

SECTION 1: DNA EVIDENCE

Editor's Note: *This paper is the full version of the executive summary available at http://www.fairlds.org/DNA_Evidence_for_Book_of_Mormon_Geography/. This paper was last updated 3 September 2008.*

This document is an analysis of the scholarly merits of the theories proffered by Rodney Meldrum¹ in his firesides and DVD presentation, *DNA Evidence for Book of Mormon Geography*.² Neither FAIR nor this document take any position on the geographic location of Book of Mormon events.³ It is important, however, that Meldrum's theories be analyzed according to the same standards by which other Book of Mormon geography theories are evaluated. To avoid confusion, this paper refers to Meldrum's geographic model as the Limited North American Model, or LNAM.⁴ This document is just one in a series of such analytical documents.

For an explanation of how the analysis should occur, see the section entitled "Part II: An Approach to Scholarship," in the overview analysis (*Misguided Zeal and Defense of the Church*) provided on the FAIR Web site.⁵ In starting this analysis, we echo the sentiments of Dr. John Clark:

Once one publishes a proposed [Book of Mormon] geography, however, he or she moves from the realm of recreation into scholarship and must be held

¹ This paper follows the scholarly custom of referring to an individual, at first reference, by full name and then subsequently referring to the individual by last name only. We fully recognize Rodney as a brother in the gospel, but in discussing secular issues (such as scholarly research and geographic models) it was felt that continually prefacing his name or the name of any other referenced scholar or individual with "Brother" or "Sister," while accurate, would distract from the readability of the paper.

² Rodney Meldrum, *DNA Evidence for Book of Mormon Geography: New scientific support for the truthfulness of the Book of Mormon; Correlation and Verification through DNA, Prophetic, Scriptural, Historical, Climatological, Archaeological, Social, and Cultural Evidence* (Rodney Meldrum, 2008). The DVD is in sections; citations in this paper reference the DVD's section number and title, followed by an approximate time stamp from the DVD.

³ FAIR recognizes that faithful individuals and scholars can honestly disagree on where Book of Mormon events took place; there is no revealed or officially accepted geography. FAIR provides an online reference to over 60 different geographic models at http://en.fairmormon.org/Book_of_Mormon_geography (click on Book of Mormon Geographical Models). That being said, this paper may occasionally make reference to a Mesoamerican model for Book of Mormon geography. Such reference is not made to argue for that particular geographical model, but because (1) the presentation often criticizes Mesoamerican models through misrepresentation and (2) the presentation often makes a claim that is equally true of the Mesoamerican model. If both models make the same claims and meet the criteria necessary for those claims, it stands to reason that both models would be equally viable relative to such claims.

⁴ Meldrum's model places Book of Mormon peoples in an area roughly covering the Atlantic seaboard to the Rocky Mountains. This name was chosen as descriptive of the general model. We recognize that Meldrum may pick a different name at some point and would invite him to do so.

⁵ See http://www.fairlds.org/DNA_Evidence_for_Book_of_Mormon_Geography/.

responsible for this action. All such scholarship should be evaluated against a high standard—preferably a higher standard than detractors of the Church of Jesus Christ would use in debunking such claims. I attempt to treat all such geographies with scholarly seriousness and hold their authors to appropriate standards. Have they set forth the facts? Have they cited all the relevant sources? Do their inferences flow logically from accepted facts? Is the argument convincing and interesting? Are the illustrations appropriate? Is the work a contribution? Is the book well written?⁶

The first part of the DVD presentation is entitled *Section 1: DNA Evidence*. This section is, ostensibly, the heart of the LNAM—after all, the title of the presentation is *DNA Evidence for Book of Mormon Geography*. It should be noted, as well, that this section, only one out of eighteen parts on the DVD, occupies approximately 49 minutes of the four-hour total.

LOOKING FOR ANSWERS

In the introduction to the DVD presentation it is explained that in the Spring of 2003 when the presenter first became aware of critical claims against the Church relative to DNA studies, he was “totally confident that the LDS scholarly community would find the answers.”⁷ Just a few moments later he indicated that “I kept looking and I kept looking. There were several LDS scholars who were attempting to address the issue, but didn’t really have an answer to this.”⁸

Meldrum indicates that he is a professional researcher, so claims that LDS scholars didn’t provide answers to the DNA issue are troublesome. In 2003, when Meldrum first became aware of the Book of Mormon DNA problem, LDS scholars had already published several responses to the supposed DNA dilemma. This information was available, at the time, both online and in print.

In fact Meldrum, who started his firesides in the middle of 2007 and published his DVD in early 2008,⁹ is a relative latecomer to the dialogue. The issue first came to the fore in LDS studies because of a May 2002 book, *American Apocrypha*.¹⁰ By the time critics’ signs were seen at General Conference in 2003 announcing that DNA had proved the Book of Mormon false, there were already several responses available online.¹¹ Before 2003 was

⁶ John E. Clark, “Evaluating the Case for a Limited Great Lakes Setting,” *FARMS Review of Books* 14:1-2 (2002), 9-10. It is interesting that Dr. Clark was, in this article, reviewing four proposed Great Lakes settings for Book of Mormon geography—similar in nature to the LNAM.

⁷ Meldrum, *DNA Evidence*, Introduction, 1:08.

⁸ *Ibid.*, 2:13.

⁹ The earliest fireside listed on Meldrum’s website was on Saturday, June 30, 2007 (see <http://www.bookofmormonevidence.org/page.php?page=seminars>). According to Amazon.com, Meldrum’s DVD was released in January 2008.

¹⁰ See Thomas W. Murphy, “Lamanite Genesis, Genealogy, and Genetics,” *American Apocrypha: Essays on the Book of Mormon*, edited by Dan Vogel and Brent Lee Metcalfe (Salt Lake City: Signature Books, 2002), 47-77.

¹¹ See, for instance, a 2001 presentation by Dr. Scott Woodward posted on FAIR’s website (<http://www.fairlds.org/pubs/woodward01/>) on 24 December 2002. Also see “The Tempest in a Teapot: DNA Studies and the

out, there were other responses available online and in print.¹² In the subsequent years even more information has come forth, both from critics and the faithful alike.¹³

It appears that Meldrum was unaware of these scholarly studies when he began his fireside presentations. In August 2007, for instance, he told one FAIR volunteer that he was unfamiliar with *The FARMS Review* and that he knew nothing of the responses to the DNA issue within its pages.¹⁴ According to some who have attended his firesides—even those presented since 2007—Meldrum doesn't tell his audiences about the LDS scholarly articles that address DNA and the Book of Mormon.

In the six years since the critics tried to use DNA evidence against the Book of Mormon, many articles have appeared in the pages of *The FARMS Review* on this very issue. While a few of these articles were written by FARMS scholars, most were written by world-class geneticists and researchers completely independent of FARMS. For example, Dr. John Butler is an internationally renowned researcher on the use of forensic DNA; he literally wrote the textbook on the subject.¹⁵ Other authors published by FARMS are equally eminently qualified. Similar articles have appeared in the *Journal of Book of Mormon Studies*, as early as 2000.¹⁶ Meldrum seems to have missed all of these articles in his research and his audiences do not hear about them.

Although Meldrum told the FAIR volunteer that he was unfamiliar with *The FARMS Review* articles, he quotes Matthew Roper, without attribution, from an article in an issue

Book of Mormon" (http://www.fairlds.org/Book_of_Mormon/DNA_Studies_and_the_Book_of_Mormon.html) posted 20 January 2003. Also see "A Brief Review of Murphy and Southerton's 'Galileo Event'" (http://www.fairlds.org/Book_of_Mormon/Brief_Review_of_Murphy_and_Southerton_Galileo_Event.html) posted on 25 February 2003.

¹² See, for instance, D. Jeffrey Meldrum, "The Children of Lehi: DNA and the Book of Mormon," August 2003 FAIR Conference presentation (http://www.fairlds.org/FAIR_Conferences/2003_Children_of_Lehi_DNA_and_the_Book_of_Mormon.html). See also David A. McClellan, "Detecting Lehi's Genetic Signature: Possible, Probable, or Not?," *The FARMS Review* 15:2 (2003), 35-90; Matthew Roper, "Nephi's Neighbors: Book of Mormon Peoples and Pre-Columbian Populations," *The FARMS Review* 15:2 (2003), 91-128; Matthew Roper, "Swimming in the Gene Pool: Israelite Kinship Relations, Genes, and Genealogy," *The FARMS Review* 15:2 (2003), 129-164; and Brian D. Stubbs, "Elusive Israel and the Numerical Dynamics of Population Mixing," *The FARMS Review* 15:2 (2003), 165-182.

¹³ The Neal A. Maxwell Institute for Religious Studies has collected several responses together in *The Book of Mormon and DNA Research: Essays from the FARMS Review and the Journal of Book of Mormon Studies* (Provo, Utah: Maxwell Institute for Religious Studies, 2008).

¹⁴ Louis Midgley, "The Midgley/Meldrum Encounter," personal notes of telephone conversation (August 2007).

¹⁵ Forensic DNA is the use of DNA evidence to help in the identification of suspects or bodily remains. See John M. Butler, *Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers* (New York: Elsevier Academic Press, 2005). This is the second edition of a book that originally was published in 2001. Dr. Butler, who works for the National Institutes of Standards and Technology and led the government's forensic efforts to identify remains from the wreckage of the 9/11 terrorist attacks in New York City, wrote "Addressing Questions Surrounding the Book of Mormon and DNA Research," *The FARMS Review* 18:1 (2006), 101-108. Several other articles in *The FARMS Review* 18:1 (2006) were written on this very subject by other genetic experts, none of whom are on the staff or payroll of FARMS.

¹⁶ See John L. Sorenson, "The Problematic Role of DNA Testing in Unraveling Human History," *Journal of Book of Mormon Studies* 9:2 (2000), 66-74; John L. Sorenson and Matthew Roper, "Before DNA," *Journal of Book of Mormon Studies* 12:1 (2003), 6-23; Michael F. Whiting, "DNA and the Book of Mormon: A Phylogenetic Perspective," *Journal of Book of Mormon Studies* 12:1 (2003), 24-35; John M. Butler, "A Few Thoughts from a Believing DNA Scientist," *Journal of Book of Mormon Studies* 12:1 (2003), 36-37; and D. Jeffrey Meldrum and Trent D. Stephens, "Who Are the Children of Lehi," *Journal of Book of Mormon Studies* 12:1 (2003), 38-51.

of *The FARMS Review* that was largely devoted to the issue of DNA and the Book of Mormon.¹⁷ Perhaps he forgot that he had read at least parts of this issue of *The FARMS Review*, or perhaps he didn't feel that the information in this volume was worth mentioning to his audience. In either case, it is troubling that Meldrum would assert that LDS scholars "didn't really have an answer"¹⁸ to the perceived DNA conundrum and not provide his audience with information about the many articles (both in print and online) that were devoted to this very subject by faithful LDS scholars and researchers.

