The Problematic Role of DNA Testing in Unraveling Human History

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Over the last century, new techniques of scientific analysis have been developed that have been applied with the intent to clarify the course of human history. Immediately after World War II, blood group data seemed to provide a magic key to open up the history of the world’s populations, but by the 1960s such studies were shown to be unrealistic and misleading. The new tool in human biology and anthropology is DNA analysis. Despite cautions from the best scientists about the limits the new findings have for interpreting human history, some enthusiasts continue to claim too much for DNA study.
The Problematic Role of DNA Testing in Unraveling Human History

Much in the news these days is the “DNA method” for calculating affinities of individuals or populations. FARMS regularly receives inquiries from members about the validity and significance of the results of such studies that have been reported in the press. A general characterization and evaluation of the use of this source of “new light” is given here for JBMS readers.

New Tools, New Zeal

From time to time over the last century, new techniques of scientific analysis have been developed that have been applied with the intent to clarify the course of human history. These techniques characteristically exhibit a life cycle consisting of six stages.

First, the technique is applied experimentally and produces certain results that seem to sharply modify the conventional picture. Second, these preliminary findings lead developers or proponents of the new tool to loudly proclaim that their technique will revolutionize the interpretation of history once it is widely applied. Third, it is announced that sweeping modifications must be made to established views, while in quieter tones the qualification is added, “although further research is needed.” Fourth, basing their views especially on apparent flaws in logic and methods used in the early studies, critics point out problems with the claims that have been made. Fifth, more critics join the counterattack, and some of the early enthusiasts grant that they may have overstated their case. Sixth, expectations and use of the “new” technique gradually sink until it occupies a specific, highly qualified place in the kit of previously developed tools for the study of history, or it may even drop out of use altogether because seemingly superior tools have been developed.

Two past cases exhibit this pattern. In the late 1950s linguist Morris Swadesh announced the development of “glottochronology,” a special version of “lexicostatistics.” He claimed that the basic vocabulary (defined as a standard list of 100 or 200 everyday words, like hand, water, or night) evolves at a constant rate of about 13 percent of the terms changing per 1,000 years; the rate was calculated from historical cases like Latin. So if two languages share a certain percentage of the basic vocabulary, the elapsed time since they split from their common ancestral tongue could be approximated in years. A flurry of excitement and reinterpretation of linguistic history followed; then critiques began appearing on the heels of the enthusiasm. Before long it became clear that the method, which had appeared to be quite objective, actually involved subjective steps (when are words “the same”?) that rendered the result far more uncertain than it had first appeared. Nowadays the scheme is rarely used, because the resulting dates are not generally seen as trustworthy or significant.

A parallel case in the development of a technique involved the identification of human blood groups. All of us are acquainted with the fact that the blood of any human falls into one of four broad classes or groups, AB, A, B, or O, according to the specific substances contained in the blood that cause clumping of the cells when blood serum from a person of one type is injected into a sample of blood of a different type. These groups become significant in a practical sense since the differences prevent successful blood transfusions between groups. The four classes
are inherited by simple (Mendelian) rules of heredity. Early in the 20th century it was noted that different population or ethnic groups were characterized by the frequencies with which the blood types occur among their members (e.g., one people might show 13 percent having type B and 67 percent with type O, while a second person has 41 percent B and only 9 percent O). Subsequently, the frequencies of other factors—M, N, and S as well as numerous Rh features—were found to distinguish the blood of various groups.

