

Genetics and the History of Latin America

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Given that we live in the much-vaunted era of the “genomics revolution,” one cannot help but wonder whether those long strands of DNA will ever wash up on the historian’s lonely shore. Sure, we are all aware of one or two high-profile instances when genetic evidence was able to change a historical interpretation. The case that most readily comes to mind is the Y-chromosome DNA test conducted by a retired pathologist in Charlottesville, Virginia, in 1998—intended to settle the question of whether Thomas Jefferson had fathered a child by his slave Sally Hemings.¹ Among other things, the ensuing furor and soul-searching produced a spate of works reexamining slavery, miscegenation, and the connections between the private and public spheres in early America.²

Still, we (professional historians) ordinarily regard DNA work as a mere curiosity. For one thing, this type of inquiry has been carried out by outsiders: retired physicians, forensic experts, history buffs, and the like. But more to the point, DNA’s strong suit is “whodunit” types of questions—such as whether President Jefferson sired any children with his slave or whether the famous outlaw Jessie James faked his own death, attended his funeral, and went on to live quietly for many years. (Disappointingly, DNA evidence fails to support this legend.) Such projects, dreamed up mostly by amateurs and designed to solve lingering historical mysteries, appear far removed from the more sweeping and ethereal social, political, economic, and cultural explanations that are the hallmark of our academic discipline today.

At the other end of the spectrum, those of us working on topics pertaining to the history of Latin America in the last five hundred years may be aware of

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1. The original story appeared in the *U.S. News & World Report*, 9 Nov. 1998.

2. On the many ripples created by the Jefferson–Hemings relationship, see Gordon S. Wood, “Slaves in the Family,” *The New York Times Book Review*, 14 Dec. 2003.

the work being done by geneticists and molecular anthropologists on ancient America. Since DNA yields information that no historical, archaeological, or linguistic source can provide, it is not surprising that much of the pioneering genetic work has been focused on the remote past, broaching subjects such as the peopling of the Americas, the early process of group formation, and the assessment of ancestor-descendent relationships among pre-Columbian indigenous groups. Even so, DNA scholarship has occasionally moved squarely into the historians' turf. The work of Juan Carlos Martínez Cruzado and his group of researchers at the University of Puerto Rico is a case in point.³ This team started out in the 1980s by studying the mitochondrial DNA (mtDNA) of some pre-Columbian skeletal remains found on the island. To contextualize this data, the group also conducted mtDNA tests among living Puerto Ricans. Astoundingly, Martínez Cruzado and his collaborators concluded that 53 percent of islanders have indigenous ancestry through the maternal line. To say the least, these results contradict the dominant historical narrative of annihilation of the indigenous population of Puerto Rico by the middle of the sixteenth century. Can these findings be somehow explained by subsequent indigenous migration to the island, or is it time to critically reassess the standard historical narrative and the colonial sources on which it rests?

In this report, we will survey the DNA literature most relevant to historians of Latin America (especially those working in Mexico and the American Southwest) and discuss how the genetic evidence jibes with our socially constructed notions of race and ethnicity. We will be selective in our coverage by necessity, but we also point readers to a fairly comprehensive list of references available at <http://resendez.ucdavis.edu>. We hope this piece can serve as a bibliographical resource for all historians curious about how their own interpretations square with the DNA evidence.

One prefatory clarification is in order here. We do not take the view that DNA data should take precedence over other kinds of textual, linguistic, or archaeological evidence. This is an especially important and sensitive matter in these heady times, when DNA is accorded so much authority that it can single-handedly condemn or exonerate individuals accused of serious crimes. Instead, we advocate a brand of methodological eclecticism in which different lines of evidence are cross-checked against each other and used to advance interpretations consistent with multiple sources of data.

3. Martínez-Cruzado et al., "Mitochondrial DNA Analysis in Puerto Rico," *Human Biology* 73 (2001): 491–511.

An Emerging Genetic Map of the Continent

DNA may well be the ultimate archival repository, containing clues about large-scale population movement, conquest, sexual and reproductive patterns, and even group identities—after all, with whom we have children constitutes one important way to define community. Historians may be put off by DNA's focus on sample sizes and statistics. But on the positive side, while oral and written sources limit us to the most literate social groups and to the last five or six hundred years (two thousand or so if we include Maya glyphs), DNA evidence sheds light on the most numerous and ordinary individuals—representing a bottom-up approach as it were—and at the same time extends our scope to the first inhabitants of the Americas and beyond.

For historians, DNA scholarship's most significant contribution comes in the form of a genetic map. Virtually all indigenous peoples of the Americas have been found to cluster into one of four founding maternal lineages—haplogroups—determined by mutations in the mtDNA.⁴ These four founding lineages are so widespread and ancient that they can be identified among contemporary Native Americans as well as in samples from individuals who lived thousands of years ago. DNA scholars conveniently—if somewhat unimaginatively—call them haplogroups A, B, C, and D.⁵ These four founding lineages can be traced back to Asia, where they coexist with others, but are quite different from those of Europe and Africa.⁶ This simply indicates that the early inhabitants of the Americas came originally from Asia but that not all Asian

4. We are hesitant to use “mutation” because the term may have negative connotations. DNA scholars often use the more neutral but mystifying “polymorphism.” In this paper we will continue to refer to mutations but in the understanding that they do not generally affect the performance of the individuals or lineages that have them. Although much of the early work has been conducted on the mitochondrial genome, it is possible to create other genetic maps based on Y-chromosome information or on nuclear DNA, as discussed later.

