

# THE CASE FOR DNA EVIDENCE: POSSIBLE, PLAUSIBLE, OR PROBABLE?

What types of DNA markers might we reasonably expect to find from a population with the background of Lehi's group? The answer to this question can be quite complex, so we will begin from the most obvious.

First: We should expect to find DNA markers in the Native American populations consistent with known Caucasian lineages stemming from Shem at the very least. We would not expect to find significant levels of Asian or African DNA profiles within Lehi's group. Later admixture with an established Asian population could have diluted much of their unique DNA characteristics away, but probably not completely, skewing their genetic profiles heavily towards Asian lineages.

We would then expect to find profiles that were predominantly Asian, with lower frequencies of European markers among at least some populations within a large sampling. As a result of the three known genetic bottlenecks, even if there was a large Nephite or Lamanite population that did not intermix with Asian populations, it seems likely that their overall genetic contribution to modern Native American populations would be relatively small. If we were to find such "Caucasian" markers, termed "European" in DNA nomenclature, we could then make the claim that there is the potential for DNA evidence supporting the claims of the Book of Mormon. This would indicate that the Book of Mormon story is historically *possible*.

Second: To narrow it down further, we may hope to find DNA markers common to or consistent with those found more specifically among known Jewish or Israelite lineages. Should such DNA markers be found, we may be able to more reasonably claim that there is stronger evidence that actually favors the Book of Mormon position and that the Book of Mormon history is *plausible*.

Third: Additional refinements to the probabilities could include the following, each level becoming progressively more robust as evidence:

- If Native American markers consistent with progressively more specific lineages such as Semitic (good), Israelite (better), or Jewish (best) lineages were found and/or
- If such lineages could be shown to have existed in the correct region or area anciently and/or
- If such lineages were found to have existed near the time that Lehi left the old world and/or
- If markers were found linking Native Americans to a specific population from the same time frame and area from which Lehi's group left

If any or all of these refinements can be made, then a stronger case can be assembled and a more robust claim made that the Book of Mormon story may actually be *probable*. We must remember that without actual DNA samples from both a source and a control population, no one can make a claim of "proof" for or against the Book of Mormon. We are only dealing with probabilities here.

## Genetic background of the other two Book of Mormon migration groups

What do we know of the genetic background of the two other groups spoken of in the Book of Mormon, the Jaredites and the Mulekites?

### *The Mulekites*

Mulek was a son of Zedekiah (Helaman 8:21) who was a king of Judah in Jerusalem when it was conquered by Babylonian forces led by King Nebuchadnezzar in 586 BCE (2 Kings 25:7). His people, called Mulekites, left Jerusalem prior to its destruction and traveled by boat to the Promised Land. The Mulekite group shared a common ancestry with Lehi, Ishmael, and their group, in that Mulek was a son of the King of Judah, a Jewish royal lineage going back to Jacob (Israel), the father of both Joseph and Judah. The fact that Zedekiah was a Jewish King indicates that his lineage was not likely to have intermarried with non-Israelites, because had any of his fathers done so, they may have been stripped of their familial rights resulting in loss of their societal rights to authority within the Israelite community.

From a DNA perspective, they would have had DNA markers remarkably similar to Lehi's group in the general sense because they could both trace their ancestry back to Jacob or Israel, although from differing sons, Judah and Joseph. What we could expect from their genetic lineages is roughly similar to what we could expect from those of the Lehi group...that is that they should harbor some DNA markers consistent with Caucasian/European, Israelite or Jewish lineages.

### *The Jaredites*

The Jaredites consisted of several families that migrated to the Promised Land in enclosed ships or barges (Ether 2:16-17) near the time of the Tower of Babel (Ether 1:33). Their lineage and heritage is obscure. The Jewish historian Flavius Josephus, in his book *Antiquities of the Jews* written circa 94 AD, claims that it was Nimrod, the son of Ham that instigated the building of the tower and of "turning men from the fear of God" that ultimately caused the confusion of languages resulting in the great building project being thwarted.

Now it was *Nimrod* who excited them to such an affront and contempt of God. He was *the grandson of Ham, the son of Noah*, a bold man, and of great strength of hand. He *persuaded them not to ascribe it to God*, as if it were through his means they were happy, but to believe that it was their own courage which procured that happiness. He also *gradually changed the government into tyranny, seeing no other way of turning men from the fear of God, but to bring them into a constant dependence on his power...* Now the multitude were very ready to follow the determination of Nimrod, and to *esteem it a piece of cowardice to submit to God*; and they built a tower,... When God saw that they acted so madly, he did not resolve to destroy them utterly, since they were not grown wiser by the destruction of the former sinners [in the Flood]; but he caused a tumult among them, by *producing in them diverse languages*, and causing that, through the multitude of those languages, they should not be able to understand one another. The place wherein they built the tower is now called Babylon, because of the confusion of that language which they readily understood before; for *the Hebrews mean by the word Babel, confusion...* <sup>Ref 5</sup>

Historical sources such as the works of Josephus and the Midrash teachings claim it was Nimrod that caused the building of the tower; however, other Rabbinical sources give a somewhat different account, stating only that he separated from those who were the builders. It is also unknown if the brother of Jared was of the same lineage as Nimrod or not. If so, then the Jaredite people may have been descended from Ham, if not, then we simply don't know what his lineage might have been.

### Finding a European Lineage in the Americas

Getting back to the controversy over mtDNA findings we begin from the initial research conducted on Native American populations throughout the Americas that found that they all could be categorized into four primary haplogroups, identified as A, B, C, and D. All four of these "founding Haplogroups" were correspondingly found in native populations in Asia, lending support for the dominant theory of the peopling of the

Americas over the Bering Strait land bridge during the last ice age. Confirming this concept is an article in the journal *Science* in 1998.

Researchers had already identified four common genetic variants, called haplogroups A, B, C, and D, in the mitochondrial DNA (mtDNA) of living Native Americans (*Science*, 4 October 1996, p. 31). These haplogroups turned up in various Asian populations, lending genetic support for the leading theory that Native Americans descended primarily from these peoples. But researchers also found a handful of other less common variants, one of which was later identified as X. [Ref 29](#)

The end of this quote makes reference to an interesting find among a handful of Native Americans that was originally thought to be an insignificant outlier and categorized as "other" for its markers were not found among the other four haplogroups.