For a couple of decades immediately after World War II, blood group data seemed to provide a magic key to open up the history of the world’s populations. To illustrate, in the wake of Thor Heyerdahl’s Kon Tiki voyage, much attention went to the question of possible relationships between American Indians and Polynesians based on blood group frequencies. J. J. Graydon in 1952 claimed that the blood group systems in the eastern Pacific “are all consistent with Heyerdahl’s theory.”7 R. I. Murrill in 1965 explained at length the difficulty, exhibited in most previous studies, of drawing a sample of “pure” natives unmixed with Europeans.9 Further, it was increasingly recognized that during the period of European expansion and colonization throughout much of the world, the blood group composition of surviving populations changed by a process of, apparently, natural selection because of exposure to new diseases.10 Furthermore, the notion had been held that scientists could draw their sample for say, “Polynesians” with “American Indians.” In this case the former “group” was defined only in linguistic or geographical (not biological) terms while the genetic makeup of speakers of the same language turned out to be highly variable13 and the basis for an American Indian sample might be as much geographical as biological.14

So doing historical reconstruction today using blood group comparisons is essentially passé. D. Allbrook felt that studies have shown but little historically sensible patterning when viewed against linguistic and archaeological data.15 Rubén Lisker decided that only an integrated analysis of all the known blood group systems would serve to justify statements as to the origins and relationships of New World populations.16 This has not yet been attempted on a comprehensive scale. L. Cavalli-Sforza...
and associates tried something of the sort in 1994; however, much of their synthesis has proved to be tentative and flawed by numerous qualifications about the use of outdated archaeology, contradictions in their explanations, and gaps in the data.

These two cases suggest that adopting a fashionable new scientific technique is something like a youth receiving a telescope for Christmas. At first it is enthusiastically turned in all directions, until the owner finds that effective use of the instrument actually requires investing heavily in an increased study of astronomy and mathematics and a discomforting exercise of critical judgment in interpreting what is observed. At that point the initial fervor to apply the tool indiscriminately palls, particularly if some new “toy” comes on the scene to divert attention.

The new toy in human biology and anthropology is DNA analysis. Despite cautions from the best scientists about the limits the new findings have for interpreting human history, some enthusiasts without adequate critical acumen claim too much for DNA study. DNA is usually obtained from a sample of body fluids in a population. It occurs in the nuclei of all cells. Examination of the DNA sequence from a person shows the presence or absence of certain mutations at particular identified points in the coded gene sequence. If another population group has the same mutation record in its members’ DNA, it is certain that the two groups shared a common ancestor. Or, in general terms, the number of mutations by which samples differ allow estimation of the approximate time since the two populations separated.

**The Trend from Simple Interpretive Schemes to Complex Puzzles**

But DNA information never interprets itself. The meaning or significance of—the story behind—the data is necessarily furnished by the minds of the scientists who examine the information.

The temporary, even faddish, nature of historical reconstructions based on DNA analysis is illustrated by what happened with one widely publicized interpretation early in the development of present methods. The proposition was put forward that an ancestral human female, dubbed “Eve” for journalistic pizzazz, must have lived in Africa very long ago. Here is how the notion came about. Unlike most DNA, which occurs in the nuclei of all cells, DNA found in cellular structures called mitochondria acts somewhat differently. Mitochondria are special bodies within a cell that serve as power sources for the cell’s contents. DNA in the mitochondria (mtDNA) were involved in the analysis that led to the idea of “Eve.” That DNA passed to the next generation only from mother to daughter. All mtDNA is reproduced in a daughter unchanged, except for rare random mutations that may occur. If a female suffers a mutation, she will pass on that disruption in her DNA to her daughters. Thus the daughters’ DNA sequence provides a kind of biological record of their entire female ancestry.

In 1989 an analysis of samples of mtDNA from 147 women from diverse parts of the world was interpreted by Dr. Rebecca Cann and colleagues as indicating that all the present-day women tested descended from the same ancestress, for they all shared certain mtDNA features that they could have received only from a common female ancestor. Using estimates of the rate of mutations in mtDNA as a basis, the investigators reasoned that this hypothetical common ancestor of the women from four continents had lived about 200,000 years ago in sub-Saharan Africa. This postulation, fertilized by journalistic simplification and hype, was parlayed into unhesitating statements in the

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press to the effect that “all human beings alive today shared one female ancestor—a kind of ‘Eve’—in Africa 200,000 years ago.”

