



## CHAPTER TWELVE

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# A SECOND LOOK

**T**he field of genetics is in a constant state of flux as it goes about sequencing and interpreting DNA data, continuing to gain additional insights from larger and more robust sampling groups and methods. One of the most exciting things for members of The Church of Jesus Christ of Latter-day Saints is that these findings may provide additional validation for the historical claims of the Book of Mormon and also potentially lend supporting evidence in favor of Joseph Smith's understanding and revelations involving the geography that is outlined within the prophecies and promises of the Book of Mormon.

Those taking issue with the Book of Mormon lineage claims did so based on the assumptions explained above. For example, it was assumed that the Book of Mormon descendants would have Israelite or at least European type DNA markers and these markers would be found in the Americas. It was specifically thought these genetic markers or lineages would be found in Mesoamerica because a general consensus among LDS scholars had been reached by this time. Since no such lineages were found in the initial studies and all founding lineages found in Mesoamerica were Asian-based, it was believed that this *proved* that the Book of Mormon claims

have no basis and are therefore false. Such were the assumptions of those who were a little too eager to attempt to discredit the Book of Mormon and the Church.

These groups relied on the incomplete preliminary findings of DNA research and assumed that DNA research would predict the demise of Book of Mormon claims. Not only were the non-members premature in their assumptions but also the LDS scholarly community was perhaps a little hasty in defending their positions in the DNA controversy, trying to explain why there wouldn't be any Israelite DNA found in the generally accepted Mesoamerican setting for the Book of Mormon.

Researchers and geneticists working on Native American DNA sequencing did, however, find a new genetic strain that didn't match with any of the established Asiatic lineages. Initially, it was relegated to the "other" category until further sampling could be done. As early as 1998 these new findings were beginning to surface in the professional journals and literature. Genetic research in Europe was by this time in full stride and the journals were flowing with information on their findings. Scientific investigators were beginning to unravel some of the mysteries behind the migrations of the ancient peoples of Europe. Populations were being sampled and linkages and groupings of European peoples were being procured from the data found. Investigators on both sides of the Atlantic began to share their findings with each other in unprecedented cooperation. Consequently, unexpected links between the old world and the new world began to be found.

The predominate theory of the peopling of the Americas, known as the Bering Strait theory or hypothesis, claims that ancient Asian people crossed a land bridge sometime during the last ice age into what is now Alaska. They then worked their way down through Canada into the United States, Mexico, and Central America, finally pushing their way into South America. This theory assumed that there would be no *founding* of European descent until the more recent admixture with Vikings and other European explorations into the Americas.

The initial research conducted on Native American populations throughout the Americas 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 native to populations in Asia, lending support for the dominant theory of the peopling of the Americas over the Bering Strait land bridge or Beringia during the last ice age. Confirming this concept, an article in the journal *Science* appeared in 1998 with a surprise twist in the genetic makeup of Native Americans.

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, 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.<sup>90</sup>

The end of this quote makes reference to an interesting find among a handful of Native Americans that was originally thought to be insignificant and categorized as “other,” as its markers were unique from the other four haplogroups. David Smith refers to this group stating, “The remaining few Native Americans that do not exhibit one of these four haplogroups have been termed ‘others’...”<sup>91</sup>

It wasn't until DNA testing got underway in Europe and comparisons could be made between the Native American populations in the Americas and the newly developed European DNA databases that there was discovered a genetic relationship between some Native American and European lineages. When these lineages were further analyzed it was found that a particular set of markers existed in some European populations which correlated with some Native American markers in prehistoric North America. An article by science writer Virginia Morell introduces these findings, reporting on the remains that came to be known as Kennewick Man:

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, 1990). 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.<sup>92</sup>

This article started a firestorm of excitement and controversy among geneticists and archaeologists conducting DNA and archaeological research. Many scientists feared that these findings could be contrary and damaging to the dominant theory of an Asian migration if the markers of this “other” haplogroup could not be found in the Asian populations. The identification of this other DNA source was designated “haplogroup X” as outlined by David Smith, which suggested the possibility of a fifth founding haplogroup<sup>93</sup> that was unrelated to the Asian haplogroups A, B, C, and D.

