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Is Decrypting the Genetic Legacy of America's Indigenous Populations Key to the Historicity of the Book of Mormon?

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Is Decrypting the Genetic Legacy of America's Indigenous Populations Key to the Historicity of the Book of Mormon?

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Abstract: *Some critics of the Book of Mormon suppose that the DNA characteristics of modern Native Americans should be compatible with "Israelite" rather than with Asian genetics. The authors point out that while DNA is a valid tool to study ancient and modern populations, we must be careful about drawing absolute conclusions. They show that many of the conclusions of critics are based on unwarranted assumptions. There are specific limitations that cannot be ignored when using the available genetic data to infer conclusions regarding the DNA of Book of Mormon peoples. Such conclusions are not founded on solid science but are the interpretation of a few, as genetic data fails to produce conclusive proof weighing credibly in favor of or against the historicity of the Book of Mormon.*

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See Ugo A. Perego and Jayne E. Ekins, "Is Decrypting the Genetic Legacy of America's Indigenous Populations Key to the Historicity of the Book of Mormon?," in *Ancient Temple Worship: Proceedings of The Expound Symposium 14 May 2011,* ed. Matthew B. Brown, Jeffrey M. Bradshaw, Stephen D. Ricks, and John S. Thompson (Orem, UT: The Interpreter Foundation; Salt Lake City: Eborn Books, 2014), 259–94. Further information at https://interpreterfoundation.org/books/ancient-temple-worship/.]

Background

Members of The Church of Jesus Christ of Latter-day Saints (i.e., Mormons or LDS) consider the Book of Mormon a volume of divine origin comparable in scriptural sacredness to the Bible (Article of Faith #8). They believe it to be an historical record originally engraved on golden plates, covering a period of approximately one thousand years (600 BC to 400 AD) and dealing with ancient people who lived in the American continent hundreds of years before the arrival of the Europeans. A small part of the Book of Mormon describes a different group of people of unknown Old World origin, called the Jaredites, disappearing (at least as a civilization) by the time the second group of migrants made their journey to the Western Hemisphere.

The main narrative of the Book of Mormon begins in Jerusalem with a family who escapes, by divine warning, the destruction of the Kingdom of Judah at the hands of the Babylonians approximately six centuries before the birth of Jesus Christ. With a few others, they are eventually guided on a journey to a non-specified region of America's double continent.[1] The descendants of this small original group later divided into two opposing factions, called the Lamanites and the Nephites, and the rest of the volume focuses mainly on the spiritual and social dynamics between these two groups, including their warfare. The recurring theme of the Book of Mormon is the coming of the Savior Jesus Christ first to the Old World, as witnessed in the Bible, followed by a brief ministry after his resurrection to a group of disciples who received him in the Americas. The book itself does not claim to be a complete history of these people but rather an abridgment made by Mormon, one of the last prophets in charge of the records, after whom the whole volume was eventually named. Further, the explicit purpose of many of the contributors to the records compiled in the Book of Mormon was to focus on spiritual rather than historical matters regarding the doings of their people.

Honest seekers of truth are invited to receive a spiritual confirmation of the truthfulness of the Book of Mormon within the scriptural text itself (Moroni 10:3-5). Still, at times some have wondered about the compatibility of the record put forth in the Book of Mormon with academic studies (archaeological, linguistic, anthropological, etc.) of the indigenous people and area of the Americas. There are some who promote strong criticism in this arena in an attempt to discredit the divine origin of the volume.

Recent attention has been paid to DNA data reported in scholarly papers written by scientists external to the Book of Mormon debate but

interpreted by some as the ultimate proof against the book's historicity. Others are even making claims about specific genetic lineages found in the Americas as a confirmation that the record is true. Overall, the complexities and limitations of the discipline of population genetics cannot be dismissed when attempting to use these tools to reconstruct the history of past civilizations. The questions treated herein examine the historical origins of the people described in the records of the Book of Mormon from a genetic point of view, making use of key principles of population genetics that cannot be neglected when undertaking such a study.

Introduction

The arguments of some critics of the Book of Mormon suppose that the DNA characteristics of modern Native Americans should be compatible with "Israelite" rather than with Asian genetics, as reported in scientific data demonstrating a strong affinity with the latter. In response to such criticisms, others have jumped at reports of pre-Columbian genetic lineages found in the Americas that could be ascribed to a Near Eastern origin as physical evidence of the existence of Book of Mormon people.[2] A key point is that arguments in favor or against the Book of Mormon narrative rely on genetic data gathered by researchers uninvolved with the Book of Mormon historicity issue. These studies were designed to offer new perspectives on the prehistoric origin and migrations of Native Americans. Contrary to the claims of critics, they fail to address historical events pertaining to the Nephites' record.

The stated time frame of The Book of Mormon covers ca. 600 BC to 400 AD, and the text explicitly states itself to be a record of the religious dealings of the people rather than a purely historical document. Scholarly studies on the genetic origin of the ancestors of Native Americans have been concerned most with the first waves of migrations that took place several thousands of years ago, toward the end of the Last Ice Age, across the exposed land-bridge called Beringia that once connected Siberia to Alaska. Thus the genetic data used by critics of the Book of Mormon address a time period many thousands of years before the time of the actual record. One may compare this case of "interpretive anachronism" to searching for news about the landing of man on the moon in ancient Egyptian papyri. However, it should be noted that if there were a large genetic contribution by a group of Middle Easterners, it would stand out in these sorts of analyses because they are analyzed in comparison to modern populations sampled from diverse geographical regions.

Nevertheless, these analyses have not ruled out a comparatively small contribution of ancestry from Middle Eastern groups.

Another factor worth considering in this context is that many Native American samples have some amount of post-Columbian European mixture. This mixture could confound putative evidence in support of the Book of Mormon narrative for some analyses (researchers often ignore any non-Asian DNA as definitively post-Columbian). In addition, recent publication of preliminary data from the remains of an individual dated 24,000 years ago, found in south-central Siberia and showing a possible ancient connection between Native Americans and Central/West Eurasia, is further complicating the admixture issue.[3] Nonetheless, the possibility of an arrival of a small group of migrants approximately 2,600 years ago to an already populated continent is not excluded by the reported genetic data.

Critics incorrectly insist that the LDS Church has taught for years that the American continent was uninhabited until the arrival of Book of Mormon people and that only recently, following the DNA debate, this position has changed. However, the LDS Church has not expressed an official opinion with regard to either Book of Mormon geography or population dynamics.[4] This, of course, does not preclude LDS leaders and scholars from sharing their personal opinions one way or the other, including several instances in which the concept of an already inhabited continent was shared prior to bringing forth the so-called DNA evidence.[5]

The main argument seems to stem from the introduction added in 1981 at the beginning of the Book of Mormon, which read that "after thousands of years, all [people] were destroyed except the Lamanites, and they are the *principal* ancestors of the American Indians" (emphasis added). Although the term "principal" already presupposes the existence of other ancestors without specifying whether the idea of ancient or modern ancestral contribution was intended in this statement, this was recently changed. The current edition of the Book of Mormon now reads "… all [people] were destroyed except the Lamanites, and they are *among* the ancestors of the American Indians" (emphasis added).

Although this change does not drastically affect the concept of heritage and ancestry of modern Native Americans in relation to ancient Lamanites, of greater importance is to understand the meaning of the term *Lamanite* as used in the latter part of the Nephite history. In the book 4 Nephi, the writer explains that following the visitation of the Savior to the Americas, the formerly warring people became united, without genetic or ethnic distinction among them: "There were no robbers, nor

murderers, *neither were there Lamanites*, nor any manner of -ites; but they were in one, the children of Christ, and heirs to the kingdom of God" (4 Nephi 1:17, emphasis added).

The record continues by stating that eventually there "were a small part of the people who had revolted from the church and *taken upon them the name of Lamanites; therefore there began to be Lamanites* again in the land" (4 Nephi 1:20, emphasis added). It is very likely that this choice of designation was social or religious rather than genealogical in nature, based on the character of the Lamanites prior to Christ's visit. In fact, 4 Nephi 1:36-39 reports that in a similar fashion, others decided to use the term *Nephites* again to distinguish them as "true believers of Christ" and restating that those that "rejected the gospel were called Lamanites" and were "taught to hate the children of God, *even as the Lamanites were taught to hate the children of Nephi from the beginning*" (emphasis added).[6] Here the use of the word "even" underscores the practice of choosing a name that had a specific social meaning in the past.