The remaining few Native Americans that do not exhibit one of these four haplogroups have been termed "others." [Ref 30](#)

It wasn't until DNA testing got underway in Europe and comparisons could be made with newly developed European DNA databases that it was discovered the set of markers found in this smattering of Native Americans were the same set of markers also found in some European populations.

This same article goes on to say:

Anthropologists have long assumed that the first Americans, who crossed into North America by way of the Bering Strait, were originally of Asian stock. But recently they have been puzzled by surprising features on a handful of ancient American skeletons, including the controversial one known as Kennewick Man—features that resemble those of Europeans rather than Asians (*Science*, 10 April, p. 190). Now a new genetic study may link Native Americans and people of Europe and the Middle East, offering tantalizing support to a controversial theory that a band of people who originally lived in Europe or Asia Minor were among the continent's first settlers. [Ref 29](#)

This article started a firestorm of excitement and controversy among geneticists and archaeologists conducting DNA and archaeological research. They found that in a few ancient American remains there were features that more closely resembled Caucasian populations than Asian ones. This would be contrary to the dominant theory if these markers could not be found in the Asian populations, thought to be the source populations for the peopling of the Americas. Originally denoted "other," now this particular lineage received a designation: Lineage or Haplogroup X, which is technically defined as follows.

Bailliet et al. (1994) suggested the possibility of a fifth haplogroup, defined by a C = T transition at np 16278 and the absence of the mutations that characterize haplogroups A, B, C or D. Haplogroup X is also characterized by *Dde* I site losses at np 1715 and np 10394, mutations that are otherwise rare in North America. [Ref 30](#)

Upon investigation it was initially found that no such markers turned up in Asia, suggesting that a separate migration may have taken place by an ancient European population into the Americas. The suggestion was made that a possible link had been found between European populations and Native Americans.

The new data, from a genetic marker appropriately called *Lineage X*, suggest a "definite -- if ancient -- link between Eurasians and Native Americans," says Theodore Schurr, a molecular anthropologist from Emory University in Atlanta, ... [Ref 29](#)

Further investigation into the source population for this lineage found in Native Americans revealed that indeed, this was a European lineage, as this same set of mtDNA markers were confirmed in the European populations of Italians, Finns, and most interestingly for this research, Israelis. It was still not found in the source populations of Asia.

Haplogroup X was different: It was spotted by Torroni in a small number of European populations. So the Emory group set out to explore the marker's source. They analyzed blood samples from Native American, European, and Asian populations and

reviewed published studies. "We fully expected to find it in Asia," like the other four Native American markers, says Brown. To their surprise, however, haplogroup X was only confirmed in the genes of a smattering of living people in Europe and Asia Minor, including Italians, Finns, and certain Israelis. The team's review of published mtDNA sequences suggests that it may also be in Turks, Bulgarians, and Spaniards. But Brown's search has yet to find haplogroup X in any Asian population. "It's not in Tibet, Mongolia, Southeast Asia, or Northeast Asia," Schurr told the meeting. "The only time you pick it up is when you move west into Eurasia." [Ref 29](#)

### What Native American populations have haplogroup X?

What Native American populations were found to have these markers, known today as Haplogroup X? The *American Journal of Physical Anthropology* published an article titled "Distribution of mtDNA Haplogroup X Among Native North Americans" in 1999 that reported finding the markers designating Haplogroup X in seven "unrelated language families."

Why is the fact that they are unrelated language groups important? If a group of populations share a common genetic ancestry, but their languages have had time to diverge one from another, then that gives some indication that this lineage existed a very long time ago—long enough that their languages had diverged from each other. Human language changes much more rapidly than does DNA. If the DNA is the same, and the languages have changed, then that DNA lineage must have arrived a very long time ago to give sufficient time for the changes and resultant diversity in languages.

These seven language families are today found throughout North America. The markers were found in highest concentrations in the Canadian Subarctic/Great Lakes region, the Southwestern region, the Southern Plains, and the Central and Northwest Coasts of North America. The broadest language group

is known as Algonquian, which encompasses over 100 Native American tribal groups.

*Haplogroup X has now been reported in contemporary members of seven specific unrelated language families (Athapaskan, Algonquian, Kiowa-Tanoan, Wakashan, Plateau Penutian, Northern Hokan, and Siouan) which are distributed throughout markedly noncontiguous geographic regions of the Canadian Subarctic/Great Lakes region, the Southwestern U.S., the Southern Plains and the Central and Northwest Coasts,... confirming its legitimacy as a founding haplogroup.* [Ref 30](#)

Such wide distribution then justified "X" being classified as a "founding haplogroup" taking its place with the other four founding groups. Today these remain as the five founding haplogroups: four Asian based bloodlines, and only one European based bloodline. Haplogroup X is the only founding European lineage in the Americas to date, and it is highly unlikely that any other "founding lineages" will be found, as there have now been tens of thousands of mtDNA samples taken from among every known Native American group. It requires large distribution to qualify for "founding" status, and there are simply no haplogroups with large distributions except these five groups. Of course things in science can change, but in this case it is very highly unlikely that any additional haplogroups will reach "founding" status. If there were other such founding haplogroups, they would already have been found.

The producers of the anti-Mormon DNA documentary completed their research near the end of 2002 and began distribution early in 2003. Not long before their DVD was completed, scientific journals such as the *American Journal of Human Genetics* and the *American Journal of Physical Anthropology* began publishing new findings from mtDNA sequencing that verified the existence of one lineage that had been found in Italians, Finns and Israelis, making it a "European" group. It was later verified to be among the Algonquian speaking Native American tribes in the Canadian Subarctic and Great Lakes region of

the United States, establishing it as a "founding haplogroup." This lineage was denoted Haplogroup X but was not recognized in the earlier Native American DNA results until DNA sequencing of Europeans got underway which provided a "link" that was previously classified as "other" among the Native American population.