5. Although much of the discussion in the DNA literature revolves around haplogroups A, B, C, and D, about 3 percent of Native Americans belong to a fifth haplogroup called X. Interestingly, haplogroup X has also turned up in Europe and in Central Asia, thus fueling speculation, until quite recently, about whether Europeans may have contributed to the genetic makeup of the New World before Columbus. The latest work indicates that haplogroup X, as found among Native Americans, is not closely related to the European haplogrup X variant. See M. Reidla et al., “Origin and Diffusion of mtDNA Haplogroup X,” *American Journal of Human Genetics* 73 (2003): 1178–90.

6. The main haplogroups in Asia are A, B, C, D, F, G, and Z; in Europe, they are H, I, J, K, T, U, V, W, and X; and in Africa, they are L1, L2, and L3.

haplogroups made it to America, thereby resulting in reduced genetic diversity in the New World.⁷

Two features make mtDNA ideally suited for historical and anthropological investigations.⁸ First, it is passed down solely from mother to child and without recombination. A woman gets an identical copy of her mother's mtDNA, and, in turn, she will pass it on to her children. In other words, when we determine a mtDNA lineage, we are in fact peering at a genetic legacy passed through an unbroken line of female ancestors going back for millennia. In this sense, we can conceive of haplogroups A, B, C, and D as the indelible imprints of four pioneering native women whose progenies gave rise to nearly all of the indigenous peoples of the New World.⁹ It is important to emphasize that while the time depth revealed by mtDNA is astonishing, its ability to predict physiognomic or racial traits or capture genetic mixture is limited at best, because it traces only one line of descent (from grandmother to mother to daughter, etc.) while ignoring all other genetic contributions to the individual. In other words, a person may look—and indeed be—decidedly African or European and still possess one of the four Native American matrilineal lines or vice versa.

The second feature that makes mtDNA especially relevant for historians is that one region of the molecule mutates rapidly.¹⁰ As mtDNA is copied with each succeeding generation, slight copying errors (mutations) are inevitably introduced. Bases can be added, deleted, changed, or simply jumbled. As mutations accumulate, patterns emerge in branchlike fashion. Due entirely to chance, certain mutations become associated with certain populations and are absent in others.

We cannot know for sure *when* a particular mutation first occurred, and therefore DNA provides only a crude historical clock. But we do know that some lineages are more widespread and basic than others, indicating that the former occurred earlier than the latter. We can thus think of mtDNA as a large, sprawling tree. At the trunk we will find mutations that are common to all liv-

7. There is a large literature devoted to the origins and initial peopling of the Americas. For an insightful and recent survey, see Herbert S. Klein and Daniel C. Schiffer, "The Current Debate about the Origins of the Paleoindians of America," *Journal of Social History* 37, no. 2 (2003): 483–92.

8. Mitochondria are elliptical-shaped organelles that provide energy to the cell. Each mitochondrion carries two copies of a small circular strand of DNA.

9. This does not mean that the continent was peopled by four women only. It simply means that the mtDNA lineages of the other women became subsequently extinct.

10. Called the "hypervariable region," this feature allows one to make differentiations between closely related populations, such as Native Americans.

Table 1. Haplogroup Frequencies of Selected Populations in the Hemisphere.

| <i>Population</i> | <i>N</i> | <i>%A</i> | <i>%B</i> | <i>%C</i> | <i>%D</i> | <i>%X</i> |
|----------------------------------|----------|-----------|-----------|-----------|-----------|-----------|
| Kuna (Panama) | 89 | 79.8 | 20.2 | 0 | 0 | 0 |
| Nahua-Cuetzalán (central Mexico) | 31 | 61.3 | 32.3 | 6.5 | 0 | 0 |
| Tohono O'odham (Arizona) | 37 | 0 | 56.8 | 37.8 | 5.4 | 0 |
| Yanomama (Brazil and Venezuela) | 110 | 2.7 | 11 | 39 | 47.3 | 0 |

Source: Compiled from a list of sources available at <http://resendez.ucdavis.edu>.

ing humans and that must have been present when our ancestors still constituted one single group in Africa, prior to the momentous dispersal to the other continents. Or we may choose to train our sight on more recent branches, such as the founding lineages of the indigenous peoples of the New World, associated with mutations introduced just prior to or immediately after the initial peopling of our continent. It is further possible to look at subbranches and even twigs on the basis of even more recent mutational events that may be associated with the formation of populations or language groups. Indeed, each haplogroup can be further subdivided to a level of resolution that can give us clues about events in a time horizon more consistent with that commonly employed by historians.¹¹

What can the geographic distribution of mtDNA variation teach us about the history of Latin America? Thus far, scholars have studied genetic markers of indigenous groups in all major areas of Latin America, including South America, Central America, the Caribbean, Mexico, and the American Southwest, and they have found that haplogroups A, B, C, and D are widely dispersed throughout the hemisphere.¹² Even a cursory look at the mtDNA of such diverse populations as the Yanomama of Brazil and Venezuela, the Kuna of Panama, the Nahua of central Mexico, and the Tohono O'odham of Arizona (just to name a handful) shows that each population contains at least three and often all four founding lineages, although the proportions vary widely from one population to another as a result of their separate histories (see table 1).

