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Abstract This paper debunks the myth that the Book of Mormon has been proved false by modern DNA evidence. Critics have tried to apply American Indian DNA-based research to the Book of Mormon without designing a study specifically for that purpose. It is extraordinarily difficult to use DNA sequence information to track the lineage of any group with such a complex lineage history as the Nephites and Lamanites. Possible hypotheses about the populations from the Book of Mormon include the global colonization hypothesis (in which the three colonizing groups came to a land void of humans) and the local colonization hypothesis (in which the land was already occupied in whole or in part by people of an unknown genetic heritage). The latter hypothesis, generally viewed by Book of Mormon scholars as a more accurate interpretation, is much more difficult to investigate by way of DNA evidence. Issues such as genetic introgression, genetic drift, and the founder effect would seriously hamper any attempt to produce a funded, peer-reviewed study of Book of Mormon genetics.



DNA AND THE BOOK OF MORMON: A PHYLOGENETIC PERSPECTIVE

Michael F. Whiting

THE PAST DECADE HAS SEEN A REVOLUTION in the way in which biologists collect data and proceed with their research. This revolution has come about by technological innovations that allow scientists to efficiently sequence DNA for a wide range of organisms, resulting in vast quantities of genetic data from a diverse array of creatures. From estimating the genealogical relationships among fleas to understanding the population genetics of crayfish, DNA sequence information can provide clues to the past and allow scientists to test very specific hypotheses in a way that was unapproachable even a few years ago. The announced completion of the Human Genome Project is not really a completion of DNA work at all, but simply one step on the road toward a better understanding of ourselves as biological organisms, our shared genetic history as humans, and the genetic history we share with all living organisms. Work is under way in many fields to generate DNA sequences from a wide variety of organisms for a spectrum of genes to address an almost dizzying array of scientific and medical questions. As it stands, there is possibly no other data source that holds more potential for biological inquiry than DNA sequence data, and this information is currently one of the most powerful tools in the arsenal of scientists.

However, as with all scientific tools, there are bounds and limits to how this tool is applied and what questions it can adequately address. This is because DNA sequence information is useful for only certain classes of scientific questions that need to be properly formulated and carefully evaluated before the validity of the results can be accepted. There are many interesting questions for which DNA sequence data is the most appropriate data source at hand, as

current scientific investigations attest. But there are some classes of problems for which DNA may provide only tangential insight, and some very interesting biological questions for which DNA is altogether an inappropriate source of information. Moreover, there are certain biological problems that scientists would love to answer but that are complicated and resist solution, even given DNA information. Within the scientific community, DNA-based research is carefully scrutinized to be certain that underlying assumptions have been tested, that data have been correctly collected and analyzed, and that the interpretation of the results are kept within the framework of the current theory or methodology. DNA research is only as good as the hypotheses formulated, data collected, and analyses employed, and the pronouncement that a certain conclusion was based on DNA evidence does not ipso facto mean that the research is based on solid science or that the conclusion is correct. The National Science Foundation rejects literally hundreds of DNA-based research proposals every year because they are lacking in some way in scientific design. The inclusion of a DNA component does not necessarily guarantee that the study was properly designed or executed.

Recently, some persons have announced that modern DNA research has conclusively proved that the Book of Mormon is false and that Joseph Smith was a fraud.¹ This conclusion is based on the argument that the Book of Mormon makes specific predictions about the genetic structure of the descendants of the Lamanites and that these descendants should be readily identifiable today. These critics argue that when the DNA is put to the test, these descendants lack the distinctive genetic signature that the critics claim the Book of Mormon predicts. They



bolster their arguments by appealing to DNA research, claim that their conclusions are thoroughly scientific, and pronounce that the Church of Jesus Christ of Latter-day Saints must now go through a Galileo event, in reference to the 17th-century astronomer who discovered that the sun, not the earth, was the center of the solar system, much to the consternation of the prevailing religious view. They have trumpeted this conclusion to the media and have gained a modicum of press coverage by playing on the stereotype of modern science being suppressed by old religion. Moreover, they argue that the silence at Brigham Young University over this topic is evidence that their arguments and conclusions are above reproach. However, these claims err scientifically in that they are based on the naive notion that DNA provides infallible evidence for ancestry and descent in sexually reproducing populations and that the results from such analyses are straightforward, objective, and not laden with assumptions. Moreover, proponents of this naive view blindly ignore decades of theory associated with DNA sequence evolution and data analysis and rarely speak to the extremely tentative nature of their conclusions.

The purpose of this paper is to debunk the myth that the Book of Mormon has been proved false by modern DNA evidence. What I put forth here is a series of scientific arguments highlighting the difficulty of testing the lineage history given some of the known complicating events. This paper should not be regarded as a summary of current research on human population genetics nor as an extensive analysis of all possible complicating factors; rather, it focuses on the current attempts to apply DNA information to the Book of Mormon.

What Is the State of DNA Research on the Book of Mormon?

The first point that should be clarified is that those persons who state that DNA evidence falsifies the authenticity of the Book of Mormon are not themselves performing genetic research to test this claim. This conclusion is not coming from the scientists studying human population genetics. It is not the result of a formal scientific investigation specifically designed to test the authenticity of the Book of Mormon by means of genetic evidence, nor has it been published in any reputable scientific journal open to scientific peer review. Rather, it has come



Galileo's controversial but correct scientific observation that the earth rotates around the sun was consistent with good science. (*Galileo*, by Justus Sustermans, 1597–1681, oil on canvas; Scala/Art Resource, New York)

from outside persons who have interpreted the conclusions of an array of population genetic studies and forced the applicability of these results onto the Book of Mormon. The studies cited by these critics were never formulated by their original authors as a specific test of the veracity of the Book of Mormon. To my knowledge there is no reputable researcher who is specifically attempting to test the authenticity of the Book of Mormon with DNA evidence.

Is DNA Research on the Book of Mormon Fundable?

As I am writing this article, I am sitting in an airplane on my way to Washington, D.C., to serve as a member of a scientific review panel for the Systematic Biology program of the National Science Foundation. The NSF is a major source of basic research funding available to scientists in the United States, and every six months the NSF brings in a panel of researchers to review grant applications and provide recommendations for funding. Each research proposal is a 15-page explanation of what research is to be performed, how the research project is designed, the specific hypotheses to be tested through the proposed work, preliminary data

indicating the feasibility of the particular scientific approach, careful analyses of these data, preliminary conclusions based on those analyses, and a justification for why the proposed research is scientifically interesting, intellectually significant, and worthy of funding. As someone who has received a half-dozen NSF grants and has written even more research proposals, I recognize how much time and effort go into writing a successful research proposal and how carefully thought out that research must be before funding will ever be made available. While anyone can claim to do scientific research, it is widely accepted within the scientific community that the touchstone of quality in a research program is the ability to obtain external funding from a nationally peer-reviewed granting agency and to publish the results in a reputable scientific journal. To be funded at the national level means that a research proposal has undergone the highest degree of scrutiny and been approved by those best able to judge its merits.

Given that no research program thus far has been designed to specifically test the authenticity of the Book of Mormon, I would like to center my discussion on the following question: *If one were to design a research program with the stated goal of testing the validity of the Book of Mormon based on DNA information, what specific hypotheses would one test, what experimental design is best suited to test each of these hypotheses, what sort of assumptions must be satisfied before these tests are valid, and what are the limitations of the conclusions that can be drawn from these data?* In other words, would a proposal to test the validity of the Book of Mormon by means of DNA sequence information have a sufficiently solid base in science to ever be competitive in receiving funding from a nationally peer-reviewed scientific funding agency such as the NSF?

Is the Authenticity of the Book of Mormon Testable by Means of DNA Information?