### *Haplogroup X, Verified as an Ancient Founding Lineage*

This European type mtDNA was initially thought to have been the result of recent admixture of Europeans with Native American populations which is known to have occurred after the time of Columbus. It became necessary to determine if this set of markers arrived in the Americas anciently or more recently, after the 1492 arrival of Columbus to the New World and the European explorers began their incursions. If it was found to be ancient, then this lineage could hold some tantalizing new clues to the peopling of the Americas.

Archaeologists submitted ancient remains for radiocarbon and mtDNA testing. Their findings confirmed that *not only was there a European type of DNA in the Americas, but it was in the Americas long before European exploration and settlement.* This verified the prehistoric presence of haplogroup X in North America.

The most convincing evidence that haplogroup X is not the result of Viking or even more recent European admixture would be its presence in ancient Native Americans. *We confirmed the presence of Haplogroup X in one prehistoric sample excavated at a site on the Columbia River near Vantage, Washington and radiocarbon dated to 1,340 [+/-] 40 years BP [before present]. To the best of our knowledge, this is the first evidence of haplogroup X in prehistoric America to be confirmed using both control region markers and the diagnostic restriction site gain in the coding region. This verifies a prehistoric presence of haplogroup X in North America ...* [Ref 31](#)

Later, another set of remains from west-central Illinois was tested, again confirm-

ing a pre-Columbian presence of haplogroup X in the heartland of America.

*...haplogroup X also have been found in two individuals from the Norris Farms Oneonta burials, a 700-year-old cemetery in west-central Illinois...the Norris Farms sequences are virtually identical to those of modern Algonquians from the Great Lakes region confirmed to be members of haplogroup X.* [Ref 3](#)

These remains were recovered near what is called the Dixon Mounds about 40 miles east of present day Nauvoo, Illinois. This is also near the site of what has become known as the "Zelph Mound" (or archaeologically denoted as Naples-Russell Mound #8), from an event during Zion's Camp march, (see History of the Church Vol. 2:79-80) wherein Joseph Smith claimed to have received a revelation about the remains of a "white Lamanite" who died in one of the last battles between the Lamanites and Nephites and whose bones were found in an ancient burial mound overlooking the Illinois River.

Five specific mtDNA markers differentiate this lineage from other European lineages, and its existence in ancient North American native populations was verified by DNA sequencing of remains pre-dating European exploration and conquest. Remains radiocarbon dated to 1300 or more years before present were found to harbor this lineage; other ancient remains have confirmed that Haplogroup X was among the ancient American inhabitants of North America. To date, it is the only "European" lineage known to be a "founding" or primary genetic contributor to Native American populations.

### *Haplogroup X Not Found in Asia*

A fundamental difficulty with this particular haplogroup when it came to conformity with the dominant Bering Strait theory of the peopling of the Americas is that any trace for its passing through Asia was missing. The theory had shown that all of the other four founding haplogroups could be traced back

into Asia as the theory would suggest; haplogroup X, however, was different. If the theory is correct, that all Native American populations came from or at least through Asia, there should be some genetic evidence left behind from such a long migration. It is thought that populations large enough to sustain a new civilization would mate with other populations along their journey, thereby leaving traces of their genetics along their path. However, at first, such a trace for haplogroup X appeared to be completely absent, unlike the other four founding haplogroups.

*Haplogroup X is an exception to this pattern of limited geographical distribution. It is found, generally at low frequencies, in both West Eurasians and some northern groups of Native Americans, but, intriguingly, it is absent in modern north Siberian and East Asian populations, which are genetically and geographically closest to those of Native Americans. Among Siberians, haplogroup X mtDNAs have only been detected in some Altaian populations of southwestern Siberia.* [Ref 32](#)

After further investigation it was found that haplogroup X had indeed been located in the Altaian population of southwestern Siberia and critics of the Church again made a flurry of claims that this now proved that haplogroup X did come through Asia as was shown for the other founding haplogroups. Unfortunately, again they were premature, jumping to their conclusions.

*To extend the survey of Asian mtDNAs for the presence of haplogroup X, we screened the mtDNAs of a total of 790 individuals for the RFLP markers that define this lineage. Haplogroup X mtDNAs were detected only in Altaians, at a frequency of 3.5%.*

*It should also be noted that none of the Altaian X mtDNAs harbored the 225A variant, which is a marker for a major part of haplogroup X.*

*However, the X mtDNAs that we detected in the Altaian sample do not bear the 16213A and 200G variants that are characteristic of most American Indian haplogroup X mtDNA.* [Ref 33](#)

This article in the prestigious *American Journal of Human Genetics* reports extensive

surveying of the Asian mtDNA data, looking for traces of haplogroup X, which was found in a few Altaian samples. However, upon closer examination they were found not to have particular markers common to Native American haplogroup X carriers, and that their markers were more likely explained by a much later incursion of European bloodlines, making the Altaian group unrelated to the Native American groups.

*...the few Altaian and Siberian Haplogroup X lineages are not related to the Native American cluster, and they are more likely explained by recent gene flow from Europe or from West Asia.* [Ref 32](#)

An explanation for the detection of the Altaian haplogroup X was given in a 2005 article in the journal *Annals of Human Genetics*.

Several "west" Eurasian haplogroups, including H, V, J, U4, U5, W, and X, were also detected. Their confinement to the southwest part of Siberia might be indicative of an Upper Paleolithic dispersal from the Middle East/southeastern Europe, the traces of which have not been erased by subsequent migrations and gene flow. Alternatively, a relatively recent gene flow mediated by women of European/West Asian ancestry could have occurred at the time of the expanding Mongolian Empire. [Ref 34](#)

The explanation given is that the haplogroup X strain found among the Altaians was most likely a result of the conquests by the Mongol warrior Genghis Khan who dominated this region between 1206 and 1405 AD. It was confirmed that the Native American haplogroup X mtDNA lineages were not derived from this group.

The Bering Strait theory is so prevalent that researchers were still trying to find some sort of trace in Asia, rather than accepting the idea that another (possibly European) migration had actually occurred. However, as of 2009, Haplogroup X is still not found in Asia, and continues to frustrate the theory, causing researchers to invoke the "it got lost" explanation.