History is repeating itself, but the genetic distinction most likely no longer applies to the masses. Of note in this context are instances in the text of the Book of Mormon where Mormon himself twice declares his ancestry [as a genealogical descendant of Nephi (Mormon 1:5) and a "pure descendant" of Lehi (3 Nephi 5:20)], possibly supporting by inference the existence of outside populations contributing to the social dynamics of the people of the Book of Mormon.[7] As the term *Lamanite* loses its genetic meaning in the latter part of the Book of Mormon narrative, attempts to define an original *Lamanite* genetic signature are highly suspect, as the modern remnant of this ancient population would have to include both true descendants of Lehi's original party as well as others already inhabiting the land.

Critics who conclude the Book of Mormon to be fictitious in nature due to genetic data which fails to show "Israelite DNA" in the Americas must also consider logical and scientific reasons why such DNA could have existed in Native Americans at some point in history but may not be present or as easily detected in today's population. To rigorously examine the history of a people using genetics, all the tools of the discipline of population genetics must be embraced.

What some may refer to as the absence of genetic evidence does not preclude at all the real possibility that Lehi and his family were real people who actually left Jerusalem and established themselves on the American continent. In fact, as will be examined, it is very likely that either their DNA has disappeared over time, or it is present at such a low frequency

(due to mixing with other peoples) that the genetic methods to date have not detected it. In the event such DNA is found, it will most likely only be possible to ascribe it to these migrant groups only speculatively. Regardless, a DNA approach does not decisively and definitively fill in our void of knowledge of the happenings on the American continent during the time frame of the Book of Mormon. Both critics and apologists utilize speculations and assumptions to support their views. However, both sides of this controversy fail either to support or reject the authenticity of the Book of Mormon on the basis of DNA.

Evidence or Proof?

Stating that DNA evidence stands as the conclusive proof that the Book of Mormon is a fabricated historical account is not a convincing argument. Scholarly studies indicate that the majority of DNA observed in Native Americans has a common origin or ancestry with Asian populations, thus suggesting an ancient split between Paleo-Indians and their Eurasian source population sometime before the Last Ice Age. These population studies do not consider, however, the possibility of other migrations that could have taken place between the first entries of the early ancestors of Native Americans and the more recent documented European colonization after 1492.

The concept of additional, small-scale contacts and migrations to the Americas throughout the millennia is not dismissed by scientists. In fact, in recent years, genetic data was successfully sequenced from hair belonging to a well-preserved, 4,000-year-old, Paleo-Eskimo individual belonging to the Saqqaq culture discovered in Greenland.[8] This research has contributed greatly to the current understanding of events that led to the peopling of the Americas. The authors concluded that the genetic makeup of the ancient Saqqaq individual was very different from that of Inuit or other Native American populations. Instead, he was closely related to Old World Arctic populations of the Siberian Far East, separated from them by approximately two hundred generations (roughly 5,500 years).

These data suggest a distinctive and more recent migration across Beringia by a group of people who were not related to the first ancestors of modern-day Amerindians. In an interview, one author emphasized that the lack of genetic continuity between the ancient Saqqaq individual and the modern population of the New World Arctic stands as a witness that other migrations could have taken place that left no contemporary genetic signals.[9] In commenting about the findings of this project, population geneticist Marcus Feldman from Stanford University said

that "the models that suggest a single one-time migration are generally regarded as idealized systems, like an idealized gas in physics. *But there may have been small amounts of migrations going on for millennia*" (emphasis added).

He went on to explain that "just because researchers put a date on when ancient humans crossed the Bering Bridge, that doesn't mean it happened only once and then stopped."[10] This concept has also been included in the volume *The Origin of Native Americans* by Michael H. Crawford, molecular anthropologist at the University of Kansas. In his lengthy review of data supporting the ancient Asian origins of the Amerindians, he stated that "this *evidence* does not preclude the possibility of some small-scale cultural contacts between specific Amerindian societies and Asian or Oceanic seafarers" (emphasis added).[11]

Lastly, in discussing the difference between "evidence" versus "proof" Professor Daniel C. Peterson wrote that,

> The claims of Mormonism are, I think, … [n]ot so obviously true as to coerce acceptance, and not so obviously false as to make acceptance illegitimate.
>
> I can't agree with my fellow believers who imagine that the evidence for Mormonism is so strong that only deliberate, willful blindness can explain failure to be persuaded. But I also reject the claim of detractors of Mormonism, that its falsehood is so transparently obvious that only naked dishonesty or ignorance can account for failure to recognize it.[12]

Dr. Peterson's paradigm is easily adapted to the current discussion of "genetic evidence" vs. "genetic proof." The lack of genetic evidence or absence of strong affinity for "Israelite" genetic markers in Native American populations in no way approaches the level of *ultimate proof* of falsehood of the Book of Mormon. The lack of genetic evidence as examined in modern populations does not demonstrate proof of an absolute historical absence. This issue will be discussed in detail later in this essay.

Some critics propose a straw man construct superimposing an empty continent theory (i.e., the Americas were completely unpopulated prior to the arrival of the Book of Mormon people in 600 BC) as the basis of belief from which Mormonism stems regarding Book of Mormon populations and their origins. By such reasoning the lack of a pervasive Israelite genetic profile in pre-Columbian Native American populations must be viewed necessarily as the ultimate proof that the Book of Mormon is a product of

nineteenth-century fiction. With this strategy, critics purposely engineer the background they want others to accept at the outset in order to have a strong case based on genetic evidence. Many fallacies arise from this approach that will be treated in detail herein. Suffice it to say, as with archaeological, linguistic, and anthropological evidence, DNA cannot be used to support or to discredit the true historical nature of Joseph Smith and his purported acquisition and translation of ancient gold plates.

Honest seekers of truth will be wary of dogmatic statements that proclaim absolute authority on a topic and call it closed. Often these statements are based on personal interpretation that can be shown to have logical lapses and are given without careful regard for the complexities of the topic at hand. At times it is helpful to understand something about the nature and motives characterizing those bringing forth such claims.

What Does Science Say About the DNA of Native Americans?

The early 1990s marked the beginning of the genomic era with regard to the study of human diversity and the elucidation of the relationships and origins of different world populations. With the best technologies available in those early days, scientists for the first time were able to analyze segments of the female-inherited mitochondrial genome and to identify small but important genetic markers uniquely linked to specific populations.

Subsequent to this novel use of mitochondrial DNA (mtDNA), new technologies ushered in the study of genetic markers found on the male-inherited Y chromosome and the autosomes, giving sometimes distinct insights into populations origins and migrations. With regard to mtDNA, the first samples analyzed came from Native American populations. The data showed that nearly all the mtDNAs could be clustered into one of four groups, which were initially labeled A, B, C, and D, and later groupings identified in other populations proceeded through the subsequent alphabetical nomenclature.[13]

These earlier studies utilized a small section of the mitochondrial genome, often limited to just a few hundred DNA bases. Among others, three significant findings were published during the 1990s based on mtDNA diversity with some implications to our understanding of Native American origins:

1. The highest level of mtDNA variation was observed in sub-Saharan African groups, thus indicating that all humans shared a common female ancestor from Africa and that human colonization of the planet started from there;

2. Lineages A, B, C, and D were observed in the Americas as well as in modern Asian populations, thus supporting the theory that the ancient maternal ancestors of Native Americans were Paleo-Indians of Asian origins who survived the Last Ice Age on the continent-sized land-bridge called Beringia that once connected northeast Siberia to Alaska;[14]
3. A fifth lineage was observed in Native American populations from the Great Lakes area and in a few other North American groups. This new mtDNA was termed X, and differently from the previously known Native American mtDNA lineages, it was also observed in many modern European, African, and Middle Eastern populations[15] as well as in a small region of Central Asia.[16]

These three points have strong implications with respect to the Book of Mormon debate, but the most emphasized in early disputes was point 2 — the common presence of lineages A, B, C, and D in both the Asian and American continents. Each of these three findings deserves its own treatment in detail.

The existence of a common maternal ancestor from Africa for all mtDNA lineages has many significant implications; of relevance for the current question is the fact that this woman was not the only female alive at that time, but merely lucky in perpetuating her genetic lineage through millennia to the present time. (This was due to several factors, including her own success and the happenstance successes of her descendants.) The phenomenon of chance transmissions will be addressed in detail when we introduce the population genetic principle of *genetic drif*t. For the current discussion, it is sufficient to realize that the genetic variation present in modern populations does not give a complete picture of the variation that existed in the past.

