

“A Tool to Recover Past Histories”
Genealogy and Identity after the Genome

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The Occasional Papers of the School of Social Science are versions of talks given at the School's weekly Thursday Seminar. At these seminars, Members present work-in-progress and then take questions. There is often lively conversation and debate, some of which will be included with the papers. We have chosen papers we thought would be of interest to a broad audience. Our aim is to capture some part of the cross-disciplinary conversations that are the mark of the School's programs. While members are drawn from specific disciplines of the social sciences—anthropology, economics, sociology and political science—as well as history, philosophy, literature and law, the School encourages new approaches that arise from exposure to different forms of interpretation. The papers in this series differ widely in their topics, methods, and disciplines. Yet they concur in a broadly humanistic attempt to understand how, and under what conditions, the concepts that order experience in different cultures and societies are produced, and how they change.

“A Tool to Recover Past Histories”: Genealogy and Identity after the Genome

In January 1997, the journal *Nature* published “Y chromosomes of Jewish priests” (Skorecki, et al. 1997). The first of several Y-chromosome studies of Jewish male descent, this publication launched a new field of historical studies, one that attempted to reconstruct the origins, relatedness and migration patterns of Jewish communities on the basis of evidence of patrilineal origin and descent.

The 1997 *Nature* paper, however, did not study Jewish descent. Rather, it announced the results of a study of descendants of the male priestly line-known in Jewish tradition as the Cohanim. “According to biblical accounts,” the paper begins, “the Jewish priesthood was established about 3,300 years ago with the appointment of the first Israelite high priest. Designation of Jewish males to the male priesthood continues to this day, and is determined by strict patrilineal descent” (32). If priestly descent (the Cohen lineage) has been passed from father to son originating with the biblical figure of Aaron, Karl Skorecki reasoned, it should be possible to confirm the biblical account through genetic analysis. A nephrologist at the Ramban Medical Center in Haifa who started this project as a hobby, Skorecki contacted Michael Hammer at the University of Arizona because of Hammer’s expertise in using the Y-chromosome to trace the origins of specific population groups.

The Y-chromosome, like its mitochondrial DNA (mtDNA) counterpart, possesses specific characteristics conducive to this kind of a historical-genealogical quest. Both the Y-chromosome and mtDNA are passed down unilineally. One inherits one’s mtDNA from one’s mother; men inherit their Y-chromosome from their father. As explained by Mark Jobling, a leading scholar in Y-chromosome research: “Neither of these segments of DNA recombines at meiosis¹ and this means that they each contain a particularly simple record of their past” (449).² As a result, the biological principles of descent can now be pried apart: it is possible to track one’s lineage up the maternal line or paternal line. The two lines remain fully independent of one another and the “history” of each can radically diverge. Researchers produce genealogical trees that reify specific Y chromosome and mtDNA haplotypes³ and their descent lines. By deciphering the actual sequence of nucleotides,⁴ a relatively recent technological possibility in the wider field of genomics, geneticists track population histories by delineating lines of descent believed to be archived in the history of genetic polymorphisms (a variation or, mutation in the sequence of nucleotides among individuals) as they are passed down from mothers to their children and from fathers to their sons. Evidence of origins and kinship, in other words, are now understood as recorded in one’s genetic code.

Research projects seeking to track histories of Jewish origins and migrations are part and parcel of a larger field of genetic anthropology that has turned to the genome in order to reconstruct the history of human evolution and population expansions in general, and of contemporary population groups more specifically. In what follows, I make initial forays into analyzing this emergent domain of genetic research. First, I analyze the scientific publications, considering the evidentiary assumptions and logics through which such “population histories” are recreated. I then turn to speculate about the forms of social classification, self-

identification, normativity and politics that such research might enable or entail.

I. Priestly Descent

Given that “there is no procedure other than paternal descent by which male Jews are assigned to the priesthood” (Skorecki 1997:39), Karl Skorecki turned to the Y-chromosome in order to test the veracity of the oral tradition of priestly descent. Researchers collected DNA samples from 188 Israeli, British and North American Jewish men. They compared the Y-chromosomes of Jewish men who self-identified as Cohanim (n=68) with men who self-identified as either Levites (a second priestly line) or as “lay-Jews”—named in the study, in accordance with biblical tradition, “Israelites.” If the biblical tradition were historically accurate, the study proposed, “observable” differences should exist between the Y-chromosome haplotypes of “Jewish priests and their lay-counterparts.”

It was just such an observable difference that the 1997 *Nature* paper announced. Excluding Levites from the final analysis (they showed no pattern of patrilineal descent from a single ancestor), researchers compared Cohanim and Israelites. On the basis of a haplotype constructed out of polymorphisms at two genetic loci,⁵ Skorecki concluded that there is a distinct difference in the Y-chromosome haplotypes of priests versus that of lay Jews, thus “confirm[ing] a distinct paternal genealogy for Jewish priests.” To further explore these initial results, Skorecki designed a second, more expansive study. Joined by several colleagues at University College London and the School of Oriental and Asian Studies in London who would all emerge as central figures in this genealogical genetic quest, Thomas and Skorecki published a follow-up paper in *Nature* the following year. A study of 306 Jewish men and based upon a haplotype constructed out of 12 genetic loci,⁶ this second study produced similar results: “despite extensive diversity among Israelites,” they explain, “a single haplotype ([now named] *the Cohen Modal Haplotype*) is strikingly frequent in both Ashkenazi and Sephardi Cohanim” (Thomas et al. 138, emphasis added). The Cohen modal haplotype is present in approximately 50% of Cohanim (0.449 of the Ashkenazi Cohen sample, and 0.561 of the Sephardi Cohen sample). And “given the relative isolation of Ashkenazic and Sephardic communities over the past 500 years, the presence of the same modal haplotype in the Cohanim of both communities strongly suggests a common origin” (139).

Delineating “descent” is but one aspect of this project of historical reconstruction. The question of time is at least as important to the historical theses of the authors: “To the extent that patrilineal inheritance has been followed since some time around the Temple period (roughly 3,000-2,000 years before present), Y chromosomes of present day Cohanim...should derive from a common ancestral type no more recently than the Temple period” (138). In other words, the “coalescence time” (the time of origin) of the Cohen modal haplotype must date to before the “dispersion of the priesthood following the Temple’s destruction” (ibid).