Upon investigation, it was initially found that no such markers turned up in Asia, suggesting that an alternate migration route may have been taken by an ancient European population into the Americas. The suggestion was made by Morell that a possible link had been found between European populations and Native Americans as she quotes Theodore Schurr, a molecular anthropologist from Emory University in Atlanta: “The new data, from a genetic marker appropriately called Lineage X, suggest a definite—if ancient—link between Eurasians and Native Americans.”<sup>94</sup>

Further investigation into a possible source population for this set of markers found in these Native Americans revealed that indeed this was a European lineage and had the same set of mtDNA markers that were confirmed in such European populations as Italians, Finns, and most interestingly for this research, Israelis.

Haplogroup X was still not found in any populations in Asia as reported in the journal *Science*.<sup>95</sup>

Haplogroup X was found to be concentrated among seven Native American Language groups. These seven language families are today found throughout North America. Haplogroup X mtDNA markers were found in highest concentrations in the Canadian Subarctic/Great Lakes region. The broadest language group is known as Algonquian, which encompasses over 100 Native American tribal groups. Smith explains this distribution by stating that:

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.<sup>96</sup>

Such wide distribution, combined with the fact that these groups shared a common genetic lineage, justified haplogroup X being classified as a “founding haplogroup,” taking its place with the other four Asian-based founding groups. Today haplogroups A, B, C, D, and X remain as the only five founding haplogroups of Native Americans found in the Western Hemisphere: 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 a large distribution to qualify for founding status, and there are simply no other haplogroups with large and widely dispersed distributions. If there were other such founding haplogroups, they would have been found long ago.

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 *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.

### ***Haplogroup X, a Founding Lineage***

The discovery of this European type mtDNA was initially thought to have been the result of recent contact of Europeans with Native American populations which would have occurred after the time of Columbus. It became necessary to determine if this set of five specific markers arrived in the Americas before or after 1492 and the arrival of European explorers to the New World. 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 historic 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.<sup>97</sup>

Recently, several sets of remains from west-central Illinois, near the site of the Naples-Russell Mound #8 or what has become known as the Zeph Mound of Zion's March were sequenced. This is the same area where Joseph Smith declared that the last great struggle (not battle) between the Nephites and Lamanites took place.<sup>98</sup> The remains from this area, near what is today known as the Dixon

Mounds, just east of present-day Nauvoo, Illinois were sequenced and analyzed confirming a pre-Columbian presence of haplogroup X in the heartland of America. This is described in *Evolutionary Anthropology*, which makes a direct connection between prehistoric North American remains and modern Algonquians, confirming both as having this European-based haplogroup.

...haplogroup X also have been found in two individuals from the Norris Farms Oneota 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.<sup>99</sup>

A series of specific mtDNA markers distinguishing haplogroup X from other European lineages and its existence in ancient Native North American populations was verified by DNA sequencing. This lineage and other ancient remains have confirmed that haplogroup X was among the ancient American inhabitants of North America. To date, this haplogroup X is the only European lineage known to be a founding or primary genetic contributor to Native American populations throughout the Western Hemisphere. This genetic lineage provides at least a possibility of supporting the claims of Book of Mormon history, the “remnant,” and the statements of Joseph Smith.

### *Haplogroup X Not Found in Asia*

A fundamental difficulty between the haplogroup X lineage and the dominant Bering Strait theory 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, but haplogroup X 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 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. At first, such a trace for haplogroup X

appeared to be completely absent, unlike the other four founding haplogroups. However, a “clade” or strain of haplogroup X was found in the Altaian populations of southwestern Siberia.<sup>100</sup>

An article in the *American Journal of Human Genetics* reports extensive research of the Asian mtDNA data, looking for traces of haplogroup X. The Altaian samples, upon closer examination, were found not to have those particular markers common to Native American haplogroup X carriers. The study indicated that the Altaian markers were more likely explained by a much later incursion of European bloodlines, making the Altaian group unrelated to the Native American groups and as such they could not have been the source population for the haplogroup X carriers in North America.

The conclusion was that “...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.”<sup>101</sup> An explanation for the detection of the Altaian haplogroup X was given in a 2005 article in the journal *Annals of Human Genetics* that attributed the Altaian group to the Mongolian Expansion.<sup>102</sup> It was confirmed that the Native American haplogroup X mtDNA lineages were unrelated to the Altaian lineages and could not have derived from the same group.