Before long, however, another investigator, Alan Templeton, pointed out serious problems with this “Eve Hypothesis.” He argued that the analysis was invalid because it used improper statistical tests and sampling methods biased in favor of an African origin. Its results, he said, were actually dictated by the order in which the information was fed into the computer! When the same mtDNA data was treated according to different procedural rules, instead of producing one family tree pointing back to ancient Africa, that data could produce thousands of simpler descent trees, some of which did not have African roots. Others compounded the criticism. Today the only correct answer to the question, “Does mtDNA analysis demonstrate that there was a shared common ancestress in Africa for all human beings?” is, for the moment, “We don’t know.” And the chances are slim that we will ever know.

Another highly publicized reconstruction of the past involving genetics, this time for the settling of the Americas, was put forward in 1985 by a trio of anthropologists. Joseph Greenberg, a prominent linguistic anthropologist at Stanford, argued that there were three, and only three, language groups who entered the New World via the Bering Strait (later he softened to say “at least” three). Christy G. Turner cited studies of unique tooth forms to support Greenberg’s three-group theory.

Stephen Zegura interpreted blood group and related genetic studies based on blood groups (though none was on DNA) to come to the same conclusion: there were three distinct peoples who entered the northwestern gateway to America and all American Indians descended from them. A subsequent small-scale DNA analysis also claimed to find “three distinct migrations across the Bering land bridge.” Such follow-the-leader studies soon provided the basis for sweeping popularized statements like, “Recent genetic research . . . has helped to reconstruct native American population history, and to confirm the hitherto controversial classification of the native American languages into just three major macrofamilies.” But other scientists were much less kind to the proposition. Many commentators on Greenberg, Turner, and Zegura’s major article were mostly unsupportive verging upward to outraged. By 1998 Michael H. Crawford concluded that the triple-migration hypothesis had “slowly unraveled.”

What had happened is that the early work was followed with more comprehensive sampling and more sophisticated analysis that have yielded results far more complicated than anything Greenberg and his associates detected. M. S. Schanfield and fellow workers found significant markers that genetically distinguished four Amerindian groups that they considered to represent four migrations, not three, and Joseph G. Lorenz and David G. Smith found a broadly comparable fourfold grouping. Yet another group of scientists was led to conclude that there were nine founding mtDNA sequences behind native American peoples. A more elaborate study went on to sequence 403 nucleotides in the mitochondrial control region that were drawn from seven tribes and that omitted South America from consideration at all. They identified “30 distinct lineages,” from which they inferred that “mitochondrial variability within Amerindian populations” is greater than many researchers had previously claimed.

For the moment many geneticists choose to simplify the confusion by talking about four Amerindian haplogroups—A, B, C, and D. (A haplogroup is composed of those descent lines that share the major characteristics in their mtDNA sequences.) Yet a significant “other” category remains beyond the accepted A-to-D set. A miscellany of odd mtDNA haplotypes have been dumped into this vague category, often because their presence in America is suspected to be due to the intrusion of European or black slave genes among American Indians in the last few generations. But that assumption may be wrong. From the “other” rubric a fifth haplogroup has now been extracted, called X. Haplogroup X has been found in the DNA of certain North American groups such as the Ojibwa of eastern Canada as well as in some very early American skeletons on this continent. But the more interesting development is the discovery that X is also found in scattered populations in the Old World—in Italy, Finland, and especially Israel, and probably nearby areas. (Some have suggested
that the “European-like” characteristics exhibited by the notorious skull from Kennewick, Washington, and related ancient remains from western North America could be due to haplogroup X people from Europe who reached America, perhaps across the ice-covered North Atlantic Ocean, tens of thousands of years ago. At least T. Schurr is confident that “haplogroup X was brought to the New World by an ancient Eurasian population in a migratory event distinct from those bringing the other four lineages to the Americas.”28 Yet X may not be the last new haplogroup to be winnowed from the residual “other” category. A haplotype among the Maya Indians has already been noted that appears to be the same as European haplogroup H, the most commonly observed mtDNA lineage in populations of Europe and the Caucasus.29