Estimating coalescence time is a complex process in genetic anthropology. It depends on “knowing” the “normal” rate of mutations in the Y-chromosome, specifying what is referred to as the “molecular clock.” In addition, it requires an assumption about the proper span of “generation time”—should it be 15, 20, 25, or 30 years? Moreover, calculations regarding coalescence time generally assume that both of these rates—mutation rate and generation time—remain constant over time. In the 1998 *Nature* paper, researchers determined the number of generations to coalescence at 106 generations. Multiplying that number of generations by 25 (30) years (a standard choice of generation time in population genetics), they concluded that the Cohen modal haplotype dates to 2650 (3,180) years before present—an era that roughly corresponds to the chronology traditionally ascribed to the biblical

accounts of Aaron and the beginnings of his priestly line. As they note, “ignoring uncertainty in the mutation rate,” there is a 95% confidence interval that the coalescence time of the Cohen modal haplotype is 2,100-3,250 years before present, “sometime during or shortly before the Temple period in Jewish history” (139).⁷

The conclusions of the 1998 paper went much farther than that, however. Might the Cohen modal haplotype be indicative of more than just priestly descent?

[T]he identification of haplotypes with restricted distributions may provide ‘signatures’ of ancient connections *that have been partially obscured by subsequent mixing with other populations*. Gene flow⁸ from the Cohanim could account for the presence of the Cohen modal haplotype in both Ashkenazi and Sephardi Israelites, or it could be a signature of the ancient Hebrew population. The Cohen modal haplotype *may* therefore be useful for testing hypotheses regarding the relationship between specific contemporary communities and the ancient Hebrew population (139, emphasis added).

While not definitive, the Cohen modal haplotype—found in approximately 10 percent of Ashkenazi and Sephardi “Israelites” (0.132, 0.098 respectively; n=9 and 5 respectively [Thomas et al., Supplementary Information])—may well indicate ancient Hebrew, and not just priestly, origins. With the identification of a possible indicator of common (Jewish) ancestry, the opportunity to use genetic information to study the patrilineal origins and descent of contemporary Jewish communities was opened up. Further examinations of Jewish origins and histories would rely, at least initially, on the Cohen modal haplotype-determining its geographic origin, using it as the normative measure of ancient Hebrew descent. In short, researchers turned to the Cohen modal haplotype and, increasingly, to a search for other Y-chromosome types shared or, “prevalent” in contemporary Jewish populations, in order to evaluate the historical relatedness of contemporary Jewish communities, the veracity of the history of the Jewish people as a history of diaspora borne out of exile from ancient Palestine, and to test the claims of “potential” Jews, groups of Jews who believe themselves to be descendants of Hebrew ancestors.

II. In search of population histories

The turn to DNA to pursue a “curiosity about origins” is not new, as Mark Jobling remarks. DNA “has been passed down to us from our ancestors, accumulating mutations along the way.” As such, “the DNA of modern humans are. . .different from each other, and these differences, or polymorphisms, provide a record of our relatedness and genetic history” (Jobling 1995:449).

Nevertheless, the use of Y-chromosome analysis is quite new. Because of its particular character-that the Y-chromosome can be used to trace paternal lineages and, thus, that it is potentially useful for illuminating one aspect of both the origins of modern humans as well as subsequent population movements-the Y chromosome was long considered potentially valuable to genetic anthropological research. And yet, as Mark Jobling wrote in a paper published in 1994, “The human Y chromosome is poor in conventional DNA polymorphisms,” hindering “studies of the paternal lineage”(107). In other words, for the Y chromosome to be useful in understanding “an aspect” of either the origins of anatomically modern humans or, more specifically, in illuminating the genetic history of particular populations (Mathias 1994:115), sufficient genetic diversity must be present in human Y-chromosomes-and it must be sought, categorized, and mapped into phylogenetic trees.

Genetic anthropology seeks to understand the history of human migrations and population-specific genealogies and relationships by analyzing "diversity" at the molecular level. Using genetic data to make inferences about population histories involves starting with the principle that, under certain circumstances or assumptions, "genetic similarity reflects common ancestry" (Relethford 68). But genetic similarity—this is not a quest for genetic matches—is derived from an analysis of polymorphisms, of genetic differences. As explained by Relethford, there is a paradox at the heart of genetics and evolutionary theory. Take the case of the use of mtDNA in the search for "Eve," the female (genetic) ancestor of all modern humans. If we all trace back to a single ancestor, must not our DNA—in this instance, our mtDNA—be identical? If so, how could one use mtDNA to untangle the different genetic relationships or degrees of relatedness among individuals—or among groups? Descent from a common ancestor, however, does not imply identity. Rather, it implies a presumably decipherable matrix of genealogical relationships "visible" in genetic polymorphisms. According to classical evolutionary theory, as organisms reproduce mutations are randomly generated—some deleterious, some positive, most neutral. Researchers decipher (the chain of) those mutations in order to reconstruct genealogies, using genetic differences among pairs of individuals to evaluate their relatedness: "the greater the length of time separating two individuals, the more mutations will accumulate, and the greater the genetic difference between them" (72). At its simplest, that is the underlying assumption of phylogenetic analysis. Genetic distance is a measure of the relationship of one population to another: the more genetically similar, the more recently two populations had a common ancestor; the more genetically dissimilar, the more remote the common ancestor. And it is by identifying specific polymorphisms, on the basis of which distinct (compound) haplotypes are constructed, that one individual or group of individuals (population) is compared to another: for example, what is the relative frequency of the Cohen modal haplotype in Jewish priests versus lay Jews? What is the relative frequency of the Cohen modal haplotype in Jewish versus non-Jewish populations? What is the origin of the Cohen modal haplotype? In other words, in what other populations does one find either the same haplotype or a haplotype closely related to it? And what might all this information tell us about the geographic origins of the contemporary Jewish "diaspora?"

"Diversity," of course, has long played a central role in biological thought.⁹ In the late 19th century, Darwin recast both the meaning and the significance of diversity for an understanding of the natural world. As Evelyn Fox Keller put it: "The living world became a world in time, and both its occupants and its relational structure were reconfigured as products of its evolutionary history" (7). Darwin's evolutionary theory offered his readers a mechanism for the origin and transformation of species in which natural selection acted upon individual variation. This shift to individual variation emerged as central to biological and anthropological projects to come: race, for example, would come to be deconstructed on the basis of arguments that most genetic variation occurred at the level of individuals and not between so-called racial groups—differences that are, moreover, *biologically* insignificant.