Ongoing research then indicated that the strain of haplogroup X found among the Native Americans came to the Americas by a different route other than the Bering Strait.<sup>103</sup> Of course the Book of Mormon declares that a migration by boat did occur, long before Columbus, and that the genetic makeup of this founding group should be of a European-type haplogroup that would be genetically connected to the Middle East.

The Bering Strait theory continues to be so prevalent and pervasive—almost dogmatic—that researchers are still trying to find some sort of trace for haplogroup X in Asia rather than accept the indications that another possible European migration had actually occurred. However, as of 2009, haplogroup X strains of mtDNA



found in Native Americans are still not found in Asia which continues to frustrate the theory, causing researchers to invoke “it got lost” or “it evolved in a place that no longer exists” explanations.

Geneticist Ugo A. Perego writes “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.”<sup>104</sup> Although Perego falls into the land bridge camp, he like many others finds it difficult to provide an answer or conclusion that might be *contrary to scientific dogma and consensus*. He offers an unverifiable theory for an Asian migration across a land bridge that “got lost” rather than accept the data that would lead to an unpopular secular conclusion but would possibly support the claims of the Book of Mormon.

To be accepted in the scientific world a scientist or geneticist cannot go against well-entrenched theory and the Bering Strait theory is the most widely accepted genetic theory for the peopling of the Americas at this time. The current and popular presumptions are founded in an “evolutionary model” that would postulate that these population movements occurred long before the scriptural chronology of the Book of Mormon and even the Bible.

### *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, Lenni 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. Haplogroup X has also been found to be geographically widespread throughout nearly all of North America among groups that share no close historic or linguistic ties, indicating an expansion and subsequent diffusion from the Great Lakes region.

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 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...The presence of a daughter clade in northern Native Americans testifies to the range of this population expansion.<sup>105</sup>

This 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 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 and subtype 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?

The wide dispersion of haplogroup X over the entire North American continent provides additional clues as to when this lineage arrived in the New World. Such a wide dispersion of this lineage indicates that it arrived long enough ago for it to have been dispersed amongst many native populations in the Americas.

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.*<sup>106</sup>

This article amazingly not only confirms that haplogroup X is a “founding” American Indian or Amerindian group, but that it is geographically widespread throughout North America. It is found in highest frequency in the Great Lakes region, which is precisely where Joseph Smith recovered the ancient record, and sent the very first missionaries of the church “unto the Lamanites” (D&C 28, 30, 32) 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 has been found there to date.

The latest results in mtDNA research reaffirm that haplogroup X2a continues to be restricted to North America in the January 2009 article in *Current Biology*. The author, 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.<sup>107</sup>

A few summary statements would explain that haplogroup X, which is a European-based lineage of mtDNA, is the only European haplogroup now confirmed among the founding populations of North America. It is found in highest frequencies in the Great Lakes area among present-day Native American Algonquin-speaking language groups, yet is widespread throughout North America, including groups that apparently have no cultural or linguistic ties. Remains from west-central Illinois, which is near where Joseph Smith's Zephr 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 it is important to recognize that the modern Algonquin Indians from the Great Lakes area have nearly identical DNA sequences as those found in ancient burial mounds in Illinois. These mounds and the remains that were tested are considered to be the remnants of the Hopewell culture. Charles C. Mann states in his book *1491* that the Algonquin-based languages originated in a civilization known today as the Hopewell Mound Building culture, which flourished between 300 BC and 400 AD, when it ended abruptly archaeologically. These Algonquin languages are thought to have existed as a single language about 200 years before Christ.<sup>108</sup> Mann continues by stating that the Hopewell culture spread not because of conquest but the "vehicle for transformation" of this culture "may have been Hopewell religion."<sup>109</sup>

### *No Haplogroup X in Mesoamerica*

An article in *American Journal of Physical Anthropology* in 2005 provides additional insight into the question of whether or not a Mesoamerican setting for the Book of Mormon provides a similar level of potential evidence in favor of the claims of the Book of Mormon. The article "*Is Haplogroup X Present in Extant South American Indians*" provides a stark answer to the question, stating that haplogroup X is not present in Central or South America.<sup>110</sup>

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 or any other European founding lineages among Native South American populations. They are all members of haplogroups A through D, the Asian lineages found throughout the Americas.