While Meldrum doesn't engage this scholarship in his presentation, his website acknowledges that other LDS scholars have sought to engage the issue, but he brushes those attempts aside:

For the first time other Christian denominations have something for which we, the members of the church, have no answers. While some have attempted to address the issue (including FARMS or Foundation for Ancient Research and Mormon Studies) their apologist attempts fall short of providing a solid answer that validates the claims of *The Book of Mormon*. Rather, their attempts are simply to attempt to discredit DNA science in general or grasp some 'reason' why DNA studies have not (as yet) vindicated the truthfulness of *The Book of Mormon*.¹⁹

There are multiple problems with such a statement. First of all, the DNA issue does not represent the "first time" critics have tried to use arguments for which some members of the Church did not have ready answers. Most members learned Nephi's lesson long ago: "I know that the Lord loveth his children, nevertheless, I do not know the meaning of all things" (1 Nephi 11:17). We should, of course, prepare ourselves to answer criticisms, but DNA is neither the first nor the last time that the critics will come up with something new that may catch some members by surprise.

Secondly, the website claims that other LDS scholars have tried to "discredit DNA science in general..." As noted above, however, many of those LDS scholars are DNA experts. They make no attempt to "discredit DNA science" but rather they show how critics have misapplied DNA science to the study of Book of Mormon historicity.

Thirdly, the website claims that some responses attempt to "grasp some 'reason' why DNA studies have not (as yet) vindicated the truthfulness of *The Book of Mormon*." The arguments of these scholars have obviously been misunderstood. Their articles dealing with DNA and the Book of Mormon do not attempt to vindicate the truthfulness of the Book of Mormon simply because they do not believe DNA can do so. Instead, they address the critics' claim that DNA science has shown the Book of Mormon to be fictional. There is a subtle yet distinct difference—and it seems that distinction was missed.

¹⁷ Meldrum, *DNA Evidence*, section 3, "Joseph Smith," 36:45. The presentation cites, without attribution, Matthew Roper, "Nephi's Neighbors: Book of Mormon Peoples and Pre-Columbian Populations," *FARMS Review of Books* 15:2 (2003), 91–128.

¹⁸ Meldrum, *DNA Evidence*, Introduction, 2:13.

¹⁹ Meldrum, "Frequently Asked Questions," <http://www.bookofmormonevidence.org/FAQ.php> (accessed July 6, 2008).

The fact is, while the website asserts that the members of the Church have no answers, many responses have been offered by LDS scholars with advanced degrees related to DNA science. Anyone is certainly free to disagree with the conclusions drawn by these scholars, but it is misleading to claim in firesides, on a website, and in DVD presentations that other LDS scholars have either failed to address the issue or that their responses are nothing more than “apologetic attempts” that “fall short” of actually engaging the problem. If the person disagrees, he or she must demonstrate why the scholars’ answers are in error.

MISTAKEN EXPECTATIONS

What does the presentation expect in the way of answers? Unfortunately, it begins with faulty expectations:

Where did Lehi come from? Where did he leave from? From Jerusalem, that’s right. Then he came to the Americas someplace. That would mean that he and his wife and Ishmael and his family would have come here and then, the Book of Mormon talks about how they covered the face of the land. That DNA would have to still be here someplace.²⁰

The faulty expectation is that Lehi’s DNA would still need to “be here someplace.” Such statements are reminiscent of the expectations of critics, who argue that if Lehi and his party lived here and covered the Americas, then their DNA must be someplace. The majority of LDS researchers have also considered this very expectation and concluded that it would be overwhelmingly unlikely to find DNA from Lehi’s party:

- **Dr. Michael F. Whiting:** “I would suggest that the Book of Mormon can neither be corroborated nor refuted by DNA evidence and that attempts to do so miss the mark entirely. *I would be just as critical of someone who claimed that current DNA testing proves the Book of Mormon is true as I would of those who claim that DNA evidence proves it is not true.*”²¹
- **Dr. Whiting:** “Is testing the Book of Mormon by means of genetic information a fundable research project? I do not think so. Given the [difficulties] it is very unclear what would constitute sufficient evidence to reject the hypothesis that the Lamanite lineages were derived from Middle Eastern lineages, since there are so many assumptions that must be met and so many complications that we are not yet capable of sifting through.”²²
- **Dr. John M. Butler:** “The majority of people living today in Iceland had ancestors living only 150 years ago that could not be detected based on the Y-chromosome and mitochondrial DNA tests being performed and yet the

²⁰ Meldrum, *DNA Evidence*, Introduction, 3:00.

²¹ Michael F. Whiting, “DNA and the Book of Mormon: A Phylogenetic Perspective,” *Journal of Book of Mormon Studies* 12:1 (2003), 27, emphasis in original. At the time of writing this article, Dr. Whiting was the Director of BYU’s DNA sequencing center.

²² Michael F. Whiting, “DNA and the Book of Mormon: A Phylogenetic Perspective,” *Journal of Book of Mormon Studies* 12:1 (2003), 35.

genealogical records exist showing that these people lived and were real ancestors...[therefore] it certainly seems possible that the people who are reported in the Book of Mormon to have migrated to the Americas over 2,600 years ago *might not have left genetic signatures that are detectable today.*"²³

- **Dr. David A. McLellan:** "Those who have attempted to draw conclusions regarding the validity of the Book of Mormon based on the current body of human genetic data...*reveal their ignorance of scientific principles by drawing conclusions that are inappropriate.* They ignore pertinent information because they do not know that it may be important, or they fail to probe the primary literature, opting instead to use summaries or popular scientific literature exclusively because *they have a difficult time interpreting much of the data for themselves.*"²⁴

These experts do not share the presentation's faulty expectation, and they possess training and qualifications in genetics that are not evident in the presentation. They run DNA sequencing labs, teach biology at BYU, write textbooks about the use of DNA in police work, and advise the U.S. government on genetics issues. If they don't share the presentation's expectation about finding Lehi's DNA, is such an expectation reasonable?

The presentation seems to insist that DNA must validate the Book of Mormon, that Lehi's DNA signature must be somewhere. But what if DNA does not validate the Book of Mormon? What if, as the experts believe, DNA cannot prove or disprove the Book of Mormon? Unfortunately, it appears that the answer is simple—like some critics, the presentation attempts to utilize DNA research to fit a purpose for which it was never intended.

EVEN THE CHURCH'S CRITICS AGREE WITH THE LDS SCIENTISTS

One vocal critic that has used DNA evidence to question the veracity of the Book of Mormon is Dr. Simon Southerton, author of a book entitled *Losing a Lost Tribe*.²⁵ Meldrum makes mention of Southerton's book:

There was a molecular biologist down in Australia, he was the bishop of the church. He saw what was happening with this and became very concerned. He had some other issues with the veracity of the Bible and so forth, as well. But his name was Simon Southerton and he ended up leaving the church.²⁶

²³ John M. Butler, "Addressing Questions Surrounding the Book of Mormon and DNA Research," *The FARMS Review* 18:1 (2006), 105-106, emphasis added.

²⁴ David A. McClellan, "Detecting Lehi's Genetic Signature: Possible, Probable, or Not?," *The FARMS Review* 15:2 (2003), 86-87, emphasis added. Dr. McLellan is assistant professor in the Department of Integrative Biology at BYU.

²⁵ Simon G. Southerton, *Losing a Lost Tribe: Native Americans, DNA, and the Mormon Church* (Salt Lake City: Signature Books, 2004).

²⁶ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 15:00.

The facts, as presented, are not quite right. Southerton is a geneticist by trade and was, indeed, a bishop. According to him, he resigned as bishop and became inactive because of the DNA issue. He did not, however, end up “leaving the church.” While still a member he confessed to adultery in the press²⁷ and was excommunicated for that sin.²⁸

In their more candid moments, some critics admit that their criticisms relative to DNA and the Book of Mormon require that a key assumption be made. Southerton writes of how some LDS (like those at The Maxwell Institute) have argued that

Bottleneck effect, genetic drift, Hardy-Weinberg violations and other technical problems would prevent us from detecting Israelite genes [in Amerindians].²⁹

This is a technical way of explaining a relatively simple fact: if a small group is placed in contact with a larger group and allowed to intermarry, it becomes harder to detect the small group’s “genetic signature.” Southerton then goes on to say:

I agree entirely. In 600 BC there were probably several million American Indians living in the Americas. If a small group of Israelites entered such a massive native population it would be very, very hard to detect their genes 200, 2000 or even 20,000 years later.³⁰

This is really quite astonishing—he admits that there are many genetic objections to his argument, unless we accept that Native Americans are *only* descendants of Lehi and Mulek. Indeed, Southerton went on to insist that this was the *only* way in which members of the Church can read the Book of Mormon, because it is how some past leaders have read it. He is, of course, mistaken and is not entitled to tell members what they must believe.³¹ It would appear, then, that the debate is about theology—how statements within the text of the Book of Mormon are to be interpreted—not about the science of DNA.

²⁷ Linda Morris, “Mormons Challenge Apostate Scientist,” *Sydney Morning Herald*, July 21, 2005.

²⁸ Southerton confessed his adultery in the press and on the Internet, but says he refused to discuss it with the high council and stake president at his disciplinary council. He wanted the focus to be on DNA and the Book of Mormon, instead of his admitted adultery. (Simon Southerton, “Feeling the Love...Disciplinary Council report version 2,” e-mail dated August 2, 2005.)

²⁹ Simon Southerton, “Answering the DNA apologetics,” e-mail dated February 15, 2005.

³⁰ *Ibid.*

³¹ Ideas on these lines have been present for over a century. An excellent review is Matthew Roper, “Nephi’s Neighbors: Book of Mormon Peoples and Pre-Columbian Populations,” *The FARMS Review* 15:2 (2003), 91-128. Specific examples of statements include Levi Edgar Young, *Conference Report* (October 1928): 103-106; Janne M. Sjødahl, “Suggested Key To Book of Mormon Geography,” *Improvement Era* 30:11 (September 1927); Anthony W. Ivins, *Conference Report* (April 1929): 15; William E. Berrett, Milton R. Hunter, Roy A. Welker, and H. Alvah Fitzgerald, *A Guide to the Study of the Book of Mormon* (Salt Lake City: LDS Department of Education, 1938), 47-48; Roy A. West, *An Introduction to the Book of Mormon: A Religious-Literary Study* (Salt Lake City: LDS Department of Education, 1940), 11; Dallin H. Oaks, “The Historicity of the Book of Mormon,” (Provo, Utah: FARMS, 1994): 2-3, republished in Dallin H. Oaks, “The Historicity of the Book of Mormon,” *Historicity and the Latter-day Saint Scriptures*, edited by Paul Y. Hoskisson (Provo, Utah: BYU Religious Studies Center, 2001), 238-239; Richard L. Evans, “What Is a ‘Mormon?’” *Religions of America*, edited by Leo Rosten (London: Heinemann, 1957), 94, reprinted as *Religions of America: Ferment and Faith in an Age of Crisis: A New Guide and Almanac* (New York: Simon and Schuster, 1975); John L. Sorenson, “I Have a Question,” *Ensign* (September 1992), 27; John A. Widtsoe and Franklin S. Harris, Jr., *Seven Claims of the Book of Mormon: a collection of evidences*, (Independence, Missouri: Press of Zion’s Printing and Publishing Company, 1937), 15, 84; Milton R. Hunter, *Archaeology and the Book of Mormon* (Salt Lake City: Deseret Book

Unfortunately Meldrum, like some critics, insists that the issue is about DNA. DNA is only an issue when one starts with a faulty premise—that Lehi and his party were the main or only sources of DNA in the New World. Ironically, this is an assumption that the LNAM does not require. The model indicates that the Book of Mormon peoples were confined to a restricted area.³² So, why would he believe an absence of Lehi DNA was a problem when his own geography argues otherwise?