But if genetic diversity only accounts for a tiny percentage of the diversity among human individuals, that diversity has nevertheless long been the stuff of population genetics and, more recently, of a growing field of genetic anthropology (population genetics at the molecular level). It is through a focus on genetic diversity at the level of population groups—diversity "observed" on the genomes of individuals classified according to ethnicity or "geographic origins"—that new kinds of questions about human history and population-specific origins and migrations can be asked. In short, for the field of genetic anthropology and its efforts at evolutionary and historical reconstruction, the analytic importance of

group-based “genetic diversity” far outstrips its statistical or, biological significance. Group-level genetic difference has become the stuff of this scientific quest.

For historical quests such as the Jewish Y-chromosome studies, “diversity” means something quite different than it did to Darwin. Not only does the term index differences among groups rather than individuals: in addition, its analytic significance has shifted. Diversity is no longer scientifically important because of the insights it lends into understanding a life-world *in time* (although one can, theoretically, address issues of broader evolutionary interest from the perspective of specific historical studies). Instead, mapping genetic diversity provides a window into a history of the truly *longue durée*. The quest for diversity, in other words, is actually a search for genetic signs that have endured through time: haplotypes with restricted distributions may be “signatures’ of ancient connections [between specific populations] that have been partially obscured by subsequent mixing with other populations” (Thomas and Skorecki 1998).

A tension between stability and change, of course, stands at the very heart of modern biological theory. Darwin’s concern with the mechanisms of transformation left a “fundamental mystery” in biological thought: “If change is the essence of life, how are we to account for the remarkable stability with which, in each generation, organisms develop and grow true to the type of their particular species, and with a certainty that endures over the lifetime of that species” (Fox Keller 12)? How can we account for *stability*, in other words? Twentieth-century biology, Fox Keller argues, focused on that task: it sought “to account for the persistence of individual traits through the genes” (13). Genetic anthropology, in turn, is beholden to the research efforts of geneticists who have sought to explain the mechanisms of stability, and not just of change. As a field, it inhabits the tension between change and stability in human biology. For genealogical descent to be traceable, variation must be detectable on the genome. For phylogenetic trees to be “clean,” for origins to be *interpretable*, however, those mutations must be rare; they must occur *only once* over the historical time-spans in which researchers are interested. If such mutations occurred more frequently, there would be no way of determining whether two populations exhibiting a similar mutation are genealogically related or whether, as a result of the repeated occurrence of random genetic mutational events, they merely *appear to be*. In fact, this emerges as a problem in mtDNA phylogenetic analysis once researchers came to realize that mtDNA has a relatively rapid mutation rate: the same mutation can occur more than once over relatively short time-spans. In short, phylogenetic analysis requires “unique event polymorphisms” (UEPs): polymorphisms which are identifiable, singular events, and which can be used to root phylogenetic trees and to delineate their most fundamental branches—“deep splits in Y-chromosome genealogy” (Nebel et al. 630-1). More commonly occurring polymorphisms-mutations that occur more than once over relatively short time-spans, such as microsatellites on the Y chromosome-can, against the background of those UEPs, be used to delineate additional population splittings that reflect “more recent genealogical events” (ibid). Microsatellites, in other words, are used to sketch a more detailed history of the migrations and branchings of specific human population or subpopulation groups.

However, this remarkable stability and, presumably, a clear understanding of the normal rate of change (the “molecular clock”), is not enough to enable the latest research into Jewish descent. This work in genetic anthropology also focuses on the *non-coding* regions of the human genome: on genetic loci that have no apparent biological function (although there is increasing debate about whether this characterization is true). Genealogical questions are being assessed on the evidentiary terrain of so-called ‘junk’-DNA. As Karl Skorecki explained to an audience at the American Museum of Natural History in June

2001,¹⁰ researchers are looking at “a set of markers on the Y-chromosome. . .They are not in genes. . .The Y-chromosome doesn’t have many genes¹¹ . . .It is very useful in terms of the fact that it doesn’t recombine and has these *neutral markers* which don’t really encode features or characteristics; however, it does serve as a tool in phylogeny,” a “tool to uncover past histories.”

Vivian Moses, the director of the Center for Genetic Anthropology at University College London, explained the importance of junk-DNA at more length to an audience at the nineteenth annual convention of the Jewish Genealogical Society:¹² “DNA is a coded message, written in [four] chemical letters . . .these 4 letters are written in groups of three. . .Buried in here is a message, a real message that you can really understand.” Those “real messages,” however, constitute only about 2% of DNA. The rest, “the parts without the message,” is called “junk.” Changes in “real message” DNA can have “deleterious consequences,” and so are often evolutionarily selected against. In other words, they don’t reliably survive from one generation to the next. However, he said, if you change a letter in the junk there is no consequence:

The point about that change in the junk is that it is inherited by the progeny because. . .it doesn’t matter whether you carry it or not. It’s junk. . .So. . .if somebody once upon a time, for some reason acquired such a change in their particular DNA, particularly if it is in the Y-chromosome of the male, then all the successive males descended from that chap will carry this particular change. . .So, for ever and a day, the person who carries that change will be marked. His progeny will be marked.

It is those enduring marks that this field of genetic anthropology seeks to find, ones that *might* indicate common (Hebrew) origins, ones that might tell us something about the religious and kinship practices of Jewish communities as they migrated and lived in the “diaspora.” Let us now turn back to the scientific studies of Jewish descent in order to further explore the workings of this field of historical research—and its implications for the future.

III. Historical Genealogy: The Search For an Enduring Trace

Following upon the studies of priestly descent, various scholars launched investigations into the origins of historical and geographic origins of contemporary Jews. If today’s Jews are descendants of ancient Hebrew and Jewish communities who lived in and then fled ancient Palestine, the CMH and other Y-chromosomes types shared by Jewish men must be closely related to other “Middle Eastern” genetic polymorphisms. Contemporary Jewish populations, in other words, must be (phylo)genetically related to contemporary Arab populations. Given the biblical stories of Israelite and Jewish origins, they must, more specifically, be related to Arabs of Palestine in particular, and of the Levant more broadly.