The article goes on to state that up to the time of publication, "haplogroup X has only been found in North America." 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 by Claudia L. Dornelles on 25 Native South American populations, looking for specific haplogroup X distinguishing markers. Their results found no evidence for haplogroup X among these populations.

A total of 1,159 mitochondrial DNA samples from two Mongolian, two Siberian, and 25 Native South 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, [totaling] 5,760 base pairs. *The results indicate that haplogroup X is not present in these samples.*<sup>111</sup>

The article above 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 strange 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.*<sup>112</sup>

Dornelles concludes the article by making it clear that haplogroup X is a lineage that is not found in indigenous South American populations, stating: "The evidence presented here strongly supports the hypothesis that haplogroup X is likely absent in modern Native South American populations."<sup>113</sup> The evidence is clear that this haplogroup with European and Middle Eastern ancestors is not a part of the founding populations of Central or South America.

In 2005 an article appeared in *Hispanic American Historical Review* titled "Genetics and the History of Latin America" which provided another witness to the previous article and conclusions. It contains a chart with the five founding haplogroups listed across the top, and Native American populations north of Panama down the side bar. In this article the author asks a question of the reader: "What can the geographic distribution of mtDNA variation teach us about the history of Latin America?"

The conclusion and answer to the question is addressed by this statement. "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."<sup>114</sup>

The article and chart indicate that both contemporary and ancient Mayan populations have zero percentage of haplogroup X, or any other European lineages among them. The Mayan populations are considered by most Mesoamerican theorists to be the most likely population to be descendants of and correlated with the Book of Mormon. The ancient Maya (Quintana Roo) were found to be of haplogroups A (87.5%), C (8.3%), and B (4.2%), which are all Asian lineages, with no evidence of European descent.

Table 2. Haplogroup Frequencies of Selected Populations in North America

Population Haplogroup	N	%A	%B	%C	%D	%X
Aztecs (Tlatelolcr, Mexico City)*	23	65.2	13	4.3	17.4	0
Cora (Nayarit)	81	28.4	51.9	16	3.7	0
Huichol (Nayarit)	52	34.6	53.8	11.5	0	0
Ancient Maya (Quintana Roo)*	24	87.5	4.2	8.3	0	0
Contemporary Maya (Yucatan)	26	53.8	23.1	15.4	7.7	0
Highland Mixe (Ayutla, Oaxaca)	16	62.5	31.3	6.3	0	0
Alta Mixtec (Nochixtlan, Oaxaca)	15	73.3	13.3	13.3	0	0
Baja Mixtec (Huajuapán, Oaxaca)	14	92.9	7.1	0	0	0
Atocpan Nahua (Milpa Alta)	49	38.8	40.8	16.3	4.1	0
Cuetzalan Nahua (Puebla)	31	61.3	32.3	6.5	0	0
Tarahumara (Durango)	72	33.3	29.2	64.9	5.6	0
Valley Zapotec (Oaxaca)	15	33.3	33.3	33.3	0	0
Akimal O'odham (Southeast Ariz.)	43	4.7	53.5	39.5	0	2.3
Anasazi (U.S. Southwest)*	25	24	60	14	0	0
Cochimi (Southern Baja Calif.)	13	7.7	46.2	46.2	0	0
Delta Yuman (Western Ariz.)	23	0	56.5	43.5	0	0
Fremont (Great Salt Lake)*	30	0	80	13.3	6.7	0
Jemez (Northwestern New Mexico)	36	0	88.9	2.8	0	8.3
Kiliwa (Northern Baja Calif.)	7	0	100	0	0	0
Pai Yuman (Northern Baja Calif.)	27	7.4	66.7	25.9	0	0
River Yuman (Western Arizona)	22	0	63.6	36.4	0	0
Tohono O'odham (Arizona)	37	0	56.8	37.8	5.4	0
Zuni (Northwestern New Mexico)	26	15.4	76.9	7.7	0	0

\* Pre-contact Population

Source: Compiled from various sources at <http://resendez.ucdavis.edu/ref.html>

As discussed by Resendez and others, the primary haplogroups in Mesoamerican indigenous populations are dominated by the Asian haplogroups A and B, with significant levels of C and minor levels of D. Haplogroup X, the only known European founding lineage, is conspicuously missing from any Mesoamerican or South American populations. Haplogroup X has only been found in North

America. At the time of this publication there is not one among the entirety of Mesoamerican populations that carries a known founding European mtDNA lineage or heritage.