The second relevant principle is the presence of mitochondrial DNA lineages labeled A, B, C, and D on both sides of the Bering Strait. As explained earlier, based on data from different disciplines, including genetics, archaeology, and linguistics, it has been postulated that anatomically modern humans were trapped in the landmass that once connected Siberia to Alaska during the Last Ice Age.[17] These Paleo-Indians most likely came from other source populations in Asia during the spread of hunter-gatherers thousands of years ago. By following and hunting large mammals, they reached the continent-sized land-bridge

Beringia but were eventually trapped there due to the worsening of climate conditions and the build-up of glaciers on either side.

During the following millennia, they probably survived in natural enclaves, living in a manner similar to modern-day Arctic natives. Population growth was probably halted because of scarcity of resources. They were physically separated from their source population, thus gradually developing their own unique linguistic, cultural, and genetic characteristics.[18] Eventually, the climate began to improve again, and the large glaciers started to withdraw.

As sea-levels began to rise again, gradually submerging Beringia and most of the world's coastlines, at least one, perhaps two entryways became available to the ancestors of American natives moving eastward into a pristine and empty continent.[19] Lack of competition for resources allowed a quick spread southward, reaching the tip of South America's southern cone (a distance greater than that from Portugal to Japan!) probably in as few as 1,000 years. Populations began to grow, and by the time the Europeans arrived after 1492, at least 20 million people lived in the Americas.[20] This summary reflects the knowledge based on genetics, archaeology, and other disciplines to the proposed understanding of the first and most significant expansions into the Western Hemisphere.

Although genetic diversity in Asia is much higher than that observed among the indigenous people of America — and also includes significantly different lineage frequencies — it is notable that those who survived the Beringia "imprisonment" were but a few compared to the larger Asian population of that time.

Once the two populations were separated, never to be reunited — first because of the deteriorating climate conditions and then by the Bering Strait — gene flow between the populations was interrupted, and their genetic histories diverged. Once populations become physically separated in this manner, powerful forces play a role in how the genetic dynamics of different populations develop over time. Even holding geographical and climate conditions constant, events that influence the genetic shaping of a group play out in a distinct story for every population.

Genetic drift and perhaps to some degree natural selection with regard to DNA transmission, gender (based on the inheritance of Y chromosome or mitochondrial DNA), and variation in number of offspring, etc., give shape to the resulting genetic profiles of populations as they develop over time. Often, if the group of founding migrants is small, the effects of drift that persist into future generations are accentuated, as the loss of even a single individual from the small founding group, or a

female bearing no children or children of just one gender, will cause the loss of genetic variability at an early stage of the colonization process. For example, when considering mtDNA passed on only by females to their children, if an original founding group is composed of four women, each carrying a different mtDNA lineage, and one of them bears only male children, 25% of the mtDNA variation in the founding population will be immediately lost from all subsequent generations.

Although the founding group of ancient Paleo-Indians trapped in Beringia for thousands of years would have included more than four women, this process can occur in subgroups of a population and could result in lost lineages that are still found among Asians but that are not currently found among Native Americans. Additionally, the separation of Paleo-Indians from their source population for such a long period resulted in the rise of novel mutations that were exclusively found in the ancestors of Amerindians.

From a strictly mitochondrial DNA point of view, a Native American mtDNA lineage is so distinct that it is easily distinguishable from those of any other world population. In fact, the level of discrimination allows clear discernment of Asian and Native American types that are relatively closely related but that have both amassed enough unique features since their divergence to give a strong degree of differentiation between the two. For example, if an mtDNA profile carrying the key mutations classified as Native American is found in Europe, one obvious argument is that early European colonists brought back indigenous women from the Americas to the Old World, whose descendants persist to the current day. These lineages are clearly not European, but neither are they Asian. They are Native American.

The opposite is also true. If mtDNA lineages are observed in the Americas, even in tribal groups considered deeply indigenous who belong to mtDNA groups known to be African, European, or even Asian, the argument most readily given is that they have been introduced more recently, after the rediscovery of the New World by Europeans.

Therefore, going back to the question posed above, a Native American lineage is an mtDNA profile that has accumulated a unique set of mutations that, although showing evidence of common ancestry with Asian populations, is different enough to be ascribed exclusively to the Americas and not to Asia. In other words, Native American mtDNA lineages are, for the most part, nested within the large family of Asian mtDNAs, and are distantly related to them (or showing an affinity) but not identical.

An increased understanding of the dynamics that characterized the mtDNA origin of Native American populations was achieved during the past decade through the analysis of complete mtDNA genomes — the highest level of mtDNA molecular resolution attainable. The original A, B, C, and D mtDNA lineages observed in the Americas were eventually renamed A2, B2, C1, and D1 to distinguish them from their Asian "cousins." Lineage X became X2a, and to this day it has been found only in North America, although there is still some uncertainty regarding its origin. These five lineages constitute the majority (approximately 95%) of all Native American lineages observed in the Americas, although in recent years, additional rare lineages also have been identified as Native American.[21]

At the present time, thanks to the complete sequencing of large numbers of mtDNA genomes, scientists performing research of worldwide populations are dissecting individual mtDNA lineages to discover important details missed in the past. This microgeographic approach is revealing a number of peculiar situations that, for the most part, are still not fully explained. For example, mtDNA lineage C1 has six known sublineages, called C1a-f. They all share a common maternal origin, but their geographic distribution is very specific: C1a is found exclusively in Asia, C1b, C1c, and C1d are found only in the American continent,[22] and C1e and C1f are two new lineages found recently in a limited number of living individuals from Iceland[23] and in ancient remains retrieved in Western Russia,[24] respectively.

The natural question is, how did the four geographically distinct clusters end up in the locations where they were observed? A possibility is that they were all in Beringia at some point, and following the Last Ice Age, carriers of the C1a and C1f mtDNA returned to Asia,[25] whereas C1b-C1d and possibly C1e moved eastwards in the Americas. Eventually, either through an Atlantic crossing along the north ice cap or, more recently, through Viking voyages,[26] a Native American female (or females) carrying the C1e lineage ended up in Iceland, where successful progeny have persisted into today's Icelandic population. However, any C1e left in the Americas either failed to perpetuate its lineage by chance due to lack of female posterity or became extinct following the massive population reduction caused by the arrival of Europeans.

Another possibility for its sole distribution in Iceland hinges on its extreme rarity as a mtDNA type, and therefore scientists have not encountered it yet on American soil.

In summary, the recent discovery of C1e in Iceland, its pre-Columbian mtDNA age, and its apparent absence among modern Amerindian groups poses some interesting questions that can be applied to the Book of Mormon debate. Would it ever have been known that an additional C1 lineage existed in America's past if it were not found in Iceland? This situation demonstrates a possible scenario in which a Beringian lineage of Asian origin could have become extinct in the Americas, and detection of the genetic type could have been accomplished only due to its having had more time to spread to outlying geographies, causing it to be external to competition with the abundant contemporary mtDNA Native American lineages.

Similarly, a more recently introduced mtDNA lineage from the Old World, as in the Book of Mormon scenario, would have been even more likely to disappear or escape detection when introduced to a large gene-pool. We will discuss this further in the section about genetic drift.

A far more puzzling story surrounds the origin of the fifth Native American lineage, called X2a. This group of mtDNAs is found exclusively in North America, with its highest modern-day concentration in the Great Lakes region.[27] While Native American mtDNAs A2, B2, C1, and D1 are clearly nested within Asian clades, lineage X2a has a hypothesized ancient Old World origin, probably in the Middle East.[28]

Although a small number of X2 samples have also been observed in Central Asia,[29] they most likely represent a recent migratory event to that region. In an mtDNA tree, the Asian X (called X2e) contains more recent mutations than the Native American X2a, and therefore it is not ancestral to the latter. Although it cannot be completely excluded that ancestors of X2a once lived in Northeast Asia and then became extinct, at the present time the closest relatives of the Native American X2a lineage have been identified in a single sample from Iran[30] and in Bedouin groups from Egypt.[31]

The potential connection between New World and Middle Eastern mtDNA X types could be seen by some as a candidate for Book of Mormon DNA in the Americas. However, some data confounds this hypothesis, as the mtDNA molecular clock[32] — the estimated average number of years before a mutation is expected to appear — dates X2a at about the same time as the arrival of all the other Asian-like lineages to the Americas (toward the end of the Last Ice Age). Data from ancient DNA studies on pre-Columbian specimens presumably belonging to lineage X are, for the most part, also inconclusive.[33]

As an additional cautionary note, mtDNA dating is concerned most with the age of divergence between two lineages sharing a common ancestor and not necessarily the location of the shared ancestral sequence. In other words, the coalescence time of X2a,[34] or of any other mtDNA lineage for that matter, reveals only how far back in time the split from the ancestral node took place, not where the split occurred and does not account for the geographic locations of these lineages today.