One could of course argue that it is impossible to directly test the authenticity of the Book of Mormon with the tools of science, since the Book of Mormon lies within the realm of religion and outside the realm of science. It would be like asking a scientist to design an experiment that tests for the existence of God. There are no data that one could collect to refute the hypothesis that God exists, just as there are no data that one could collect to refute the hypothesis that he does not exist: science simply

cannot address the question, and one might argue that the same is true for the Book of Mormon. If one holds this view, and there may be some very good reasons why one might, then there is no need to read any further: DNA can tell us nothing about the authenticity of the Book of Mormon.

However, one might argue that it is possible to indirectly judge the validity of the text by testing the authenticity of the predictions made within the text. If one can demonstrate that some predictions are specifically violated, then perhaps one would have some basis for claiming that the text is false. This is the line of reasoning followed by those who pursue the genetic argument. They suggest that the Book of

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.

Mormon makes specific predictions about the genetic structure of the Nephite-Lamanite lineage, that this genetic structure should be identifiable in the descendants of the surviving Lamanites, and that if the Book of Mormon is “true,” then these predictions should be verifiable through DNA evidence. The critics argue that the Book of Mormon predicts that the Lamanite lineage should carry the genetic signature of a Middle Eastern origin and that the genetic descendants of the Lamanites are Native Americans. They then scour the literature to show that current DNA research suggests that Native Americans had an Asian origin. These results are then trumpeted as invalidating the authenticity of the text.

However, by simply applying the results of population genetic studies, which again were never intended to test the Lamanite lineage history put forth in the Book of Mormon, these critics have ignored crucial issues that any reputable scientists designing a research program would have to consider. My thesis is that it is extraordinarily difficult, if not impossible, to use DNA sequence information to track the lineage of any group of organisms that has a historical population dynamic similar to that of the Nephites and Lamanites. This is not an argument



that the Nephite-Lamanite lineage is somehow immune to investigation through DNA evidence because its record is a religious history, but simply that the Nephite-Lamanite lineage history is an example of a class of problems for which DNA evidence provides—at best—ambiguous solutions. It does not matter to me whether we are talking about humans or fruit flies; you could substitute the term *Lamanite* with *Drosophila* and the argument would be the same. The lineage history outlined in the Book of Mormon is a conundrum from a DNA perspective; the critics have grossly underplayed or are ignorant of the complications associated with testing this history. Further, because of the complicated nature of this lineage history, 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.* The Lamanite lineage history is difficult to test through DNA information, DNA provides at best only tangential information about the text, and anyone who argues that it can somehow speak to the authenticity of the text should consider the following complicating factors.

What Hypotheses Emerge from the Book of Mormon?

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. Good science consists of formulating specific hypotheses that can be directly tested from a particular data source. The problem is that, unlike a good NSF research proposal, the Book of Mormon does not explicitly provide a list of null and alternative hypotheses for scientific testing. For instance, the spiritual promise offered in Moroni 10:4 is not open to scientific investigation because it does not put forth a hypothesis that can be tested with any sort of scientific rigor. Likewise, the entire text of the Book of Mormon was meant for specific spiritual purposes and was not intended to be a research proposal listing an explicit hypothesis that is open to scientific investigation. Hence, any hypothesis that emerges from the Book of Mormon is entirely a matter of interpretation, and any specific, testable hypothesis is

based very much on how one reads the Lamanite history and considers the degree to which external forces may have influenced the composition of the Lamanite lineage. A person cannot test the authenticity of the Book of Mormon by means of genetics without making some statement about the specific hypotheses that are being tested, why these hypotheses are an accurate interpretation of the text, and how these hypotheses somehow speak to the authenticity of the text. At the very best, one might demonstrate that the predictions have been violated, but the question remains as to whether the supposed predictions were correct to begin with.

From my perspective, there are two possible basic lineage histories—differing in scope, magnitude, and expectation—that one might derive from the Book of Mormon. These histories make predictions that could possibly form the basis of hypotheses that may be tested to varying degrees by means of DNA evidence. I have set these up in a dichotomy of extremes, and certainly one could come up with any combination of these two scenarios, but the extremes are useful for illustrating difficulties associated with applying DNA sequence information to the Book of Mormon. For lack of better terms, I will refer to these as the global colonization hypothesis and the local colonization hypothesis.

The Global Colonization Hypothesis

The global colonization hypothesis is the simplest view of the Lamanite history and the one most readily testable through DNA evidence. This is the view that when the three colonizing groups (Jaredites, Mulekites, and Nephties + Lamanites) came to the New World, the land they occupied was entirely void of humans. It presumes that these colonizers were able to form a pure and isolated genetic unit of Middle Eastern origin living on the American continent and that this genetic heritage was never “contaminated” by the genetic input from any other non-Middle Eastern sources or peoples during the time recorded in the Book of Mormon. It also assumes that the colonizers accurately carried the genetic signature of the Middle Eastern source population and that such a signature indeed existed both within the source population and the migrants. It further requires that genetic input from the time when the Book of Mormon record ends to the present day was negligible or absent and that the direct genetic descendants of these colonizers exist today



Figure 1. Simplistic representation of population genetics

Each candy store (A and B) represents a human population that may be distinguished on the basis of genetic information. The gumballs represent a particular genetic marker (or locus), such as an entire gene, a portion of DNA, or a specific position along a strand of DNA. Each gumball color represents a variant of the genetic marker, such as a particular form of a gene (allele) or a different nucleotide (A, G, C, or T) at a specific site on the DNA strand. Each gumball machine represents a collection of all of the variants for a single genetic marker across the entire population. If gumball machine A1 contains 100 gumballs, this means that within population A all 100 individuals possess the red variant (and no others) for that particular genetic marker. Most organisms (including humans) carry a large number of genetic markers, so think of the candy store as a giant warehouse stretching out as a seemingly endless line of gumball machines. Most populations consist of a large number of individuals, so think of the gumball machines as being much larger than illustrated.

One population (= candy store) may be distinguished from another by characterizing the particular combination and frequency of genetic variants (= gumball colors) for every genetic marker (= gumball machine). For instance, candy store A may be distinguished from candy store B by carrying only red gumballs for genetic marker 1, a high frequency of green gumballs for genetic marker 2, and a high frequency of yellow gumballs for genetic marker 3. In relation to genetic marker 1, the differences between candy store A and B are discrete differences. That is to say, in candy store A there is only a single genetic variant (red), and in candy store B there is also only a single genetic variant (green). In relation to genetic markers 2 and 3, the differences between candy stores A and B are frequency differences. While both store A and B contain blue variants for genetic marker 2, blue is present in a much higher frequency in store B than it is in store A. The majority of population genetic studies rely on such frequency differences to characterize populations.

and can be identified prior to any genetic analysis. This hypothesis also incorporates the notions that these groups expanded to fill all of North and South America, that there was a tremendous population explosion from these single colonization events, and that any subsequent genetic input, if it occurred, would be swamped out by the strength of the Middle Eastern genetic signal present in the majority of the population. This hypothesis requires that introgression (i.e., gene flow from an external population to the one under study) of genetic signal from other sources be negligible or absent and that the

genetics of the individuals compared in an analysis have remained largely pure since the time of colonization. This interpretation of the lineage history of the Book of Mormon is the most easily tested hypothesis by way of DNA analysis.