Michael Hammer et al. published the first study comparing Jewish and “Middle Eastern non-Jewish” populations on the basis of Y-chromosome haplotypes. As with studies to follow, Hammer’s paper begins with an historical account:

Jewish religion and culture can be traced back to Semitic tribes that lived in the Middle East approximately 4,000 years ago. The Babylonian exile in 586 B.C. marked the beginning of major dispersals of Jewish populations from the Middle East and the development of various Jewish communities outside of present-day Israel (2000).

Due to “numerous migrations of Jewish populations” a complex set of “genetic relationships” now exists among “the Jewish populations and their non-Jewish neighbors” (2000). As with previous genetic studies, Hammer’s goal is to unravel “the numerous evolutionary factors”—common ancestry, genetic drift, natural selection, admixture—that have “come into play during the Diaspora:” “Given the complex history of migration, can Jews be traced to a single Middle Eastern ancestry, or are present-day Jewish communities more closely related to non-Jewish populations from the same geographic area?” That is the question that frames this research.

To date, genetic studies of Jewish populations had been unable to adequately resolve that question, as Hammer explains. Some studies concluded that Jewish communities are more genetically similar to one another than to their host populations; others demonstrated “substantial non-Jewish admixture” (2000). *Depending on the locus investigated*, the degree (or, mathematical calculation) of genetic similarity among Jews shifts: “This observation raises the possibility that variation associated with a given locus *has been influenced by natural selection*” (2000). More recent genetic-genealogical studies, such as work on the non-recombining Y (NRY), have aimed to “circumvent some of the complications associated with selection” (2000). According to Hammer, in the current study “the DNA results. . .are less likely to be *biased* by selective effects” (2000, emphasis added).

What precisely are the “complications” that such work is trying to circumvent? Why does selection constitute bias? To propose an answer to those questions we must take a detour into an earlier domain of biological practice and consider the way in which genetic anthropology configures the relationship between culture and biology in comparison to the relationship posited in a race-science of old.

In scholarly and popular conceptualizations of race, the relationship of culture to biology has always been complex. Race is a category of social classification that relies on the presumption of biological difference. As Anthony Appiah and Henry Louis Gates Jr. have argued, “racial identities, like those along the dimensions of gender and sexuality, are defined in a peculiarly corporeal way”(3). And the ascription of such corporeal—or biological—difference has been, in practice, inextricably enmeshed with cataloguing and identifying cultural distinctions.

At the turn of the twentieth century each race was understood to possess particular mental and moral characteristics. There were no clear distinctions between cultural and physical elements, between social and biological heredity (see, for example, Stocking 1968). Race theory was concerned with the “inherited capacity” of human groups (Barkan 187). The size of one’s brain, the shape of one’s head, for example, all those measurements for which physical anthropologists became famous, did far more than classify groups: they *explained* racial-cultural distinctions. In fact, the study of the *shapes* of plants and animals was cardinal to nineteenth century biology, as Richard Lewontin has illustrated. Shape and biological function were understood to be inseparable: “The nineteenth century sciences of phrenology and criminal anthropology,” for example, “were based in the belief that character and cognitive function would leave their mark in the shape of skulls and noses” (82). During the first two decades of the twentieth century the focus of biological work began to turn inwards, all the while continuing the logic of the racial quest. Geneticists sought to isolate single genes (in true Mendelian fashion) that were understood as coded for specific characteristics—height, color, intelligence (Barkan 5). As articulated in the science of eugenics, there was “a direct translation between superior genes and superior culture” (Marks 356). Nature trumped nurture: the idea of genetically encoded differences formed the foundation of race science as it sought to distinguish human groups and to place them

along an evolutionary grid.

The analysis of non-coding regions of the human genome, so-called junk-DNA, does a different kind of work, one that re-imagines the relationship between culture and biology and so generates a different kind of history to be unraveled on the terrain of "biological" evidence.

Today, researchers in genetic anthropology struggle to create a firewall between the realms of culture (which extends to questions about ability or behavior) and nature. They are not interested in external form or phenotypic effects. Instead, they insist that their work is a matter of tracing *descent*; this is nothing more than a mark and it has no bearing on the question of inherited characteristics. *This is not race science*, in other words. Genetic anthropology is a quest for "inheritance" stripped of the question of "capacity"—an inheritance, moreover, no longer visible on the body itself. These are haplotypes "signifying nothing" in the biological domain, to borrow Kath Weston's term. These are neutral markers; this is junk-DNA.

Much has been written about the significance of the shift in biology from a science that conceived of organisms as organic and integrated systems to one that imagines life as a code. As Donna Haraway has written: "The organism has been translated into a problem of genetic coding and read-out. Biotechnology, a writing technology, informs research broadly. In a sense, organisms have ceased to exist as objects of knowledge, giving way to biotic components, i.e., special kinds of information processing devices" (1997:164). Yet better than 90% of that genome is currently understood to be a code that, in effect, doesn't code for any biological function at all. It is a code that has no meaning that can be either read or, in turn, re-written, through biotechnological interventions.

What happens to our understanding of that code when one shifts research domains? In particular, what happens to the analytic significance of the genome's non-coding regions in the context of genetic-genealogical quests? For researchers in genetic anthropology to refer to these markers as either "neutral" or as "junk" is certainly a misnomer. But it is one that is perhaps crucial to sustaining the *difference* between contemporary genetic anthropological inquiries and a race-science of old. *Vis-à-vis* the functioning of organisms, *vis-à-vis* the mechanisms of evolution, *vis-à-vis* phenotypic effects, these so-called neutral markers have, apparently, no genetic function, no biological meaning. Most mutations are, after all, *biologically* neutral. Junk-DNA is the residue of random evolutionary events. To borrow the terms through which François Jacob understands the dual nature of a (computer) program, neutral markers are carriers of "memory" (the traits of the parents, now purely *genotypic* traits) minus the capacity for "design" (the program's ability to control the formation of the organism and to determine its specific traits). As neutral markers, they cannot generate cultural, behavioral, or for that matter, truly biological differences between human groups. This is not—quite—"nature."