As seen with the C1e example, there could have been closer relatives of X2a in other parts of the world, but either they became extinct or have not yet been found. The Egyptian and Iranian X2* samples share one of the three coding region mutations that define X2a in the Americas. Their existence indicates that potential "relatives" of the X2a lineage could be found elsewhere, assuming they still exist in contemporary individuals.

However, in this particular example, it is important to note that the Old World X2* haplotypes share additional mutations that would increase the genetic distance between the Amerindian and Middle Eastern branches of X2, even with the shared common conservative mutation. The story of X2a is a likely example of an mtDNA lineage found in the Americas that to this date cannot be completely ascribed to an Asian origin and is a subject worth further investigation.

Perhaps the greatest challenge faced by scientists is to be able to assign clearly and unequivocally any European or African lineage found in the Americas to the pre-Columbian era. The generalized view among population geneticists is that after the initial arrival of Paleo-Indians toward the end of the Last Ice Age, no other migrations took place until the discovery of the double-continent by Europeans in 1492.

Together with a drastic indigenous population reduction (addressed in detail in the section dealing with the effect of *population bottleneck*), first the European and later the African gene-pool were introduced to the Americas, thus altering forever the original genetic landscape of the Western Hemisphere. Therefore, the common consensus, whenever any DNA is found that does not fit with the classic Native America genetic types, is an automatic assignment of such DNA to the post-Columbian migration wave of European or African migrants.

Although this assignment may be accurate in most instances, few tools are available to test the assumptions underlying this assignment; this means that even in the unlikely scenario that a few genetic lineages survived to modern times from additional migrations that occurred in the pre-Columbian era, they would not be strongly differentiated from contemporary DNA profiles found in modern Europe and Africa.

This is a critical and often overlooked limitation in using DNA to try to isolate a migration by a small group to the Americas in the recent past. If we take mtDNA, for example, it is correct to say that more than 95% of lineages identified are of Asian origin for the simple reason that they are similar to — but at the same time sufficiently different from — Asian lineages due to the fact that they have been separated for enough time to develop their own set of unique mutational motifs. If a modern Asian lineage were to be found in the Americas, it would most likely be assigned to a post-Columbian arrival, just like any other non-indigenous mtDNA profile. The root of this issue lies with the so-called "molecular clock" used to determine the age of lineages.

Scientists have been able to calibrate the estimated time of entry of the first Paleo-Indians based on the number of mutations that separate the Native American lineages from those found in Asia today (using molecular clocks).

Dating of the genetic data supporting this first arrival coincided with the geological evidence from the improvement of climate conditions toward the end of the Last Ice Age, at about 15-18,000 years ago. This molecular clock is based on the number of mutations accumulated in each mtDNA lineage, and it is calibrated on the assumed common ancestor between modern humans and chimpanzee, a split from their common unknown ancestor (the "missing link") that would have occurred approximately 6.5 million years ago.

The mutation rate of mtDNA is roughly 3,000-9,000 years per mutation, depending on the section of mtDNA analyzed and the molecular clock applied.[35] Therefore, with few exceptions, it is only possible to infer migrations and other events that occurred thousands of years ago and not more recent ones.

Moreover, scientists in general are extremely cautious to make statements based on the available data that unequivocally point to a single conclusion and leave no room for an alternative hypothesis. Nearly all scientific papers published on population migration subjects offer new clues or revisit old ones, with the objective of furthering scholarly work by contribution of new perspectives and data that other researchers will utilize in their own work.

However, this is often not the case when the same information is then represented by the media or by others with a specific agenda, as they tend to sensationalize such discoveries in order to attract greater attention from the public. Unfortunately, as with any sub-specialized topic, a relatively small percentage of the population has the necessary

background to fully grasp the original scientific work, and therefore they often have to rely on how this information is interpreted and propagated, and this includes all the involved biases.

In summary, it is an oversimplification to assert that all DNA in the Americas is provably Asian. The large majority shows Asian affinity simply because it is similar enough to demonstrate a more recent shared ancestry with Asian populations than other worldwide populations but has enough accumulated differences to be distinctively identifiable as Native American DNA. Based on scientific investigation, this main genetic component was introduced in the Americas at the end of the Last Ice Age thousands of years ago.

A particular lineage called mtDNA X does not appear to be of Asian origin: it is more closely related to ancient Near Eastern lineages, but there is not enough evidence to link it definitively to Book of Mormon people. Unless retrieved from ancient specimens, any other unusual DNA types found in the Americas are generally ascribed by scientists to later colonization events. However, as the following points will clearly show, the hypothesis that makes the fewest assumptions (*lex parsimoniae*) based on the principles of populations genetics is that any unusual DNA types that arrived in a recent small migration to the Americas would most likely not be detectable in our present time.

What Did Lehi's DNA Look Like?

A major limitation that prevents the identification of genetic signatures that could be tied to Book of Mormon people is the obvious fact that this genetic signature is not known in the first place, although based on modern and ancient DNA studies, it is possible to determine a genetic lineage that could approximate a "typical" Near Eastern type.

While this may be the case, it must still be acknowledged that virtually any individual DNA profile could be found in any population, although at different frequencies. For example, the male Y chromosome type known as lineage J and the female mitochondrial DNA family U/K are found at high frequencies in the Middle East. However, these lineages are also found in smaller numbers in other countries, and conversely non-typical Middle Eastern lineages are also found in the Holy Land and surrounding countries, albeit in low frequency.

From a genetic viewpoint, there are a larger number of distinct mtDNA lineages observed in a single population than there are unique lineages in a particular population when comparing two or more groups.

This means that anyone from any region of the Old World could have carried virtually any mtDNA lineage to the Americas.

As an example, one of the authors of this paper, Ugo Perego, is nearly 100% European based in his overall DNA makeup (autosomal),[36] but his paternal line belongs to the Y chromosome family C, which is typical of Asia, North America, and Oceania.

The frequency of this particular genetic lineage in the Mediterranean Basin approaches zero. It appears that the introduction of this DNA marked as Asian in Ugo's family is quite ancient and perhaps attributable to the invasion of barbaric groups to Europe between 400 and 600 AD.[37]

There is no genealogical record to confirm this information, only speculation based on history and the available DNA in his particular family. If he were to relocate to Asia today, and someone were to find his skeleton and extract his DNA two thousand years from now, based on the Y chromosome data alone, they would believe that he was indigenous to Asia and not a migrant from Europe.

Additionally, this is also a helpful example that demonstrates the presence of an ancestor of Asian origins (through the Y chromosome) whose autosomal DNA failed to survive in Ugo's current genetic makeup. If a single individual or a relatively small number of people mixed with a large pool of Southern Europeans, their DNA would likely disappear over time, even though their genealogical ancestry would remain.[38]

The problem with not knowing the DNA of Lehi and his group is a situation that in forensics would be categorized as the absence of specific information. First, it would be impossible to recognize their DNA even if it survived genetic drift and population bottleneck. It could be something similar to other Asian lineages, or it could be European or Middle Eastern. It could be nearly anything.

It is possible that the DNA of Lehi's group is one of the most prominent lineages in the American continent but that we do not recognize it as such due to lacking knowledge of their mtDNA profile. Second, any attempt to link DNA in the Americas that might look like a potential candidate for Book of Mormon people (e.g. mtDNA lineage X found in northern North America) would likewise result in further speculation for the same reason. The small group that left Jerusalem to embark on a journey to a new land was not selected based on their genetic uniqueness, or because they represented the typical genetic signature found in their homeland.

These people were unaware of their genetic profile, and so are we. This fact alone would seriously compromise any effort to bring forth

DNA as evidence that they never existed or that the Book of Mormon is not the religious and historical record it claims to be. One could ask, "What would Lehi's DNA have looked like?" but no testable hypothesis answers this question.

Population genetic studies are based on statistical evidence, but they are weak when evaluating rare occurrences in the sampled population. If we were trying either to detect or measure the amount of genetic contribution from Book of Mormon people, the hypothesis to be tested would be not how much Middle Eastern DNA is observed in the pre-Columbian native population, but rather how much DNA from Lehi's or other groups survived to our day. In other words, what is the frequency of rare lineages that could be confidently assigned to them? We can attempt to determine a Middle Eastern DNA contribution to the Americas (a population-based approach), but we don't have the tools to determine the contribution of Lehi's family DNA in the same area (a family/pedigree-based approach). Therefore, we have to be careful to avoid confusing the absence of confidently recognizable Old World DNA in the Americas with the assertion that Lehi's party never existed.