Thus so many disagreements have arisen as new discoveries have complicated previously simpler interpretations that linguist Greenberg now chooses simply to ignore the new genetic data: “Every time, it [mtDNA research] seems to come to a different conclusion. I’ve just tended to set aside the mtDNA evidence. I’ll wait until they get their act together.”30 But it is in the nature of scientific research that new discoveries will continue; who knows if a time will come when “they get their act together” to his satisfaction? Rather, what we can look forward to is reiteration of that catchall slogan of the scientist—“More research is needed”—rather than final consensus. A recent assessment of “progress and perspectives” in DNA studies concluded that any comprehensive solution to questions about the relationships among and origins of the American Indians must await a substantially larger, and more costly, suite of tests on DNA than those now in use.31

Clearly the DNA technique is not the ultimate answer to the problems of ancient population movements that lay people (and some experts) have hoped it might be. In general, we have seen, the advent of new tools or techniques in a scientific field leads to overexpectation. That has certainly been so with DNA study. Yet short of any full consensus, fascinating new information of value in untangling the threads of history has come forth when research has been done right.

A case in point is the surprising identification of a group of black South Africans as descendants of Jewish priests, a development that press and television coverage has brought to the attention of many. Oral tradition among the Lemba people had long maintained that they were of Jewish origin. A few years ago a unique genetic signature was discovered by a group of Jewish geneticists; it occurs in the Y chromosome (which passes only from male to male) and has been identified in a majority (about 53 percent) of Jewish Cohanim, or holders of the priesthood that is passed on from father to son in certain families. Researchers set out to determine if the Cohen-line genes showed up among the Lemba. They did indeed! Lemba males carried the unique Y-cell haplotype previously shown to have been possessed only by traditional Jewish priests. Interpretation of documented Jewish

history and of Lemba tribal traditions, combined with the biological findings, led to the conclusion that a group of Jews that included Cohen priests migrated to Yemen in southern Arabia some 2,700 years ago, then moved to southern Africa more than 20 centuries ago. Although the members of this group have lost most of their Jewish cultural characteristics and have taken on the external characteristics (the racial or biological features and language) of surrounding black groups, they still identify themselves as of Israelite origin, and the DNA data has decisively confirmed their tradition.32

All genetic data does not come from tests on living persons. The ability to recover substances from mummies and skeletons has opened new vistas for the exploration of the human past. For instance, a quarter century ago Marvin Allison and fellow researchers working in Peru found that all four ABO blood groups occurred in mummies dated from 3000 B.C. to A.D. 1450, while in the last 500 years only A and O were seen. But mummies

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Are there “Mongoloid” Jews? Yes. This gentleman is from Afghanistan.
from present-day Chile as early as the second century A.D. showed no B or AB, although in modern times those groups often show up in that area. Meanwhile, studies of mummies from Peru contrast sharply with those from Chile; that is, prior to the Spanish conquest the natives who lived in Peru were genetically different from those living in the territory of today’s Chile. DNA samples have also been taken from remains of the dead in other areas, including Egypt, and may prove equally instructive about unsuspected relationships.

It begins to look like a great deal of previously undetected travel, migration, and gene mixing must have been going on throughout the world in the past. For instance, studies of Polynesians have recently shown that those included under that ethnic label actually fall into at least three descent groups. Group I includes about 95 percent of Hawaiians, 90 percent of Samoans, and 100 percent of the Tongans sampled. This group’s characteristic pattern of mutations first appeared in Taiwan many generations before Polynesia was settled. A second group among nominal Polynesians includes a small minority in Hawaii, Samoa, and the Cook Islands that shows “an interesting possible phylogenetic connection between Group II and a group of African pygmy sequences from central Africa” (possibly transmitted by way of New Guinea). Group III links some Samoans to Indonesia. Still, some 2 percent of the “Polynesians” studied do not fit any of the three recognized groups; they belong to 14 other distinct DNA lineages, each represented by a single individual. The 14 individuals display remarkable diversity, some, though probably not all, possibly springing from mixture with Europeans in the islands in recent generations (much care was taken in drawing the sample to try to avoid such cases). Two of the 14, for instance, have genetic markers that closely compare with those in American Indians (“which may be the first genetic evidence of prehistoric human contact between Polynesia and South America”). Another study found one Samoan who shared the same DNA sequence as a Native American.