It would appear that Meldrum also believes that DNA evidence would make the LNAM stronger. But, as is shown shortly, he unfortunately gets the DNA science wrong on many counts, which actually weakens his argument.

HOW TO TRACK GENEALOGY WITH DNA: AN EASY GUIDE

Genetics is an exciting subject. It is also a relatively new field of study and knowledge is exploding. Most of us do not have the background to understand the sometimes complex details. This can be frustrating.³³

Here's an easy way to understand how scientists use DNA to understand human relationships, using everyday examples. Follow along and you'll soon know enough to understand how the presentation gets the science of DNA wrong.

A COPYING BUSINESS

Let's imagine that you run a business. The service you provide is copying—there are no computer printers, no typewriters, no photocopiers, and no printing presses in this imaginary world. So, your business does things the old-fashioned way—by hand. Any document that anyone wants to copy has to be copied by hand, one letter at a time.

This is just like DNA. Each “base pair” of DNA corresponds to a letter in what you are copying. Long strings of the letters make words and sentences, corresponding to strands of DNA. These words and sentences tell your cells how to do their job. When a cell divides, it needs to send a copy of the instructions to the new cell, and it needs to keep a copy for itself.

There's no photocopier inside the cell, so a series of complex chemical reactions make a copy of the instructions. This happens every time a cell divides.

Company, 1956), 53; James R. Christiansen, *Book of Mormon: the Keystone scripture*, edited by Paul R. Cheeseman (Religious Studies Center, Brigham Young University, 1988), 232–233; Hugh W. Nibley, *Lehi in the Desert and the World of the Jaredites* (Salt Lake City: Bookcraft, 1952), 253, reprinted in *Lehi in the Desert/The World of the Jaredites/There Were Jaredites*, vol. 5 in *The Collected Works of Hugh Nibley* (Salt Lake City: Deseret Book and FARMS, 1988), 251; Hugh W. Nibley, *Since Cumorah: the Book of Mormon in the Modern World* (Salt Lake City: Deseret Book Company, 1967), 249; Hugh W. Nibley, “The Book of Mormon and the Ruins: The Main Issues,” F.A.R.M.S. paper, 1980.

³² The LNAM posits a geography in which the Lamanites and Nephites covered an area extending from approximately the Great Lakes on the north to the Gulf of Mexico on the south and from the eastern seaboard to the Rocky Mountains.

³³ A more detailed discussion of basic genetic principles for non-experts can be found in David A. McClellan, “Detecting Lehi’s Genetic Signature: Possible, Probable, or Not?,” *The FARMS Review* 15:2 (2003), 35-90.

TO ERR IS HUMAN—AND DNA DOES IT TOO

Just like human copyists, DNA copying isn't perfect—there will sometimes be mistakes made during the process. So, one cell gets the “old” instructions, and the other cell gets the “new” instructions, the one with the mistake.

So, let's look at your business. Imagine you have four employees—Alice, Bob, Claire, and Dan. Alice starts things out and begins copying a sentence. After she finishes, she passes her copy on to Bob, who makes a copy, and passes *his* copy on to Claire, and so on.

Remember, though, that Alice, Bob, Claire, and Dan aren't perfect. They get bored or careless and make mistakes. None of them pays a lot of attention to detail, so they can't tell if what they're copying is right or not—they just copy what is put in front of them and pass it on to the next person. *Every person makes one error in what they copy, every time.*³⁴

Let's pretend you want them to copy a page that says, “THE CAT SAT ON THE MAT.” Here's what happens:

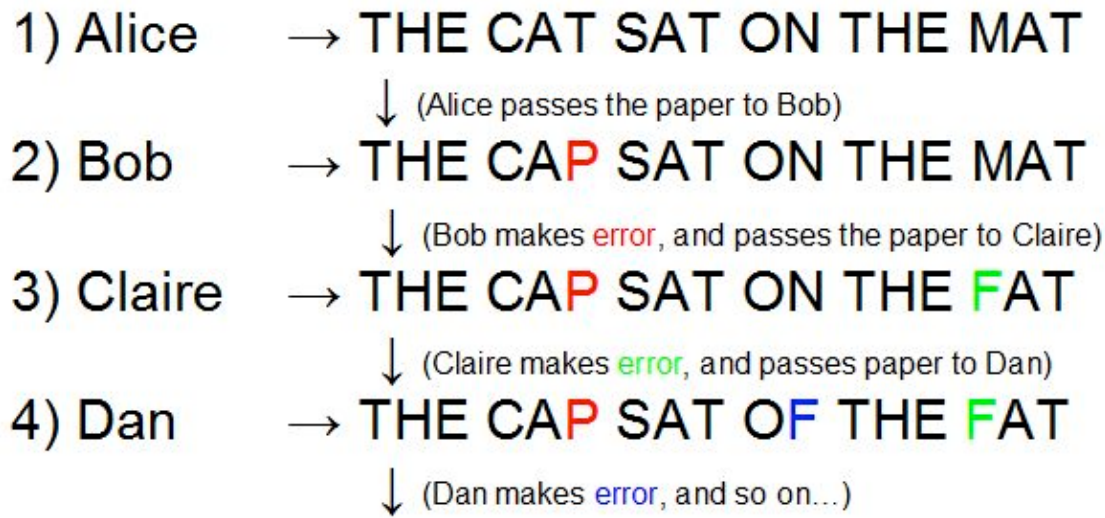


Figure 1: Copying errors

Alice writes “THE CAT SAT ON THE MAT,” and hands it to Bob. But Bob makes a mistake. He passes his mistake on to Claire, who keeps his mistake (because she doesn't *know* it's a mistake—remember, she doesn't see what was passed to Bob). So, she copies his mistake, but makes a mistake of her own. So, now there are *two* mistakes (in red and green).

Claire passes her paper with two mistakes to Dan, who doesn't know that there are mistakes. He copies them exactly as he receives them, but also adds one error of his own (in blue). Now, the sentence has *three* mistakes, even though each person only made one error.

³⁴ The rate of error in DNA copying varies. For simplicity, this example assumes one error is made every generation. The key point is that the rate of error must be known, and it must be more or less constant.

Exactly the same type of thing happens with DNA. Each cell copies its DNA, but not perfectly. Sometimes, the error is fatal and it kills the cell. But sometimes the sentence still “makes sense,” even though it isn’t exactly what we started with. Each of the sentences above contains real English words, and makes a kind of sense. But, they don’t match the first sentence.

Now, let’s see how this helps us figure out genetics.

GENEALOGY OF ERRORS

Imagine now that you have a fifth employee—let’s call him Eddie. Eddie starts work, but no one tells him he’s supposed to come after Dan. So, Eddie gets one of the other copyists to let him use *their* copy of the message. So, there’s a “fork” in our system. One person’s copy will be used by both Eddie and someone else as the basis for their copies.

You find out about this, and are very upset—Eddie is spoiling your whole system! You march into the copying room, and demand to know: Who has been letting Eddie copy from them? Since everyone is afraid of being fired, no one will speak up.

Can you use your detective skills to figure out whom Eddie copied from? Of course! You take his copy, and see that it looks like this (we’ve highlighted the errors to make it easy to pick out):

?) Eddie → THE CAP RAT ON THE FAT

Figure 2: Who did Eddie get his paper from?

Well, Eddie has some errors. Let’s try to eliminate our suspects. Remember that each copyist makes one (and only one) error. Is his copy based on Dan’s work?

Dan → THE CAP SAT OF THE FAT
? ↓ (Did Eddie copy Dan ??)

Eddie → THE CAP RAT ON THE FAT

Figure 3: Did Eddie Copy Dan?

The red “P” certainly looks like it came from Dan. And, the green “F” also fits. And, Eddie made his error by changing the “S” in “SAT” to “R” to make “RAT.” But, there’s another difference—Dan made an error that Eddie has corrected. The blue “F” didn’t get copied by

Eddie. Remember, Eddie (like all your employees) doesn't know what the original said, so he shouldn't be able to correct Dan's error.

So, Dan's job is safe. He's not the person who Eddie was copying from, since the errors don't match: Dan has an error that Eddie doesn't have (the blue "F").

What about Claire? As it turns out, she's the guilty party, as the next figure shows:



Figure 4: Solving the mystery of Eddie.

As you can see, both Dan and Eddie keep *all* of the mistakes made by Claire (the red "P" and the green "F"). And, they each add a mistake to what they receive from her—even though they each make a *different* error.

Bob can't be the source of Eddie's copy since Eddie has *two* errors compared to Bob, and each copyist only makes one error. Alice certainly can't be the source of Eddie's copy, since Eddie has *three* errors compared to hers. So, you've proved beyond a doubt that Claire is the one who messed up your system. Whether you fire her is up to you.

This is a very simple version of how scientists use DNA to decide how closely humans are related to each other. Just like the “CAT ON THE MAT” copies, all humans are related to each other *somewhere*. But, some humans are a lot more closely related than others. Alice and Bob’s copies are very closely related while Alice and Eddie’s copies are much further apart—and, it’s the errors, not the correct parts, that show us this.

Imagine now that we add a whole bunch of other employees. You decide to keep Claire and have her share her copy with Dan *and* Eddie. Dan makes a copy and passes it on to Fred. Eddie makes a copy and passes it to Georgia, and so on. Eventually, you’d have a long “genealogy of copies.”