No matter how large or small they eventually became as a people in the American continent, we are still talking about a very small initial group with extremely limited genetic variation that would not constitute a large enough sample of their native population to ensure that the genetics of the Middle East would be properly represented in the New World.

What is Genetic Drift?

While several genetic principles, limitations, and possibilities have been explored at length herein, possibly the single most influential factor that would prevent detection of Lehi's DNA in both modern and ancient samples is the concept of genetic drift.

For the sake of modeling, assume that Lehi and the members of his family carried the most representative modern Middle Eastern genetic profiles, a paternal Y chromosome belonging to lineage J for the males, a mtDNA K female lineage, and nuclear DNA packed with genes and markers typical of the Old World.

The only way these Middle Eastern markers would have survived past the first few generations in the American continent would be in the unlikely event that they were successful in being an isolated population with limited mixing with the hosting population.

The abridged history contained in the Book of Mormon gives only a few sporadic details about the whereabouts of its people with regard to

potential interactions with any other groups.[39] If the hypothesis we are trying to test is whether the party from Jerusalem really existed, we must take into the account their group size and the estimated population count in the Americas at their arrival.

Exact information on both issues is unknown, but a fair guess about proportions can be attempted. Lehi, his family and the others who came along were probably no more than 30-40 individuals, representing two, perhaps three family nuclei:

1. Lehi, his wife Sariah, and their children Laman, Lemuel, Nephi, Sam, Jacob, Joseph, and some sisters;
2. Ishmael's widow and her children;
3. Zoram, the servant of Laban.

It is even more speculative to infer much about the genetics of surviving Jaredites (if any) and Mulek's group, since the Book of Mormon is silent about their population of origin.

Mulek is presented as one of the geneaological heirs to the Jerusalem throne, but nothing is recorded about the number and origins of those who eventually sailed with him to the Americas. Since many assumptions are already made about the group size and the genetics of the main characters of the Book of Mormon, the following considerations will be based exclusively on the hypothesis that these were real people and made it to the American continent.

What would have happened to their DNA after their arrival? A well-considered argument comes from Henry C. Harpending, Distinguished Professor of Anthropology at the University of Utah. When asked, "If a group of, say, fifty Phoenicians (men and women) arrived in the Americas some 2,600 years ago and intermarried with indigenous people, and assuming their descendants fared as well as the larger population through the vicissitudes of disease, famine, and war, would you expect to find genetic evidence of their Phoenician ancestors in the current Native American population? In addition, would their descendants be presumed to have an equal or unequal number of Middle Eastern as Native American haplotypes?"

Professor Harpending's reply was, "I doubt that we would pick up [evidence of the Phoenicians] today at all, but it does depend on how they intermixed once they were here. If they intermixed freely and widely, and if there were several millions of people here in the New World, then the only trace would be an occasional strange stray haplotype. Even if we found such a haplotype we would probably assume it was the result of post-Columbian admixture."[40]

The natural process of DNA markers disappearing in populations over time is called *genetic drift*. The concept of genetic drift is partly based on the inheritance properties of DNA. With regard to markers received from one parent only (Y chromosome and mitochondrial DNA), inheritance is contingent on whether or not you have offspring of the "right" gender. If a couple has only girls, none of them (and therefore no posterity) will receive the father's Y chromosome. If a couple has only boys, they will all receive the mother's mitochondrial DNA, but none of the grandchildren will inherit it.

The situation is different for autosomal DNA, the twenty-two pairs of chromosomes, excluding the X and Y chromosomes. This part of the nuclear genome is subject to reshuffling at each generation, with the loss of substantial components of the parents' genetic make-up. In fact, when a man and a woman have a child, she will receive fifty percent of each of her parents' autosomal DNA. Consequently, the remaining part of her parents' DNA will be lost unless the couple has more children.

Over just a few generations, potentially all of a couple's genetic material will be diluted and lost, as they will represent an ever-smaller percentage of the ancestors contributing to the DNA of a single descendant. Simply stated, as with the previously-mentioned example of Ugo's autosomal DNA, there is a considerable difference between being genealogically related and having a genetic inheritance. In fact, it is estimated that at the tenth generation level, and given an equal chance to propagate their autosomal DNA, a person would carry only 12% of his or her 1,024 ancestors' DNA.[41]

This phenomenon can be observed in as few as a couple of generations at a family level, but the effects of genetic drift at the population level are even more drastic. Depending on the population size and the variety of DNA present in that population, over a time measured in generations, some of that variation will inevitably be lost due to chance.

Even when a hypothetical population made up of only two ancestral lines, lineage A and lineage B, are found with the same frequency in a given hypothetical population (therefore having the same initial probability of perpetuating through future generations), over time one or the other may disappear completely. It is comparable to the probability of tossing a coin and knowing you have a fifty percent chance of obtaining heads or tails. The probability is based on the number of potential outcomes (either head or tail), but with one hundred actual tosses it would be unlikely that the final result would be exactly fifty heads and fifty tails.

With DNA, you start with a specific set of genetic markers at one generation, and through mating and random segregation of variants, generation 2 will have a somewhat different representation of the DNA markers than generation 1. Generation 2 will provide the only gene-pool available, which will be responsible for the variation of generation 3 and so on. If we could compare DNA variation of a starting gene-pool to one hundred marbles of two colors, fifty red representing lineage A and fifty blue representing lineage B, where marbles are drawn randomly, recorded, and placed back in their box with the purpose of determining the colors of a new box of marbles, chances are that the new box would have a different color composition than the one used to create it.

For example, during the first one hundred draws, sixty blue and forty red marbles may be obtained. To create a third box, we would repeat the exercise using the marbles of the second box. Drawing one hundred times from box 2 could very easily produce an even larger number of blues for box 3 than reds. As we continue this exercise, box after box, or generation after generation, it would not be an unusual outcome to end up with a box with all blue and no red marbles.[42]

While the example of the marbles is a purely statistical approach to what could happen to a population made of only two different lineages having equal starting frequencies, when modeling the dynamics of questions of DNA and the Book of Mormon, we face even more confounding variables. In fact, it is estimated that at the time of its rediscovery, the American double-continent may have had a larger population than Europe. It is difficult to guess the population size of the Western Hemisphere at the time of Lehi's arrival, but it probably would have been in the order of a few millions, considering that humans have been here at least since after the Last Ice Age.

From a numerical point of view, the arrival of Lehi and his group would be comparable to a drop of ink in a swimming pool. However, in the swimming pool, although nearly impossible to detect, the actual drop of ink is present. The difficulty in recognizing the drop of ink is determined by the availability of instruments sufficiently sensitive to detect its minuscule presence within the much larger body of water. This analogy does not extend perfectly to DNA and inheritance at the population level. Although the group of Old World migrants was small (a drop of ink), the DNA may have survived (or not) to the present time — due to the forces of genetic drift. If it disappeared, it would be as if someone removed the drop of ink from the swimming pool such that it seemed never to have been there in the first place. Of course, this would

be heavily dependent on the level of isolation the Book of Mormon party experienced — something not clearly stated in the narrative.

In the case of almost immediate admixture with locals, returning to the model of the colored marbles, the earlier exercise would be repeated, drawing from a box with one million blue marbles and five red ones. As marbles are randomly selected to create the second generation, what is the likelihood that red marbles are selected by chance to perpetuate their color to future generations?

From a cultural or linguistic point of view, even a small group of migrants may play a significant and lasting impact on the host population, but genetic signatures are different. Even if we know the family lines several generations in the past, the DNA of a specific ancestor, depending on the markers studied, can readily disappear. This can happen even in a single generation.

For example, in just three generations, both the Y chromosome of the paternal grandfather and the mitochondrial DNA of the maternal grandmother could not be transmitted to their descendants. On average, twenty-five percent of the grandparents' autosomal DNA will be inherited by their grandchildren, with a range that would go from zero to fifty percent. Some traces of the autosomal DNA may persist over generations, but this will become more diluted over time and, depending on the roll of the dice with each new generation, may be nearly extinguished at some point.

In other words, genetic lineages were and are continually lost randomly in the world among all living species, even when there is no selective factor operating or the environment would not favor any specific lineage to be the likely surviving candidate in future generations. However, when dealing with a disproportionately larger hosting population, the odds are against the chances of genetic survival in the colonizing population. Depending on the size of the migrant group and the timing of admixture, the probability approaches zero. This of course also depends heavily on the level of intermixing between hosting and colonizing groups, which will be addressed when discussing the process of *natural selection*.