Unlike in the case of all other Native American haplogroups, a close molecular counterpart for X2a has not been found in Asians, suggesting that its X2 ancestor became lost in Asians after entry in Beringia, most probably because of genetic drift. [Ref 35](#)

In summary, haplogroup X was not initially found in modern populations of Asia, but in 2001 it was thought to have been found among Altaians in Mongolia. It was later shown not be directly related to the Native American Haplogroup X groups, but to have been possibly related to the conquests of Genghis Khan around 1206-1405 AD. No DNA matching with Native American haplogroup X has yet been found in Asia, indicating that it may have arrived via a different mode of transport than walking over the Bering Strait during an ice age, which is the current dominant theory of the peopling of the Americas.

### Haplogroup X Distribution

Haplogroup X was found at highest frequencies among Native American Algonquian speaking language groups. These include such tribes as the Arapaho, Blackfoot, Cheyenne, Cree, Gros Ventre, Illini, Kickapoo, Leni Lenape, Delaware, Lumbee, Mohican, Menominee, Sac and Fox, Miami, Micmac, Ojibwa, Shawnee, Sioux, Wiyot, and Yurok along with many others. This language group today consists of more than 100 individual tribes. It has also been found to be geographically widespread throughout nearly all of North America, present among groups that share no close historic or linguistic ties.

An article titled "Origin and Diffusion of mtDNA Haplogroup X" in the *American Journal of Human Genetics* in 2003 provided significant additional evidence of this relationship. It states that Haplogroup X could be separated into two distinct groups called clades, denoted as X1 and X2. X1 is restricted to North and East Africa, whereas X2 appears in greatest frequency in populations of the Near East and Mediterranean Europe. The article states that the Native American populations having the X haplotype derive

from X2, the Mediterranean group, distinguished by a unique combination of five mutations. The article ends by stating that the subgroups of haplogroup X suggest that the Near East (which includes the Levant area and Israel) is the likely geographical source for the North American Indian X2 mtDNA lineages.

The results of this study point to the following conclusions. First, *haplogroup X variation is completely captured by two ancient clades that display distinctive phylogeographic patterns—X1 is largely restricted to North and East Africa, whereas X2 is spread widely throughout West Eurasia.* Second, it is apparent that *the Native American haplogroup X mtDNAs derive from X2 by a unique combination of five mutations.* Third, *the few Altaian and Siberian Haplogroup X lineages are not related to the Native American cluster, and they are more likely explained by recent gene flow from Europe or from West Asia.* Finally, phylogeography of the subclades of haplogroup X suggests that *the Near East is the likely geographical source for the spread of subhaplogroup X2, and the associated population dispersal occurred around, or after, the LGM (Last Glacial Maximum) when the climate ameliorated. The presence of a daughter clade in northern Native Americans testifies to the range of this population expansion.* [Ref 32](#)

The findings of this research article are compelling. The haplogroup X subgroup, denoted as X2, which stems from the Mediterranean area of Europe is the same type of haplogroup X that is found in modern and ancient Native Americans. The question then is how did the haplogroup X lineage get from the Mediterranean (region around Israel) to the Americas at least 800 years before Columbus and the ensuing European colonization?

It is notable that X2 includes the two complete Native American X sequences that constitute the distinctive X2a clade, a clade that lacks close relatives in the entire Old World, including Siberia. [Ref 32](#)

Once haplogroup X had been discovered and its subgroup or "clade" brought out, a search for matching mtDNA X2 resulted in no exact matches with the subgroup. This suggested that it may have been in the Americas,

and evolved, over a still longer period of time, possibly dating much further back than 1340 years ago as indicated by the Kennewick man remains in Washington State. Without an exact match, but with close genetic relationships, haplogroup X must have arrived in the New World long enough ago to allow some changes, called mutations, to occur making this sub-lineage distinct from other haplogroup X lineages. Such changes could provide new clues to the arrival time of haplogroup X from the Mediterranean into the Americas.

*These findings leave unanswered the question of the geographic source of Native American X2a in the Old World, although our analysis provides new clues about the time of the arrival of haplogroup X in the Americas.*  
Ref 32

Haplogroup X had been found in the mtDNA of Native American tribes distributed geographically over the entire North American continent, which provides additional clues as to when this lineage arrived in the New World. Such a wide dispersion of this lineage must surely indicate that it arrived long enough ago for it to have been dispersed among many populations in the Americas, an obvious sign that it came a very long time ago. However, it was not long enough ago that it spread throughout all the Americas as did the other four Asian haplogroups as will be seen.

*Although apparently sharing a matrilineal ancestor with the European haplogroup X at some point deep in time, the Native American sequences formed their own branches independent of European representatives of haplogroup X. The distribution of haplogroup X is also consistent with a pre-Columbian source. Though presently thought to be most common among speakers of Algonquian languages, haplogroup X, which reaches a frequency of 20% in some Algonquian populations, is geographically widespread throughout North America among groups sharing no close historic or linguistic ties.*  
Ref 3

This article amazingly not only confirms that Haplogroup X is a "founding" American Indian or "Amerindian" group, but that it is geographically widespread through-

out North America. It is found in highest frequency in the region surrounding the Great Lakes and the Great Plains, which is precisely where Joseph Smith sent the very first missionaries of the Church "unto the Lamanites" (D&C 28:8-9, 30:5-6, 32:1-3) with original copies of the Book of Mormon. It also establishes that this haplogroup or lineage did not come from Asia as Bering Strait theory would predict, as no matching Haplogroup X population has been found there to date.

The very latest results in mtDNA research reaffirm that haplogroup X2a continues to be restricted to North America. In a January 2009 article in *Current Biology*, LDS geneticist Ugo Perego confirms that haplogroup X2a is found primarily in the Great Lakes and Great Plains areas of North America.