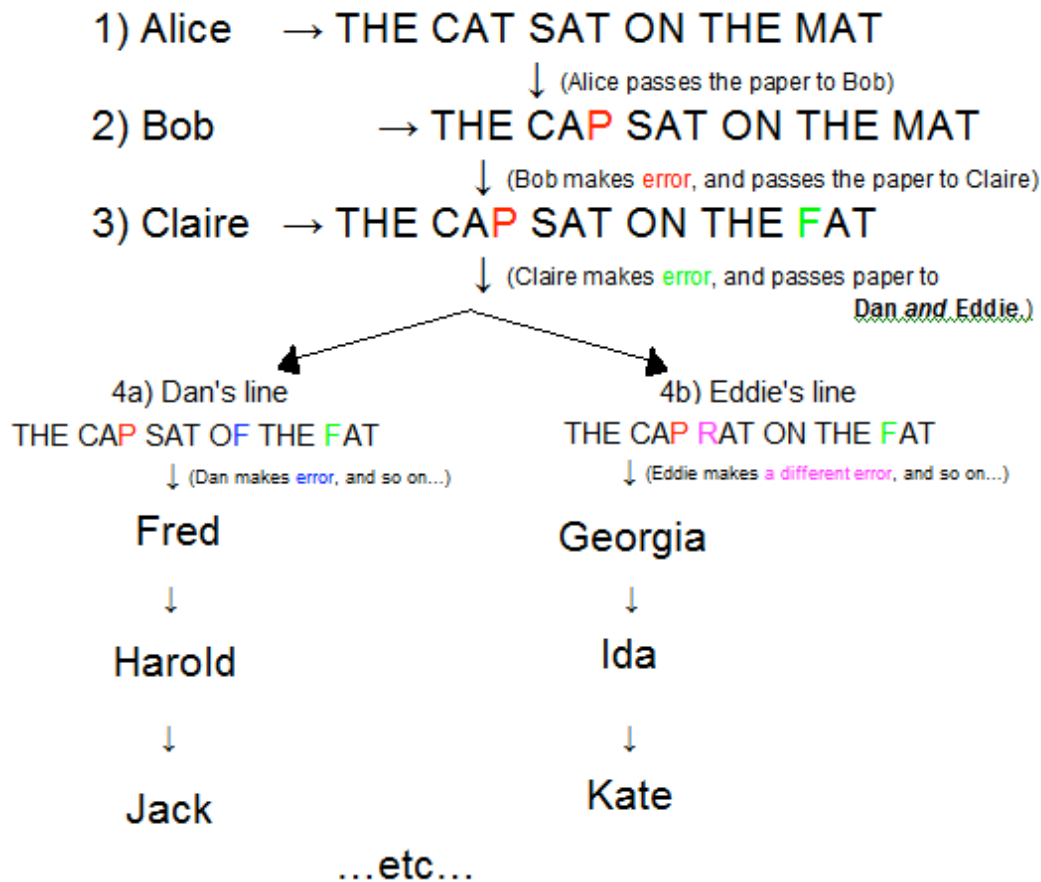


Figure 5: Two "lines," which can be traced by errors. Claire is the "last common ancestor." All the copies are related *somehow* but some are closer than others.

Because Claire’s work is the last one that all of Dan’s line and Eddie’s line had in common, she is called the “last common ancestor.”

When DNA error patterns are studied, scientists can be very confident about how closely related two people—or groups of people—are. You would not believe someone, for example, who tried to tell you that Bob and Jack were as closely related as Fred and Jack. You certainly wouldn’t believe that Kate and Jack were closer than Alice and Bob. Because

of what you know about how the copies are made—and how the *errors* are made—that just doesn’t add up.

Something like this process—only far more complicated, with many more “letters” and many more copies—can be used to determine the relationships between living people.

DNA “CLOCKS”—USING ERRORS TO MEASURE TIME

What if, though, scientists wanted to measure *how much time* had passed since two people’s ancestors had been in the same family? We understand intuitively that someone from France has a better chance of being closely related to someone else from France than someone from Japan. Is there a way to measure this sort of thing scientifically?

Let’s go back to your imaginary copy business to see how we might do this. What if we wanted to know how long it had been between Bob’s copy and Dan’s copy, for example?

This can be done—if we know how often an error occurs. Let’s use just your original four employees. You remember that each makes one (and only one) mistake. They aren’t very fast, so it takes each of them 10 minutes to copy out their line.

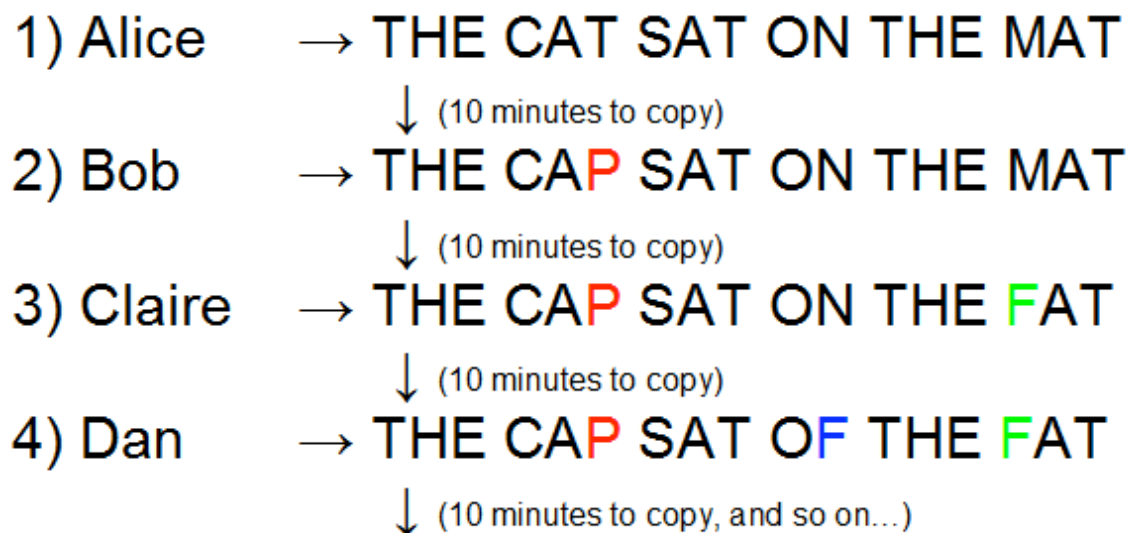


Figure 6: How long since an error was made?

Once you know how many errors have been made from your starting point, it is easy to tell how long it has been. Since Bob has one error compared to Alice, and each copy takes 10 minutes to make, you know that 10 minutes passed between Alice’s copy and Bob’s copy.

There are three errors in Dan’s copy, so $3 \times 10 = 30$ minutes since Alice’s copy.

Note that this will only work if the copyists make errors at the same rate: they have to make *one error every ten minutes*. If sometimes they make lots of errors and sometimes they don’t make any errors, then our “error clock” won’t keep time.

So, scientists want to find DNA that accumulates errors at a *constant* rate. That lets them compare two living people and estimate how much time has passed since those people had a common ancestor.

Believe it or not, you now know enough to understand the DVD presentation is talking about and how much it gets wrong.

GETTING THE SCIENCE WRONG

Dr. David McLellan, of BYU, warned us about those who

*reveal their ignorance of scientific principles by drawing conclusions that are inappropriate. They ignore pertinent information because they do not know that it may be important, or they fail to probe the primary literature, opting instead to use summaries or popular scientific literature exclusively because they have a difficult time interpreting much of the data for themselves.*³⁵

Unfortunately, the presentation's conclusions exhibit this very problem. Note the conclusions about mitochondrial clocks:

This led to, in the journal *Science* 1998 in an article called "Calibrating the Mitochondrial Clock" it said, "...researchers have calculated that 'mitochondrial Eve'—the woman whose mtDNA was ancestral to that of all living people—lived [100,000 to] 200,000 years ago in Africa. Using this new clock (this new calibration), she would be a mere 6,000 years old."

Brothers and sisters, how close is that to what we understand from the scriptures? This is DNA showing at least the preponderance of an Eve that lived 6,000 years ago. But then, I love this next sentence here: "No one thinks that's the case."³⁶

Science is a prestigious journal, and the evidence in the presentation relies on a news article summarizing some then-recent research.³⁷ Meldrum has apparently not read the original article upon which this news article is based. Had he done so, and understood it, he would not be so enthusiastic. Even the news article itself contains information that the presentation does not reveal, which we will now examine.

IS THE CLOCK WRONG?

First, some background: You will remember in the imaginary example about your employees how you could use copying errors to determine how much time had passed between copies. DNA clocks work on the same principle. DNA copies are passed with each

³⁵ David A. McClellan, "Detecting Lehi's Genetic Signature: Possible, Probable, or Not?," *The FARMS Review* 15:2 (2003), 86-87, emphasis added.

³⁶ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 5:50.

³⁷ Ann Gibbons, "Calibrating the Mitochondrial Clock," *Science* 279:5347 (1998), 28-29.

generation. When we know how *often* an error occurs in the DNA, we can then determine *how long* since two people—or animals or plants—shared an ancestor. We can, in a sense, find out how many generations it has been since our ancestors were siblings. When we know how long a generation is (roughly twenty years for humans) we can then know how long it has been since the two populations separated.

Mitochondria are small structures within cells that help cells produce energy. While most of the cell relies on the DNA in the cell's nucleus (often called *nuclear DNA*), there is a small amount of DNA in the mitochondria (called *mitochondrial DNA* or mtDNA) that is passed from a mother to all her children. Since mitochondria all come from the mother and don't combine with the father's DNA in any way, they form a particularly clear "signal" for populations.³⁸

Until the late 1990s, regions of this mtDNA called the "control region" had been used as a DNA clock because it didn't contain any code for proteins. It was thought that this would make it a better area to use as a clock, since errors wouldn't disrupt the codes needed to make proteins. If an error in the mtDNA altered a vital protein, the cell could die, and its DNA wouldn't be passed on.

So, the assumption was that errors in the control region of mtDNA would not be lethal to the cell if it had errors because it didn't code for proteins. The research that is discussed in *Science's* news article called these ideas into question.³⁹ The error rate in the control region, rather than being 1 change per 600 generations, was found in *some* living groups to be 1 change every 33 generations. It is as if, in our example, your employees made an error every 3 seconds instead of every 10 minutes. Clearly, this causes problems with a clock based on the rate of change.

But, the problem wasn't seen in all groups of people. As even the news article cited in the presentation states, "[t]he fact that we see such relatively large differences among studies indicates that we have some unknown variable which is causing this."⁴⁰ Meldrum conveys incredulity concerning the line that says, "No one thinks this is the case," but he stops there. He doesn't tell his audience *why* no one thinks that it's the case. And, it has nothing to do with refusing to accept that Adam and Eve only lived 6,000 years ago, as he concludes.

The news article points out at least two possible options: "[1] if the noncoding DNA in the control region is not entirely immune to selection," then the clock is based on faulty assumptions. Remember, the assumption was that errors in the control region wouldn't affect proteins and so wouldn't affect survival. But, if that isn't true, then the errors aren't happening at a constant rate, and using the control region as a clock is a bad idea. A second option for the rejection of the 6,000 year figure is that "[2] the oldest non-controversial archaeological sites [in the Americas] are 12,500 years old."⁴¹ The mtDNA clock is not the

³⁸ Fathers have a similar "signal" in the Y-chromosome, which also doesn't combine with anything from the mother. (Women don't have a Y-chromosome at all.)

³⁹ T.J. Parsons, *et al.*, "A High Observed Substitution Rate in the Human Mitochondrial DNA Control Region," *Nature Genetics* 15:4 (1997), 365.

⁴⁰ Ann Gibbons, "Calibrating the Mitochondrial Clock," 28-29.

