

picture is not only provocative but confirmatory about the arrival of non-indigenous populations in ancient Mesoamerica.

One thing we can conclude from this brief examination of research on the ethnic variety present among the ancient Americans is that the human biological history of both North and South America, as far as we can see it at present, was more complex than is usually supposed in the interpretations offered by the majority of anthropologists. This situation requires seeing a variety of ethnic or physical types and points to immigrants coming from overseas by boat, who also brought with them the diseases and plants already discussed.

The Indeterminate Nature of Molecular Genetic Data and the Origins of Amerindians

What do the genetic data say about whether Near Eastern people were involved in the Mesoamerican gene pool? Results obtained so far do not provide enough evidence to be certain.

Scientists who specialize in DNA analyses present results similar to those who used other approaches. They generally believe that the American Indians originated from initial colonizing populations that carried only four genetic haplotypes (sets of genes so closely linked as to be inherited as a complex). Those four are supposed to have arrived via the Bering Strait more than 10,000 years ago.³⁷ In the conventional interpretation, it is assumed that other genes did not come into the Americas until Europeans arrived in the late 15th century. But that picture is incomplete. In recent years an additional haplotype ("X") has been identified that was anciently distributed among several New World groups, as well as in European and Asian populations.³⁸ Further discoveries of unsuspected haplotypes in small populations could modify the confidence with which the experts currently—prematurely, I believe—count and characterize ancient American genetic

37. Michael H. Crawford, *The Origins of Native Americans: Evidence from Anthropological Genetics* (New York: Cambridge University Press, 1997).

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): 1852–61; and Virginia Morell, "Genes May Link Ancient Eurasians, Native Americans," *Science* 280 (1998): 520.

structures as though they were fully known. Furthermore, the significance of the "basic" four haplotypes remains in question because only certain peoples have survived and have had their members' DNA tested.

Of even greater significance is the fact that serious methodological difficulties or limitations are inherent in all such studies. Jones, for example, has pointed out a large number of these. They hinge on assumptions made in the construction of the models employed in interpreting the historical significance of the majority of studies, which rely on data from mtDNA and Y-chromosome samples almost exclusively. The problems are compounded when one considers the limited size and nature of the DNA samples of American Indians used in almost all studies.³⁹

As an example of the kind of data that may yet be revealed by carefully designed DNA studies, consider a report by the Cherokee DNA Project conducted by DNA Consultants, a firm that has been taking DNA samples from Cherokee Indians in the United States for over 10 years as a means of establishing tribal membership, an affiliation of considerable economic and social significance. Their report under the heading "Anomalous Mitochondrial DNA Lineages in the Cherokee" says that "a sample of 52 individuals who purchased mitochondrial DNA tests to determine their female lineage was assembled after the fact from the customer files of DNA Consultants. All claim matrilineal descent from a Native American woman, usually named as Cherokee. The main criterion for inclusion in the study is that test subjects must have obtained results not placing them in the standard Native American haplogroups A, B, C or D, hence the use of the word 'anomalous.' Most subjects reveal haplotypes that were unmatched anywhere else [in the New World] except among other participants. There proves to be a high degree of interrelatedness and common ancestral lines. Haplogroup T emerges as the largest, followed by U, X, J and H. Similar

39. 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* (2002): 1-32; and Jones, *American Indian mtDNA, Y and Chromosome Genetic Data, and the Peopling of North America* (Boulder, CO: The Bäu Institute, 2004).

proportions of these haplogroups are noted in the populations of Egypt, Israel, and other parts of the East Mediterranean."⁴⁰

Part of the problem in this area of research lies in trying to draw conclusions from restricted sorts of genetic data. Almost the entire conjectured genetic history published and accepted thus far is based on data derived either from mtDNA (passed only from mother to child, though only daughters pass it to the next generation) or from Y-chromosome (paternally transmitted) genetic material. But these two sources constitute only a minuscule sample, less than 0.01 percent, of the total human genome.⁴¹ An "individual's strictly maternal and strictly paternal lines are just two of a vast number of possible paths back through his or her ancestors."⁴² A result of confining studies mostly to the two conveniently accessible sources of gene data has been to ignore the far greater mass of evidence of human ancestry that potentially is, or may eventually become, available beyond the nuclear data.