Most immediately, the wide distribution of haplogroups has a bearing on discussions about the initial peopling of the Americas. Studies in the 1980s and 1990s, based on early mtDNA findings, as well as linguistic and craniomet-

11. For example, in another context Stephens has established a link between a nuclear DNA mutation in the CCR5 gene and the bubonic plague in Europe. See J. C. Stephens et al., "Dating the Origin of the CCR5-Delta-32 Aids-Resistance Allele by the Coalescence of Haplotypes," *American Journal of Human Genetics* 62 (1998): 1507-15.

12. For a comprehensive list of DNA articles of each of these regions, readers can turn to <http://resendez.ucdavis.edu>.

ric evidence, argued for three distinct migration events from Asia to the New World.¹³ More recent DNA scholarship has cast doubts on multiple-migration models. While no scholarly consensus has been reached, many DNA researchers now favor explanations that involve a single migration and subsequent expansions or radiations throughout the hemisphere.¹⁴ The most obvious objection to multiple-migration models is the widespread distribution of the four founding lineages throughout the Americas. Moreover, the four haplogroups evince a similar amount of accumulated diversity, suggesting a common time depth in the New World for all. In short, it is unlikely that multiple migrations—totally unrelated to one another, taking place thousands of years apart, and possibly originating in different places—would have given rise to a scenario in which four haplogroups were so widely distributed among virtually all of the native populations of the continent.¹⁵

The History of Mexico and the American Southwest as Revealed by Genes

Studying genetic markers in narrower regions has much to add to our understanding of history. Some tantalizing patterns emerge in the case of Greater Mexico, for example. In the core regions of Mexico—roughly coterminous with the extent of Mesoamerica—haplogroup A predominates, with additional but smaller percentages of the other haplogroups. DNA studies conducted among Nahua, Maya, Mixe, Zapotec, and Mixtec populations show significant genetic similarities (see table 2).¹⁶ The similarity of haplogroup frequencies across these

13. Joseph H. Greenberg, Christy G. Turner II, and Stephen L. Zegura, “The Settlement of the Americas: A Comparison of the Linguistic, Dental, and Genetic Evidence,” *Current Anthropology* 27, no. 5 (1986): 477–97. Interestingly, Zegura—one of the three authors who originally launched the “three-wave model”—has come back full circle and now supports a single migration. S. L. Zegura et al., “High-Resolution Snps and Microsatellite Haplotypes Point to a Single, Recent Entry of Native American Y Chromosomes into the Americas,” *Molecular Biology and Evolution* 21 (2004): 164–75.

14. See especially W. A. Silva et al., “Mitochondrial Genome Diversity of Native Americans Supports a Single Early Entry of Founder Populations into America,” *American Journal of Human Genetics* 71 (2002): 187–92.

15. Thus far, we have largely been concerned with mtDNA-based studies. DNA scholars have also begun investigating Y-chromosome DNA, as well as autosomal (i.e., nuclear) DNA markers. Like mitochondrial DNA, the Y chromosome has a nonrecombining region—that is, a region that is passed down unchanged—this time through the paternal line. For a review of recent Y-chromosome literature, see Klein and Schiffner, “The Current Debate,” 485–88.

groups is remarkable if we bear in mind that they represent all four major linguistic families of Mesoamerica—Uto-Aztecan, Mayan, Mixe-Zoquean, and Otomanguan, respectively. Linguists believe that each of these language families has a time depth that runs in the thousands of years and that they are thus not closely related. Moreover, comparisons of ancient and modern DNA data show that haplogroup frequency distributions have remained relatively stable for at least six hundred years (the demographic catastrophe of the early colonial period notwithstanding) and perhaps considerably longer. How can we explain these long-term genetic similarities in the face of profound linguistic differences? One possibility is that all major indigenous civilizations that flourished in Mesoamerica descend from a single ancient population that already bore a large frequency of haplogroup A. Recent mtDNA testing of the skeletal remains of an 11,000-year-old individual found in Mexico City lends some support to this idea.¹⁷ Alternatively, one can theorize that the continuous human interaction within Mesoamerica in the form of warfare, trade, and successive macroregional political arrangements—including those centered at sites like La Venta, Teotihuacán, Tula, and Tenochtitlán—may have, over time, blurred whatever genetic differences originally existed.