The possibility of an American Indian-Polynesian connection is of unusual interest to some of our readers. Regarding the two persons in the Polynesian study whose DNA patterns match that of American Indians, the researchers held open the possibility that the pair represented survivors of ancestors who “came into the Pacific as a result of secondary contact [from America] of the kind that also introduced the Andean sweet potato.” Dr. Rebecca Cann recently observed: “More and more people are thinking there’s a group of native Americans that may have closer genetic ties to Pacific Islanders. That would make a lot of sense. Why would the Polynesians get to Easter Island [from the west] and [just] stop [there]?” Evidence has surfaced that Polynesians may have sailed to Chile or Peru and returned home, she continued.
South America and the Nuuchal Nulth [Nootka] of Vancouver Island, British Columbia.” These findings are “consistent with direct but low levels of gene flow across the entire Pacific Ocean [to America],” as well as with the likelihood of some westbound voyages that brought a few Amerindians into Polynesia. Unexplained gene connections are not as rare as one might think. They reflect the historical potpourri of gene mixing that apparently was more characteristic of prehistoric peoples than is acknowledged by our normal supposition that “a people” are biologically homogeneous. For example, Sykes and his colleagues found that one person in their Polynesian sample showed a DNA mutation history that was closely related to that of Basques of western Europe! How does history as we know it handle that? James L. Guthrie, not a geneticist but a careful scientist nonetheless, has reexamined the data in the massive work by Cavalli-Sforza and associates, The History and Geography of Human Genes (1994), in the light of accumulated cultural data that suggests specific ancient migrations. In an unpublished monograph Guthrie has identified a substantial number of cases in which unexpected Old World gene features show up about where and when some of the migrations indicated by cultural evidence also occurred. More sophisticated studies of this type could at least multiply the number of interesting questions still facing geneticists as they try to interpret human history through the lens of DNA/molecular studies.

DNA Studies and the Book of Mormon

The interest of most readers of this journal will be on the relation that DNA analysis might have for the Book of Mormon. Is there a way in which sound DNA research could shed new light on the peoples and history described in the Book of Mormon? This ancient record, which Latter-day Saints hold sacred, reports the arrival by sea, apparently to Mesoamerica, of three different Near Eastern groups, one in the third or second millennium B.C. and the other two soon after 600 B.C. So is there evidence from DNA studies of populations in America having Near Eastern/Jewish characteristics?

It may be helpful to shift to a dialogue format at this point. Suppose that a DNA scientist were talking with a wealthy person anxious to fund a study of “DNA and the Book of Mormon.” Their hypothetical conversation can bring out important issues.

DNA expert: I appreciate your anxiety and enthusiasm to have a study carried out, but we have to get some things straight before I can seriously consider being involved. First, what result would you expect to see for the money you put out?

Donor: I’d like to see you get in there and prove that the genes of the Nephites and maybe the Lamanites were like those of the Jews. That ought to prove that the Book of Mormon is true.

DNA expert: I see. But, hold on a minute. Lehi and his folks left Jerusalem about 2,600 years ago. Over that period of time the biological characteristics of both the Jews Lehi left behind and those of his own party would have changed, possibly dramatically. If Lehi, Ishmael, their wives, and Zoram were not genetically “typical” of the Jews in Jerusalem in his day—and five people could never be “typical” of a gene pool of thousands—then the unique features in those Lehites would skew the characteristics of all their descendents in unknown ways. We call that “founder effect.” Adaptation to conditions in the new promised land as well as mutations would further shift their gene patterns away from whatever had been Jewish in their day.