Dillehay reminded scientists that some groups who settled in America may have become extinct because of environmental problems such as disease.⁴³ Sheer lack of investigation is also an issue. For example, the only evidence historians have for the routine assumption that the Vikings did not leave genes behind among native peoples of northeastern North America is negative; that is, investigators have *not* found any Norse-specific features so far. However, the possibility has hardly been raised among geneticists, let alone carefully studied.

Sadovszky produced substantial evidence from linguistics and ethnology that Indian populations in central California spoke languages and retained cultural characteristics that belonged to populations at home in western

40. "Anomalous Mitochondrial DNA Lineages in the Cherokee," abstract available at DNA Consultants website, <http://dnaconsultants.com/Cherokee/index.htm>.

41. Susanna C. Manrubia, Bernard Derrida, and Damián H. Zanette, "Genealogy in the Era of Genomics," *American Scientist* 91 (2003): 158.

42. Douglas L. T. Rohde, "On the Common Ancestors of All Living Humans" (unpublished manuscript dated 11 November 2003, in possession of author). Compare Joseph T. Chang, "Recent Common Ancestors of All Present-Day Individuals," *Advances in Applied Probability* 31 (1999): 1002–26.

43. Tom D. Dillehay, "Disease Ecology and Initial Human Migration," in *The First Americans: Search and Research*, ed. Tom D. Dillehay and David J. Meltzer (Boca Raton, FL: CRC, 1991), 231–64.

Siberia.⁴⁴ He argued persuasively that their ancestors arrived in California from the Ob River area probably over 2,000 years ago. Yet no search for specific genetic evidence of such a migration has been conducted, or even conceived of, to confirm or disconfirm the extensive linguistic and cultural evidence.

In addition, according to González C. on the basis of his direct observation of thousands of figurines from Olmec sites in the Isthmus of Tehuantepec, San Lorenzo Tenochtitlán, and nearby La Venta, he has identified faces that show three distinct racial/ethnic groups: (1) a bearded white race with aquiline noses, probably Mediterranean in origin; (2) an oriental race, probably Han Chinese; and (3) a black race. At all Olmec sites other than San Lorenzo, the Chinese features are completely absent, while the white type predominated at La Venta.⁴⁵ To the extent that there is a basis in fact for his observation, DNA tests of living groups in the vicinity could well be made to see whether special characteristics of the Chinese or European genomes can be detected to match the images. But such tests neither have been nor are likely to be carried out as long as molecular anthropologists' curiosity is not whetted in that unorthodox direction. In fact, only a fraction of the various contemporary peoples in Mesoamerica have been tested and analyzed for mtDNA or Y-chromosome DNA. Further studies should be undertaken to look for the genes of descendants of the people who were the ancient models for the foreign faces known from art.

Evidence has also been found that changes in a population's DNA come about for unknown reasons. One of the most extensive historical genetic studies ever made was a study of over 131,000 Icelanders and their ancestors back to 1789.⁴⁶ It showed that the majority of people living today in Iceland had ancestors "that could not be detected based on the Y-chromosome and

44. Otto J. von Sadowszky, *The Discovery of California: A Cal-Ugrian Comparative Study* (Los Angeles: International Society for Trans-Oceanic Research, 1996). For a more complete discussion, see chapter 10 herein.

45. González Calderón, *Jade Lords*, 48, 51, 135; and González Calderón, *Cabecitas olmecas*.

46. Agnar Helgason et al., "A Populationwide Coalescent Analysis of Icelandic Matrilineal and Patrilineal Genealogies: Evidence for a Faster Evolutionary Rate of mtDNA Lineages than Y Chromosomes," *American Journal of Human Genetics* 72 (2003): 1370–88.

mitochondrial DNA tests being performed and yet the genealogical records exist showing that these people lived and were real ancestors."⁴⁷