In stark contrast to the mtDNA profile of Mesoamerica, in the American Southwest haplogroup A is generally absent while haplogroup B predominates (see table 2).¹⁸ Indeed, populations in the Southwest exhibit some of the highest frequencies of haplogroup B to be found anywhere in the New World. For instance, among River Yuman in southwestern Arizona, fully 63 percent of the population exhibits haplogroup B, while among the peoples of Jémez Pueblo in New Mexico an overwhelming 88 percent do so.¹⁹ With the limited mtDNA information at our disposal, it would thus appear that substantial genetic dif-

16. Admittedly, sampling is still spotty, and sample sizes are generally small. Larger and more comprehensive studies carried out in the future may qualify these sweeping results.

17. Description and dating of these ancient remains in Silvia González et al., “Earliest Humans in the Americas: New Evidence from Mexico,” *Journal of Human Evolution* 44 (2003): 379–87. Angélica González-Oliver (personal communication) has performed the mtDNA analysis and concluded that it belongs to haplogroup A.

18. For a comprehensive survey of mtDNA in the Southwest, see R. S. Malhi et al., “Native American mtDNA Prehistory in the American Southwest,” *American Journal of Physical Anthropology* 120 (2003): 108–24.

19. Joseph G. Lorenz and David G. Smith, “Distribution of Four Founding mtDNA Haplogroups among Native North Americans,” *American Journal of Physical Anthropology* 101 (1996): 307–23; David G. Smith et al., “Distribution of mtDNA Haplogroup X among Native North Americans,” *American Journal of Physical Anthropology* 110 (1999): 271–84; and Malhi et al., “Native American mtDNA Prehistory.”

Table 2. Haplogroup Frequencies of Selected Populations in North America

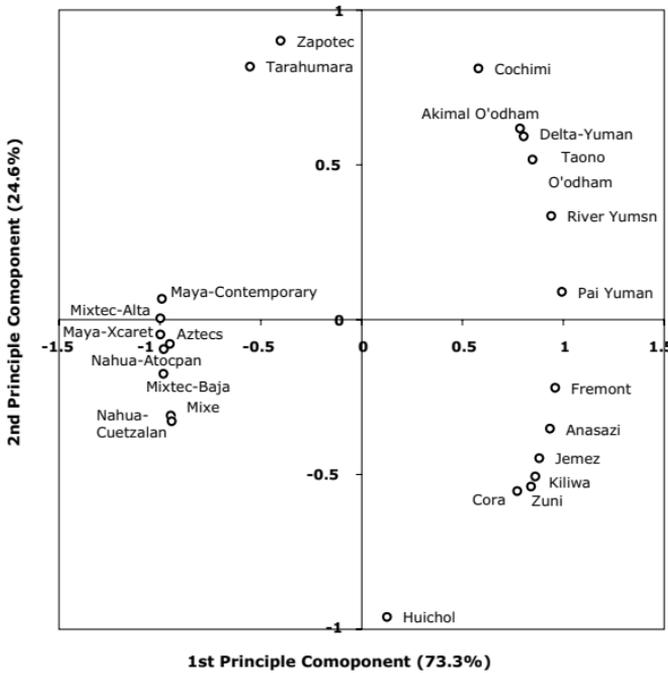
| <i>Population</i> | <i>N</i> | <i>%A</i> | <i>%B</i> | <i>%C</i> | <i>%D</i> | <i>%X</i> |
|---|----------|-----------|-----------|-----------|-----------|-----------|
| Aztecs (Tlatelolco, Mexico City) ¹ | 23 | 65.2 | 13 | 4.3 | 17.4 | 0 |
| Cora (Nayarit) | 81 | 28.4 | 51.9 | 16 | 3.7 | 0 |
| Huichol (Nayarit) | 52 | 34.6 | 53.8 | 11.5 | 0 | 0 |
| Ancient Maya (Quintana Roo) ¹ | 24 | 87.5 | 4.2 | 8.3 | 0 | 0 |
| Contemporary Maya (Yucatán) | 26 | 53.8 | 23.1 | 15.4 | 7.7 | 0 |
| Highland Mixe (Ayutla, Oaxaca) | 16 | 62.5 | 31.3 | 6.3 | 0 | 0 |
| Alta Mixtec (Nochixtlán, Oaxaca) | 15 | 73.3 | 13.3 | 13.3 | 0 | 0 |
| Baja Mixtec (Huajuapán, Oaxaca) | 14 | 92.9 | 7.1 | 0 | 0 | 0 |
| Atocpan Nahua (Milpa Alta) | 49 | 38.8 | 40.8 | 16.3 | 4.1 | 0 |
| Cuetzalán Nahua (Puebla) | 31 | 61.3 | 32.3 | 6.5 | 0 | 0 |
| Tarahumara (Durango) | 72 | 33.3 | 29.2 | 31.9 | 5.6 | 0 |
| Valley Zapotec (Oaxaca) | 15 | 33.3 | 33.3 | 33.3 | 0 | 0 |
| Akimal O'odham (southeast Arizona) | 43 | 4.7 | 53.5 | 39.5 | 0 | 2.3 |
| Anasazi (U.S. Southwest) ¹ | 25 | 24 | 60 | 16 | 0 | 0 |
| Cochimi (southern Baja California) | 13 | 7.7 | 46.2 | 46.2 | 0 | 0 |
| Delta Yuman (western Arizona) | 23 | 0 | 56.5 | 43.5 | 0 | 0 |
| Fremont (Great Salt Lake) ¹ | 30 | 0 | 80 | 13.3 | 6.7 | 0 |
| Jémez (northwestern New Mexico) | 36 | 0 | 88.9 | 2.8 | 0 | 8.3 |
| Kiliwa (northern Baja California) | 7 | 0 | 100 | 0 | 0 | 0 |
| Pai Yuman (northern Baja California) | 27 | 7.4 | 66.7 | 25.9 | 0 | 0 |
| River Yuman (western Arizona) | 22 | 0 | 63.6 | 36.4 | 0 | 0 |
| Tohono O'odham (Arizona) | 37 | 0 | 56.8 | 37.8 | 5.4 | 0 |
| Zuni (northwestern New Mexico) | 26 | 15.4 | 76.9 | 7.7 | 0 | 0 |

