hmg.oxfordjournals.org/cgi/content/full/13/11/1139

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