If we grant that the global colonization hypothesis is the correct lineage history emerging from the Book of Mormon, this hypothesis predicts that the modern-day descendants of the Lamanite lineage should contain the Middle Eastern genetic signature. Since current population genetics suggests that Native Americans (presumed by some to be the direct

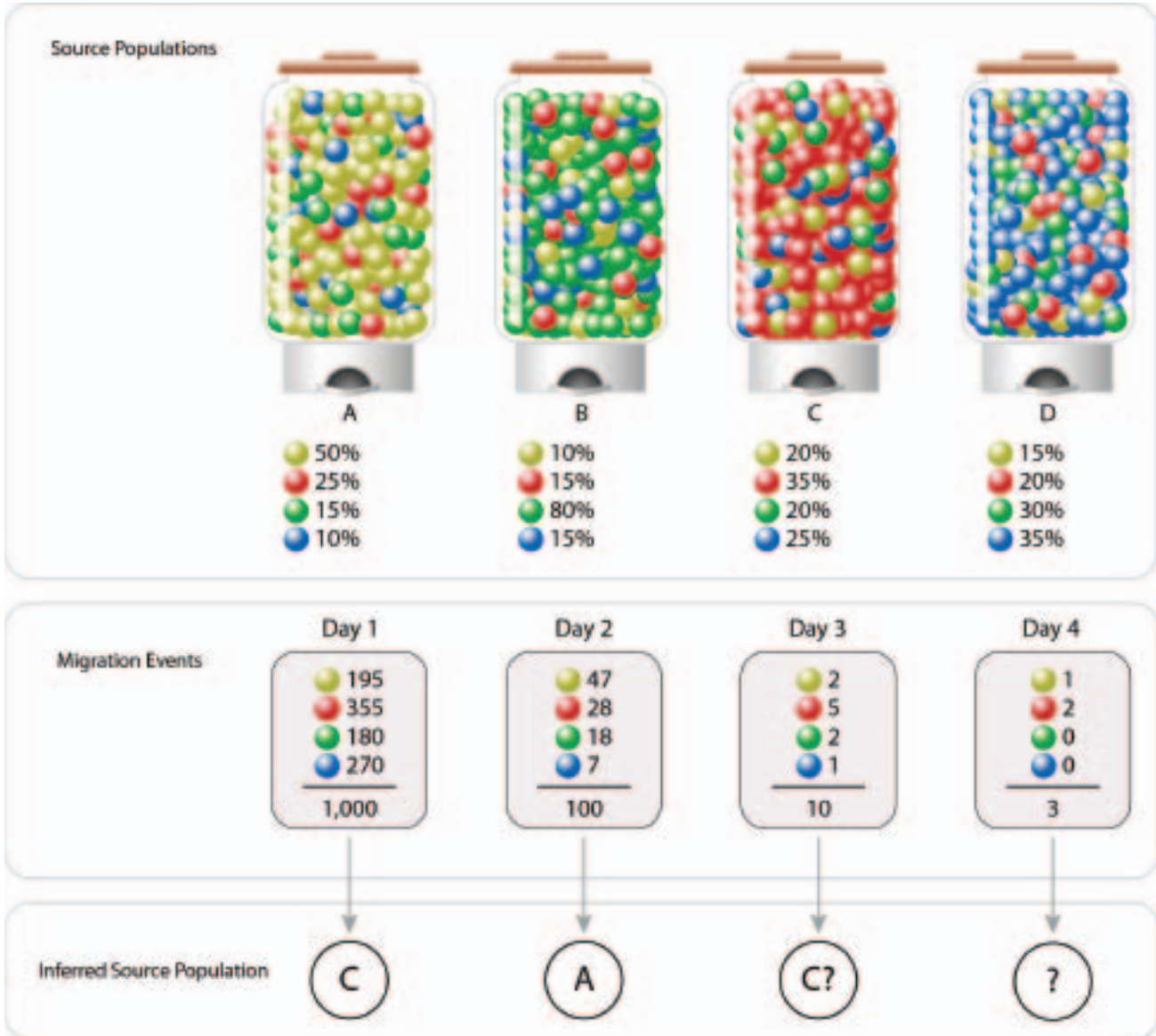


Figure 2. Influence of founder effect on frequency distributions of genetic variants

Each gumball machine (A–D) represents a potential source population for a single genetic marker. Each source population can be distinguished by a unique frequency of genetic variants (= gumball colors); for example, half of the individuals in source population A possess the genetic variant yellow. Now assume that the mechanism for releasing gumballs from one machine is broken, so that when you return in the morning you find gumballs on the floor. This represents a migration event from an unknown source. Suppose this happened three more times. Your task is to determine which gumball machine was the source population of spilled gumballs for each day in a four-day period.

On day 1, 1000 gumballs spill onto the floor. The inference is that population C was the source population since the frequency of gumballs on the floor is very close to the frequency in the original population. On day 2, 100 gumballs spill onto the floor and you infer (with less confidence) that the source population is A since the frequency of the spilled gumballs is similar to the frequency of population A. On day 3, only 10 gumballs spill. The source population might be C, but this inference carries a great degree of uncertainty since the frequencies are markedly different. On day 4, only 3 gumballs spill, and you cannot determine with any degree of confidence the identity of the source population. Thus as the sample size decreases, the probability that it will not reflect the frequencies in the original population increases. Undersampling of populations is caused by the migration of few individuals and results in a major shift in frequency distributions of genetic markers, thereby obscuring the genetic link to the source population.