¹Precontact population

Source: Compiled from a variety of sources found in <http://resendez.ucdavis.edu>.

ferences exist between the indigenous peoples of Mexico and those of the Southwest, even though we know that architectural fashions, cultigens, trade goods, and at least some population groups have historically moved across these regions. Have the great deserts of northern Mexico constituted a real barrier through the ages preventing the widespread movement and mixing of peoples (see graph 1)?

Additional research on the biological connections between Mesoamerica and the American Southwest adds new twists. Given the apparent lack of shared matrilineal markers, scholars have studied other genetic markers to confirm or challenge these results. David Glenn Smith and his team have studied a unique type of human serum known as albumin Mexico. Although exceedingly rare, albumin Mexico is found in several linguistically unrelated groups throughout Mexico and also in various communities of the Southwest, thus providing clear evidence



Graph 1. Principal Component Analysis of Haplogroup Frequencies of Selected Groups from Mexico and the American Southwest.

of a biological connection. Smith and his collaborators believe that albumin Mexico may have originated more than three thousand years ago somewhere in central Mexico and subsequently moved northward along the Tepiman corridor, spreading to various groups associated with the Hohokam culture in what is now the American Southwest.²⁰ If this analysis is correct, then how can we reconcile the cross-regional distribution of albumin Mexico with the apparent lack of shared matriline between Mexico and the Southwest? One possible explanation is that much of the human interaction between the two macroregions has occurred via males—such as long-distance merchants (like the Aztec *pochteca*), all-male armies, or predominantly male migrations.²¹ It is also possible that more thorough sampling of Mexican and Southwestern indigenous groups and investigation of mtDNA on a finer scale will eventually reveal the elusive shared matriline.

These results are especially relevant in light of the recent discussion among ethnohistorians, linguists, and archaeologists concerning the origins and spread

20. David G. Smith et al., "Implications of the Distribution of Albumin Naskapi and Albumin Mexico for New World Prehistory," *American Journal of Physical Anthropology* 110 (1999): 271–84.

21. Precisely this scenario is advanced in R. S. Malhi et al., "Native American mtDNA Prehistory."

of the Uto-Aztecan language family. When Spanish conquistadors made their way into Central Mexico in the early sixteenth century, they found that Nahuatl (a member of the Uto-Aztecan family) was the most common language within the Aztec Empire, functioning as a lingua franca in the core region of Mesoamerica. But while contemporary scholars agree on the preeminence of Nahuatl at the time of contact, they disagree about its origins. Most scholars subscribe to the notion that Proto-Uto-Aztecan (and therefore Proto-Nahuatl) speakers originated outside of Mesoamerica—in northwestern Mexico or farther north—and moved south, populating central Mexico in successive migratory waves that took place roughly over the thousand-year period prior to the Spanish arrival.²² Linguist Jane Hill has called this interpretation the northern origin model. Yet some scholars, including Hill, have recently proposed an alternative southern origin model, arguing that Proto-Uto-Aztecan peoples lived within Mesoamerica at least since the beginnings of maize domestication more than five thousand years ago.²³ The supporters of this interpretation reverse completely the direction of the language spread and contend instead that it started out in central Mexico and subsequently expanded to the northwest and beyond on the basis of agricultural technology. These scholars, who have not overturned current scholarly consensus favoring a northern origin, have nonetheless produced relevant linguistic evidence that merits further investigation. More DNA evidence would help elucidate this ongoing debate that is so fundamental to the overall history of early Mexico.

The efforts of our own research team at the University of California, Davis, have also been geared toward further exploring the genetic connections between Mesoamerica and the Southwest. Specifically, we have studied the mtDNA of geographically intermediate populations, including Coras, Huicholes, and Tarahumaras (see table 2). We have found that these groups have high frequencies of both haplogroups A and B, as befits “frontier” or “contact” populations. Yet, our preliminary findings indicate that the transition of haplogroup frequencies from the Southwest to Mesoamerica does not occur uniformly and smoothly following a north-south gradient. Instead, we have discovered nota-

22. Christopher S. Beekman and Alexander F. Christensen have cogently and concretely laid out this interpretation in “A Synthetic Analysis of the Nahua Migrations” (ms).