The absence of any European or Middle Eastern mtDNA in Central America has formed the basis of the attacks against the historicity of the Book of Mormon by anti-Mormon critics. There is simply no genetic evidence in Central or South America to support the claims of those who adhere to a geographic setting which excludes North America.

This reinterpretation of scripture is much like the “two Cumorah theory” which was postulated to explain and maintain consistency with a Mesoamerican-centric view. In recent years many books, tapes, DVD’s and tour packages have appeared, which state or imply that Mesoamerica is, without question, the defacto setting for the Book of Mormon.<sup>115</sup>

Because of this “unofficial” but culturally accepted trend in LDS culture, and the growing support for the “consensus” theories coming from scholars of the Church, Anti-Mormon groups have adopted the view that this popular theory has become accepted as doctrinal fact among Latter-day Saint scholars and therefore Latter-day Saints in general subscribe to the prevailing view that the Book of Mormon occurred in the proposed limited Mesoamerican setting. The mtDNA research conducted thus far has revealed that no supporting evidence has yet or is likely to ever be found in Central America for a genetic “remnant” which disconcerting fact continues to fuel direct anti-Mormon attacks.

Every significant indigenous population in the Americas has now undergone at least some DNA testing. It is also true that of the entire DNA testing completed thus far, most of it has been done by focusing primarily on the control region and other segments of the mtDNA itself and not on complete mtDNA sequences. However, enough has been accomplished that it is very highly doubtful that any new founding lineages will be found or accepted. While it may be possible that there remains some small, hidden population deep



in a mountain jungle in Central or South America that has not as yet been tested, it would be insufficient to establish another founding European lineage such as haplogroup X even if found among such a population. Such a small population is not what would be expected by a population group the size described in the Book of Mormon in the first place. Those who study the scriptures are not looking for a tiny insignificant remnant of the Book of Mormon peoples.

Haplogroup X, which is the only founding European lineage known to have occurred anywhere in the Americas anciently, is found only in the Native American populations in North America. Because of this, haplogroup X is the most likely, and most qualified or suitable candidate lineage for establishing a possible, plausible, and probable case for the historicity of the Book of Mormon.

### *A Curious Finding*

Haplogroup X lineages have been reported in Europe and Western Eurasia. 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, a religious order that has strict rules pertaining to many areas of their lives, including matrimony, do not proselyte and the only method of becoming a Druze is by birth.

In a May 2008 article it was concluded that the “Galilee Druze” provide a “*sample snapshot of the genetic landscape of the Near East prior to the modern age.*”<sup>116</sup> According to geneticists, the Druze population genetics could be considered a sample population of Israel before the modern age. This finding further strengthens the genetic connection between the old world populations of the Mediterranean area and the American Indian populations of North America.

Haplogroup X is found among the Druze population in such high frequencies, it was stated, that “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%)."<sup>117</sup> Although a geographic region for the origin of haplogroup X among the Druze has not been defined, researchers surmise it might be Israel.

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.<sup>118</sup>

The article also implies that "The Druze population has a unique historical, social and demographic structure, which is closely connected with their religion."<sup>119</sup> This is unique because it involves religious and social policies regarding marriage to those outside of their order.

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.*<sup>120</sup>

This type of genetic refuge found among the Druze is similar to the genetic findings of Jewish populations scattered in the Middle East that tend not to mix or intermarry with their host populations. These genetic ties to haplogroup X provide "a sample snapshot of the genetic landscape of the Near East [Syria, Lebanon, Israel and Jordan] prior to the modern age" [before 1400 AD].<sup>121</sup>

This statement should even include the Jewish communities that existed in the same area before modern times. The authors of this article 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. For a more in-depth discussion pertaining to the Druze and haplogroup X, see *Rediscovering the Book of Mormon Remnant through DNA* by Rod Meldrum.