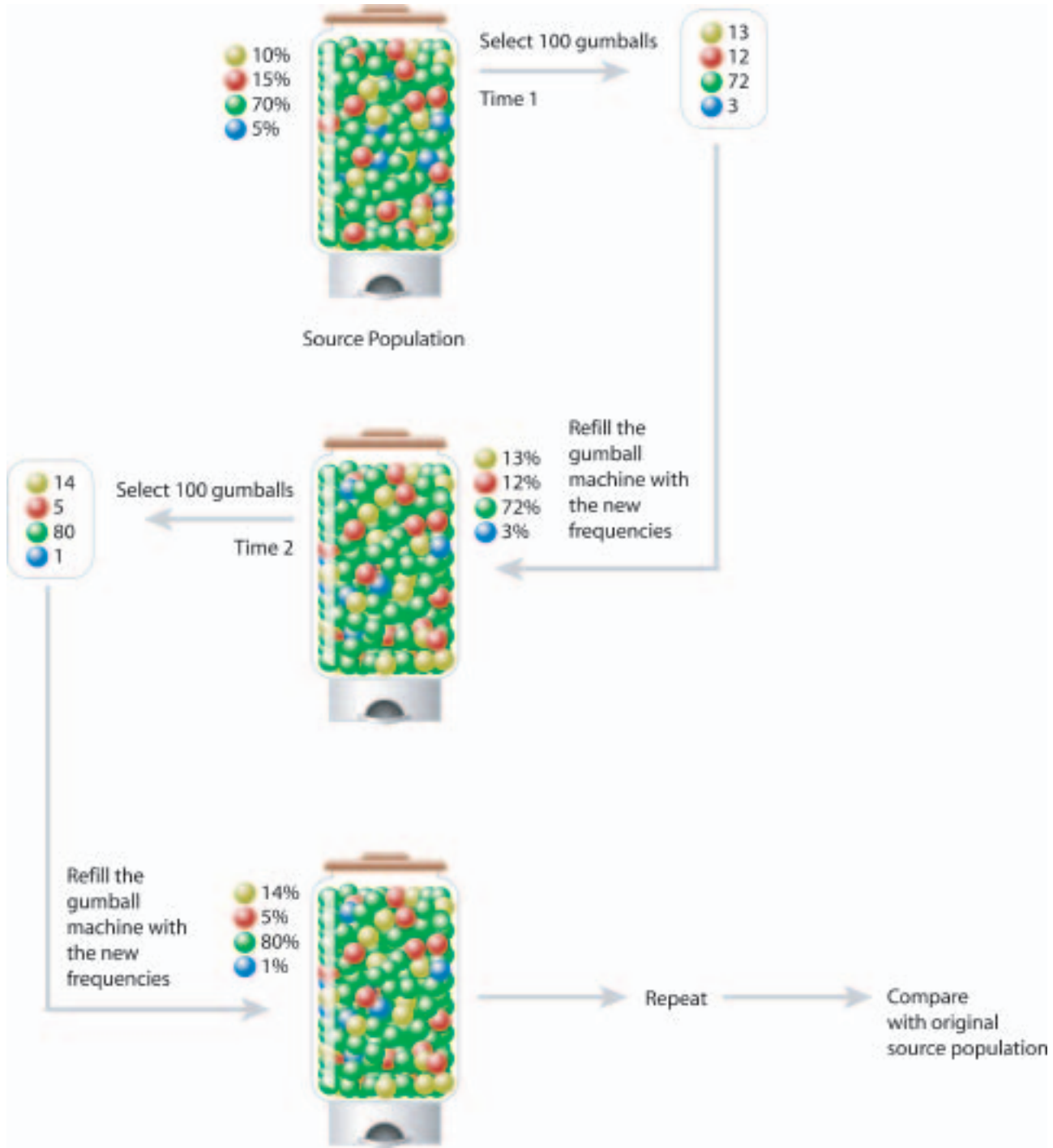


Figure 3. Effects of genetic drift

Assume that a source population consists of 1000 gumballs with the frequencies as illustrated. Sample 100 individuals from the source population and the frequency of gumballs will shift (for reasons given in fig. 2). Now establish a new population of 1000 gumballs with frequencies identical to those of the selected sample at time 1. Sample 100 individuals from this new population at time 2. The frequency of the gumballs will shift again. Reestablish the population of 1000 gumballs and repeat the process multiple times. When, after repeated rounds of sampling, you compare the population frequencies with those of the original source population, the frequencies will have drifted over time, thus limiting the ability to accurately infer the source population.



genetic descendants of the Lamanites) have an Asian genetic signature,² the above hypothesis is indeed incorrect. To this point all we have shown is that the global colonization hypothesis appears falsified by current genetic evidence. But is the global colonization hypothesis the only hypothesis emerging from the Book of Mormon? This is the crux of the matter. Critics who argue that DNA analysis disproves the authenticity of the Book of Mormon need to demonstrate that the global colonization hypothesis is the only way to interpret the Lamanite lineage history and the only hypothesis under question. *The authenticity of the Book of Mormon is in question only if this is an accurate interpretation of the historical population dynamics inferred as existing before, during, and after the Book of Mormon record takes place.* However, if the above description of the lineage history in the Book of Mormon is oversimplified, then these genetic results demonstrate only that this oversimplified view does not appear correct. But Book of Mormon scholars have been writing about certain complicating factors for decades, so this conclusion about oversimplification really comes as no surprise.³

The Local Colonization Hypothesis

The local colonization hypothesis is more limited in scope, includes many more complicating factors from a genetic perspective, is much more difficult to investigate by way of DNA evidence, and, in my view and that of Book of Mormon scholars, is a more accurate interpretation of the Lamanite lineage history. This hypothesis suggests that when the three colonizing parties came to the New World, the land was already occupied in whole or in part by people of an unknown genetic heritage. Thus the colonizers were not entirely isolated from genetic input from other individuals who were living there or who would arrive during or after the colonization period. The hypothesis presumes that there was gene flow between the colonizers and the prior inhabitants of the land, mixing the genetic signal that may have been originally present in the colonizers. It recognizes that by the time the Book of Mormon account ends, there had been such a mixing of genetic information that there was likely no clear genetic distinction between Nephites, Lamanites, and other inhabitants of the continent. This distinction was further blurred by the time period from when the Book of Mormon ends until now, during which there was an influx of genes from multiple genetic sources. Moreover, the

hypothesis suggests that the Nephite-Lamanite lineage occupied a limited geographic range. This would make the unique Middle Eastern genetic signature, if it existed in the colonizers at all, more susceptible to being swamped out with genetic information from other sources.

The problem with the local colonization hypothesis (from a scientific standpoint) is that it is unclear what specific observations would refute it. This is because it makes no specific predictions that can be refuted or corroborated. For instance, there is no expectation that the descendants of the Lamanites should have any specific type of genetic signal, since their genetic signal was easily mixed and swamped out by other inhabitants of unknown genetic origin. Hence, this hypothesis can be neither easily corroborated nor easily refuted by DNA evidence, since any observation could be attributed to genetic introgression, drift, founder effect, or any of the other complicating factors described below.

Local Colonization Hypothesis: Complicating Factors

Suppose you threw caution to the wind and believed that the local colonization hypothesis was the correct one emerging from the Book of Mormon, you really think it is testable, and you are specifically seeking funding to test it. Further, suppose that someone with knowledge of modern population genetics, phylogenetic systematics, molecular evolution, and the Book of Mormon was sitting on the NSF panel reviewing your proposal. Below is a short description of some of the complicating factors that you would have to address in your proposal before the research could be funded. This is not meant to be complete or exhaustive, but just an example of some complicating factors. More detailed descriptions of these basic concepts can be found in standard population genetic, molecular systematics, and molecular evolution textbooks.⁴

1. *Was there a unique, Middle Eastern genetic signature in the source population?* In order for the colonizers to carry a Middle Eastern genetic signature with them, that signature needed to first exist in the source population. It is possible that the Middle Eastern population may not have had a single genetic signature that would allow one to unambiguously identify an individual as being from the Middle East and from no other human population. This is an important consideration because there are many

cultural and racial groups today for which there are no discrete markers unambiguously identifying an individual as a member of that group. Moreover, typically the larger the population and the greater that population tends to migrate, the smaller the probability that a unique, discrete genetic marker exists for that group.

2. *Were genetic variants present in the colonizers?* In order to perform your study, you would need to present evidence that each of the colonizing groups possessed the unique and defining Middle Eastern traits and did not possess any genetic variants that were atypical of this Middle Eastern genetic heritage.

The DNA Fallacy

- DNA analysis does not require careful experimental design.
- DNA provides straightforward, unambiguous, and internally consistent information about the past.
- DNA can be used to infer the genealogy of any organism or any species, regardless of circumstance or historical population dynamic.
- DNA conclusions are final, decisive, and free of assumptions.

3. *How do you know that small founder size does not confound your results?* The Book of Mormon makes clear that each colonization event involved a very small number of founders. Such small population sizes would have had profound effects on how the genetic markers changed over time. In fact, moving a few individuals of any species from one population to a new locality can have such a profound effect on the underlying genetic profile that it is considered to be a major mechanism in the formation of new species. This is called founder effect, which is caused by undersampling genes from a much larger population of genes and is closely tied to the concept of genetic drift (described below). In other words, founder effect describes the evolutionary process that results in the colonizing population

having a gene pool that is not likely to reflect the gene pool of the original source population.

4. *What are the effects of genetic drift?* Genetic drift is the well-established evolutionary principle that in small populations random sampling biases will cause certain genetic markers to disappear and other markers to become widespread in the population just by chance. As an example, suppose you go to the grocery store to purchase a container of 1,000 jelly beans in 10 flavors. When you bring the jelly beans home, you determine that each of the 10 flavors is present in equal frequency; that is, you have as many tangerine-flavored jelly beans as you have lime-flavored jelly beans. Now from that container of

The DNA Fact

- DNA is a very important tool for inferring history, but
 - experiments must be properly designed,
 - hypotheses must be formulated,
 - assumptions must be tested,
 - analyses must be appropriate for the data at hand,
 - conclusions are the best current estimate but are open to revision with additional data or analytical tools.