23. Jane H. Hill, “Proto-Uto-Aztecan: A Community of Cultivators in Central Mexico?” *American Anthropologist* 103, no. 4 (2001): 913–34. The basic notion is that large linguistic families such as Indo-European, Austronesian, and Uto-Aztecan must have grown at the expense of other languages and on the basis of technological advances such as plant domestication.

ble frequency differences and have even detected the presence of haplogroup enclaves. For instance, while haplogroup A tends to predominate in Nahuaspeaking populations, such as those of precontact Tlatelolco and modern-day Cuetzalán, Puebla, we have been able to identify at least one Nahua community—San Pedro Atocpan, right outside Mexico City in the district of Milpa Alta—where haplogroup B constitutes the largest percentage. Our long-term goal is to add sufficient detail to this rough genetic map to enable scholars to pinpoint instances in which haplogroup-A-bearing Mesoamerican groups made inroads into the Southwest and, conversely, identify cases where haplogroup-B-bearing peoples of the Southwest (conceivably Chichimecs, Teochichimecs, and their forebears) migrated south into the core regions of Mesoamerica.

One final way to tackle this problem is by focusing on specific mutations that arose recently and can be credibly linked to historical phenomena. We have identified what we believe is a particularly promising genetic marker—a derived form of haplogroup A that carries a nine base-pair deletion in the mitochondrial genome. Our interest in this marker was sparked after studying the remains of 27 “Aztec” individuals from precontact Tlatelolco. Three of these individuals carried this derived form of haplogroup A.²⁴ A literature search reveals that this particular mutation has been reported only for populations located within the present-day Mexican states of Chihuahua, Puebla, and Yucatán, as well as in Costa Rica and Puerto Rico.²⁵ Although the 9-bp deletion has occurred previously in Asia and Africa, its association with haplogroup A constitutes an independent New World mutational event that most probably arose in Mesoamerica relatively recently.²⁶ Given that this mutation appears at a significant frequency among the Aztecs of Tlatelolco and that its general distribution corresponds roughly with that of Nahuatl-speakers—from northern through central Mexico with additional pockets in Central America—it is tempting to theorize that this derived form may be related to the spread of Nahuatl, even though considerably more data would be required to substantiate this interpretation.

In addition to tracking large-scale population movements, the distribution of mutations will also serve to address some vexing problems of colonial fron-

24. B. M. Kemp et al., “An Analysis of Ancient Aztec mtDNA from Tlatelolco: Pre-Columbian Relations and the Spread of Uto-Aztecan,” in *Biomolecular Archaeology: Genetic Approaches to the Past*, ed. David M. Reed. Forthcoming.

25. Relevant citations can be found in <http://resendez.ucdavis.edu>.

26. A. Torroni et al., “Asian Affinities and Continental Radiation of the Four Founding Native American mtDNAs,” *American Journal of Human Genetics* 53 (1993): 580; and B. M. Kemp et al., “An Analysis of Ancient Aztec mtDNA from Tlatelolco.”

tier history. The case of New Spain's northwest illustrates well the formidable challenge that historians have faced. This area was first described by Spanish conquerors in the 1530s and 1540s. These early *entradas* provide glimpses of the numerous and varied peoples that inhabited the region and give us a sense of the social world as it existed prior to contact. But it is only with the advent of the mission system, well into the seventeenth century, that we are able to count on more substantial and regular sources. Unfortunately, it is precisely between the conquest and the spread of the mission system—a period for which we lack adequate sources—when indigenous communities underwent enormous upheavals and precipitous population declines, resulting in displacements, amalgamations, and disappearances, as well as remarkable survivals.²⁷ As historians come to grips with these events, DNA evidence will be instrumental in addressing some specific problems. First, genetic markers will help archeologists and historians establish links and sort out relationships between pre-Columbian sites and their colonial descendants. For instance, Phil C. Weigand has proposed that the ancestors of the Tepecanos once inhabited the Cerro de Colotlán in the Bolaños Valley of Jalisco. As he wrote in the mid-1980s, “It seems that the dozen old Tepecanos who still use the Cerro de Colotlán circle may be among the last remnants of the entire Teuchitlan Tradition which dominated much of western Mesoamerica during the Classic period.”²⁸ Such concrete lines of inquiry can now be pursued through DNA analysis. More generally, the slow but continuous accumulation of archeological data from northern Mexico now puts us in a better position to connect the pre- and postcontact pasts in more credible ways; DNA evidence will be a crucial tool in this monumental task.²⁹

Second, DNA work can also help us revisit the issue of the magnitude of population decline among different indigenous groups. This is a subject vigorously debated since colonial times and more recently in the classic works of Sherburne F. Cook and Woodrow Borah. The controversy arises largely

27. For an overview, see Susan M. Deeds, “Northwest Mexico,” in *The Cambridge History of the Native Peoples of the Americas*, ed. Richard E. W. Adams and Murdo J. MacLeod (Cambridge: Cambridge Univ. Press, 2000) 2:52–53; and Cynthia Radding, *Entre el desierto y la sierra: Las naciones O’odham y Tegüüma de Sonora, 1530–1840* (Mexico City: CIESAS-INI, 1995), chaps. 2 and 3.