⁴¹ *Ibid.*

only measure of time. There are other methods of dating (like carbon dating or dating rocks) and if the mtDNA is getting an answer that is wildly different from the other methods, then the problem is probably with the mtDNA clock.

SUSPECTING THE CLOCK WAS WRONG

To understand why the mtDNA clock was questioned, let's imagine that a group of athletes want to have a race. They want to time themselves, and find out who runs the fastest, and how fast they run. Unfortunately, no one has a watch that is exactly accurate. So, they decide to use five watches to time the race. The race happens, and the times for the fastest runner are measured:

Watch	Time Measured	
#1	1 hour, 50 minutes	
#2	1 hour, 55 minutes	
#3	1 hour, 43 minutes	
#4	5 minutes, 3 sec	(Notice the huge error)
#5	1 hour, 59 minutes	

Notice that none of the watches match exactly—none of them is perfect. But, there is one watch that is vastly different than the others. The racers have used the other clocks before, and suspect that though they aren't perfect, they're relatively good. And, they may not know exactly how fast the winner was, but they're pretty sure that he didn't run the whole race in only 5 minutes.

Now, the athletes have two choices—they can decide that *all* the other clocks are wrong and adopt the fastest time. (This is what Meldrum proposes.) Or, the athletes can decide that something went very wrong with clock #4. Maybe the person using it read it wrong; maybe it is completely broken, and so isn't any good as a clock at all.

Meldrum should have been able to get this much from the news article. If he had read the actual research paper, he would have also seen the authors say:

- an age for mitochondrial Eve of 6,500 years ago is “clearly incompatible with the *known age* of modern humans” (emphasis added). Again, there are other reasons for the dating.
- “it remains implausible to explain the known geographic distribution of mtDNA sequence variation by human [movement] only in the last ~6,500 years.”⁴²

⁴² T.J. Parsons, *et al.*, “A High Observed Substitution Rate,” 365.

The authors, contrary to the suggestion in the presentation, do not simply reject the 6,500 year period because of religious bias, but spend considerable time offering suggestions as to why the error may have occurred. Significantly, they challenge the idea that the control region of the mitochondria is an area where errors can happen without causing problems.

Once the scientists realized something was going on, they checked a variety of other mammals' mtDNA. They found that one spot in the control region was identical in all the species they checked. This suggests that the control region is not free to have any sort of error—and, if that assumption is false, then using the control region as a clock may well fail. As they point out, “the [control] region has crucial regulatory functions and internal sub-regions display quite different levels of variation, both within and between species.”⁴³

The research cited in the DVD presentation is over ten years old. That is an eternity in some branches of science, and particularly in genetic science. The presentation implies that the mtDNA dating evidence has rested here—but nothing could be further from the truth. Scientists were now aware that the control region was perhaps not a good region for a clock. They set out to find out why.

UNDERSTANDING AND FIXING THE CLOCK

Less than a year after the *Science* news article cited in the presentation, more evidence was presented. Another type of genetic clock was explored, using part of the X-chromosome. The area of the X-chromosome chosen was known not to code for proteins and didn't seem to have any function—it was even a long way from the nearest gene, so errors in the nearest gene would hopefully not even affect it, nor would accumulated errors in the clock affect the gene and cause selection.⁴⁴ The scientists compared the same area in chimpanzee and gorilla DNA, and found no evidence that errors made any difference in survival of the cells with errors. So, this part of the X-chromosome was a good site to use as a genetic clock because errors there would have no effect on survival (unlike, they now suspected, the control area of the mtDNA).

The next year, the same team of researchers presented evidence about the mtDNA clock. They checked the precise idea that the 1997 article had suggested—that the control region was not a good place for a DNA clock and that's why the results were so far off. And, they were right. The researchers found that “the [control region of mtDNA] has not [changed] at a constant rate across all human lineages...and is consequently less suitable for dating...” In contrast, the areas “*outside* of the [control region change] in a roughly ‘clock-like’ manner, enabling a more accurate measurement of mutation rate, and therefore improved estimates of times to evolutionary events.”⁴⁵

Researchers then performed a check on their X-chromosome and mtDNA clocks. They knew that nuclear DNA (where the X-chromosome is located) changes about three times

⁴³ T.J. Parsons, *et al.*, “A High Observed Substitution Rate,” 365.

⁴⁴ H. Kaessmann, *et al.*, “DNA Sequence Variation in a Non-Coding Region of Low Recombination on the Human X Chromosome,” *Nature Genetics* 22:1 (1999), 78-79.

⁴⁵ M. Ingman, *et al.*, “Mitochondrial Genome Variation and the Origin of Modern Humans,” *Nature* 408:6813 (2000), 708, 712, emphasis added.

slower than mtDNA, which would put the last common ancestor about three times further back in time than mtDNA calculations would.

Their X-chromosome DNA clock put the last common ancestor at $535,000 \pm 119,000$ years. A third of that would be about 178,000 years $\pm 40,000$ years. Their mtDNA clock gave a last common ancestor at 171,500—once the faulty “control region” was left out. This is an impressive match, and since it comes from two separate, unrelated techniques, they confirm each other—yet more evidence that something was wrong with the mtDNA clock that used the control region.

So, within two years of the article used in the DVD presentation, the problem had been defined and a solution found. Meldrum must have been unaware of this updated information because his assumptions and conclusions are based on a misreading of the outdated data presented in the *Science* news summary.

WHAT IS MTDNA GOOD FOR?

The answers to Meldrum’s confusion are in the papers he cites, but he has not appreciated their implications. He says in his presentation:

In fact this is from *Annual Views of Genomics and Human Genetics*, 2005 article. It said that they showed “a model that includes a rate variation in mitochondrial control region that gave an estimate for the age of the human mitochondrial DNA ancestry that was **half** of that that was obtained from a single mutation rate when that was assumed.”

I know that’s a lot of scientific mumbo-jumbo maybe. But what that’s basically saying is that when they checked one individual and then checked it against the population, the individual was, or that the population ends up being half of what the original individual person’s dating was. Well, how can that be happening? Half—that’s a huge difference, OK?⁴⁶

In 2005, however, it was well known that the mitochondrial DNA control region is not the best place to use as a clock—as discussed above and as was scientifically demonstrated five years earlier. Since Meldrum appears to be unaware of this updated information, these important details are not passed on to his audience.

Unfortunately Meldrum also misunderstands the information in the 2005 article that he chooses to use. The phrase he quotes occurs after an extensive discussion of the variations on mtDNA mutation rates. The paper upon which the news article that started Meldrum’s discussion is based (Parsons, 1997) is even cited. The 2005 paper cited by Meldrum is *not* saying that mtDNA cannot be used for dating—rather, the article spends considerable time explaining that the observed mutation rates are different in the short term compared to the long term. Therefore, one should exercise care relative to which rate one is using, depending on the timeframe one is interested in. Here is the concluding paragraph from

⁴⁶ Meldrum, *DNA Evidence*, section 1, “DNA Evidence,” 35:50. Underlining and bolding are in the PowerPoint slide used in the presentation.

which Meldrum took the one phrase. His material is underlined, with comments in brackets to translate some of the “mumbo-jumbo,” as he calls it:

In any event, because a significant number of the mutations observed in pedigree data have arisen recently [i.e., they have occurred in the *short term*] and will probably not become fixed [i.e., they will not become features of the mtDNA of their descendants in the *long term*, for a variety of reasons already discussed in the paper], the phylogenetic rate (which represents mutations that have reached an appreciable frequency in the population [over the *long term*]) may be preferable for studies of *deep history*, whereas it may be advisable to use the pedigree rate for studies of *recent history*. Alternatively, studies of population history could incorporate models that allow for different classes of [mtDNA] sites with different evolutionary rates. For examples, Hasegawa *et al.* showed that a model that includes rate variation in the mtDNA control region gave an estimate for the age of the human mtDNA ancestor that was half that obtained when a single mutational rate was assumed. Therefore, average estimates of the mutation rate for human mtDNA do not reflect the true state of affairs, and should be viewed as simplistic tools for phylogenetic [i.e., evolutionary, or long time scale] studies.⁴⁷

Note, then, that the authors are arguing that mtDNA is still useful—in the short and long term. What matters, though, is that there seem to be two different rates of change: the short-term rate that gets somewhat cancelled out over time, and the longer-term rate that is lower.

An average of these rates is useless. To illustrate, consider a school class with two students: if one student gets 100% on a test, and the other gets 0% on a test, the class average is 50% (100+0 divided by 2 equals 50). But, this average score tells us very little about how the students are doing. One must pick one mtDNA error rate or the other, depending on what timeframe one wishes to explore.

The presentation then returns to the scientific research and interprets what it means:

“Therefore average (age) estimates of the mutation rate for human mitochondrial DNA do not reflect the true state of affairs and should be viewed as simplistic tools for phylogenetic studies.” In other words, for establishing relationships, but not for establishing dating.⁴⁸

Unfortunately, this interpretation is completely wrong. The authors are not saying mtDNA is good for establishing relationships but not dating; they are saying that average rates of mtDNA change are misleading—as you have already seen. But, if the short- and long-term rates of error are known, then we can use them, provided we know the timeframe in which we are interested. It makes no sense whatsoever for Meldrum to claim that mtDNA

⁴⁷ B. Pakendorf and M. Stoneking, “Mitochondrial DNA and Human Evolution,” *Annual Review of Genomics and Human Genetics* 6 (2005), 169.

⁴⁸ Meldrum, *DNA Evidence*, section 1, “DNA Evidence,” 36:28.

can't cast light on dating issues when the authors are advocating its use for matters of "deep history" or in models that use variable rates.

The authors go on to specifically discuss the use of mtDNA for dating events. Here's the presentation's use of their material:

And then finally he says, "This means that care must be taken when using mitochondrial DNA to date phylogenetic events, as the underlying assumption of neutral clock-like evolution may not hold."⁴⁹

After a long discussion of the sorts of things we've been discussing (the portion used in the presentation is again underlined), the authors in fact conclude that:

This means that care must be taken when using mtDNA data to date phylogenetic events [i.e., deep history] as the underlying assumption of neutral clock-like evolution may not hold. However, the basic results of mtDNA studies, such as a recent initial migration out of Africa and subsequent world-wide dispersal of modern humans, are not affected by [the problems we've discussed], and, furthermore, are supported by a wide array of other loci.⁵⁰

"A wide array of other loci" means that there are many other genetic markers that confirm the general picture and time scale provided by mtDNA when it is used appropriately, despite its problems. Thus, while mtDNA is not the technique of choice—especially by itself—the "6,000 years ago" figure that Meldrum concludes from the study is based on a faulty reading of the actual scientific arguments. The other clocks don't match it, and we know why.

The misunderstandings evidenced in the presentation go from one faulty assumption to another:

So what they're saying is don't use DNA for dating old things. It's great for current day stuff but not for old things. You can't use it for dating.⁵¹

The scientists disagree with this assertion. They are saying we should not use mtDNA (especially the control region) as the *only* source of dating without being aware of all the factors in play. But, other DNA dating methods work very well and they are part of how we know that the mtDNA is wrong in some situations. It is erroneous to claim that these authors do not think that DNA can be used to date "old things."