Nevertheless, junk-DNA is considered deeply meaningful in an *historical* register. This junk may not code for disease or behavior or phenotype. But some of it does, apparently, "code" for ancestry, at least from the interpretive perspective of researchers seeking to establish points of geographic origin and specific lines of descent. And these now not so neutral markers, inscribed within the body, configure a specific relationship between biology and culture, one quite distinct from the biology-culture nexus that stood at the heart of race science. I turn to the opening paragraph of Thomas and Skorecki's 1998 *Nature* article:

According to Jewish tradition, following the Exodus from Egypt. . . male descendants of Aaron were selected to serve as Priests (Cohanim). *To the*

extent that patrilineal inheritance has been followed since sometime around the Temple period (roughly 3,000-2,000 years before present), Y chromosomes of present-day Cohanim. . . should not only be distinguishable from those of other Jews, but—given the dispersion of the priesthood following the Temple’s destruction—they should derive from a common ancestral type no more recently than the temple period. (138, emphasis added)

One can *derive behavior from DNA evidence*, in other words. If the tradition of passing the priesthood from father to son has been adhered to in practice then, in the words of Vivian Moses, “from the Y chromosome point of view, the descendants of Aaron form a progressively separate group through the ages.” This “biology” is the *consequence* of a particular set cultural practices. The causal relationship is inverted: causal mechanisms move from culture to biology. In turn, one derives the truth of culture—of oral tradition, of religious or kinship practices—from biological data. Those data, as natural-cultural artifacts, comprise a genealogical code that bears witness to one’s geographic origins and cultural past.

The problem with selection—the “bias” introduced by coding regions of the human genome—thus, has to do with the problem of biology, strictly understood. In focusing on junk-DNA one controls for the biological dynamic of natural selection whereby groups of self-identified Cohanim in different regions of the world, for example, become progressively more genetically different from one another and more similar to the populations with which they reside, not just because of “admixture” (which, along the paternal axis, is what is being investigated), but because of selective advantage. Certain genotypes (in the coding regions of DNA) are more fitted to certain environments and, thus, survive and, moreover, proliferate. Take, for example, the phenotypic differences central to race-science at the turn of the 20th century. Luca Cavalli-Sforza (a leader in the field of population genetics) has argued that racism is “a fallacy” first, because although genetics is “instrumental in shaping us,” so too are “the cultural, social and physical environments in which we live.” Second, the genetic differences between populations, or “so-called ‘races,’” are small. They are “*superficial*,” “attributable mostly to responses to the different climates in which we live” (Cavalli-Sforza’s example here is skin pigmentation, see Cavalli-Sforza viii, emphasis added). Contrary to racial theories of old that understood phenotypic differences as important, Cavalli-Sforza understands these distinctions to be biologically insignificant and, moreover, as adaptive. Minus the influence of environment, they don’t tell us anything truly important about the differences between population groups.

But consider how the language of admixture and superficiality plays out in the following exchange between Karl Skorecki and a member of the audience during the session at the American Museum of Natural History in New York. A woman commented that she was very glad that “genetics has put to rest the question of race which is clearly a social construct.” She then asked: “How can you claim that Jewish communities are really endogamous and don’t intermarry given that when you go to different parts of the world, Jewish population groups resemble the population groups with which they reside?” Skorecki responded:

That is an excellent question. . . If there is common ancestry in the Jewish Diaspora from India to Eastern Europe to Northern Africa, what explains the phenotypic differences and the closeness in those appearances to the local, and not to Jewish communities. The answer? Recombination and admixture. This work that has enabled tracing back common ancestry has been based either on the Y chromosome or on mitochondrial DNA. Those

are two segments of the genome that don't recombine...[They] don't swap genetic material with the other parental contribution. Therefore they maintain a *fidelity, a trace that goes back in history*, and therefore they are less affected by admixture. . . But if you study admixture and its effects on phenotypes, a little bit of admixture goes a long way in a few generations. It doesn't take much admixture to have a change of phenotypic appearance and that also speaks to the issue of how superficial those phenotypic differences are. *Even though it looks striking to the eye, it doesn't reflect something very deep and one can see through it by using non-recombining regions of the genome* (emphasis added).

In other words, the goal of these genealogical-genetic quests is, precisely, to "see through" all the genetic noise—the noise of recombination, of admixture, of genetic drift and of natural selection—in order to uncover a truth about origins. In search of "ancestry," genetic markers that would necessarily render Jewish populations genetically *more similar* to "the local populations" with whom they have long lived are sidelined in favor of the search for an enduring "trace" believed to embody a history of the truly *longue durée*. And that historical *longue durée* is a distinctly internal matter. It is a genomic sign carried within the body, through time; it remains decipherable regardless of what is added from without via selection, via admixture, or, for that matter, via drift.

Distinguishing between the "internal" and the "external"—between the organism and the environment—was cardinal to Darwinian thought. While Lamarck insisted on the inheritance of acquired characteristics, Darwin "created a dramatic rupture in this intellectual tradition by alienating the inside from the outside, by making an absolute separation between the internal processes that generate the organism and the external processes, the environment, in which the organism must operate" (Lewontin 42). That "internal process" comes to be understood, in the 20th century, as gene mutation and recombination: random biological processes, internal to the organism that, in turn, produce organisms more or less "fit" for the existing environments in which they live. Thus, built into the logic of genetics is a distinction between internal and external, between the organism and environment. In addition, there is a commitment to the autonomy of the gene itself. Genes came to be understood as "particulate, self-replicating elements" that determine the "properties of the organism" (Fox Keller 17). In the words of E. B. Wilson, "As far as inheritance is concerned the body is merely the carrier of the germ-cells, which are held in trust for coming generations" (quoted in Fox Keller 17). Not only would these units—initially referred to as the "germ plasm," eventually as genes—serve as the "fundamental units of biological explanation" (18) or as independent units determining the outcome of biological development. They would, in addition, be conceptualized as fundamentally stable. Despite important shifts in understandings or definitions, as Evelyn Fox Keller explains, certain assumptions that underlay late-19th century conceptions of the germ plasm were carried over into conceptualizations of the gene: "whatever they were made of. . .the capacity for faithful transmission from generation to generation remained built into the very notion" (19). In effect, the post-Darwinian concern to understand the biological mechanisms of "intergenerational stability" structured the very concept of the gene and its precursors: "The problem of stability was answered by assuming the existence of an inherently stable, potentially immortal, unit that could be transferred intact through the generations" (Fox Keller 14).

What happens when this conception of the gene—as code, as autonomous and self-generating, as stable, immortal, intact, and internal—gets carried over into historical domains of research? From the perspective of genetic anthropologists, the turn to nucleotide

sequences as a way of investigating history or, more accurately, historical genealogy involves merely the addition of a novel domain of evidence to answer long-standing questions about population origins and migrations. Nevertheless, I want to consider what kinds of assumptions are carried in tow. For now, I will do so by switching fields of analysis.¹³ How does this conceptualization of the gene, and through it, of history, origins, and ancestry, intersect with contemporary forms of politics, in particular, with the politics of identity, of recognition and with conceptualizations of authenticity?