Practical and strategic problems with the DNA specimens used in genetic studies of American Indians remain to be dealt with. Jones warned, "It is evident that the population groups [that] 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 from a contemporary American Indian reservation to arrive at an unequivocal haplotype for that group, either presently or prehistorically."⁴⁸ Merriwether and his colleagues added, "With the exceedingly spotty sampling of Native American populations, it may be a long time until we have sampled enough populations truly to tell how localized or widespread any polymorphism [genetic identifier] really is."⁴⁹

Support from gene studies for the arrival of voyagers from the Old World may yet be increased and clarified. For example, Douglas Wallace, one of the leading scientists working in the field, believed that a particular pattern of mutations found in Native American populations as well as in Southeast Asia and Pacific Islands (but not in Siberia) hints at "one of the most astounding migrations in human experience." On the basis of the data he had available, he postulated that anciently a group of people moved out of China into Malaysia, where they became sailors and then proceeded to populate the islands of the South Pacific. Some 6,000 to 12,000 years ago these mariners made it to the Americas, although "I don't know how they came," Wallace went on. "They either came across the Pacific to Central and South America or they went [by sea] up the east coast of Asia and across the northern Pacific to Alaska and Canada."⁵⁰ His timing of the movement of those voyagers across the Pacific could account for the arrival of hookworms

47. John M. Butler, "Addressing Questions Surrounding the Book of Mormon and DNA Research," in *The Book of Mormon and DNA Research*, ed. Daniel C. Peterson (Provo, UT: Neal A. Maxwell Institute, 2008), 75.

48. Jones, "American Indian Demographic History," 17.

49. Andrew Merriwether 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, England: McDonald Institute for Archaeological Research, 2000), 117.

50. Bishop, "Strands of Time," A1.

in America (see the section “Old World Diseases in the New World” above), and perhaps it also relates to the transoceanic linkage that Neves and colleagues saw for early Brazilian skeletal specimens.⁵¹ Testing such hypotheses deserves serious research, but that hardly seems imminent.

One of the most recent syntheses of genetic studies on the origin of Amerindians reaches very different conclusions from ideas considered current only a few years past. Arnaiz-Villena et al. have found that (1) the Bering Strait was probably not the only entrance to America; Pacific Ocean boat trips may have contributed as well. They have also concluded that (2) American Indians share most genetic characteristics with Pacific Islanders, and (3) they have created a model that does not support the classic picture of “three waves” of population entering via Alaska but, rather, calls for immigration also via the Pacific coast.⁵² At the least, these results demonstrate that the comprehensive biological history of human settlement in America when it is soundly documented is going to be much more complex than previously thought.

A considerable to-do has been made about a supposed lack of Jewish DNA in American Indians in the light of the Book of Mormon report of migrations from Jerusalem to Mesoamerica.⁵³ Such assertions have been discussed at length by DNA scientists and other scholars.⁵⁴ Their views suppose that attempts to answer the question are premature at best and possibly futile. The key problem is still the same as Mourant pointed out some time ago; that is, we don't know the genetic composition of the Jews at the

51. Neves et al., “Extra-continental Morphological Affinities,” 260.

52. A. Arnaiz-Villena et al., “The Origin of Amerindians and the Peopling of the Americas According to HLA Genes: Admixture with Asian and Pacific People,” *Current Genomics* 11/2 (April 2010): 103–14.

53. Simon G. Southerton, *Losing a Lost Tribe: Native Americans, DNA, and the Mormon Church* (Salt Lake City: Signature Books, 2004); and Thomas W. Murphy, “Simply Implausible: DNA and a Mesoamerican Setting for the Book of Mormon,” *Dialogue* 36/4 (2003): 109–31.