It is important to remember that genetic drift is a natural phenomenon that is central to study of the population genetics of all organisms. It is not exclusive to the Book of Mormon discussion. It affects all genetic markers: mtDNA, the Y chromosome, and autosomal DNA. A powerful example of the effect of genetic drift on a population was described in a classic study of the Icelandic people, where genealogical and historical

records have been available for the past three centuries, providing opportunities for comparison to the genetic data observed in the modern population.[43] This study demonstrated that the majority of individuals living in the eighteenth century did not have any living posterity, whereas a small percentage of the population during the same time period is responsible for nearly all living Icelanders today. The findings gleaned in the Icelandic study can be extrapolated to any population around the world, including Native Americans, keeping in mind that genealogical and historical records are often not available elsewhere. The impact of the European conquest in the shaping of the genetic dynamics and demographics of the New World would have exponentially accentuated and aggravated the effects of genetic drift in the Americas.

The Effect of Population Bottleneck

By the time Christopher Columbus discovered the Americas in 1492, perhaps as many as one hundred million inhabitants could have populated the entire double-continent.[44] The clash with Europeans settlers, followed by disease, slavery, and warfare, resulted in a population decline of tremendous proportions.

Molecular anthropologist Michael Crawford states in his volume *The Origin of Native Americans: Evidence from Anthropological Genetics* that "the conquest and its sequelae squeezed the entire Amerindian population through a genetic bottleneck. The reduction of Amerindian gene pools from 1/3 to 1/25 of their previous size implies a considerable loss of genetic variability."

He also added that "it is highly unlikely that survivorship was genetically random."[45] Eventually, starting in the eighteenth century, native groups began to increase in size again, even reaching some of the original numbers in certain areas. However, the variation previously seen in pre-Columbian genetic lineages would never be replicated again.

Simply stated, a population bottleneck is the decrease in number of individuals (or genetic lineages) in a population following migration, natural disasters, disease, or warfare. The small number of survivors will carry only a fraction of the genetic diversity from the original population. Their posterity, no matter how large it could become in subsequent generations, will carry the DNA of only those living through the catastrophic event, thus not representing all the genetic variation once found in the whole population.

The arrival of Europeans to the Americas in the fifteenth century was orders of magnitude worse than the combined effect of the Black

Plague and the Spanish Influenza on Europeans. The consequences of rapidly reduced population and displacement has forever altered the demographic landscape of pre-Columbian America such that scientists from many disciplines are considerably limited in their ability to draw conclusions about the history, including the genetic history, of the New World. To model such an event, suppose that after an epidemic of smallpox, a hypothetical village of a thousand individuals experienced a ninety percent reduction; the one hundred surviving subjects may or may not include at least one representative of all the original group genetic lineages. Although survival of many diseases also involves a genetic component,[46] Y chromosome and mitochondrial DNA variance have little known or no influence at all on the immunity of an individual affected by one of the several diseases Europeans brought to the New World.

With selection playing little or no recognizable role on specific ancestral lines, the drastic population reduction in the hypothetical village inevitably would have affected the number of surviving genetic lineages. Of course, the initial impact with Europeans was so severe that entire tribal groups, particularly on the Atlantic side of the Americas, were completely decimated, leaving no genetic trace of their existence. Native Y chromosomes were quickly replaced by those from the Old World, and mitochondrial DNA variation was greatly reduced.[47]

In the unlikely scenario that the descendants of the few migrants described in the Book of Mormon were able to "survive" genetic drift and therefore transmit a modest genetic signal to future generations, the devastating conquest by Europeans in the 16th and 17th centuries has created a situation in which even the most experienced researchers admit the limited knowledge available to properly infer the complete history of the pre-Columbian era.

However, this would not be the only event affecting population bottleneck among the Nephites. In fact, the Book of Mormon itself describes at great length two additional major events that, presuming historical accuracy, would have had a tremendous impact on the survival of any genetic lineages carried to the Americas by any of its original groups.

The first event took place after the biblical account of the crucifixion of Jesus Christ in Jerusalem. Only one of the Gospels of the New Testament briefly mentions the geological events experienced in the Holy Land following the death of Christ.[48] Concomitantly, in the Western Hemisphere, far greater destructive natural forces were witnessed as

recorded in 3 Nephi chapter 8, with entire cities being destroyed and the geographical landscape becoming greatly changed. The extent of destruction over the whole American continent is not known, as the writer in the Book of Mormon was likely mostly limited to his immediate radius. However, since this debate concerns the genetics of Book of Mormon people, it is not unreasonable to think that such devastation and loss of life would also have had a great effect on the survival and transmission of any Old World genetic lineages to future generations.

Finally, in conjunction with the natural destruction described in the Book of Mormon at the time of the death of Jesus Christ in the Holy Land is the targeted elimination of people referred to as Nephites through massive warfare starting in the 4th century AD.

It is a difficult task to estimate the level of admixture experienced by the descendants of those that came from Jerusalem around 600 BC, but from the population growth described occasionally in the Book of Mormon, it could be that the Lamanites were more consistently absorbed with locals than the Nephites.[49]

The Bible itself perhaps supports this assertion, as it is rich with examples of those who placed little importance on covenants with God and how they were more easily infiltrated and adopted practices, often mixing with the people surrounding them. This may allow suggestion that because of the religious character of the Nephite people as a whole, they may have had some success in maintaining a fraction of their ancestors' genetic integrity. The great war that resulted in their nearly complete annihilation would also have had a negative effect on the survival of their Old World DNA, if any at all persisted to the time of the end of the Book of Mormon narrative. Of course, at that time, as already discussed, the terms *Nephite* and *Lamanite* were mostly used as cultural rather than genetic terms.

Natural Selection

Although genetic drift and population bottlenecks are likely the two primary causes of why DNA from a purported Old World migration 2,600 years ago is not found in modern-day American natives, another perspective should be considered, albeit probably not as influential as the previous two. Consider that early humans have migrated from place to place for thousands of years in a process that resulted in the colonization of the whole planet. The initial driving force to move was simply the need for survival. If a population nucleus outgrew the resources of a particular

area, they would probably starve or become a few people left searching for new means of survival.

A gradual expansion into new unoccupied regions allowed the newcomers to adapt to different environments and master new survival skills. Naturally, some individuals would have characteristics better suited to adaptation than would others. In genetics, this is known as degree of fitness, or in other words, possessing the right genes for the right surroundings so that climate, food tolerance, etc. would allow some to live longer and become stronger, thus increasing their chances for reproduction and passing their "more-fit" genes to future generations.

However, as climate conditions changed, or a move was necessary, those more fit in the previous environment may have later become genetically disadvantaged. Through this process of gene selection, the best genetic make-up for a specific environmental background would end up as the predominant gene pool for a specific population. Less fit genes would tend to disappear over time.

Natural selection is a well-established population genetic principle which has been observed among many species and organisms, including humans. This natural process has recently been recognized as influential in the Black Death that was responsible for the death of one out of four Europeans in the 14th century. Recent genetic studies on remains from that period revealed that the bacteria that caused the bubonic plague are still in existence today.[50] However, together with other factors, the subsequent generations of humans since that time are not dying in such large numbers as in the past because those who survived the first devastating pandemics had a stronger genetic resistance to it, and they passed those successful genes to their progeny.

Likewise, after the publication of the complete sequence of the Neandertal genome, scientists reported that a small percentage of hominid DNA was found also in modern humans but not the other way around. The Neandertal genome is also relevant, as some have pointed out that since we are able to sequence ancient DNA samples dating tens of thousands of years ago and to observe admixture between two related species, in turn we should also be able through the same technology to detect Middle East DNA in the genome of indigenous individuals from the Americas (and consequently, failure to find any should be a further proof that Book of Mormon migrants never existed).[51] However, as explained by a researcher who helped produce the Neandertal genome, this is not always the case,

> We detect gene flow from Neandertals into modern humans but no reciprocal gene flow from modern humans into Neandertals. Although gene flow between different populations need not be bidirectional, *it has been shown that when a colonizing population* (such as anatomically modern humans) *encounters a resident population* (such as Neandertals), *even a small number of breeding events along the wave front of expansion into new territory can result in substantial introduction of genes into the colonizing population* as introduced alleles can "surf" to high frequency as the population expands. *As a consequence, detectable gene flow is predicted to almost always be from the resident population into the colonizing population, even if gene flow also occurred in the other direction*.[52]

The example of Neandertal and anatomically modern human gene flow can safely be applied to the Book of Mormon and New World scenario. The indigenous inhabitants of the Western Hemisphere had lived here for thousands of years prior to the arrival of the small group of migrants from the Old World. Environmental conditions were likely dramatically different from those of their homeland as they adjusted to their new conditions. Surely food supplies and other technologies available to them allowed for their initial survival while they adapted to the features of the new land. However, although many markers used in population studies do not contribute directly to cellular processes, it is plausible that the change in climate and food resources, among other factors, may have caused a selection against their genes over time, especially in the case of potential admixture with locals. Mitochondrial DNA in the population could have experienced the same effect, since the mitochondria are organelles responsible for the cell respiratory cycle and energy production, crucial to the health and proper function of the cells making up the human body.