IV. Genealogy, Identity and Recognition

Following a lecture given by Vivian Moses at the 19th annual conference of the International Jewish Genealogical Society, in which he spoke about the Ancestry of European Jews project being run out of UCL, a woman in the audience said:

I would just like to make a comment about the question of are we genetically Jewish. We get half of our genes from each camp. So that means we have potentially one-fourth from each grandparent, one-eighth from each great grandparent, one-sixteenth, you understand that? So once you introduce a non-Jewish ancestor, some of that DNA we inherit. And, in order to figure out if we are really Jewish, we are all probably partially Jewish, you know depending on how clear and precise our ancestry is.

Vivian Moses replied: “We are not partially Jewish. Those of us who are Jews are all Jewish, but our ancestors may not have been Jewish.” Jewishness, he insisted, is a matter of self-designation.

The relationship between “ancestry” and the question of who is a Jew, however, is far more complex than Moses’ reply suggests. What is the relationship between genealogy and Jewishness, and for whom and with what consequences might that relationship be mediated on the evidentiary terrain of DNA?

In “Diaspora: Generation and the Ground of Jewish Identity,” Daniel and Jonathan Boyarin argue that group identity (a process of self-construction) can be either “a product of a common genealogical origin” or, it can be generated with reference to “a common geographical origin” (1995:305). (Both of those traditions exist within Judaism, they argue, and stand in tension with one another.) While the latter has “a generally positive ring” in contemporary social theory, the former tends to be regarded pejoratively. The Boyarins argue that the more obvious reason for the contemporary denigration of genealogy as a grounds for identity is the history of modern racism (305-6), but they less predictably insist there is also a second source: a disdain for genealogy that characterizes the Letters of Paul which “lie at the fountainhead of Christianity” (306). In brief, the Pauline letters substituted “an allegorical genealogy for a literal one”: through baptism, one would be born anew, into the family of Christ. Theologically then “the physical connection of common descent from Abraham and the embodied practices with which that genealogy is marked off as differences are rejected in favor of a connection between people based on individual re-creation and entry *de novo* into a community of common belief” (307). But “descent from a common ancestor” is essential to the construction of a Jewish identity, they argue, a “myth” of descent that operates “on the semantic field of the body” and not “on the semantic field of status through land” (329).

I want to think about how generation, genealogy, identity, and community are (re)configured within the logic of genetic anthropology. On the one hand, many of these researchers work to disentangle those terms. They insist that genealogy or the generational

connection demonstrable via the genome adjudicates neither the question of whether or not one is a Cohen nor, more broadly, the question of whether or not an individual or a community is Jewish. As was emphasized many times following the “discovery” of the Cohen-modal haplotype, the presence or absence of the haplotype on an individual’s Y-chromosome has no bearing on whether or not a particular man is a Cohen, although many a self-identified Cohen has contacted these researchers in order to take the test.¹⁴ As argued by Vivian Moses, “[t]here is a significantly greater frequency of this genetic pattern in the Cohanim than there is among the others. This is not diagnostic for being Cohen. People keep asking us, let me give you a bit of my DNA and you tell me whether I am a Cohen. It doesn’t work like that. There isn’t a Cohen gene. It is a statistical phenomenon that among the Cohanim you find this pattern. Whether it is indicative of Cohenism is another matter. If someone has this pattern, but doesn’t think he’s a Cohen does it mean he really is? That is a thing one can debate about. . .” This discovery confirms the veracity of an oral tradition, *in general*. As a *statistical* fact, it characterizes an aggregate of individuals—a population—identified as members of the priestly lineage. But the Cohen-modal haplotype is not found on the Y-chromosome of every self-identified Cohen. (In the two research samples, the CMH was identified in approximately 50% of Cohen men, with variations in percentage between self-identified Ashkenazi versus Sephardi Cohanim.) Nor is the Cohen-modal haplotype not found on the Y-chromosomes of Jewish men who do not believe themselves to be Cohanim or, on the Y-chromosomes of non-Jewish men.¹⁵ The Cohen-modal haplotype, in other words, cannot be used to *test* whether or not a particular man is a Cohen. Genomic facts of generational connection and Halachic traditions of priestly status remain, and should remain, distinct, or so insist the researchers.¹⁶

But what might such evidence say about more marginalized persons or *groups*? Specifically, what might genetic anthropology have to say about the status of so-called “would-be Jews”? (Kleiman)

In Search of Lost Tribes:

Tudor Parfitt, an anthropologist at the School of Oriental and African Studies in London, decided that he might be able to use the results of the Cohanim study in order to solve what he considered the “riddle” of the Lemba. A group in southern Africa, the Lemba have long claimed to be descendants of Jewish ancestors who migrated out of Judea millennia ago. As Parfitt recounts his foray into this research, he found Lemba claims to Jewish descent hard to believe. Upon the publication of results from the initial Cohen study, Parfitt reasoned that the Cohen modal haplotype could be used to assess the Lemba’s historical claim. Parfitt and his colleagues decided that if the CMH could be found in a similar percentage of the Lemba as it was in the *lay* Jewish population (or among “Israelites”) (between 9 and 10%), the Lemba’s assertion of Jewish ancestry might be plausible. In other words, adopting the Cohen-modal haplotype as an indicator of ancient Hebrew origins, that genetic marker could be used to evaluate the Lemba’s claim to Jewish ancestry that is not recognized as credible by the mainstay of the world’s Jewish community (see Parfitt; NOVA 2000). This normative genetic measure, in other words, could be used to experimentally test other populations.