*... the latter [X2a] being restricted to northern North America, with no instances detected south of the United States. ...An analogous query for the X2a control-region motif confirmed that this haplogroup is confined to northern North America, with a frequency peak in the Great Lakes area. ... the other rare Native American haplogroup, X2a, despite a similar expansion time, is restricted to northern North America, with a focus in the Great Lakes and the Great Plains regions.*  
Ref 35

In summary, haplogroup X, a known European based mtDNA lineage, is confirmed. It is found in high frequency in the Great Lakes and Great Plains areas among present day Native American Algonquin-speaking language groups, yet is widespread throughout North America, among distantly related groups. No European mtDNA lineages have been deemed as a founding lineage except haplogroup X. Two individual sets of remains from west-central Illinois, which is near where Joseph Smith's Zephrus mound experience took place, were found to possess this European DNA lineage, again confirming haplogroup X's ancient, pre-Columbus and pre-Viking heritage. Also very importantly, modern Algonquin Indians from the Great Lakes area have nearly identical DNA sequences as those found in ancient burial mounds in Illinois.

*Any Haplogroup X in Mesoamerica?*

The question arises of whether or not DNA evidence for a Mesoamerican setting for the Book of Mormon exists. An article in *American Journal of Physical Anthropology* in 2005 provides additional insight. The article "Is Haplogroup X Present in Extant South American Indians" gives a stark answer: "The results indicate that *haplogroup X is not present in these samples.*" [Ref 36](#)

This survey of 1,159 samples from 25 South Native American populations that include Central America, found no evidence for the presence of haplogroup X in Native South American populations. They are all members of haplogroups A through D; the Asian lineages found throughout the Americas. It goes on to state that up to the time of publication, "*haplogroup X has only been found in North America.*" [Ref 36](#) Thus, *no evidence for an ancient founding European lineage migration has been found in the native populations of Central or South America through DNA research and analysis.* This is the region generally accepted through consensus by the LDS scholarly community to have been the location of the lands of the Book of Mormon.

The study was conducted on 25 South Native American populations, looking for a particular haplogroup X distinguishing marker. Their results found no evidence for haplogroup X among these populations.

*ABSTRACT: A total of 1,159 mitochondrial DNA samples from two Mongolian, two Siberian, and 25 South Native American populations was surveyed for the presence of the C16278T mutation, frequently found in haplogroup X. The tests involved all the control region, as well as the presence of characteristic mutations in seven coding fragments, totalling [totaling] 5,760 base pairs. The results indicate that haplogroup X is not present in these samples.* [Ref 36](#)

The article continues by stating that haplogroup X is not restricted to Europe, but is found throughout West Eurasia, which comprises both Europe and the Mediterranean

region. They also mention that because of its ancient arrival, and status as a founding lineage, it is anomalous that its distribution is restricted to North America.

Despite some initial speculations that haplogroup X in modern Native North Americans may have its origin in Europe, *subsequent research found it actually widely distributed in West Eurasia*, although it is not yet possible to answer the question of the more exact geographic origin of this haplogroup in the Old World. *Its presence in ancient Native North Americans and its ancient coalescence time also helped to corroborate its position as a major founder haplogroup. However, this haplogroup has an anomalous distribution pattern in the New World, apparently being restricted to North America.* [Ref 36](#)

Finally, this article makes it clear that haplogroup X is a lineage that is not found in indigenous South American populations.

The evidence presented here strongly supports the hypothesis that *haplogroup X is likely absent in modern Native South American populations.* [Ref 36](#)

Another 2005 article in *Hispanic American Historical Review* titled "Genetics and the History of Latin America" provides a second witness to the previous article. It contains a chart with the five founding haplogroups listed across the top, and Native American populations north of Panama down the side bar. It indicates that both contemporary and ancient Mayan populations, which are considered by most Mesoamerican theorists to be the most likely population to be descendants of the Book of Mormon, have zero percentage of haplogroup X, or any other European lineages among them. The ancient Maya (Quintana Roo) were primarily of haplogroups A (87.5%), C (8.3%), and B (4.2%), which are all Asian lineages. Are there any large indigenous populations in the Americas that have not yet had mtDNA testing performed?

What can the geographic distribution of mtDNA variation teach us about the history of Latin America? *Thus far, scholars have studied genetic markers of indigenous groups in all major areas of Latin America,*

including South America, Central America, the Caribbean, Mexico, and the American Southwest, and they have found that haplogroups A, B, C, and D are widely dispersed throughout the hemisphere. [Ref 37](#)

Every significant indigenous population in the Americas has now undergone DNA testing. While it may be possible that there remains some small, hidden population deep in a mountain jungle in Central America that has not yet been tested, it is highly unlikely. Such a small population is not what would be expected by a population group the size described in the Book of Mormon. We are not looking for a tiny, insignificant remnant because the Book of Mormon itself testifies otherwise. We are not looking for every indigenous people to have these lineages either, as set forth by the First Presidency in the change to the introduction page of the current Book of Mormon.

Haplogroup X, which is the *only* founding European lineage known to have occurred anywhere in the Americas anciently, is found only in Native American populations in North America, making it the most likely, qualified, or suitable candidate lineage for establishing a possible, plausible or probable case for the historicity of the Book of Mormon according to the findings of DNA research.

*Although haplogroup X is now accepted as a pre-Columbian Native American haplogroup, controversy still surrounds its origin. ... This has led to the hypothesis, fueled by morphometric studies of the Kennewick Man remains in Washington state and other Paleo-Indian remains, that there was a prehistoric migration of Europeans to the New World.* [Ref 3](#)

### Old World Populations having Haplogroup X mtDNA

What Old World populations have Haplogroup X mtDNA? Haplogroup X lineages have been reported in Europe and Western Eurasia, but what specific populations were they found in?

### *The Mediterranean Druze Population*

A 2007 article in *BMC Evolutionary Biology* studying Saudi Arabian populations reported haplogroup X in high frequency among a population known as the Druze. The Druze population is found primarily in Syria, Lebanon, and Israel according to the Israel Central Bureau of Statistics.

The Druze is a religious order that has strict rules pertaining to many areas of its members' lives, including matrimony. They do not proselyte and the only method of becoming a "Druze" is by birth or through the death of a member, for which a replacement is permissible. An article in *PloS ONE* of May 2008 concludes that the "Galilee Druze" provide a "sample snapshot of the genetic landscape of the Near East prior to the modern age." According to geneticists, the Druze population is the sample population for Israel before the modern age, further strengthening the genetic connection between the old world populations of the Mediterranean and the American Indian populations of North America.