Donor: Well, I see that. But “the Jews” continued on as a group, didn’t they?

DNA expert: Many were killed in the Babylonian conquest and captivity that followed on the heels of Lehi’s departure. Others surely died off in captivity. There is a good chance that the demographic crisis of the Babylonian conquest was also a genetic crisis for “the Jews.” We can’t tell how those massive deaths may have varied the pattern of biology in those who came back from Babylon with Ezra and Nehemiah.

You see, just because a group keeps its ethnic name over centuries does not mean that its biology has stayed anywhere near constant. The later history of the Jews offers a lesson on this point. The Ashkenazim, those Jews from eastern Europe who constitute the largest proportion of the identifiable Jewish people existing today, have actually descended from a group of only a few thousand ancestors who lived in and around the territory of
Poland about five centuries ago. The characteristics of those few thousand have come to define the biology of “the Jews” of today—far out of proportion to their number in relation to all Jews before A.D. 1500. The Lembas, the “Black Jews” of southern Africa, show “thoroughly Negroid blood groups.” The Falasha Jews from Ethiopia also differ little from their neighbors in their blood groups. Likewise, the Bene-Israel group of Jews that developed in the Bombay area of India descended from a mere seven founding families settled there hundreds of years ago. By early in the 20th century their descendants numbered in the tens of thousands, and some of them were absorbed into the population of the state of Israel. But in Bombay they were essentially similar in biological features and speech to their non-Jewish neighbors. The modern Jewish population as a whole will show a mix of the genes of various subgroups like the Ashkenazim, Lembas, Falashas, and so on developed historically and biologically in different regions of the world. We have no way to tell how any sample of modern Jews we might select would relate to the Jews of Lehi’s day, except that there is no reason to think today’s sample would be very similar.

Donor: But I understand that you can get DNA from old bones. Couldn’t you get some of those from tombs of about 600 B.C.? Their DNA would give you approximately what Lehi’s DNA was, wouldn’t it?

DNA expert: Unfortunately, tombs or burials from that date in the land of Israel are very scarce, and those that have been found almost never contain bones, for whatever reasons. Besides, just imagine the problems involved in overcoming the objections of orthodox Jews to having a scientist meddling with the bones of their ancestors!

Donor: Hmm.

DNA expert: From what I have been told about the Americas, the problem of getting a useful sample is just as much a problem, if not worse. The Book of Mormon text does not make clear just how and when Lehi’s descendants got mixed up with other peoples in their new land of promise, but it is clear that they did. That complicates terribly our forming any idea of what they became genetically over the thousand-year history recorded in Mormon’s account. After A.D. 400 the problem would be still more complicated.

Tell me, do you have any idea where I would go to get a DNA sample of Lehi’s direct descendants? No one I know seems to have a specific idea.

Donor: Haven’t LDS archaeologists found evidence among some tribes in Mexico that they descended from the Israelites?

DNA expert: Not according to what they have told me. At the level of culture and language there is evidence indicating that people from the Near East were involved in Mesoamerica, but that wouldn’t help the particular problem I’d face. A 1971 paper showed that there is a large, detailed body of parallels between the civilizations of the Near East and Mesoamerica in sacred architecture and practices, astronomy, calendar, writing, beliefs, symbolism, and other aspects of culture. A Jewish scholar, Cyrus H. Gordon, and other notable researchers have compiled interesting data on that point. A man named Alexander von Wuthenau published images of ceramic figures from Mesoamerica that definitely show Jewish faces. And linguists have some evidence for possible connections between Semitic languages and Mesoamerican Zapotec and related tongues on one hand and Uto-Aztecan on another.