54. See essays by Butler, Whiting, McClellan, Sorenson, Roper, and others in Peterson, *Book of Mormon and DNA Research*; also Terryl L. Givens, “Common Sense Meets the Book of Mormon,” in *Revisiting Thomas F. O’Dea’s ‘The Mormons’: Contemporary Perspectives*, ed. Cardell K. Jacobson, John P. Hoffman, and Tim B. Heaton (Salt Lake City: University of Utah Press, 2008), 88–89.

time of the Diaspora when the Lehite and Mulekite parties left the land of Israel.⁵⁵ Given that basic lack of data, no valid comparison can be made. Even in the unlikely case of such information becoming available, formidable methodological problems would make fruitful investigation of the issue unlikely.⁵⁶

A quite different type of genetic analysis than the usual mtDNA/Y-chromosome treatment provides support for challenging the scholarly view of an Amerindian gene pool uncontaminated by transoceanic voyagers. Guthrie examined human lymphocyte antigens (HLAs) as evidence for the intrusion of Old World human biological characteristics into the New World.⁵⁷ HLAs are proteins on white blood cells that function to produce antibodies. At least 29 families of these substances have been identified, and their distributions among some of the world's population groups have been determined.⁵⁸ Their distribution shows that certain HLA alleles are common in the Old World among a certain percentage of many populations, yet groups in America often display the same features, but with lesser frequencies. This could mean that the American peoples share in the descent from the Old World groups. Few scientists have paid attention to explaining how or when these proteins arrived in American populations. The usual explanation for the exotic (in the New World) HLAs that are much more frequent in the Old World has been that they came from an admixture of genes that European and African people produced in American Indian populations after Columbus. Guthrie argues that a much more likely explanation for the presence of many Old World HLAs is that some Amerindian populations

55. Arthur E. Mourant, "The Jews in Palestine," in *The Genetics of the Jews*, ed. Arthur E. Mourant et al. (Oxford: Clarendon, 1978), 17.

56. See John M. Butler, "A Few Thoughts from a Believing DNA Scientist," *Journal of Book of Mormon Studies* 12/1 (2003): 36–37; Michael F. Whiting, "DNA and the Book of Mormon: A Phylogenetic Perspective," *Journal of Book of Mormon Studies* 12/1 (2003): 24–35; and David A. McClellan, "Detecting Lehi's Genetic Signature: Possible, Probable, or Not?," in Peterson, *Book of Mormon and DNA Research*, 99–155.

57. James L. Guthrie, "Human Lymphocyte Antigens: Apparent Afro-Asiatic, Southern Asian, and European HLAs in Indigenous American Populations," *Pre-Columbiana: A Journal of Long-Distance Contacts* 2/2 (2000): 90–163.

58. L. Luca Cavalli-Sforza et al., *The History and Geography of Human Genes* (Princeton, NJ: Princeton University Press, 1994), appendix 2.

assimilated a significant number of foreigners from across the oceans prior to the 1492 European discovery of America.

He also reviews data on the differential presence of transferrins, immunoglobins, and other blood features in Old and New World populations. These data provide additional support for his interpretation of the arrival of human lymphocyte antigen material: "The distributions of HLA types, combined with supporting data from other genetic systems, provide strong evidence that some American populations have assimilated significant numbers of foreigners"⁵⁹ anciently into the base population (the nominal ancestors of the American Indians) who had come from Northeastern Asia.

Practically the entire body of data used to this point for the genetic study of American Indian populations has come from gene samples taken from living natives (usually self-identified "Indians"). Very little information has been gained from *ancient* specimens (compare the statement above from Mourant). With present information, we do not know enough about the actual genetics of Mesoamerica's early inhabitants to allow general statements to be made as to whether transoceanic voyagers may or may not have entered into the hemispheric gene pool. At the present limited rate and scope of research on this sensitive topic, it will be years before reliable generalizations will be possible using DNA samples from the bones of a large number of actual ancient persons. But the combination of present knowledge of genetics added to other (nongenetic) evidence of human biological immigration from the Old World already reviewed (plant and disease transfers from overseas, art representations of foreign phenotypes, confirming morphological indicators, and traditions of incoming voyagers) convincingly shows that some Old World peoples definitely lived as minorities among the inhabitants of the New World. The data to which attention has been drawn in this chapter do not contradict that possibility but directly support it.

It is a rational conclusion that this picture of human physical variation within the Americas, limited as it is, points to Old World populations having reached this hemisphere by sea voyages. This constitutes a fundamental correspondence or convergence between the scientific evidence and the historical account in the Book of Mormon, regardless of any unanswered questions.

59. Guthrie, "Human Lymphocyte Antigens," 91.