In cooperation with Neil Bradman, a biologist at University College London, Parfitt and his colleagues set off to southern Africa, collected DNA samples and concluded that the distinctive Cohen marker appears in the Lemba with same frequency that it occurs in the general Jewish population (in just under 1 out of every 10 men). Moreover, that Y-chromo-

some type was found with a far higher frequency (50%) in one particular clan, the Buba (n=13 of whom 7 carried the CMH). The Cohen-modal haplotype shows up in approximately 10% of the general Jewish population, but in approximately 50% of the self-identified priests. The Buba clan, he speculated, are perhaps the Cohanim of the Lemba tribe. (NOVA 2000; see also Parfitt; for subsequent research on the Lemba, see Thomas and Parfitt et al.).¹⁷

Does the presence of the Cohen-modal-haplotype in the Lemba population, however, make the Lemba Jewish, even if one does accept the CMH as the modal haplotype of an ancient Hebrew population? “Being Jewish is a spiritual, metaphysical state and DNA is a physical characteristic, like nose size,” Karl Skorecki has argued, invoking an earlier race science in his choice of phenotypic traits. “But,” he continued, “we wouldn’t dare go around saying we’re going to determine who is Jewish by the length of their nose. Similarly we’re not going to determine who is Jewish by the sequence of their DNA” (quoted in Epstein). The discovery of this genetic trace of Jewish ancestry does not render the Lemba (recognized) Jews. As argued by Shaye Cohen, a professor of Jewish studies at Brown University, “As a historian, I find the whole enterprise rather silly. Are the Lemba descendants of the lost tribes who disappeared from the face of the earth? The answer, of course, is no” (quoted in Greenberg). They might well be, however, “a kind of modern lost tribe”—“a group of people unbeknownst to us and to themselves carrying Jewish genetic material.” Cohen explains: the Lemba will “be accepted as Jews ‘if the Jewish people want them to become Jews. And that’s the way it’s been since Moses and Aaron.”

Clearly, Parfitt and Bradman’s study did not simply transform the Lemba community into (recognized) Jews either in the eyes of Lemba (for whom it might have “confirmed” a long-standing belief in their own Jewish origins, however the meaning of that ancestry is configured)¹⁸ or in the eyes of “mainstream” Jewish individuals or groups whose own claims to being Jewish are unlikely to be called into question regardless of the results of genetic anthropological work. Nevertheless, this research has far-reaching implications for the question of recognition. On the basis of what criteria might “the Jewish people want them to become Jews,” to return to Shaye Cohen’s words?

In contrast to the paradigm developed by Daniel and Jonathan Boyarin, this work in genetic anthropology mediates genealogy and territorialism on bodily terrain. As was true of race-science, a geographic grammar undergirds the classificatory distinctions between social groups: a shared genetic marker is a sign of a shared geographic origin and it is that geographic origin that delimits distinguishable population groups. As John Relethford has argued, in these quests for population origins and descent lines, “geography” is to genetic anthropology what “species” is to evolutionary biology. Within the workings of genetic anthropological research into Jewish origins, Y-chromosome haplotypes are emerging, to borrow Daniel and Jonathan Boyarin’s characterization of circumcision, as a “diacritic that symbolizes the biological status of Jewishness,” a biological status that marks *both* “a biological difference between Jews [or, more accurately, those of Jewish ancestry] and others” as well as “the biological connection that filiation provides.” Genealogy, in this configuration, is neither mythical nor rhetorical. It is a bodily *mark*—physical and literal, scientifically knowable and visible, now with the help of biotechnological instruments and techniques. And given a long history of the centrality of genealogy to Jewish identity, while that empirical terrain does not produce, in any straightforward manner, the truth of Lemba Jewishness, it does make possible a *reasonable debate* about whether or not they are, about whether or not ancestry and identity are distinct (particularly when we are talking about patrilineal ancestry and Jewishness), and about whether or not the Lemba can or should be recognized as Jews.

During the discussion that followed the screening of the NOVA video, "The Lost Tribes of Israel," a woman in the audience, clearly a bit frustrated, asked: "Given the discussion, and the distinction between ancestry and identity being made, I'm still not clear as to whether or not the Lemba really are Jewish, and who gets the final word?" Tudor Parfitt responded:

That's the point. Who decides. Does Tudor Parfitt decide. In which case, if they say they are Jewish, and *they are practicing some kind of religion that looks like Judaism*, and everyone around them says, ah, yes, these are the black Jews, in that sense yes, they are Jewish. Whether the DNA evidence changes their status, I don't think it does. Particularly, all that it shows is that probably at some time in the past, Jews went to Central Africa. And we didn't know that and that is a remarkable finding. . . But if you were to take this film or our discussion or any number of papers that have been written on the subject to the chief Rabbinate in Israel and ask them to decide on the basis of this whether the Lemba are Jewish or not. . . the answer would be no. Because none of these features has got anything to do with the Halachic definition of what a Jew is [which of course is defined matrilineally] (emphasis added).

It was precisely on the grounds of a particular set of religious practices that another member of the audience objected to this whole discussion of whether or not Lemba are Jews and to Tudor Parfitt's willingness to accept the Lemba as Jews. "Another feature of what determines Jewishness is belief in the bible and the use of certain prayers," and neither is demonstrated by the Lemba, he said. In other words, Jewishness requires the demonstration of a normative set of practices and beliefs. Parfitt responded: "The fact is that the Lemba do have a whole range of practices and prayers which, while not being very similar to those used by mainstream Judaism, nevertheless do appear to be Jewish in some way. They look rather like Old Testament practice, and they certainly seem to predate the coming of the Christian missionaries."

But the question of recognizable—or normative—religious belief and practice may well be more convoluted than this interchange suggests. After all, in the wake of genetic evidence of Jewish ancestry, there have been efforts to "integrate" the Lemba—who are, for the most part—self-identified practicing Christians—into the Jewish community. Kulanu,¹⁹ an American Jewish group that specializes in the discovery and integration of "lost tribes," has funded various education programs in Lemba communities. As explained by their representative in South Africa, "Kulanu has been very supportive of the youth program because the Lemba have not had much exposure to Judaism. . . This will provide a means for them to experience the Jewish way."

Recognizing the Lemba's Jewishness was made possible (even if in its most sustained form by a group described to me by the director of public outreach for one New York-based Jewish cultural institution as "a bit kooky") by the results of Parfitt and Bradman's genetic study. It was only in light of the discovery of the Cohen-modal haplotype on the Y-chromosomes of a certain percentage of Lemba men that white South African Jewish groups as well as Kulanu have initiated relationships with Lemba communities *as fellow Jews*. Culture and descent are inextricably intertwined (see Benn Michaels): suddenly Judaism becomes their religion and Jewishness becomes *their* culture by virtue of *their* genealogical descent, even if they don't, at present, engage in the doing of "Jewish things."²⁰ In turn, now recognizable Jews by virtue of their descent, *their* culture (and *their* religion) is something

that they need to be taught. Identity, in this formulation, is not only something that people or groups “have;” it can be “discovered” by (social) scientists and it can be “*mistaken*” (Brubaker and Cooper 10, emphasis added). And it is in the wake of scientific research that demonstrates that Lemba ancestry claims are not simply a “mistake” that the press²¹ has reported on the “discovery” of a “lost Tribe” in, as one headline put it, “unlikely places,” that other Jewish groups and individuals have become willing to discuss the Lemba’s possible Jewishness, and moreover, in the case of Kulanu and certain associations of South African Jews, that some Jewish groups and communities have been willing to champion their “integration.”