1,000 jelly beans, randomly sample 100 jelly beans and place them in a new container. If you count the jelly beans in the new container, you will realize that the frequency has changed; some flavors happened to be selected 11 or 12 times, some were sampled only 3 or 4 times, and some might not be sampled at all. Now instead of sampling 100 jelly beans, this time sample 30 from your original container. You would find that the frequency of flavors is more greatly skewed with the smaller sample size and that you have lost more flavors. As you reduce your sample size, you increase the probability that the frequency of jelly beans in the new sample will be all the more different from the original population. If each flavor represents a unique genetic heritage, this means that the sampling of genes from one generation to the



next can cause certain genetic markers to go extinct and others to be present in higher frequency due entirely to random sampling. When the colonizers left the Middle East, they brought with them only a sample of the genetic heritage of that population that may not have accurately represented the markers present in the whole population; and when they arrived in the New World, the frequency of those genetic markers was likely to continue to change as the population was established.

5. *What were the effects of the colonizers' arriving to a locality that was not a complete genetic island (i.e., other humans were present and could contribute to the gene pool)?* If there were other inhabitants al-

this could have occurred early in the colonization process or later as the Nephite and Lamanite nations flourished, but the swamping-out effect would be very similar in either case.

6. *What were the effects of gene flow after the Book of Mormon ends?* Certainly there was gene flow from the time when the Book of Mormon record closes to when DNA samples are obtained in the present day. It is preposterous to suppose that there has been complete genetic isolation in the Lamanite lineage during this time period. As the designer of the scientific experiment, you would need to account for the effects of gene flow in this undocumented time period and provide a justification for

What I am NOT saying is . . .

- All population genetic studies are bogus.
- DNA is an unreliable tool.
- The science has so many assumptions that results are never believable.

ready present on the American continent when the colonizers arrived, then it becomes extremely difficult to distinguish whether the genetic signature a descendant carries is due to its being carried by the original colonizers or due to gene flow from the other, original inhabitants. This is especially problematic if the colonizing population is small and the native population is large once gene flow commences, since it will speed up the swamping-out effect of the colonizers' genetic markers with those of the native inhabitants. John L. Sorenson, among others, has presented evidence suggesting that the colonizers were not alone when they reached the Americas; and as I read the Book of Mormon, I can find no barriers to gene flow between the native population and those who formed the Lamanite lineage. Note that

What I AM saying is . . .

- The local colonization hypothesis is hard to test because of complications associated with the Lamanite lineage history, such as founder effect, genetic drift, and extensive introgression.
- DNA evidence is not likely to unambiguously refute or corroborate this hypothesis.
- This hypothesis has never been specifically tested.
- DNA evidence does nothing to speak to the authenticity of the Book of Mormon text.
- I would be just as critical of a claim that DNA evidence supports the Book of Mormon as I am of the claim that it does not.
- You cannot claim that an observation is scientific if you ignore the science.

why it did not contaminate the genetic signature of the Lamanite lineage. Simply speaking, that genetic signature, if one existed, could be obliterated by gene flow from outside groups.

7. *How do you account for the difficulties associated with a small population range?* The local colonization hypothesis suggests that the geography of the Book of Mormon was quite limited in scope and that the Lamanite lineage did not populate the whole North and South American continent.⁵ This implies that you cannot just sample anywhere in North or South America, but that you need to have some basis for deciding where you are going to sample and why it is likely that you will find pure genetic descendants of the Lamanite lineage in that specific location.



8. *Who are the extant genetic descendants of the Lamanite lineage?* If you are treating your research as a scientific test of the local colonization hypothesis, you need to identify who these Lamanite descendants are before you put them to the genetic test. When we go out to sample “Lamanite DNA,” whom do we sample to get that DNA? There is no statement within the text of the Book of Mormon identifying who these descendants might be, though later commentators and church leaders have associated them with the Native Americans and/or inhabitants of South and Central America. The introduction to the Book of Mormon states that the Lamanites were the “principal ancestors of the American Indians,” but this, again, is commentary not present in the original text and was based on the best knowledge of the time.

9. *How do you identify unambiguously the Middle Eastern population that contains the ancestral genetic signature that you will use for comparison?* Just as the genetic signature of the colonizers may have changed over time, the genetic signature of the Middle Eastern source population may have changed as well, making it unclear just whom we should sample to find that ancestral Middle Eastern genetic marker. We know that the Middle East has been the crossroads of civilization for many millennia and that many events affecting entire populations have occurred there since 600 B.C., such as the large-scale captivity of groups and the influence of other people moving within and through the area. All of these factors complicate the identification of a discrete genetic profile characterizing the original Middle Eastern source population.

10. *Has natural selection changed the genetic signature?* One assumption in performing molecular phylogenetic analyses is that the genetic markers under study are not subject to the effects of natural selection. For instance, if a particular genetic marker is closely linked to a genetic disease that reduced fitness (the number of offspring that survive to reproduce) in a population, then, over time, selection would tend to eliminate that genetic marker from the population and the phylogenetic information associated with that marker may be misleading. Likewise, a genetic marker linked to a favorable trait may become the dominant marker in the population through the results of natural selection, and the marker would then be of limited phylogenetic utility.

The above tally is not intended to be an exhaustive list of scientific concerns, and many other more

complicated ones abound. For instance, how has mutation obfuscated the identification of the original genetic signature (a process called multiple hits)? How does the shuffling of genetic markers affect your results (a process called recombination)? How do you account for the effects of groups of genes being inherited in a pattern that is not concordant with lineage history (a process called lineage sorting)? How do you deal with the well-established observation that genetic markers almost never give a single, unambiguous signal about an organism’s ancestry, but are rather a deluge of signals of varying strengths (a concept called homoplasy)? How do you know that your gene genealogy reflects organismal genealogies (a concept called gene tree versus species tree)? Researchers who use DNA to infer ancestry continually worry whether the genetic markers selected are tracking the individual’s history or the gene’s history, since one does not necessarily follow from the other.

Driving the Point Home

Let’s look at the problem another way. Suppose you were a scientist going to the NSF to get funding to study an ancient fruit fly colonization event and you want to test the hypothesis that a few thousand years ago a single female fruit fly from a Utah population was picked up in a storm and blown all the way to Hawaii to lay its eggs. You know that the offspring of this fruit fly can freely mate with the Hawaiian population and produce viable offspring, but so can all the other fruit flies blowing in from all over the world during this time period. Now suppose you use all the genetic tools in your arsenal to try to detect that Utah colonization event. Could you detect it? Perhaps, if the population dynamics were just right. But your inability to detect this event does not mean that it did not happen; it just means that given the particular population dynamics, it was extremely difficult to test because there was not a genetic signal remaining for the colonization event. Would you get funded for this study? Probably not. There are many better-designed experiments that are more worthy of funding than this shot in the dark.

Conclusion

Critics of the Book of Mormon have argued that DNA evidence has demonstrated once and for all that the book was contrived by Joseph Smith and is hence a fraud. They appeal to the precision of DNA evidence



and tout their conclusions as being objective, verifiable, assumption free, and decisive. However, these critics have not given us anything that would pass the muster of peer review by scientists in this field, because they have ignored the real complexity of the issues involved. Further, they have overlooked the entire concept of hypothesis testing in science and believe that just because they label their results as “based on DNA,” they have somehow proved that the results are accurate or that they have designed the experiment correctly. At best, they have demonstrated that the global colonization hypothesis is an oversimplified interpretation of the Book of Mormon. At worst, they have misrepresented themselves and the evidence in the pursuit of other agendas.

I return to my original question: Is testing the Book of Mormon by means of genetic information a fundable research project? I do not think so. Given the complications enumerated above, 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.