Understanding the DNA science can be tricky and it's easy for an amateur to become confused. We see this confusion in the presentation's misinterpretation of the scientific literature. As the scientists referenced in the presentation actually tell us, mtDNA will "be used less and less as the *sole* marker for...human evolution and population history." That

⁴⁹ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 36:45.

⁵⁰ B. Pakendorf and M. Stoneking, "Mitochondrial DNA and Human Evolution," 173.

⁵¹ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 37:18.

is, mtDNA should be checked against other tests and clocks. But, “it is still important for a wide range of questions...[for example] mtDNA is crucial in studies of *ancient* DNA.”⁵²

It is lamentable that Meldrum has misunderstood and misapplied this specialized science to Book of Mormon research. Unfortunately, he conveys his faulty research and conclusions to his audience—who are typically also untrained in DNA science and are therefore not in positions to recognize his many errors.

EXAMINING HAPLOGROUP X

We now come to the core of the presentation’s argument. Meldrum believes he has established that scientists are rushing to premature conclusions, and the dating of mtDNA supports a very recent “mitochondrial Eve” of about 6,000 years ago. As demonstrated earlier, these claims are not accurate. This false conclusion, however, directly influences the presentation’s primary—albeit faulty—argument regarding Haplogroup X DNA and Book of Mormon populations.

WHAT IS A HAPLOGROUP?

A haplotype is a set of DNA changes (“errors,” if you like) that are statistically associated.⁵³ In simple language, it is a group of differences in the DNA code that usually go together.

A haplogroup is a group of humans that share related haplotypes—they all have similar differences in their DNA when compared to the rest of humanity. All have a common ancestor, who experienced a change in a single DNA base pair: a single letter was copied in error, and then passed on to all descendants.⁵⁴ All those descendants form the haplogroup because they all share that original, single error. If you go back to the earlier example of your imaginary copying business, Dan and Eddie each gave rise to a haplogroup: an error unique to them which continued in all their descendants but not in the descendants of other groups.

⁵² B. Pakendorf and M. Stoneking, “Mitochondrial DNA and Human Evolution,” 173, emphasis added.

⁵³ A haplotype can also refer to a combination of alleles that are transmitted together through gene linkage, but that is a separate topic.

⁵⁴ In technical terms, the haplotype “error” is called a unique single nucleotide polymorphism (SNP).

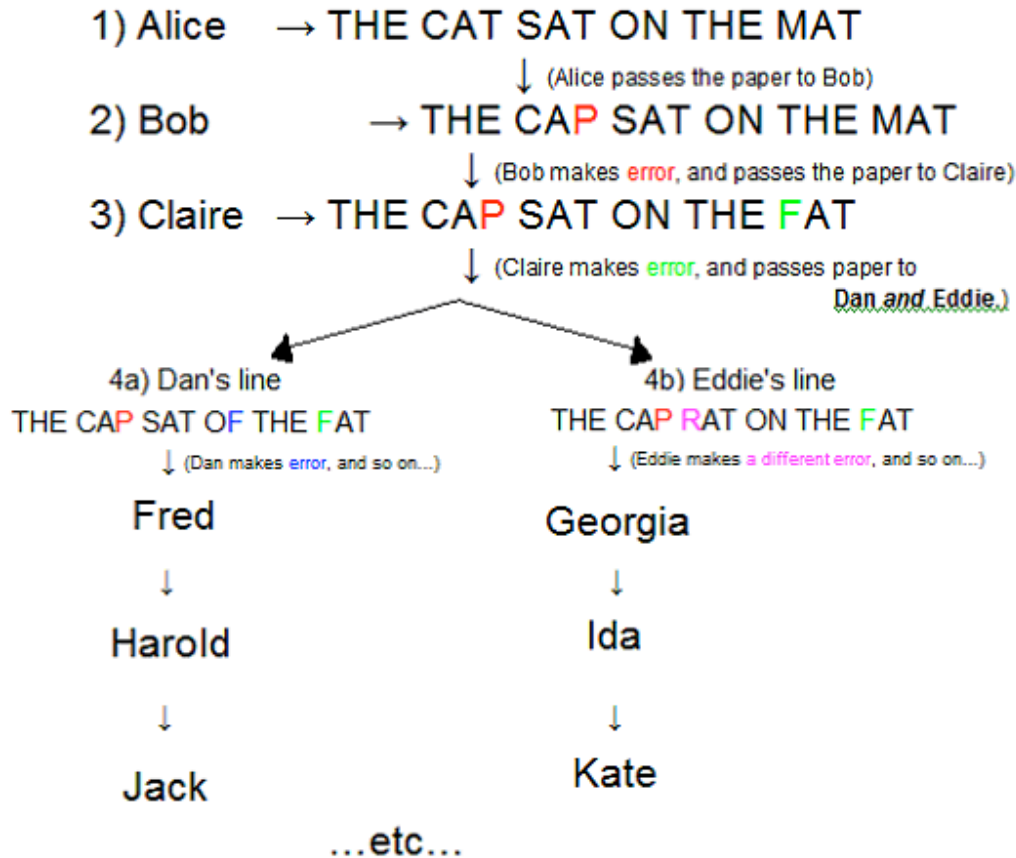


Figure 7: Dan and Eddie each make a single point error. That error is inherited by all their descendants (and no one else). We therefore have a "Dan" haplotype, and an "Eddie" haplotype.

Haplogroups are useful in population genetics because they allow scientists to determine which human groups are more closely related.

WHAT IS HAPLOGROUP X?

There are a few dozen haplogroups used for population genetics. Some haplogroups have their error in the male Y-chromosome, others (like haplogroup X) in their mtDNA. So, haplogroup X is a group of humans, all of which share a common female ancestor who had a single mtDNA error and passed it to her descendants.

Native American groups⁵⁵ consist almost completely of five haplotypes: A, B, C, D, and X. Haplogroup X is the least common haplotype in the Americas, and (as Meldrum demonstrates) there has been considerable debate about where haplogroup X comes from and to which human group the American haplogroup X is most closely related.

⁵⁵ Don't make the error of thinking that "American Indian" refers solely to natives living within the boundaries of the present-day United States of America. American Indians (Amerindians or Native Americans) are any group indigenous to North, Central, or South America.

Meldrum hopes to show that there is a high likelihood that haplogroup X came from Lehi's party⁵⁶—he wants haplogroup X to be traceable to Europe or the Middle East. And, he must prove that American haplogroup X split off from its closest ancestors around the time of Lehi's departure from the Middle East, approximately 2,600 years ago. As you begin to study the evidence yourself you'll see why Meldrum asserts that the mtDNA clock dates should be much shorter: he needs to move haplogroup X's split from their ancestor forward in time, or at least cast doubt on the more ancient dating.

BRIEF HISTORY OF HAPLOGROUP X RESEARCH

A complete understanding of the history of haplogroup X as it applies to the Americas is not necessary. The following brief timeline will demonstrate the expansion of scientific knowledge on these points. As you will see, the presentation misinforms viewers about the scientific research when it suggests there has been a steady move toward a picture that supports haplogroup X as a marker for Lehi. In fact, the opposite is the case.

- 1980 – mtDNA variability noted.⁵⁷
- 1987 – mtDNA used in studies of human evolution⁵⁸
- 1996 – Haplogroup X identified in the Americas.⁵⁹ Various explanations are eventually advanced. It may have come:
 - with haplotypes A, B, C, and D in Asian populations who crossed the Bering land bridge.
 - from European settlers after Columbus inter-breeding with Amerindians.
 - from Europeans who also crossed the Bering land bridge before Columbus.
 - from Europeans who crossed the ocean and settled well before Columbus. (This alternative has the most appeal, obviously, for the Book of Mormon.)
- 2001 – Haplogroup X identified in pre-Columbian remains. This means that the presence of Haplogroup X in Amerindians cannot be explained entirely by genes brought by European colonists after Columbus.⁶⁰
- 2001 – Haplogroup X found in the Altaians, a group from southern Siberia. This raised the possibility that X could have come to the Americas across a Bering land bridge.⁶¹

⁵⁶ Since haplotype X is based upon an error in mtDNA, it cannot come from Lehi. Genetics dictates that it must come from a female in Lehi's party.

⁵⁷ W.M. Brown, "Polymorphism in Mitochondrial DNA of Humans as Revealed by Restriction Endonuclease Analysis," *Proceedings of the National Academy of Sciences* 77:6 (1980), 3605-3609.

⁵⁸ R.L. Cann, *et al.*, "Mitochondrial DNA and Human Evolution," *Nature* 325:6099 (1987), 31-36.

⁵⁹ P. Forster, *et al.*, "Origin and Evolution of Native American mtDNA Variation: A Reappraisal," *American Journal of Human Genetics* 59:4 (1996), 127-149.

⁶⁰ R.S. Mahli, "Investigating Prehistoric Population Movements in North America with Ancient and Modern mtDNA" (University of California, 2001).

The presentation reviews this history relatively well. The interpretation of these data and the later results, however, seems driven by the need to make it fit the desired theory.

MELDRUM'S THEORY

That brings us to this, which is really a critical article. This is from the *American Journal of Human Genetics* 2003, called "Origin and Diffusion of Mitochondrial DNA Haplogroup X."⁶²

Meldrum is correct—this is a vital article. It is vital because it provides a detailed look at haplogroup X and, unfortunately, it is fatal for his theory. Yet, he quotes only those parts of the article that support his theory and ignores those that refute his theory.⁶³ As Dr. Michael Whiting, a genetics expert at BYU, reminds us,

Good science does not consist of someone dreaming up a pet theory and then quilting together pieces of evidence to support it from as many disparate sources as possible while conveniently ignoring pieces of evidence that may undercut the theory.⁶⁴

The presentation correctly notes that haplotype X is divided into two subgroups: X1 and X2. It tells us that a study states "X1 is largely restricted to North and East Africa, whereas X2 is widely spread throughout Western Eurasia."⁶⁵ Meldrum immediately comments on the study, asking, "Where is Western Eurasia? The Levant area, or Jerusalem—the Holy Land, let's put it that way."⁶⁶

The problem is that the presentation omits a crucial detail from the study cited. Meldrum does not tell his audience that X1 is "restricted to populations of North and East Africa *and the Near East*."⁶⁷ Thus, the area of interest for Book of Mormon studies—the Near East—contains *both* X1 and X2. Meldrum is eager to have a clear marker restricted to the Holy Land in X2, but he is apparently unaware that his argument is actually weakened by the evidence presented in those articles to which he refers.

The presentation is correct that the small group in Siberia that carries haplotype X is not related to the American type.⁶⁸ Meldrum's theory, however, allows him to overlook information that challenges his conclusions. He states:

⁶¹ M.V. Derenko, *et al.*, "The Presence of Mitochondrial Haplogroup X in Altaians from South Siberia," *American Journal of Human Genetics* 69:1 (2001), 237–241.