Who are the Druze and where are they located today?

*The Druze reside primarily in Syria, Lebanon, and Israel, with a smaller community in Jordan. The Israeli Druze are mostly in Galilee (70%) and around Haifa (25%), the Golan Heights...is home to about 20,000 Druze ...* [Ref 38](#)

A study of 100 Saudi Arabian populations found that haplogroup X was present, and that the Israeli Druze population had a high frequency of this particular lineage. This was significantly different from the other Saudi Arabian populations sampled. The Israeli Druze is a Saudi Arabian population living in Israel within a roughly circular area between the regions of Galilee, Lebanon, and the Golan Heights, northwest of the Sea of Galilee.

A total of 120 mtDNA Saudi Arab lineages were analyzed for HVSI/II sequences and for

haplogroup confirmatory coding diagnostic positions.

...the Druze sample was significantly different from all the other populations, mainly because of a high frequency of haplotypes (27%) belonging to the minority haplogroup X and to K (20%). [Ref 39](#)

No geographic origin had yet been found for Haplogroup X in the Old World. This article in *PLoS ONE* (Public Library of Science) suggests the Druze population as the potential source population for this lineage.

*No population or geographic region has been identified to date, in which haplogroup X and its major subhaplogroups are found at both high frequency and high diversity, which could provide a potential clue as to their geographic origin. Here we suggest that the Druze population of northern Israel may represent just such a population.* [Ref 40](#)

The article then infers that the Druze population is unique because of its religious and social policies regarding marriage with those outside of their order. This is somewhat akin to the genetic findings of Jewish populations scattered abroad that don't tend to mix with their host populations.

*The Druze population has a unique historical, social and demographic structure, which is closely connected with their religion. The contemporary Druze population constitutes a small minority in four countries of the Near East: Syria, Lebanon, Israel and Jordan. In total, the estimated population number is fewer than 1,000,000 in the Near East and fewer than 100,000 in the Druze Diaspora. The Israeli Druze population is estimated at 150,000, and is distributed over three geographical sub regions: the Carmel, the Galilee, and the Golan Heights.* [Ref 40](#)

The Druze represent a small minority of the populations of the countries wherein they reside. These countries are Syria, Lebanon, Israel, and Jordan, which are all considered to be within the eastern Mediterranean or also known as the Levant region. This is the Holy Land area where much Biblical history took place. This is the exact area where Lehi's group departed from on their journey to the Promised Land according to the Book of

Mormon. This population has genetic markers that match Native American markers today. The possibilities are intriguing.

Conclusions: Our findings suggest that *the Near East maternal genetic landscape differed substantially in the past from its current structure, and was enriched in diverse lineages of the mtDNA X haplogroup.* These findings have been uncovered due to the *unique demographic features of the Druze population, and the adjusted sampling method employed in the current study. The combination of a high frequency and diversity of the Druze mtDNA haplogroup X lineages, in a confined geographic region, and the low migration rate with nearby populations make it unlikely that this diversity was imported. It is thus likely that the global diversity of this haplogroup evolved in the Near East and adjacent regions of western Eurasia, during a long incubation period coinciding with and following the most recent out of Africa expansion as dated by mtDNA coalescence simulations. The Druze population of the Galilee represents a contemporary refugium of this past genetic landscape.* [Ref 40](#)

This quote states that in the history of the Druze, haplogroup X lineages may have been enriched in their diversity, which could help to explain any differences in the subgroups of lineage X. They clearly state that the global diversity of haplogroup X likely began from the Near East (Holy Land and Israel) region. The Druze population of the Galilee gives us a sampling of this ancient genetic landscape.

Abstract Conclusions: These findings were enabled through the use of a paternal kindred based sampling approach, and suggest that *the Galilee Druze represent a population isolate, and that the combination of a high frequency and diversity of the mtDNA X haplogroup signifies a phylogenetic refugium, providing a sample snapshot of the genetic landscape of the Near East [Syria, Lebanon, Israel and Jordan] prior to the modern age. [before 1400 AD]* [Ref 40](#)

Earlier the subhaplogroups of X, namely X1 and X2, were discussed. Haplogroup X is a unique group because it does not exhibit a geographic pattern as do the other

haplogroups. Another unique factor about the Druze population is that it has both X1 and X2 within its lineage. The explanation of this is that X subdivided within this group anciently.

Unlike other mtDNA haplogroups, X does not exhibit a geographic pattern. Its major subhaplogroup X1 is widely dispersed throughout North Africa whereas X2 is widespread from Europe to Northern America but in very low frequencies. Druze is the first population identified where both subhaplogroups are represented, and their diversity is high. A proposed explanation for these results is that Druze of Galilee represent the "refugium" population where haplogroup X remained since ancient times when it was more frequent. <sup>Ref 41</sup>

Which, then, came from which? Did X1 come from X2 or vice versa?

...thus, it cannot be completely ruled out that X1 is indeed a subset of X2 that reverted at both nucleotide positions. However, this possibility appears very unlikely, especially when one considers the time depth and the distinct geographic distribution of X1. <sup>Ref 32</sup>

It is still unknown which came first. The point is that the Druze population has both subsets of haplogroup X, which was highly surprising to those conducting this research.

In summary, the Druze population which is found in the Levant region around Israel has a high frequency of haplogroup X mtDNA. Their practice of intermarrying within their group rather than without is shown to have created a genetically isolated population (refugium) that has remained relatively unchanged over a minimum of 600 years.

It has been proposed that this population be used in the field of genetics as the "sample" genetic population of the Near East (Syria, Lebanon, Israel, and Jordan) prior to the modern age (roughly 1400 AD). This same population shares haplogroup X2 in common with Native Americans in North America. The Druze population presents a "snapshot" of the genetic landscape prior to this time. This is thought to be the source

population from which the other haplogroup X lineages stemmed, such as the Northern Native Americans who share this lineage.