A University of California linguist, Mary L. Foster, has argued for a connection between “Afro-Asiatic” languages, especially Egyptian, and old Mesoamerican languages such as Mixe-Zoquean. Those studies lead me to think that there is a distant chance that someday we might know enough to identify one group in Central America where I might go with some prospect to locate genes descended from Lehi, but today I have no informed notion. Simply to go take DNA samples at random from this or that group of Mexican Indians would be like a geologist with no geological maps in his hands looking for uranium ore by simply wandering across the landscape hoping his Geiger counter will start to click.

Donor: You’re not very encouraging, are you?

DNA expert: I must be pessimistic from the point of view of responsible scientific methods and ethics. I would like to accommodate your interest, and I wouldn’t mind having half a million dollars from you to play with, but the honest fact is, I wouldn’t know what to do with it. However, there is one little project that might be fun to try.
out. Remember the Lembas of South Africa? They have dark skins and speak a language that has no relation to Hebrew, but they do have a tradition of Jewish ancestry. In other parts of the Old World there are other little enclaves—people of yellow, brown, or white skin—that claim to have a Jewish or Israelite connection. In a number of cases there seems to be some basis for their claims.56

Well, it happens that there is, or was, a small group of Mexican Indians who claim a Jewish origin. Raphael Patai, who became one of the greatest scholars on Judaism, went to Mexico as a young man in the 1930s to see what he could learn about those people. After several months he discovered that they indeed had some customs that looked Jewish, and they claimed to have a Torah. Patai ended up saying that he did not know what to make of them, unless they were Jews who came from Spain in colonial days and found it convenient to “fade into the Indian woodwork,” so to speak.57 Now, if they really were of Jewish descent and they had priests along who carried the distinctive Cohen Y-chromosome, like the Lemba, that would be a leverage point. Maybe careful study by a modern scholar would shed more light than Patai could get on who they really were. If they came from Spain 300 years ago, that would be interesting, but not in reference to the Book of Mormon. Yet the tiniest possibility might exist that they actually descended from a pre-Spanish group of Indians. One would then like to know much more. Interestingly, Dr. Tudor Parfitt, director of the Center for Jewish Studies at the School of Oriental and African Studies in London, an expert on the Lemba who was instrumental in seeing that study made, has expressed interest in having a study made of the Mexican group—if they can still be found.58

Frankly, working with that little Indian enclave looks like the only show in town along the lines you want to see. My hunch is that there would only be one chance in thousands that it would pay off. But if you want to risk the money, maybe I could find the time.

Donor: I didn’t expect you to discourage me as much as you have, but I guess we ought to stick to what is scientifically sound. Okay, plan it out and send me a budget.

By the way, do you happen to know any explorer-type guys who’d like to look for a tribe of white Indians I’ve heard about and then write a book about it?


24. Ibid., 378.


27. See ibid., 25.

28. See ibid., 39.

29. See ibid., 101.


31. See Baugh and Cable, History of the English Language, 55.

32. See the discussion in Stubs, “Native American Languages,” 13.


42. See Rupert L. Murray, Cranial and Postcranial Skelatal Remains from Rapa Nui (Minneapolis: University of Minnesota Press, 1968), 77–79.


45. This is still assumed in a current anthropological textbook. See Colin Renfrew and Paul Bahn, Archaeology, Methods, and Practice, 2nd ed. (London and New York: Thames and Hudson, 1996), 436: “The language spoken by a community is the best predictor of what genetic characteristics . . . that community will have.”

46. See, for example, Juan Comas, “Características físicas de la familia linguística maya,” Universal Nacional Autónoma de México, Serie Antropológica 20 (México: UNAM, 1966). Comas compared the results of more than half a century of study of Maya-speaking groups to find that bio- metric differences among distinct groups within the language community, apparently due to intermarriage among non-Mayan groups, genetic drift, endogamy, and adaptive selection. See also M. Layrisse, Z. Layrisse, and J. Wiberg, “Blood Group Antigen Studies of Four Chicabal (speaking) Tribes,” American Anthropologist 65 (1963): 36–50; the tribes do not form a homogeneous genetic group.