⁶² Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 40:40.

⁶³ In academic circles, the tendency to present only favorable data and ignore contrary data is referred to as "cherry picking." See http://en.wikipedia.org/wiki/Cherry_picking

⁶⁴ Michael F. Whiting, "DNA and the Book of Mormon: A Phylogenetic Perspective," *Journal of Book of Mormon Studies* 12:1 (2003), 27.

⁶⁵ M. Reidla, *et al.*, "Origin and Diffusion of mtDNA Haplogroup X," *American Journal of Human Genetics* 73:5 (2003), 1188.

⁶⁶ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 41:10.

⁶⁷ M. Reidla, *et al.*, "Origin and Diffusion of mtDNA Haplogroup X," 1178, emphasis added.

⁶⁸ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 41:35-42:10.

But the final is really where it gets exciting, brothers and sisters. “Finally, phylogeography of the subclades of haplogroup X suggests that the Near East is the likely geographical source for the spread of sub-haplogroup X2...The presence of a daughter clade [evolutionary group] in Northern Native Americans testifies to the range of this population’s expansion. It is notable that X2 includes the two complete Native American X sequences.”⁶⁹

Note the use of ellipses (...) in this quote. Obviously the ellipses aren’t in what someone would be verbally saying (the presentation is oral), but they are in the PowerPoint slide used in the presentation. Ellipses indicate that material has been omitted from the original source. What did Meldrum leave out of the original? Here is the full quote, with the omitted material in bold type:

Finally, phylogeography of the subclades of haplogroup X suggests that the Near East is the likely geographical source for the spread of sub-haplogroup X2, **and the associated population dispersal occurred around, or after, the LGM [Last Glacial Maximum] when the climate ameliorated [improved].** The presence of a daughter clade [evolutionary group] in northern Native Americans testifies to the range of this population expansion.⁷⁰

It is true that the American subgroup of X2 *is* related to the Middle East. But it is also clear that the American group broke off from that Middle East group around the time of the “Last Glacial Maximum”—this is the last ice age, where the glaciers reached their furthest extent south about 18,000 years ago. This vital information has been snipped out from his presentation.

Now we may see why Meldrum has attempted to dispute mtDNA dating—the scientific dates, if accurate, demonstrate that the LNAM is full of holes. The scientific dates don’t match the exodus of Lehi’s group from Jerusalem, so he seems to ignore those dates or suggest that they can’t be trusted.

THE AMERICAN BRANCH BROKE OFF EARLY

The paper cited in the presentation contains further information that is detrimental to the LNAM, but it is likewise not available in the presentation. “The position of [the American branch in the family tree] suggests an *early split* from the other X2 [groups], likely at the very beginning of their expansion and spread from the Near East.”⁷¹ Thus, the Amerindian branch of X2 (referred to as X2a) is among the *oldest* of all the X2 subfamilies. It separated from the mother population very early—around the time of the recession of the glaciers, certainly not anywhere near Lehi’s time.

There is further evidence that the American branch of X2 split off from the others early because X2a has had time to begin to develop its *own* DNA errors. The same paper also

⁶⁹ Meldrum, *DNA Evidence*, section 1, “DNA Evidence,” 42:11-42:47.

⁷⁰ M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1188.

⁷¹ M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1178, emphasis added.

points out that when the branch of X2 in the Navajo and Ojibwa⁷² is examined, we see that “it began to diverge *while their common ancestor was already in the Americas*...we obtain a...time of 18,000 ± 6,800 YBP, implying an arrival time [in the Americas] not later than 11,000 YBP.”⁷³

These numbers complement the numbers calculated for the initial spread of X2 from the Middle East area. The authors use mtDNA dating by checking *both* the control region and the rest of the mtDNA, as they should. The date at which X2 populations began to spread out from the Middle East and separate is 17,000 ± 2,900 years ago based on the mtDNA control region and 21,600 ± 4,000 years ago for the rest of the mtDNA.⁷⁴ Note that the more reliable non-control region gives even older dates.

A PATTERN OF OMISSIONS

The presentation uses what Meldrum characterizes as a “second witness” for his theory—a 2003 paper from *Evolutionary Anthropology*.⁷⁵ This paper also contains information fatal to his theory, but Meldrum either fails to grasp it, or withholds it from his audience.

Although apparently sharing a [female line] ancestor with the European haplogroup X *at some point in deep time*, the Native American sequences formed their own branches *independent of European representatives of haplogroup X*.⁷⁶

Again it is pointed out that the X2a split was very early and that X2a is not “European” X2 as Meldrum claims (except in the broadest sense that *all* haplogroup X2 started in Europe at the last glacial maximum). It’s regrettable that the presentation doesn’t disclose some of the material in this article which reads, in part,

...the discovery of haplogroup X as a founding Native American lineage, fueled *premature speculation about early European migrations to the New World*. Genetic evidence *does not support such a migration*. Furthermore, the lack of other more common European haplogroups (or other nonmitochondrial genetic markers) in unadmixed Native Americans makes this scenario unlikely.⁷⁷

In other words, the genetics do not support the LNAM. Lehi and company would have brought other DNA markers besides haplogroup X. If they left a strong enough genetic signal to show haplogroup X, other such markers should be seen. They are not seen, which is supportive of the position that Lehi and company likely left no genetic trace at all. Their

⁷² It should be noted that in the LNAM both the Navajo and Ojibwa are candidates for the Lamanites of the Book of Mormon.

⁷³ M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1188, emphasis added. YBP is an acronym meaning *years before present*, a common dating reference used in the sciences. In common vernacular you could replace YBP with “years ago.”

⁷⁴ M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1187. See also the figures on pages 1179 and 1180.

⁷⁵ Meldrum, *DNA Evidence*, section 1, “DNA Evidence,” 28:10-28:45.

⁷⁶ Jason A. Eshleman, *et al.*, “Mitochondrial DNA Studies of Native Americans: Conceptions and Misconceptions of the Population Prehistory of the Americas,” *Evolutionary Anthropology* 12 (2003), 10.

⁷⁷ Jason Eshleman, *et al.*, “Mitochondrial DNA Studies of Native Americans,” 11.

group was too small and their small drop of genes have, for all practical purposes, vanished into the greater American genetic sea.

The *Evolutionary Anthropology* paper also gives a range of times based on the (imperfect) mtDNA clock for the split off of the founders in America: 40,000–11,000 years ago.⁷⁸ Even at the most optimistic, this is much too early for Lehi. But, again, the presentation does not mention this either.

An additional bit of misrepresentation occurs in a different section of the presentation:

Because in this article, *American Journal of Physical Anthropology* (2005), this article is titled “The Rapid Deployment of the Five Founding Amerind Mitochondrial DNA Haplogroups by a Coastal and Riverine Colonization.”

Now, I know that’s a mouthful, but basically what they’re saying is that Haplogroup X colonization spread up the Mississippi River. They started from here at this amount of X and they ended up here at this amount of X. There’s every indication that whoever these Hopewell mound building people were they started from down here and moved up there.⁷⁹

This is not true. The cited journal article is *a computer model*. The author does not claim it is a true model of what happened, he merely wishes to prove that such a spread is *possible* and that spreading in this way would allow the five North American haplotypes to achieve the ratio we see today:

The results of the *simulation model* demonstrate that the pattern of variation characteristic of mtDNA in the Americas *could have been established* by a [Pacific] coast route of colonization...However, the fact that the simulation model is consistent with the empirical situation does not necessarily demonstrate that it represents the actual process that generated the distribution.⁸⁰

The paper is also quite clear that the model considers haplogroup X to be part of the founding people from Asia, claiming that “a single colonization wave” best explains the haplogroup ratios observed today and puts this date long before the Nephites, from 11,000–20,000 years ago.⁸¹ These ideas are fatal to the LNAM, so they never make it into the presentation.

Meldrum’s LNAM theory seems to drive his research, rather than the other way around. Such faulty methodology leads him to make the fallacious argument that the *Anthropology* paper provides evidence for his theory of Nephites colonizing the mouth of the Mississippi River, via the Gulf of Mexico. This is not true, since the computer model studied is very clear that it assumes haplogroup X *starts* in Asia with haplogroups A, B, C,

⁷⁸ Jason Eshleman, *et al.*, “Mitochondrial DNA Studies of Native Americans,” 11.

⁷⁹ Meldrum, *DNA Evidence*, section 13, “Nephite Culture,” 2:15-2:50.

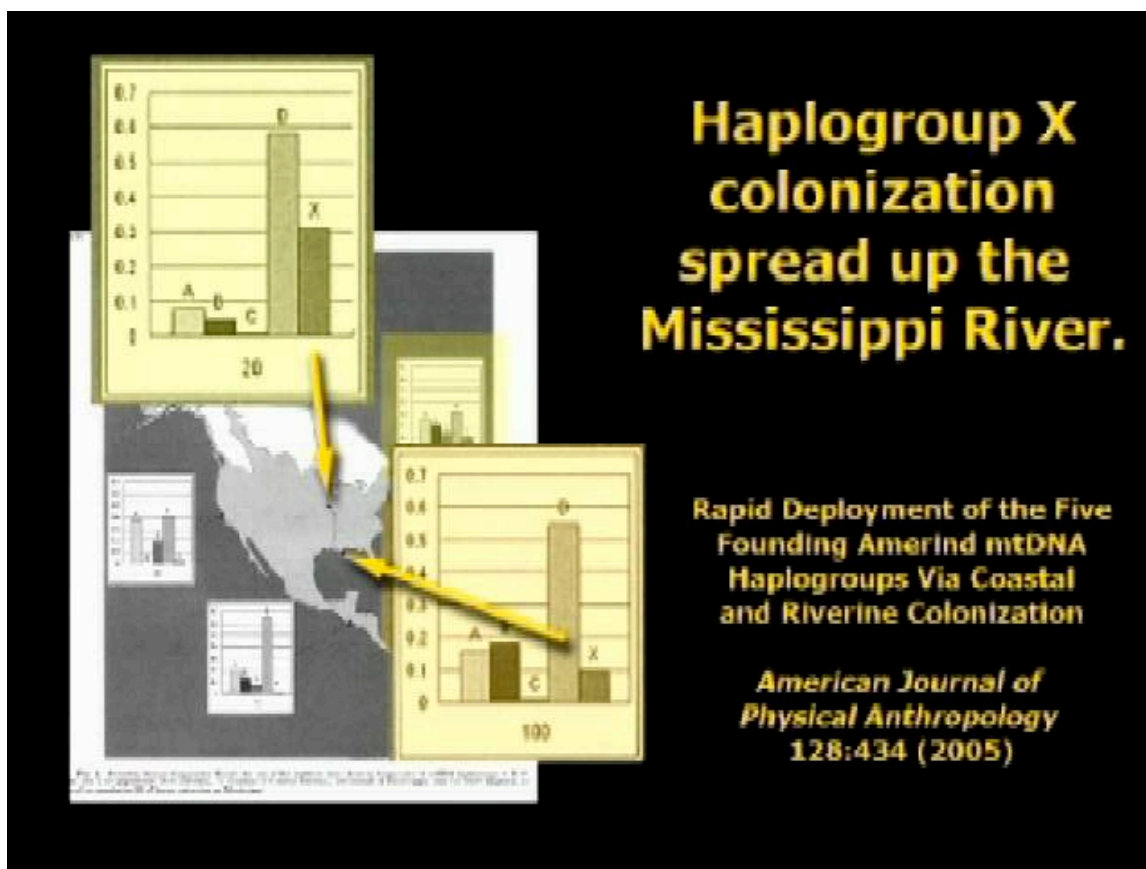
⁸⁰ A.G. Fix, “Rapid Deployment of the Five Founding Amerind mtDNA Haplogroups Via Coastal and Riverine Colonization,” *American Journal of Physical Anthropology* 128:2 (2005), 433, emphasis (italics) added, underlining in original.