It is possible that Lehi and his group may have fathered a genealogically large posterity that was eventually absorbed and became part of the current, or at least the pre-Columbian, native population. Additionally, based on a simple mathematical calculation, there are scenarios in which Lehi is potentially the genealogical ancestor of all living Amerindians,[53] contributing culturally to their contemporary indigenous neighbors, yet leaving no genetic trace of their presence in the present day.

A similar possible scenario can explain the absence of Viking DNA among modern Native Americans, although historical and archaeological evidence suggests Vikings had a significant presence which lasted a few

centuries in northern North America and had regular exchanges and contacts with native groups.[54]

Founder Effect

Another demonstrated principle that plays an important role in shaping the genetics of populations is the *founder effect*.[55] This phenomenon, which is a specific type of population bottleneck, is observed when a few members from a population source relocate to a different area, thus carrying with them a small sample of the genetic variation of the population of origin. Subsequent inbreeding and the effects of genetic drift may result in a large population displaying only the genetic lineages inherited from the founding ancestors, which may or may not resemble the frequency of the original population. An example comes from the blood types of Native Americans, which are almost exclusively group O, the least common in other world populations (where A, B, and AB are the prevalent types), including Siberia. The low blood group diversity observed in the Americas is probably attributable to a founder effect.[56]

An overly simplistic view of the Book of Mormon is that the American continent was empty at the time of the arrival of Lehi and his family and, assuming that they carried the most typical genetic lineages from the Middle East, all Native Americans today should have maintained a similar genetic make-up as their Israelite forefathers. However, this is an extremely skewed take on the Book of Mormon issue because it would imply, among other things, the following:

1. The American continent was completely empty at the arrival of Lehi's party.
2. None of the Jaredites described in the Book of Mormon would have survived;
3. Lehi and his family would carry typical and known ancient Near Eastern genetic markers (particularly those found among Jews);
4. Mulek and his group, founders of the city Zarahemla, would meet the same genetic composition criteria;
5. Middle Eastern (and more specifically Jewish) genetic makers of today's populations would be the same ones and in the same proportions as those found in the same geographic region (Jerusalem) 2,600 years ago.

Unfortunately, none of these conditions offers true testable hypotheses. For example, as already explained, neither the Book of Mormon nor the LDS Church openly teaches that the American continent

was empty in 600 BC. The summary made by Mormon on the plates does not talk explicitly about others but does not say that no one else was in the Americas. Moreover, there are different opinions on whether or not the Jaredites — whose geographic origin and genetics are unknown — became completely extinct by the time the last recorded survivor is mentioned in Omni 1:21.[57] Any Jaredite dissenters who escaped the final battle could have contributed to the complexity of identifying founding lineages from Eurasia on the American soil.

Regarding Mulek and his party, very little is written about their whereabouts and how/who arrived in the Western Hemisphere. There are too many unpredictable variables to use DNA effectively as a tool to test conclusively for the existence of Book of Mormon people.

Conclusions

In commenting on a recent article published in the scientific journal *Nature* and dealing with the number of original migrations by Paleo-Indians,[58] Professor David Meltzer of Southern Methodist University said, "Archaeologists who study Native American history are glad to have the genetic data but also have reservations, given that several of the geneticists' conclusions have changed over time. This is a really important step forward but not the last word." On the same occasion, molecular anthropologist Michael H. Crawford added, "The paucity of samples from North America and from coastal regions made it hard to claim a complete picture of early migrations has been attained."[59] These and other comments from experts in the field of ancient American history provide further evidence that DNA is a valid tool to study ancient and modern populations, but they also remind us to be careful about drawing absolute conclusions based on the genetic data. Can genetic testing and science honestly answer any of the following questions?

- What did the DNA of the Book of Mormon people look like?
- Was it the typical DNA found in the population of Jerusalem in 600 BC?
- Can their DNA be differentiated from that of Europeans arriving after 1492?
- Is the current molecular clock adequate to discern pre- from post-Columbian genetic contributions to the New World within the last three thousand years?
- What degree of mixture did the Nephites and/or Lamanites experienced with local natives?

- How long were the Nephites and/or the Lamanites an isolated population after their arrival to the American continent?

Obtaining answers to these questions would enable the design of research that could contribute to our understanding of the Book of Mormon as a historical record from a scientific approach. Without such information, we risk forming conclusions based on personal interpretation and biased assumptions. As outlined in this paper, the problems and limitations with attempting such an investigative approach are significant and cannot be overlooked by those honestly seeking for answers about the Book of Mormon through DNA. Trying to reconstruct and identify the DNA of these Old World migrants in the Americas is not a task comparable to that of finding a needle in a haystack. With time and diligence, the needle eventually will be found. With the Nephite record, the needle was once there, and then through population demographic pressures, such as drift and perhaps some degree of natural selection, the needle may have been removed from the haystack — with some people convinced that it is still there and therefore should be found. Consequently, these critics, rather than accepting the fact that the needle was once there and now is lost, prefer to take the position that it was never there in the first place. These are two very distinctive conclusions based on the same observations. Stating that the DNA of Book of Mormon people has disappeared or not been detected through time, following very basic and widely accepted population genetics principles such as genetic drift and selection, is much different from claiming that Book of Mormon people never existed because we failed to recover their DNA in the American indigenous gene pool.

The advances with DNA technologies have provided never-before attainable knowledge in many fields, such as medicine, criminal justice, etc., including the history of humanity. However, much more still needs to be investigated, and some information might never be fully revealed with a molecular approach.

We need to be wary about any statement against or in favor of Book of Mormon historicity based on genetic evidence and take the time to understand the difference between scientific data and claims people make about it. As with other religious texts and topics, science is often an inadequate tool to corroborate spiritual truths, morals, and ethics.

DNA is a powerful tool in reconstructing recent and ancient historical events. The large body of published work on the topic of Native American origins using genetic markers stands as witness that researchers are still tackling some fundamental questions surrounding the history of

the Western Hemisphere and of humanity in general. New publications provide helpful insights into the past but often pose new questions in need of further investigation.

As extensively explained herein, there are specific limitations that cannot be ignored when using the available genetic data to infer conclusions regarding the DNA of Book of Mormon people. Such conclusions are not founded on solid science but are the interpretation of a few, as genetic data fails to produce conclusive proof weighing credibly in favor of or against the historicity of the Book of Mormon.

Notes

1. For a more detailed scholarly review and summary of the Book of Mormon, see Terryl L. Givens, *By the Hand of Mormon: The American Scripture that Launched a New World Religion* (New York: Oxford University Press, 2003).
2. Rod L. Meldrum, *Rediscovering the Book of Mormon Remnant through DNA* (New York: Digital Legend Press, 2009).
3. Maanasa Raghavan and others, "Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans," *Nature* 505 (2014), 87-91.
4. Carrie A. Moore, "Debate Renewed with Change in the Book of Mormon Introduction," *Deseret Morning News* (available at http://www.deseretnews.com/article/1,5143,695226008,00.html - accessed 2 December 2012).
5. *LDS Conference Report* (April 1929), 15-16. Also see as an example, John L. Sorenson "When Lehi's Party Arrived in the Land, Did They Find Others There?" *Journal of Book of Mormon Studies* 1 (1992), 1-34; John L. Sorenson and Matthew Roper, 'Before DNA', *Journal of Book of Mormon Studies* 12 (2003); Neal Rappleye, http://www.studioetquoquefide.com/2014/08/an-open-letter-2-to-jeremy-runnells.html (accessed 20 August 2014).
6. 2 Nephi 5 is also very compelling, where Nephi in v. 6 spells out who goes with him, referring to others not on the boat, and in v. 6 and 9 he goes on to say that those who are called Nephites are those who "believe in the warnings and revelations of God" — a religious designation.
7. Note that Mormon may have been distinguishing himself from the Mulekites vs. the descendants of Lehi. Of course, the presence of Mulekites and the lack of "— ite" designations for them at this time of the narrative already shows that there is an oversimplification of the genealogy/naming.