### *The Jewish Population and Haplogroup X*

Haplogroup X has now been found to be a primary mtDNA marker for many genetically known Jewish populations. This current research solidified evidence that haplogroup X is also a primary Jewish lineage and is found among extant Jewish communities dating to the very time period of Lehi. In a 2008 medically related article on the frequency of Type 2 Diabetes among Jewish populations, haplogroup X is one of the 12 distinctive Jewish markers.<sup>122</sup>

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

Contemporary Jews, whose number is estimated at 13 million, can be divided between 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.<sup>123</sup>

The Haplogroup X lineage has now been identified in Moroccan, Libyan, and Tunisian Jews, albeit with differing sublineages represented by X2b and X2e. In one article, ten out of twenty (50%) Libyan Jews were reported to have haplogroup X2e.<sup>124</sup> 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 BCE [Before Common Era or more commonly 600 BC].”<sup>125</sup> Therefore the Jewish communities of Iraq and Iran date to the same time period as Lehi (1 Nephi 1:4). The Prophet Lehi leaves Jerusalem with his family immediately before the Babylonian captivity as recorded in the Book of Mormon.

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. These Jewish populations trace their actual ancestry to the very population to whom Lehi prophesied. An article in the *American Journal of Human Genetics* speaks of these Iraqi Jews.

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 BC.* 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.<sup>126</sup>

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, and that this population does in fact harbor haplogroup X mtDNA.

To summarize this section, 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 many Jewish communities. Almost all of these Jewish groups and communities can be traced back to the Holy Land area where Lehi, Ishmael, and their families undoubtedly lived prior to their departure to the Promised Land. It has been shown that the very people to whom Lehi preached and that were later part of the fulfillment of Lehi's prophecy concerning their being taken into captivity by Babylon have modern-day descendants that today harbor haplogroup X mtDNA.

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 underestimated by those with an understanding of Book of Mormon history.

### *A More Comprehensive View*

While LDS scholarly articles demonstrated excellent knowledge and expertise on the subject of genetic research, the arguments are biased because of an underlying assumption and deep-rooted belief that the Book of Mormon history occurred within the confines of Central or Mesoamerica. This assumption has cast their articles and statements into a defense of Mesoamerica rather than addressing the DNA issue directly. How easy would it be to say that Mesoamerica is not where Joseph Smith declared the "remnant" to be? An uncompromising belief in the Mesoamerica model has resulted in dismissal of potentially empirical evidence which

actually supports the Book of Mormon by acknowledging a direct link between ancient Mediterranean people and Native American populations in North America.

Why would the LDS scholarly community seriously consider this or any new DNA related information when they believe that they have clearly addressed the DNA issue and have concluded that there will most likely never be any evidence for or against the Book of Mormon? Their explanations certainly apply equally to North America as to Mesoamerica. Therefore, any information to the contrary may be viewed as insignificant or old news. Yet this information appears to be very recent and very exciting news to most latter-day saints.

It is hoped that this research will reopen the discussion on Book of Mormon geography and that this DNA evidence will allow a new model to be seriously considered rather than invite attempts to ignore or dismiss its authors. This information is beginning to take hold within the rank and file of church membership spurring a new level of energy and excitement not seen before. However, it remains to be seen where the scholarly community will line up in regard to this research with helpful objectivity, polite disregard, or outright disapproval.

Ironically, the greatest barrier to promulgating the information contained in this book is not the anti-Mormon faction. The greatest objection to this research comes from those whose theories, articles, papers, books and reputations are challenged by a move away from Mesoamerica. Sadly, many in the LDS scholarly community simply refuse to look objectively at the statements of Joseph Smith, the context of the Book of Mormon, and the scientific evidence, both genetic and archaeological.

Many have rightly questioned: Why have we not looked more objectively at the full text of the Book of Mormon and the inherent prophecies and promises found therein? Why has the archaeological evidence found that points to the heartland of North America been so neglected? And why can we not accept with welcome news the

genetic evidence that has recently been discovered? There are two thoughts that come to mind. One, perhaps it has been the Lord's will and wisdom to keep us focused in the wrong place for the last hundred years. Or, what could be more poetic in the "economy of heaven" than have the Book of Mormon and Joseph Smith's statements validated and verified by pure science and a community of non-LDS scholars?

Perhaps it's time to take a second look.