⁸¹ A.G. Fix, “Rapid Deployment of the Five Founding Amerind mtDNA Haplogroups,” 431.

and D. It then moves down the Pacific coast via Alaska—the very route that Meldrum has told us is impossible. The paper says:

*Entry [in the model] is by way of the Pacific coastal rim from northeast Asia, with settlement expanding along the north Pacific coast down to the narrow isthmus of Central America, crossing the isthmus, and continuing to spread up the Gulf and Atlantic coasts. The Mississippi River would have served as an entry to the continental interior.*⁸²

For the edification of readers, the author of the *Anthropology* paper even included a half-page map showing his proposed route, on the same page as the description above. It is inconceivable that Meldrum could miss such a prominent graphic. Instead, he reproduces figure 2 from the paper and uses it as a visual aid (shown below), which he claims shows that “They started from here at this amount of X and they ended up here at this amount of X. There’s every indication that whoever these Hopewell mound building people were they started from down here and moved up there.”⁸³



The paper’s figure 2 doesn’t show reality, as Meldrum seems to believe, but the results of “one of five replicate runs” of the computer model.⁸⁴ (In his use of the figure as a visual aid,

⁸² A.G. Fix, “Rapid Deployment of the Five Founding Amerind mtDNA Haplogroups,” 432, emphasis added.

⁸³ Meldrum, *DNA Evidence*, section 13, “Nephite Culture,” 2:37-2:50.

⁸⁴ A.G. Fix, “Rapid Deployment of the Five Founding Amerind mtDNA Haplogroups,” 434, Fig. 2, emphasis added.

the legend on the map is too small to be read, so there is no way for his audience to know about his misrepresentation of the data without checking the original paper.)

Contrary to Meldrum's misinterpretation of the data, the paper does not provide evidence that the Hopewell (whom the LNAM posits as Nephites) spread from the Gulf of Mexico. Meldrum is assuming that "Hopewell" and "haplotype X" are synonymous; they are not. In fact, the Hopewell culture is known to have spread from north to south, the opposite direction asserted in the LNAM. Although the origins of the Hopewell are still shrouded in historical mystery, the Hopewell culture can be considered a cultural climax:

Hopewell populations *originated in western New York and moved south* into Ohio where they built upon the local Adena mortuary tradition. Or Hopewell was said to have originated in western Illinois and spread by diffusion—perhaps carried by a religious elite—to southern Ohio. Similarly, the Havana Hopewell tradition was thought to have spread up the Illinois River and into southwestern Michigan, spawning Goodall Hopewell.⁸⁵

When the Hopewell culture is traced archaeologically, they move from northern areas into southern. The DVD presentation avoids this unpleasant fact by trying to use DNA as if it were a marker for a culture, and then resorting to a hypothetical computer model of DNA spread patterns to explain culture spread in contradiction of the archaeological record.

Sadly, Meldrum claims that a *computer model* which assumes a spread from Asia of all Amerindian haplotypes before 13,000 B.C. (every point of which he rejects) is proof *in the real world* that haplotype X spread via Nephites over the Atlantic in 600 B.C.

DO THE DRUZE HAVE ANYTHING TO ADD?

The presentation tries to tie Native Americans to the Middle East by invoking the Middle East Druze. A high percentage of Druze, like some Native American groups, are members of haplogroup X2.⁸⁶ Once again, the difficulties lie in information not disclosed in the presentation.

As you have already seen, the X2 family is divided into many subfamilies. Some Native Americans are in subfamily X2a, a very early off-shoot of X2. Meldrum wishes to squash the idea that inhabitants of eastern Siberia are the possible source of Amerindian X2a, and so points out (correctly) that they are X2e—not the same family, and so not the source of X2a.⁸⁷ What he does not tell us, however, is that the Druze are not X2a either—many of them are X2e, the exact same family that he has rejected as a DNA source from eastern

⁸⁵ William Dancy, "The Enigmatic Hopewell of the Eastern Woodlands," *North American Archaeology*, edited by Timothy R. Pauketat and Diana Dipaolo Loren (Malden: Blackwell Publishing, 2005), 114.

⁸⁶ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 43:03-44:30.

⁸⁷ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 41:46-42:00. This point is made in M. Reidla, *et al.*, "Origin and Diffusion of mtDNA Haplogroup X," 1187.

Siberia.⁸⁸ It is inconsistent to reject Siberian X2e as possible ancestors and then try to claim that X2e from the Druze prove a link to the Middle East of Lehi's day.

The Druze are also not Hebrews or Israelites, though they live in the modern state of Israel. Indeed, “the [Middle Eastern] populations with the smallest genetic distances to the Druze were: Turks, Armenians, Iranians and Egyptians”—not Jews. Researchers on the Druze believe that their DNA haplotypes are a remnant of the genetic picture from long ago.⁸⁹ While this might be initially promising for the LNAM, the authors dash any hopes we might have of linking Lehi to the Druze with the current available data. Instead, they argue that the origins of Druze genetic patterns “coincide with and follow the most recent out of Africa expansion as dated by mtDNA coalescence simulations”—i.e., around 80,000 to 150,000 years ago.⁹⁰

Of Druze males, 35% are members of Y-chromosome haplotype L, which is not present in the Americas or in modern Jews, so other genetic tests do not match the theory Meldrum proposes.⁹¹

In sum, the Druze are not relevant to Book of Mormon studies given the current state of the data—but, we are meant to think that this is one more “link” between the Israel of Lehi's day and American Indians. The science—including Meldrum's own sources—does not support this.

Yet, Meldrum wraps up his DNA argument by explaining how many Druze are in Israel and how their percentages of X2 almost exactly matches the Ojibwa Indians. Unfortunately, this information is a meaningless coincidence, since Druze are no more a part of the X2a family than are the Siberians that Meldrum and scientists have rightly rejected as Amerindian ancestors.⁹²

MELDRUM'S CONCLUSION

Meldrum summarizes his DNA presentation with this statement:

So what we have, brothers and sisters, is we have European DNA which is found right in this general area, which matches up with DNA of modern

⁸⁸ M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1187, puts Altaians in subfamily (clade) X2e. The more recent Liran I. Shlush, *et al.*, “The Druze: A Population Genetic Refugium of the Near East,” *PLoS ONE* 3:5 (2008) notes that many Druze retain X2e as well.

⁸⁹ Liran I. Shlush, *et al.*, “The Druze: A Population Genetic Refugium of the Near East,” *PLoS ONE* 3:5 (2008), 1-9.

⁹⁰ Alan Templeton, “Out of Africa Again and Again,” *Nature* 416:6876 (2002), 45-51. See, especially, figure 41.

⁹¹ P. Shen, *et al.*, “Reconstruction of Patrilineages and Matrilineages of Samaritans and Other Israeli Populations from Y-Chromosome and Mitochondrial DNA Sequence Variation,” *Hum Mutat* 24:3 (2004), 252.

⁹² That this is a coincidence is further demonstrated by the fact that Orkney Islanders [north of Scotland] also have a high frequency of X2. Reidla *et al.* argue that the high level of X2 in the Druze and Orkney Islanders is “most likely due to genetic drift and founder events,” not direct recent links such as those suggested by the LNAM. See M. Reidla, *et al.*, “Origin and Diffusion of mtDNA Haplogroup X,” 1186-1187.

Native Americans in this area. And they have no understanding of how it got there, you see, because it couldn't have come over through Asia.⁹³

This is a faulty conclusion based upon faulty data. As you have seen, the X2a subfamily in America is *not* the same as the X2 subfamilies in Europe or the Middle East. They are separate lines, with scientific evidence of separation much earlier than Lehi's migration.

The claim that it "couldn't have come over through Asia" is likewise erroneous since the time that X2a split from X2 is early enough that a crossing of a Bering land bridge is a much more likely scenario than a much later oceanic crossing. This does not mean that local populations in Siberia now carry the X2a gene, merely that a migration may have moved from the Middle East to the Americas across such a bridge. Other possible routes include a coastal spread around the Pacific Rim.

The article quoted by Meldrum from *Evolutionary Anthropology* disagrees with him further: "there is no reason to believe that [haplogroup X2a] need ever have been common in Asia in order to achieve its present distribution in the Americas."⁹⁴

CONCLUSION

The DVD presentation exhibits a consistent pattern of selective citation. Meldrum does not present information that is harmful to his case, nor does he engage it. DNA science can be difficult to navigate and Meldrum is not the first researcher to misunderstand and misinterpret the data. He, like so many others, shows little understanding of the underlying principles of the science he attempts to rally to his cause. While he is likely sincere in his attempt to bolster the Book of Mormon, his incorrect assumptions cause both him and his audience to draw conclusions that are false and contrary to the science he purports to present.

More recent work is likewise not in agreement with his theories, as indicated by a paper from 2008:

The differential pattern of distribution and frequency of haplogroup X led some to suggest that it may represent an independent migration to the Americas. Here we show, by using 86 complete mitochondrial genomes, that all Native American haplogroups, including haplogroup X, were *part of a single founding population*, thereby refuting multiple-migration models.

Our results strongly support the hypothesis that haplogroup X, together with the other four main mtDNA haplogroups, was *part of the gene pool of a single Native American founding population*; therefore they do not support

⁹³ Meldrum, *DNA Evidence*, section 1, "DNA Evidence," 42:40-43:00.

⁹⁴ Jason Eshleman, *et al.*, "Mitochondrial DNA Studies of Native Americans," 11.

models that propose haplogroup-independent migrations, such as the migration from Europe....⁹⁵

A review of the research cited by Meldrum cannot recommend his theories. While *DNA Evidence for Book of Mormon Geography* may tickle the ears of an audience that only sees the evidence through the lens Meldrum provides them, it doesn't stand up to a full examination in the light of day.

⁹⁵ N.J. Fagundes, *et al.*, "Mitochondrial Population Genomics Supports a Single Pre-Clovis Origin with a Coastal Route for the Peopling of the Americas," *American Journal of Human Genetics* 82:3 (2008), 583–592, emphasis added.