I have not made the argument that DNA is not useful for inferring historical events nor that population genetics is inherently wrong. Current research in population genetics is providing marvelous insights into our past and, when properly wielded, is a powerful tool. Nor am I disputing the inference that Native Americans have a preponderance of genes that carry a genetic signature for Asian origination. But what I am saying is that given the complexities of genetic drift, founder effect, and introgression, the observation that Native Americans have a preponderance of Asian genes does not conclusively demonstrate that they are therefore not descendants of the Lamanite lineage, *because we do not know what genetic signature that Lamanite lineage possessed at the conclusion of the Book of Mormon record.*

If you were to go back in time to when the Book of Mormon is closing and began sampling the DNA of individuals who clearly identified themselves as

Lamanites, you might indeed find a strong Asian signature and no trace of a Middle Eastern signature because of the effects, as we have noted, of genetic drift, founder effect, and especially introgression, particularly if the surrounding population was derived from an Asian origin. The point is that the current DNA evidence does not distinguish between this and other possibilities because a study has never been designed to do precisely that.

But in all this discussion of the limitations of DNA analysis, it is important to remember that science is only as good as the hypotheses it sets forth to test. If you test the veracity of the Book of Mormon based on a prediction that you define, then of course you will “prove” it false if it does not meet your prediction. But if the prediction was inappropriate from the beginning, you have not really tested anything.

In sum, the Book of Mormon was never intended to be a record of genetic heritage, but a record of religious and cultural heritage that was passed from generation to generation, regardless of the genetic attributes of the individuals who received that heritage. The Book of Mormon was written more as an “us versus them” record, with the “us” being primarily Nephites and the “them” being a mixture of the genetic descendants of Lamanites plus anyone else who happened to occupy the land at the time. This interpretation accepts as a strong possibility that there was substantial introgression of genes from other human populations into the genetic heritage of the Nephites and Lamanites, such that a unique genetic marker to identify someone unambiguously as a Lamanite, if it ever existed, was quickly lost. It would be the pinnacle of foolishness to base one’s testimony on the results of a DNA analysis. As someone who has spent a decade using DNA information to decipher the past, I recognize the tentative nature of all my conclusions, regardless of whether or not they have been based on DNA. There are some very good scientific reasons for why the Book of Mormon is neither easily corroborated nor refuted by DNA evidence, and current attempts to do so are based on dubious science. 📖



- Mosiah 24:4; Alma 7:1 and 9:21; Moroni 10:15–16; and Ether 12:23–26.
66. See the discussion in Sorenson, *Ancient American Setting*, 50–56.
 67. See P. Agrinier, “Linguistic Evidence for the Presence of Israelites in Mexico,” *S.E.H.A. Newsletter* 112 (Feb. 1969): 4–5; the report is greatly amplified by Robert F. Smith in a manuscript in possession of Sorenson and Roper. Alma M. Reed, in *The Ancient Past of Mexico* (New York: Crown, 1966), reprises information about this study.
 68. Quoted in Reed, *Ancient Past*, 10.
 69. See “Was There Hebrew Language in Ancient America? An Interview with Brian Stubbs,” *Journal of Book of Mormon Studies* 9/2 (2000): 54–63.
 70. Mary LeCron Foster, “Old World Language in the Americas” (see note 55 herein), copy in Sorenson’s possession and abstracted, including this quotation, in Sorenson and Raish, *Pre-Columbian Contact*, as item F–146B. See Foster, “Old World Language in the Americas: 2,” unpublished paper presented at the annual meeting of the Language Origins Society, Cambridge University, Sept. 1992, copy in Sorenson’s possession; see Sorenson and Raish, *Pre-Columbian Contact*, item F-146C. See also Foster’s “The Transoceanic Trail: The Proto-Pelagian Language Phylum,” *Pre-Columbiana* 1/1–2 (1998): 113.
 71. See Ruhlen, “Some Unanswered Linguistic Questions,” 171ff.
 72. Otto J. Von Sadvovsky, *The Discovery of California: A Cal-Ugrian Comparative Study* (Budapest: Akadémiai Kiadó; Los Angeles: International Society for Trans-Oceanic Research, 1996).
 73. See, for example, E. D. Merrill, “The Phytogeography of Cultivated Plants in Relation to Assumed Pre-Columbian Eurasian-American Contacts,” *American Anthropologist* 33/3 (July–Sept. 1931): 375–82, which was highly influential.
 74. See John L. Sorenson and Carl L. Johannessen, “Biological Evidence for Pre-Columbian Transoceanic Voyages,” in press in a volume of papers to be published by the University of Hawaii Press from a conference titled “Contact and Exchange in the Ancient World,” held at the University of Pennsylvania, 4–6 May 2001.
 75. Because of their length, full references are omitted from this paper; for details see the primary article when it appears.
 76. See Carl L. Johannessen and Wang Siming, “American Crop Plants in Asia before A.D. 1500,” *Pre-Columbiana: A Journal of Long-Distance Contacts* 1/1–2 (1998): 9–36. For the corn, see Ian C. Glover, “The Late Stone Age in Eastern Indonesia,” *World Archaeology* 9/1 (June 1977): 42–61.
 77. For example, see Gordon R. Willey, “Some Continuing Problems in New World Culture History,” *American Antiquity* 50/2 (April 1985): 351–63.
 78. See Wolfgang Marschall, *Influencias Asiáticas en las Culturas de la América Antigua: Estudios de su Historia* (México: Ediciones Euroamericanas Klaus Theile, 1972), 61.
 79. Julian Granberry, “Amazonian Origins and Affiliations of the Timucua Language,” in *Language Change in South American Indian Languages*, ed. Mary Ritchie Key (Philadelphia: Univ. of Pennsylvania Press, 1991), 195–242.
 80. See Emilio Estrada and Betty J. Meggers, “A Complex of Traits of Probable Transpacific Origin on the Coast of Ecuador,” *American Anthropologist* 63/5 (1961): 913–39.
 81. Clinton R. Edwards says, “From the practical seaman’s point of view Pacific crossings in such craft were entirely feasible.” See “Commentary: Section II,” in *Man across the Sea: Problems of Pre-Columbian Contacts*, ed. C. L. Riley et al. (Austin: Univ. of Texas Press, 1971), 304.
 82. See Clinton R. Edwards, *Aboriginal Watercraft on the Pacific Coast of South America* (Berkeley: Univ. of California Press, 1965); and Edwin Doran Jr., “The Sailing Raft as a Great Tradition,” in *Man across the Sea*, 115–38.
 83. See Norton, “*El señorío de Salangone*.”
 84. Dixon, *Quest for the Origins of the First Americans*, 130–31; for the changing picture, now see Heather Pringle, “Hints of Frequent Pre-Columbian Contacts,” *Science* 288/5467 (2000), 783, about “stunning new traces of the Norse . . . in the Canadian Arctic.”
 85. Swadesh (in *Culture and History*, 896) observes, in parallel, that “new languages probably came into America in the late millennia just before Columbus, but their speakers must have been absorbed . . . without leaving any language that has continued to modern times.”
 86. Joseph Needham, Wang Ling, and Lu Gwei-Djen, *Civil Engineering and Nautics*, pt. 3 of *Physics and Physical Technology*, vol. 4 of *Science and Civilisation in China* (Cambridge: Cambridge Univ. Press, 1971).
 87. Joseph Needham and Lu Gwei-Djen, *Trans-Pacific Echoes and Resonances: Listening Once Again* (Singapore and Philadelphia: World Scientific, 1985).
 88. Quoted in Caleb Bach, “Michael Coe: A Question for Every Answer,” *Américas* 48/1 (1996): 14–21.
 89. See J. Richard Steffy, “The Kyrenia Ship: An Interim Report on Its Hull Construction,” *American Journal of Archaeology* 89/1 (Jan.): 71–101. This finding was confirmed by Steffy in an e-mail message to John L. Sorenson, 18 April 2001.
 90. Ales Hrdlicka, “The Genesis of the American Indian,” *Proceedings, 19th International Congress of Americanists, Washington, 1915* (Washington), 559–68.
 91. See, for example, John L. Sorenson, *Images of Ancient America: Visualizing Book of Mormon Life* (Provo, Utah: Research Press, 2001). A larger selection can be seen in O. L. Gonzalez Calderón, *The Jade Lords* (Coatzacoalcos, Veracruz, México: the author, 1991) and three published books by Alexander von Wuthenau: *Altamerikanische Tonplastik: Das Menschenbild der neuen Welt* (Baden-Baden, Germany: Holle, 1965); *Terres cuites précolombiennes* (Paris: Albin Michel, 1969); and *Unexpected Faces in Ancient America, 1500 B.C.–A.D. 1500: The Historical Testimony of Pre-Columbian Artists* (New York: Crown, 1975). Some scholars believe the topic should not be discussed because Wuthenau and Calderón are not “accepted experts” among orthodox anthropologists. Whatever merit, if any, there might be in such an exclusivist posture, it does not eliminate the fact that the figurines actually exist and in many cases are unquestionably ancient.
 92. See, for example, Matthew W. Stirling, “Great Stone Faces of the Mexican Jungle . . .,” *National Geographic Magazine*, Sept. 1940, 327; John F. Scott, “Post-Olmec Mesoamerica as Recalled in its Art,” *Actas, XLI Congreso Internacional de Americanistas*, 2–7 Sept. 1973 (México, 1975), 2:380–86; and the discussion in Wuthenau, *Unexpected Faces*, 69–70.
 93. This point is confirmed with regard to Maya Late Classic (“Jaina style”) portrait figurines by two prominent scholars. Román Piña Chan said, “They are extraordinary because of their faithfulness to their human models” (quoted in Linda Schele and Jorge Pérez de Lara, *Hidden Faces of the Maya* [Poway, Calif.: ALTI, 1997], 11). Schele and de Lara observed that “the Maya figurines represented individual people who had readable expressions on their faces” (p. 13).
 94. See Kirk Magleby, *A Survey of Mesoamerican Bearded Figures* (Provo, Utah: FARMS, 1979).
 95. See Peter N. Jones, “American Indian Demographic History and Cultural Affiliation: A Discussion of Certain Limitations on the Use of mtDNA and Y Chromosome Testing,” *AnthroGlobe Journal*, Sept. 2002.
 96. Note this observation: “However, with the exceedingly spotty sampling of Native America populations, it may be a long time until we have sampled enough populations truly to tell how localized or widespread any polymorphism really is.” See D. A. Merrifether et al., “Gene Flow and Genetic Variation in the Yanomama as Revealed by Mitochondrial DNA,” in *America Past, America Present: Genes and Languages in the Americas and Beyond*, ed. Colin Renfrew (Cambridge: McDonald Institute for Archaeological Research, Univ. of Cambridge, 2000), 89–124, esp. 117.
 97. Jones, in his study “American Indian Demographic History,” gives a devastating critique of the typical inadequate sampling. For example: “It is evident that the population groups current studies are using to infer American Indian cultural affiliation and demographic history are not acceptable. One cannot use contemporary allele frequencies from a few individuals of a contemporary American Indian reservation to arrive at an unequivocal haplotype for that group, either presently or prehistorically.”
 98. Joseph T. Chang, “Recent Common Ancestors of All Present-Day Individuals,” *Advances in Applied Probability* 31 (1999): 1002–26.
 99. Susanna C. Manrubia, Bernard Derrida, and Damián H. Zanette, “Genealogy in the Era of Genomics,” *American Scientist* 91 (March–April 2003): 165.
 100. Manrubia, Derrida, and Zanette, “Genealogy in the Era of Genomics,” 165.