This is the area from which Lehi's ancestry arose and where he lived and preached prior to their departure to the Promised Land. The significance of the linking and interconnectedness of this ancient Holy Land region mtDNA lineage with Native North American populations cannot be overstated.

### *The Jewish Population and Haplogroup X: More Robust Evidence from the Mediterranean Area.*

There is one aspect of the Druze population that may, however, be a little unsettling. They are not Jewish. The Druze are more closely akin to Arab, Lebanese, and Palestinian lineage groups. They most certainly would be considered to be able to trace their ancestry back to Shem, making them a "European" genetic group, but they are distinct from Jewish populations both by ancestry as well as religion. If the Druze haplogroup X lineage is the source of the Native American haplogroup X lineage, could their ancestry trace back to Jacob and Joseph, thereby linking Lehi and Ishmael's wives ancestry with the Druze? The answer to this is as yet unknown.

Further research into other Old World populations that have or "harbor" haplogroup X reveals even more startling possibilities for linking this lineage with Book of Mormon people. While the Druze have haplogroup X, but are not a Jewish population per se, haplogroup X has now been determined to be a primary mtDNA marker for many genetically known Jewish populations, including one very interesting one that harkens directly back to Lehi's time and place.

In a 2008 medically related article on the frequency of Type 2 Diabetes among Jewish populations from *BMC Genomics*, author Jeanette Feder outlines the 12 most

prevalent mtDNA haplogroups in Ashkenazi Jews, which is one of the largest Jewish population groups, and haplogroup X is among the 12 distinctive Jewish markers.

Results: A total of 1,179 T2DM [Type 2 Diabetes] patients comprised of three populations (762 Ashkenazi Jews [Ash], 191 non-Ashkenazi European Jews [Seph], and 226 North African Jews [NAF]), were genotyped and assigned to different mtDNA haplogroups. Almost 90% of the subjects belonged to one of the 12 most prevalent mtDNA haplogroups in Ashkenazi Jews, i.e., K1, K2, U (non-K), H, V, J1, J2, T, N1b, I, X, W. [Ref 42](#)

Modern Jews in the following article in *PLoS ONE* in 2008 were divided into two groups: Ashkenazi Jews and non-Ashkenazi Jews. The Ashkenazi group ancestral lineages harken back to Europe, while the non-Ashkenazi Jews have continuously resided in the Near and Middle East and North Africa where they had been scattered. The article again confirms that Jewish religious practices have had a profound effect on their mtDNA genetic histories. It also states that they are probably descendants of the Babylonian exile.

*Contemporary Jews, whose number is estimated at 13 million, can be divided to Ashkenazi and non-Ashkenazi, which are each in turn comprised of numerous different constituent communities. Ashkenazi refers to Jews whose recent ancestry over the past millennium traces to Central and Eastern Europe. The geographically much more widespread non-Ashkenazi Jewish communities are also culturally more diverse, and are comprised of the Jewish communities that have continuously resided in the Near and Middle East and in North Africa and in different geographic locations to which Jews fled or to which they were deported including the Iberian expulsion in 1492-1495. These communities also share similar religious rituals, probably due to their presumed common historical origin from the descendants of the much earlier Babylonian exile. As a result of common ritual practices, they are sometimes collectively referred to as the Sephardic (Spanish) or Mizrahi (Eastern) Jews.* [Ref 43](#)

The Haplogroup X lineage has now been identified in Moroccan, Libyan and Tunisi-

an Jewish populations, albeit with differing sub-lineages represented by X2b and X2e. In one article, ten out of twenty (50%) of Libyan Jews were reported to have haplogroup X2e.

*One X2b Moroccan Jewish putative founding lineage was analyzed using 2 complete mtDNA sequences. One putative founding lineage in Hg T2 was shared by Iraqi and Iranian Jews, and was assessed by two complete mtDNA sequences. Two putative founding lineages (one in Hg H and one in Hg X2e) were shared by Libyan and Tunisian Jews, and were assessed by the same complete mtDNA information.* [Ref 43](#)

The Libyan and Tunisian Jewish communities shared among them an X2e1a1a lineage as the most frequent. [Ref 43](#)

*One-half of the Libyan Jews belong to a rare subclade of haplogroup X2e, defined by a transition at np 15310, that is widespread in the Caucasus and Central Asia.* [Ref 44](#)

The maternal founding event in *Libyan Jews* is evident, as 39.8% of their mtDNAs could be related to one woman carrying the X2e1a1a lineage, supported by an earlier observation, where ten out of twenty Libyan Jews were found to share this haplotype. [Ref 43](#)

Figure 2 in the article "Jewish and Middle Eastern non-Jewish populations share a common pool of Y-chromosome biallelic haplotypes," published in *PNAS*, in 2000, shows a dramatic demonstration of the closeness of the Druze population with several Jewish populations. The Druze are in the same quadrant as the majority of Jewish populations, including the Near Eastern Jews, Yemenite Jews, North African Jews, Kurdish Jews, and Roman Jews. This plot was based on Y-chromosome haplotype data from 29 populations made up of 22 non-Jewish and 7 Jewish populations.

*The Ashkenazi, Roman, North African, Near Eastern, Kurdish, and Yemenite Jewish populations formed a fairly compact cluster between the North African and European groups. This Jewish cluster was interspersed with the Palestinian and Syrian populations, whereas the other Middle Eastern non-Jewish populations (Saudi Arabians, Lebanese, and Druze) closely surrounded it.*

Of the Jewish populations in this cluster, the Ashkenazim were closest to South European populations (specifically the Greeks) and also to the Turks. *The close genetic affinity of Jewish and Middle Eastern non-Jewish populations was confirmed in population differentiation tests.* Pairwise comparisons between population groups indicated that only 0.8% of the total genetic variance in Jewish and Middle Eastern non-Jewish populations was attributable to between-group differences. <sup>Ref 45</sup>

The Druze population is in fact closely related genetically to Jewish populations. The Jewish population clusters were closely surrounded by the non-Jewish populations in this study such as the Druze. In other words, the Druze and Jews are genetically related if taken back enough generations in their ancestry.