28. C. Weigand, “Considerations on the Archaeology and Ethnohistory of the Mexicaneros, Tequales, Coras, Huicholes, and Caxcanes of Nayarit, Jalisco, and Zacatecas,” in *Contributions to the Archaeology and Ethnohistory of Greater Mesoamerica*, ed. William J. Follan (Carbondale: Southern Illinois Univ. Press, 1985), 165.

29. For a recent appraisal of the field see Beatriz Braniff C., ed., *La Gran Chichimeca: El lugar de las rocas secas* (Mexico City: CONACULTA, 2001), *passim*.

because works of historical demography have to rely on different population data sets that are not always readily comparable with one another. Moreover, they need to make certain assumptions about the scope and reliability of these data sets.³⁰ DNA can now offer an independent way to corroborate such analyses without having to depend on the vagaries of tribute lists and colonial censuses. In short, by comparing present-day genetic variation with that found in their precontact ancestors, DNA scholars can estimate the loss of lineages and reduction of overall diversity. One can expect a population that experienced a 95 percent reduction to be more homogeneous and exhibit fewer surviving lineages than a population that declined by only 50 percent. Population geneticists call this phenomenon a “bottleneck effect.” Assessing the magnitude of this effect for different populations will throw additional light on what is arguably Latin America’s most contentious demographic debate.³¹

Finally, DNA studies will prove very valuable in assessing long-term population dynamics and specifying more precisely the biological impact of various factors, such as the presence of missions or the proximity of mines, on indigenous communities in the immediate surroundings.³² Since the pioneering works of Edward Spicer and Gonzalo Aguirre Beltrán, much historical work has been devoted to determining why various ethnic groups disappeared from the historical record, while others endured as viable cultural, social, and political entities to the present time.³³ Scholarly concern with the “enduring peoples”

30. Especially relevant for our specific discussion is Cook and Borah, “The Population of West-Central Mexico (Nueva Galicia and Adjacent New Spain), 1548–1960,” in *Essays in Population History: Mexico and the Caribbean*, ed. Sherburne F. Cook and Woodrow Borah (Berkeley: Univ. of California Press, 1971), 1:300–75.

31. For instance, Rangel-Villalobos has concluded that present-day Huicholes and Tarahumaras show a reduced level of genetic variation, presumably due to population decline after contact. Rangel-Villalobos H et al., “Genetic Variation among Four Mexican Populations (Huichol, Purépecha, Tarahumara, and Mestizo) Revealed by Two VNTRs and Four STRs,” *Human Biology* 72 (2000): 983–95. Interestingly, DNA work to date has shown a surprising stability of haplogroup frequencies before and after the conquest. D. H. O’Rourke et al., “Spatial and Temporal Stability of mtDNA Haplogroup Frequencies in Native North America,” *Human Biology* 72 (2000): 15–34.

32. Scholars have already noted that Purépechas have more European admixture than do either Huicholes or Tarahumaras. This is attributed to the relative isolation of the latter groups. Rangel-Villalobos et al., “Genetic Variation among Four Mexican Populations.”

33. Gonzalo Aguirre Beltrán, *Regiones de refugio: El desarrollo de la comunidad y el proceso dominical en mestizo America* (Mexico City: Instituto Indigenista Interamericano, 1967); and Edward H. Spicer, *Cycles of Conquest: The Impact of Spain, Mexico, and the United States on the Indians of the Southwest, 1533–1960* (Tucson: Univ. of Arizona Press, 1962).

and their survival strategies, including forming ethnic enclaves and “zones of refuge,” continues to play a crucial role in recent scholarship, including that of Phil C. Weigand, Cynthia Radding, and Susan M. Deeds.³⁴ DNA research will inevitably engage this historiography as it provides evidence of contraction, expansion, disappearance, and endurance of lineages in the region.

Our discussion all but makes clear that DNA research will increasingly address some of our most revered categories of historical analysis: race and ethnicity. Modern DNA scholars have made strenuous efforts to distance themselves from the kind of reductionism that took place during the heyday of the eugenics movement. But notwithstanding the vast differences in sophistication, the question remains: if races and ethnicities are indeed rooted, to some extent, in biological difference, what will be the consequences of pinpointing and identifying human variation at the level of the DNA sequence? Some historians may reject the DNA research enterprise altogether on the grounds that it will ultimately serve to reify racial and ethnic categorizations. This serious issue is best addressed not by total rejection of DNA methodology but by enlightened discussion and awareness of the dangers of allowing the public at large to read too much into founding lineages and (worse still) of letting interested parties use genetic markers to further their ethnic or racial agendas.