DNA and the Book of Mormon: A Phylogenetic Perspective

Michael F. Whiting

1. The most noted is that of Thomas W. Murphy, “Lamanite Genesis, Genealogy, and Genetics,” in *American Apocrypha*, ed. Dan Vogel and Brent Lee Metcalfe (Salt Lake City: Signature Books, 2002), 47–77; see the “Editors’ Introduction” therein, vii–xvii.
2. See Peter Forster et al., “Origin and Evolution of Native American mtDNA Variation: A Reappraisal,” *American Journal of Human Genetics* 59/4 (1996): 935–45; and Santos et al., “The Central Siberian Origin for Native American Y Chromosomes,” *American Journal of Human Genetics* 64 (1999): 619–28, for reviews of the evidence.
3. For a review of studies, including some from the early 19th century, see John L. Sorenson, *The Geography of Book of Mormon Events: A Source Book* (Provo, Utah: FARMS, 1992), 7–35. Consult also Sorenson’s study *An Ancient American Setting for the Book of Mormon* (Salt Lake City: Deseret, 1985), 91–95, 138–189; and “When Lehí’s Party Arrived in the Land, Did They Find Others There?” *Journal of Book of Mormon Studies* 1/1 (fall 1992): 1–34.
4. The distinction in tracking historical relationships among sexually reproducing populations (phylogeny) versus within sexually reproducing populations (tokogeny) was best elucidated by Willi Hennig in his *Phylogenetic Systematics* (Urbana:

- Univ. of Illinois Press, 1979). For a standard textbook on molecular systematics, see David M. Hillis, Craig Moritz, and Barbara K. Mable, *Molecular Systematics* (Sunderland, Mass.: Sinauer Associates, 1996). For a textbook on molecular evolution, see Wen-Hsiung Li, *Molecular Evolution* (Sunderland, Mass.: Sinauer Associates, 1997). For a textbook on population genetics, see Daniel L. Hartl and Andrew G. Clark, *Principles of Population Genetics* (Sunderland, Mass.: Sinauer Associates, 1997).
- See John E. Clark, "A Key for Evaluating Nephite Geographies," in *Review of Books on the Book of Mormon*, 1 (1989): 20–70; and "Book of Mormon Geography," in *Encyclopedia of Mormonism*, ed. Daniel H. Ludlow (New York: Macmillan, 1992), 176–79.
- Who Are the Children of Lehi?**
D. Jeffrey Meldrum and Trent D. Stephens
- See John L. Sorenson, "When Lehi's Party Arrived in the Land, Did They Find Others There?" *Journal of Book of Mormon Studies* 1/1 (1992): 1–34.
 - See Sasha Nemecek, "Who Were the First Americans?" *Scientific American*, Sept. 2000, 81.
 - See Michael H. Crawford, *The Origins of Native Americans: Evidence from Anthropological Genetics* (Cambridge: Cambridge Univ. Press, 1998), 3.
 - Crawford, *Native Americans*, 88.
 - Crawford, *Native Americans*, 122.
 - Crawford, *Native Americans*, 3.
 - See Antonio Torroni and Douglas C. Wallace, "mtDNA Haplotypes in Native Americans," *American Journal of Human Genetics* 56/5 (1995): 1234–36.
 - Anne C. Stone and Mark Stoneking, "Analysis of Ancient DNA from a Prehistoric Amerindian Cemetery," in *Philosophical Transactions of the Royal Society of London*, series B, 354/1379 (1999): 153–59.
 - Graciela Bailliet et al., "Founder Mitochondrial Haplotypes in Amerindian Populations," *American Journal of Human Genetics* 55/1 (1994): 27–33.
 - Antonio Torroni et al., "Classification of European mtDNAs from an Analysis of Three European Populations," *Genetics* 144/4 (1996): 1835–50.
 - Peter Forster et al., "Origin and Evolution of Native American mtDNA Variation: A Reappraisal," *American Journal of Human Genetics* 59/4 (1996): 935–38.
 - Michael D. Brown et al., "mtDNA Haplogroup X: An Ancient Link between Europe/Western Asia and North America?" *American Journal of Human Genetics* 63/6 (1998): 1857.
 - Brown, "mtDNA Haplogroup X," 1853.
 - R. S. Malhi and D. G. Smith, "Haplotype X Confirmed in Prehistoric North America," *American Journal of Physical Anthropology* 119/1 (2002): 84–86.
 - Brown, "mtDNA Haplogroup X," 1857.
 - Brown, "mtDNA Haplogroup X," 1859.
 - Miroslavia V. Derenko et al., "The Presence of Mitochondrial Haplogroup X in Altaians from South Siberia," *American Journal of Human Genetics* 69/1 (2001): 237–41.
 - Richard Dawkins, *The Selfish Gene* (1976; reprint Oxford: Oxford Univ. Press, 1989), 191–92.
 - Susan Blackmore, *The Meme Machine*, (Oxford: Oxford Univ. Press, 1999), xix.
 - Blackmore, *Meme Machine*, 4.
 - Boyd K. Packer, "The Stake Patriarch," *Ensign*, Nov. 2002, 44–45.
 - John L. Sorenson, "Was There Hebrew Language in Ancient America? An Interview with Brian Stubbs," *JBMS* 9/2 (2000): 54–63.
 - Albert C. Baugh and Thomas Cable, *A History of the English Language*, 4th ed. (Eaglewood Cliffs, N.J.: Prentice-Hall, 1993), 53.
 - Review of "God as Divine Kinsman: What Covenant Meant in Ancient Israel," by Frank Moore Cross, *Biblical Archaeology Review* (July/August 1999): 32ff.; and Frank Moore Cross, *From Epic to Canon: History and Literature in Ancient Israel* (Baltimore: Johns Hopkins University Press, 1998), 8.
 - Cross, *Epic to Canon*, 3.
 - Tad Szulc, "Abraham: Journey of Faith," *National Geographic*, Dec. 2001, 96.
 - Szulc, "Abraham," 118.
 - Szulc, "Abraham," 129.
- The Word of God**
Leslie A. Taylor
- For a concise overview of the differing concepts of the Logos in Hellenism, Judaism, and early Christian theology, see J. Lebreton, "The Logos," in *The Catholic Encyclopedia: An International Work of Reference on the Constitution, Doctrine, Discipline, and History of the Catholic Church*, ed. Charles G. Herbermann (New York: Universal Knowledge Foundation, 1913–14), 9:328–31.
 - Two uses of the metaphor of the Logos-tomeus are found in sections of Isaiah quoted in the Book of Mormon. The first occurs in 1 Nephi 21:2: "He hath made my mouth like a sharp sword" (compare Isaiah 49:2), and the second in 2 Nephi 7:8: "Who is mine adversary? Let him come near me, and I will smite him with the strength of my mouth" (compare Isaiah 50:8, which omits the last clause). This image that associates the word of God with a sword is also prevalent in the book of Revelation (see 1:16; 2:12, 16).
 - See John A. Tvedtnes, "Rod and Sword as the Word of God," *JBMS* 5/2 (1996): 148–55.
 - The verb form to *divide asunder* seems to possess specific meaning in regard to both sacrifice and the power of the word of God. This construction occurs only 13 times in scripture, 7 of which are quoted in this article. Two references in the Old Testament—Leviticus 1:17 and 5:8—state that sacrificial birds should not be "divided asunder." Hebrews 4:12 (quoted earlier) is the only instance of this construction in the New Testament. The Book of Mormon contains the richest uses of this verb form. It is found in Helaman 3:29, 3 Nephi 8:6; Helaman 5:33; 12:8; and 1 Nephi 17:45 (the last two will be discussed later). All five uses of this construction in the Doctrine and Covenants were quoted earlier.
 - Tvedtnes, in "Rod and Sword," also notes that although in the Helaman passage the word of God "seems to be compared to a sword," the common language and imagery of this passage "ties [Helaman 3:29–30] to Lehi's vision, where it is the rod or the word of God that brings people safely past Satan's obstacles" (p. 154). Helaman 3:29–30 would seem to have two intertextual sources: the unidentified Old World source that it shares with Hebrews 4:12 and also Lehi's vision of the tree of life.
 - Philo, *Heres* 130, in *Philo*, trans. F. H. Colson and G. H. Whitaker (1932; reprint, Cambridge: Harvard Univ. Press, 1958).
 - Philo, *Heres* 140, in *Philo*, trans. Colson and Whitaker. For more discussion on Philo's use of the Logos-tomeus metaphor, see David M. Hay, "Philo's Treatise on the Logos-Cutter," *Studia Philonica* 2 (1973): 9–22. For a general background on Philo's life and writings, see David T. Runia, "Philo, Alexandrian and Jew," in *Exegesis and Philosophy: Studies on Philo of Alexandria* (Brookfield, Vt.: Gower, 1990), 1–18.
 - In his decision to lead a mission to the apostate Zoramites, Alma recognizes that the word of God can transmit virtue: "And now, as the preaching of the word had a great tendency to lead the people to do that which was just—yea, it had had more powerful effect upon the minds of the people than the sword, or anything else, which had happened unto them—therefore Alma thought it was expedient that they should try the virtue of the word of God" (Alma 31:5).
 - For a discussion of the striking parallels between the exodus story and Nephi's account of his family's journey in the wilderness, see Terrence L. Szink, "Nephi and the Exodus," in *Rediscovering the Book of Mormon*, ed. John L. Sorenson and Melvin J. Thorne (Salt Lake City: Deseret Book and FARMS, 1991), 38–51.
 - Richard D. Rust notes that feasting on the word is "implicitly a sacramental experience" (*Feasting on the Word: The Literary Testimony of the Book of Mormon* (Salt Lake City: Deseret Book and FARMS, 1997), 245).
 - Paul uses the phrase *past feeling* in Ephesians 4:19, but it appears nowhere else in the Bible or in other LDS scripture besides the Book of Mormon. The verb *to feel* is used to express other unique concepts in scripture. For example, *to feel after* is used to convey the meaning "to seek after Jesus Christ" in Acts 17:27 and D&C 101:8. Jesus Christ uses the expression in D&C 112:13: "Behold, I, the Lord, will feel after them." Interestingly, Exodus 10:21 and 3 Nephi 8:20 both refer to a darkness that can be "felt." Like the concept of the word of God, the verb *to feel* possesses rich and varied meanings in scripture.
 - The words *an hissing* and *hiss* in the KJV translate derivatives of Hebrew *šāraq*, meaning to hiss or whistle as a signal or summons.
 - In 2 Nephi 29 the Lord associates the gathering of his people with the gathering of his word: "And it shall come to pass that my people, which are of the house of Israel, shall be gathered home unto the lands of their possessions; and my word also shall be gathered in one" (v. 14).
- Secret Combinations and Flaxen Cords: Anti-Masonic Rhetoric and the Book of Mormon**
Paul Mouritsen
- Interestingly, William Morgan's widow, Lucinda, joined the church in 1834. Some historians claim she later became a plural wife to Joseph Smith. Regardless, there is no evidence that Joseph Smith knew William Morgan.
 - Fawn M. Brodie, *No Man Knows My History*, 2nd ed. (New York: Knopf, 1945), 65.
 - Brent Lee Metcalfe, "Apologetic and Critical Assumptions about Book of Mormon Historicity," *Dialogue* 26/3 (1993): 171.
 - Dan Vogel, "Mormonism's 'Anti-Masonic Bible,'" *The John Whitmer Historical Association Journal* 9 (1989): 29.
 - Robert N. Hullinger, *Mormon Answer to Skepticism: Why Joseph Smith Wrote the Book of Mormon* (St. Louis: Clayton, 1980), 114, n. 31.
 - My brief electronic search of the Making of America Archives at the University of Michigan (<http://moa.umdl.umich.edu>) and Cornell University (<http://moa.cit.cornell.edu/moa>) turned up over 3,000 occurrences of *secret society* or *secret societies* in 19th-century documents. Only a relative few refer to Freemasonry. (These sources were available online as of April 2003.)
 - "Remarks on Secret Societies,