### *The Iraqi Jews*

The non-Ashkenazi (Levant or Holy Land area) Jewish populations make up some of the most ancient populations of this lineage group.

*The Jewish communities of Iraq and Iran constitute the oldest non-Ashkenazi Jewish communities outside the Levant and were established during the 6th century B.C.E.* [Before Common Era, or more commonly 600 BC]. <sup>Ref 43</sup>

The oldest non-Ashkenazi Jewish communities outside of the Holy Land area were established about 600 BC and are primarily located in Iraq and Iran. Why would 600 BC and the lands of Iraq and Iran be significant?

Returning to the Book of Mormon and the account of Lehi we read.

13 And he read, saying: *Wo, wo, unto Jerusalem, for I have seen thine abominations! Yea, and many things did my father read concerning Jerusalem—that it should be destroyed, and the inhabitants thereof; many should perish by the sword, and many should be carried away captive into Babylon.*

BoM 1 Nephi 1:13

18 Therefore, I would that ye should know, that after the Lord had shown so many

*marvelous things unto my father, Lehi, yea, concerning the destruction of Jerusalem, behold he went forth among the people, and began to prophesy and to declare unto them concerning the things which he had both seen and heard.*

BoM 1 Nephi 1:18

From this vision Lehi learns that Jerusalem is about to be destroyed by the Babylonians, and that they will carry many Jews as captives back to Babylon. Lehi went among the people of Jerusalem and prophesied about what he had learned in vision. They did not believe him and sought his life (1 Nephi 1:19-20). Lehi then left with his family.

4 Yea, even six hundred years from the time that my father left Jerusalem, a prophet would the Lord God raise up among the Jews—even a Messiah, or, in other words, a Savior of the world.

BoM 1 Nephi 10:4

Lehi and his family left Jerusalem, according to this verse, 600 years before the Messiah or Christ came, making the date of his departure 600 BC. Fourteen years later, the Babylonians, according to historical sources, did in fact destroy Jerusalem and its temple, carrying these very people that Lehi had prophetically warned with them back to Babylon, now known as the country of Iraq.

To answer the previous question about the significance of this date and location regarding the non-Ashkenazi Jewish populations that were established in Iraq and Iran, it is interesting that these populations may be the actual descendants of the very people to whom Lehi prophesied. This begs the question: Is there a Jewish population still remaining in Iraq, the location of the ancient empire of Babylon? And if there is, what mtDNA lineages do they have? An article published in the *American Journal of Human Genetics* in 2002 provides additional historical insight.

*Iraqi Jews are Jews who were born—or whose parents or grandparents were born—in Iraq; Jewish tradition places the origin of this community in the exile following the destruction of the first temple in 586 B.C. Iranian Jews are Jews who were born—or*

whose parents or grandparents were born—in Iran; the origin of the community is obscure, but it is thought that it may be an offshoot of the Iraqi community. [Ref 46](#)

This 2002 article clears up these questions by stating that there is such a Jewish population in Iraq, that they are thought to be the descendants of those that were taken captive from Jerusalem just as Lehi prophesied. This population does in fact harbor

haplogroup X mtDNA. However, only one individual was sampled, resulting in haplogroup X1a rather than X2. No further information about this particular Jewish group is at present known. The extremely small sampling (one person) and the possibility of another population besides the Druze that may have both X1 and X2 clades of haplogroup X, leaves open the possibility of even closer genetic relationships between this population and Native North Americans.

TABLE 5. Distribution of mtDNA Haplogroups in 9 Israeli Populations

Populations	No. Ind.	No. Hap.	Number of individuals in each mtDNA haplogroups																							
			L0-L3	M	X	W	NI/1	R*	J	T	U1a	U3	U6	U7	U5/U2	K (preHV)	1	pre <sup>V</sup>	HV*	HV1	HV3	H*	H1			
Ethiopian	21	17	8	7	1						1												4			
Ashkenazi	20	16			1	1	2		1	1			1	1	1	9		1	1							
Iraqi	20	17		1	1	1	1		3	4	1	6													1	1
Libyan	20	13	1		10				1				1						1						4	2
Moroccan	20	19			2				3	1		1					1	1	1		3			4	3	
Yemenite	20	18	1				1	1	2		3	2					2	2			4	2			2	
Samaritan	16	6							9				1	5											1	
Druze	20	17					1	2			1								4	1					7	4
Palestinian	20	19	2	2			1			2	2		1					1	1	1					3	

Native American haplogroup X2a is unique in that to date no matching lineage in the Old World has been found. However this 2009 article in *Current Biology* by LDS geneticist Ugo Perego clarifies that the Native American lineage is considered to be associated with the Old World “branches” of X2 that include X2b-X2f.

As for haplogroup X2a, all but one of the sequenced mitochondrial genomes harbored the distinguishing X2a coding-region motif 8913-12397-14502. The exception was one of the Ojibwa sequences, which did not cluster either with X2a or any of the known Old World X2 branches (X2b-X2f). This novel X2 branch has been named X2g, and its presence in Native Americans most probably indicates an additional and very rare Native American founder. [Ref 35](#)

To summarize, haplogroup X has been established as a European lineage which has now been found throughout the Near East or Mediterranean area in both non-Jewish populations such as the Druze as well as the Jewish Ashkenazi, Sephardic, North African,

Libyan, Iraqi, Moroccan and Tunisian groups. All of these groups harken from the Holy Land area where Lehi, Ishmael and their families undoubtedly lived prior to their sojourn into the wilderness. It has been shown that the very people to whom Lehi preached and that were later a part of the fulfillment of Lehi’s prophecy concerning their being taken captive to Babylon have descendants that today harbor haplogroup X mtDNA.

Now it can be said with confidence that modern North American Native peoples do in fact share a common lineage with Jewish populations stemming from the Mediterranean area of the Old World. This fact is inescapable according to mtDNA findings, and strongly supportive of the claims of the Book of Mormon. The significance of the correlations between multiple Jewish and non-Jewish populations in the Levant or Holy Land region with Native populations in North America through mtDNA backed research cannot be mistaken by those with an understanding of the Book of Mormon history.