One way to address this profound political, epistemological, and ethical issue is by placing genetic variation in a larger context. In the first place, while DNA scholars try mightily to find variation among populations, the most obvious insight generally remains unstated: namely, that we humans are practically identical when it comes to our genetic makeup. Physical traits that we recognize at a quick glance, such as skin color, eye shape, and body size, may precondition us to believe that there exist significant genetic differences—and perhaps even commensurate cognitive and temperamental differences—between us. In fact, these physical traits are rooted in insignificant variations at the level of our DNA, which underscores the fact that we are all closely related to one another.³⁵

34. N. Ross Crumine and Phil C. Weigand, eds., *Ejidos and Regions of Refuge in Northwestern Mexico* (Tucson: Univ. of Arizona Press, 1987); Cynthia Radding, *Wandering Peoples: Colonialism, Ethnic Spaces, and Ecological Frontiers in Northwestern Mexico, 1700–1850* (Durham, NC: Duke Univ. Press, 1997); Susan M. Deeds, *Defiance and Deference in Mexico's Colonial North: Indians under Spanish Rule in Nueva Vizcaya* (Austin: Univ. of Texas Press, 2003).

35. To put it in hard numbers, out of the nearly 17,000 base pairs constituting the mitochondrial genome, the average number of base-pair differences between two human sequences is 38.5 among non-Africans, 76.6 among Africans, and 61.6 among all humans. M. Ingman et al., “Mitochondrial Genome Variation and the Origin of Modern Humans,”

To be sure, different human populations have adapted extraordinarily rapidly to different environments, much of this driven by culture. But this does not change the central fact that we are an extremely young species, having arisen in Africa only within the last 100–200,000 years.³⁶ Even if we compare the most different-looking human groups (for example, Native Americans, West Africans, and Northern Europeans), we don't need to go back too many generations to find common ancestors among them. By contrast, we will find considerably more genetic variation among gorillas or chimpanzees (even though one chimp, to our eye, looks essentially like any other chimp). These, our close cousins, have lived as distinct species for 5 million years or more, and compared to them, we humans are practically genetic carbon copies of one another.³⁷

Another way to contextualize DNA findings is by emphasizing that there are no pure races or ethnic/national groupings. The entire eugenics edifice rested on the perception that humans came in a few unadulterated varieties—most commonly Africans, Asians, and Caucasians—as well as a range of mixed or mongrel populations between them. It went without saying that these pure races were tangible, stable, and easily ascertained. Modern DNA research has shown the wrongheadedness of such discrete groupings. For one thing, DNA researchers have found heterogeneity within any given population.³⁸ Pure races simply do not exist anywhere on the planet. Moreover, racial and ethnic groups are not stable but extraordinarily dynamic. As a rule of thumb, DNA researchers have found that people tend to be more closely related to those living around

Nature 408 (2000): 708–12. Interestingly, the greater diversity within African populations—as opposed to less diversity when between African and non-African populations—may be explained by a significantly longer genetic history for humans in Africa, something that is consistent with the archaeological evidence. See also Luigi Luca Cavalli-Sforza, *Genes, Peoples, and Languages* (New York: North Point Press, 2000), chap. 1.

36. In a pioneering article, Rebecca L. Cann and her coinvestigators concluded that a common ancestor to all humans existed 200,000 years ago. Cann, “Mitochondrial DNA and Human Evolution,” *Nature* 325 (1987): 31–36.

37. For an entertaining discussion of these issues see Jonathan Marks, *What It Means to Be 98% Chimpanzee: Apes, People, and Their Genes* (Berkeley: Univ. of California Press, 2002), passim.

38. For example, a group of researchers has shown that a small indigenous community of the Pacific Northwest, the Nuu-Chah-Nulth, contains no less than 28 different lineages—equivalent to more than 60 percent of the genetic diversity observed in large ethnic groups such as the Japanese or sub-Saharan Africans. R. H. Ward et al., “Extensive Mitochondrial Diversity within a Single Amerindian Tribe,” *Proceedings of the National Academy of Sciences of the United States of America* 88 (1991): 8720–24.

them than to populations that are located farther away: in other words, that genetic variation is distributed in a clinal fashion. These two simple findings flatly contradict the existence of discrete and stable human groupings as imagined by eugenicists. All of this also indicates that an open dialogue between genetics and social scientists about the significance of biological variation among humans is the best way to prevent the kind of biological reductionism that has been so pernicious in the past.

The field of modern genetics has opened an exciting new window into our past that we've just begun to explore. Buried within our genes lies a wealth of evidence about humanity's long evolution in Africa, our momentous exodus and advance over the rest of the planet, long-distance migration patterns, warfare, disease, commerce, conquest, marriage patterns, the emergence of social groups, kinship, and a myriad of other complicated interactions in which humans engage. Historians have long been interested in these matters. New genetic tools provide an independent line of evidence, enabling us to revisit these questions and obtain more satisfactory answers. This research also opens the possibility of a dialogue between historians and geneticists, a dialogue that is desirable and badly needed, as we bring to the table complementary strengths. Historians are in a unique position to formulate sound hypotheses that fully take advantage of our accumulated knowledge about the relationships between different human groups, thereby minimizing technically competent but ultimately wasteful research. For their part, geneticists will need to educate us about what hypotheses can be feasibly tested and about the validity and scope of the results. It is up to us, historians, to become involved if we want to have a say in how genetic tools are used to investigate the past and to make sure that these tools are deployed in ways that will ultimately benefit the peoples whose trajectories we study.