8. Morten Rasmussen and others, "Ancient Human Genome Sequence of an Extinct Palaeo-Eskimo," *Nature* 463 (2010), 757-762.
9. Cassandra Brooks, "First Ancient Human Sequenced," www.thescientist.com/blog/display/57140 (accessed 4 January, 2013).
10. Brooks, "First Ancient Human." The second quotation is Brooks's paraphrase of Feldman.
11. Michael H. Crawford, *The Origins of Native Americans: Evidence from Anthropological Genetics* (Cambridge: Cambridge University Press, 1998), 4.
12. Daniel C. Peterson, "Proof and Evidence" (May 13, 2012) http://www.patheos.com/blogs/danpeterson/2012/05/proof-and-evidence.html (accessed 27 January 2013).
13. Antonio Torroni and others, "Asian Affinities and Continental Radiation of the Four Founding Native American mtDNAs," *American Journal of Human Genetics* 53 (1993), 563-590.
14. Mannis van Oven and Manfred Kayser, "Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation," *Human Mutations* 30 (2009) E386-E394 (http://www.phylotree.org Build 15 - accessed 5 January 2013).
15. Peter Forster and others, "Origin and Evolution of Native American MtDNA Variation: A Reappraisal," *American Journal of Human Genetics* 59 (1996), 935-945.
16. Maere Reidla et al., "Origin and Diffusion of mtDNA Haplogroup X," *American Journal of Human Genetics* 73 (2003), 1178-1190.
17. Jennifer A. Raff and Deborah A. Bolnick, "Palaeogenomics: Genetic roots of the first Americans," *Nature* 506 (2014), 162-163.
18. Erika Tamm et al., "Beringian Standstill and Spread of Native American Founders," *PloS One* 9(2007), e829.
19. Ugo A. Perego et al., "Distinctive Paleo-Indian Migration Routes from Beringia Marked by Two Rare MtDNA Haplogroups," *Current Biology* 19 (2009), 1-8.
20. Crawford, *Origins*.
21. Ugo A. Perego et al., "The Initial Peopling of the Americas: a Growing Number of Founding Mitochondrial Genomes from Beringia," *Genome Research* 20 (2010), 1174-1179.
22. Alessandro Achilli et al., "The Phylogeny of the Four Pan-American MtDNA Haplogroups: Implications for Evolutionary and Disease Studies," *PLoS ONE* 3 (2008), e1764; Perego, (2010).
23. Sigríður Sunna Ebenesaersdóttir and others, "A New Subclade of MtDNA Haplogrpus C1 Found in Icelanders: Evidence of Pre-

Columbian Contact?" *American Journal of Physical Anthropology* 144 (2011), 92-99.
24. Clio Der Sarkissian and others, "Mitochondrial Genome Sequencing in Mesolithic North East Europe Unearths a New Sub-Clade within the Broadly Distributed Human Haplogroup C1," *PLoS ONE* 9 (2014), e87612.
25. Tamm, "Beringian Standstill."
26. Geraldine Barnes, *Viking America: The First Millennium* (Suffolk, England: St. Edmundsbury Press, 2001).
27. Rosaria Scozzari et al., "MtDNA and Y Chromosome-Specific Polymorphisms in Modern Ojibwa: Implications about the Origin of Their Gene Pool," *American Journal of Human Genetics* 60 (1997), 241-244.
28. Shlush et al., "The Druze: A Population Genetic Refugium of the Near East," *PLoS ONE* 3 (2008), e2105; Doron M. Behar et al., "Counting the Founders: The Matrilineal Genetic Ancestry of the Jewish Diaspora," *PLoS ONE* 3 (2008), e2062.
29. Rem I. Sukernik et al., "Mitochondrial Genome Diversity in the Tubalar, Even and Ulchi: Contribution to Prehistory of Native Siberians and Their Affinities to Native Americans," *American Journal of Physical Anthropology* 148 (2012), 123-138.
30. Reidla, "Origin and Diffusion."
31. Martina Kujanová and others, "Near Eastern Neolithic Genetic Input in a Small Oasis of the Egyptian Western Desert," *American Journal of Physical Anthropology* 140 (2009), 336-346.
32. Pedro Soares et al., "Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock," *American Journal of Human Genetics* 84 (2009): 740-759.
33. Ugo A. Perego, "The Book of Mormon and the Origin of Native Americans from a Maternally Inherited DNA Standpoint," in *No Weapon Shall Prosper*, edited by Robert Millet (BYU Religious Studies Center, 2011), 171-216.
34. Perego, "Distinctive Paleo-Indian."
35. Soares, "Correcting"; Doron M. Behar et al., "A 'Copernican' reassessment of the human mitochondrial DNA tree from its root," *American Journal of Human Genetics* 90 (2014), 675-684.
36. From a commercial ancestral DNA test based on more than 500K SNPs obtained through 23andMe.com.
37. Personal conversation with Dr. Peter Underhill from Stanford University.

38. The Coop Lab: Population and Evolutionary Genetics, UC Davis, "How Many Genetic Ancestors Do I Have?" http://gcbias.org/2013/11/11/how-does-your-number-of-genetic-ancestors-grow-back-over-time (accessed 20 August 2014).
39. See for example the encounter between Sherem and Jacob narrated in Jacob chapter 7.
40. Signature Books, http://signaturebooks.com/2010/06/dna-and-the-book-of-mormon (accessed 5 January 2013).
41. "Autosomal DNA Statistics", http://www.isogg.org/wiki/Autosomal_DNA_statistics (accessed 20 August 2014).
42. Wikipedia, http://en.wikipedia.org/wiki/Genetic_drift (accessed 5 January 2013).
43. Agnar Helgason and others, "A Populationwide Coalescent Analysis of Icelandic Matrilineal and Patrilineal Genealogies: Evidence for a Faster Evolutionary Rate of mtDNA Lineages than Y Chromosomes," *American Journal of Human Genetics* 72 (2003), 1370-1388.
44. Alan Taylor, *American Colonies: The Settling of North America* (Penguin Books, 2002), 40.
45. Crawford, *Origins*.
46. See for example Kirsten I. Bos et al., "A Draft Genome of Yersinia pestis from victims of the Black Death," *Nature* 478 (2012), 506-510; Michel Samson et al., "Resistance to HIV-1 Infection in Caucasian Individuals Bearing Mutant Alleles of the CCR-5 Chemokine Receptor Gene", *Nature* 382 (1996), 722-725.
47. Ripan S. Malhi et al., "Distribution of Y chromosome Among Native North Americans: A Study of Athapaskan Population History," *American Journal of Physical Anthropology* 137 (2008), 412-424; Daniel Corach et al., "Inferring Continental Ancestry of Argentineans from Autosomal, Y-Chromosomal and Mitochondrial DNA," *Annals of Human Genetics* 74 (2010), 65-76; Ugo A. Perego et al., "Decrypting the Mitochondrial Gene Pool of Modern Panamanians," *PLoS ONE* 7(2012), e38337.
48. Matthew 27:51.
49. James E. Smith, "How Many Nephites?: The Book of Mormon at the Bar of Demography," *Book of Mormon Authorship Revisited: The Evidence of Ancient Origins* (FARMS, 1997), and references within.
50. Bos, "Draft Genome."
51. Simon Southerton, http://simonsoutherton.blogspot.com/2013/05/could-lamanite-dna-just-disappear.html (accessed 14 July 2014).

52. Richard E. Green et al., "A Draft Sequence of the Neandertal Genome," *Science* 328 (2010), 710-722, emphasis added.
53. Every person with native blood in the Americas today would have had potentially billions of ancestors 2,600 years ago, and therefore all the ancestors of one person today are also all the ancestors of everyone else in the same continent during the same period of time. See Steve Olson, "The Royal We," *The Atlantic* (May 2002) http://www.theatlantic.com/magazine/archive/2002/05/the-royal-we/302497 (accessed 8 February 2013).
54. Barnes, *Viking America.*
55. Wikipedia, http://en.wikipedia.org/wiki/Founder_effect (accessed 4 December 2012).
56. Léa Georges and others, "Molecular Characterization of ABO Blood Group Frequencies in pre-Columbian Peruvian Highlanders," *American Journal of Physical Anthropology* 149 (2012), 242-249.
57. Hugh W. Nibley, *The World of the Jaredites* (Deseret Book, 1988), 231-241.
58. David Reich et al., "Reconstructing Native American Population History," *Nature* 488 (2012), 370-374.
59. Nicholas Wade,"Earliest Americans Arrived in Waves, DNA Study Finds," *New York Times* (July 7, 2012), http://www.nytimes.com/2012/07/12/science/earliest-americans-arrived-in-3-waves-not-1-dna-study-finds.html?_r=0 (accessed 3February 2013).

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