If one has any doubt about the power of DNA in relation to the question of recognition entertain, for one moment, the counter-factual: what if Lemba men had not tested positive for the Cohen-modal-haplotype-the genetic standard against which Jewish ancestry was being measured? Their claim to Jewish descent would have remained unintelligible and/or highly unlikely, as Parfitt initially suspected.

It was precisely a fear of the counter-factual that made a group of Israeli researchers wary of publicizing some of their results. Ethiopian Jews are outliers on the Jewish genetic-genealogical map. As explained in an article in *Ha’aretz*, researchers feared that their work could be used in a racist or political manner (and this vis-à-vis a community whose integration into Israeli society has been problematic at best): “The simple reason: Ethiopian Jews were not similar from a genetic perspective with the rest of Jewish communities. Their guess is that the Ethiopians were a local tribe that adopted Judaism” (Traubman and Sini).²²

Conversion is, of course, allowed in Judaism. As Daniel and Jonathan Boyarin argue, insofar as the convert is given the name “son” or “daughter of Abraham,” she or he is “adopted into the family of Abraham and assigned a new ‘genealogical’ identity” (317). Nevertheless, one of the principle normativities that undergirds this genetic research is that of an *authentic* Jewishness measured against the genealogical principle, “a physical connection of common descent” (307), even if not from Abraham, that is now believed to be demonstrable in genomic form.

V. In the Wake of Genetics

Kinship rules have always governed the question of “Who is a Jew.” While until the Mishnaic period, Jewishness was determined by patrilineal descent, it has, since that time, been determined along a matrilineal axis. And those rules of descent, insofar as they delimit membership in the “Jewish nation,” simultaneously govern the rules of citizenship in the Jewish state: the Law of Return entitles anyone halachically recognized as a Jew to become a citizen of the Jewish state. The criteria of membership in family, nation and political society are entangled. To take but one example, while organizing the panel at the American Museum of Natural History, one museum staff member was told repeatedly by Skorecki that he wanted to steer the audience clear of political questions, never specifying exactly what he meant. I asked, what did she think he was scared of? She said, “Well for me, it always comes down to: Who does Israel belong to? For these South Africans, is the claim to identity also a claim to land?”²³

At the same time, genetic research into Jewish origins refigures the relationship between family and nation in particular ways. “Familial ties” to the nation are, after all, abstract. The nation is, in Benedict Anderson’s terms, an “imagined community,” one in which *metaphors* of lineage and birth figure in central ways. The credibility of genetic evidence, however, facilitates the shifting of registers, from the more narrow and specific to the most broad and

general categories of social classification in presumably *less abstract, less metaphorical*, ways: from family, to nation and back again, all with a newly established conceit of the concrete. The nation is, literally, an extended family.

In a different register, FamilyTree DNA, a private start up company that describes itself as "America's first DNA-driven genealogical testing company," offers tests to individuals who want to find their most recent common ancestor. As reported by Julia Fuma in an article in the *Forward*, "a 69-year-old Holocaust survivor who lost most of his family in Poland, spent more than 30 years on a quest to find his roots. For years, his search was an arduous, low-tech endeavor. He looked for people with similar last names. . .and sent letters to all of them." Only one responded and "the two men could not *prove* that they were related" (emphasis added). Until last summer, that is. Learning of FamilyTree DNA, the two men ordered DNA test kits. As one of them recounts, "Only a few weeks ago the results came! We both tested identically for the 12 tested Y chromosome markers. . .most likely, we have a common ancestor within 14 generations. . ." (emphasis added). The reporter then noted: this holocaust survivor "now feels like he has new family members."

This proof of kinship is derived from complex mathematical models that presume mutation rates (the molecular clock) and generational time in order to arrive at a coalescence time (the date of origin) for the two samples provided. And once one goes back fourteen generations, one can only imagine how many other men alive today may share a common ancestor with these newly confirmed "relatives."²⁴ Nevertheless, the results provided them with a sense of real kinship—of proof. Circulating through the logic of the market, this form of evidence, now available as "genetic testing," accrues more and more certainty. The principle of descent is empirically testable. "Proof" of relatedness—the possibility of kinship itself—can be bought. In turn, as this story indicates, credible evidence of common descent seems able to help generate affective ties. Understanding the power of genomics for identity, thus, perhaps requires that we engage not only metaphysical questions regarding the ways in which what it means to be human is becoming increasingly enmeshed in an understanding of DNA as the basic code of life and the concomitant practices of biotechnological intervention (see Haraway 1997; Kay 1993, 2000; Rabinow 1999a and b). In addition, this power might be fruitfully explored in relation to questions of epistemology: what kinds of evidence emerge as "hard," as indubitable at any moment in time, and how is that effect produced?

ENDNOTES

- 1 Meiosis refers to the cell divisions that produce gametes (a mature reproductive cell).
- 2 There is a “pseudo-autosomal” region at each end of the Y chromosome and those regions do recombine. But, those regions are not focused on in this phylogenetic Y-chromosome research. Rather, in these studies the “Y chromosome” refers to the largest region of the Y chromosome which is its non-recombining section (see Jobling 1995).
- 3 A haplotype refers to the arrangement of different kinds of polymorphisms with different rates of occurrence linked together on the same chromosome.
- 4 The nucleotides are the structural components of DNA, containing four different chemical bases-adenine, cytosine, guanine, thymine. Deciphering the nucleotide sequences involves determining the ordering of the chemical components at any stretch of a given chromosome-A, C, G, T or A, G, C, T, and so forth.
- 5 The two genetic loci were defined by a) the Y Alu Polymorphic (YAP) insert (i.e., the presence or absence of a known allele on the Y chromosome), and b) three allele frequencies of a particular microsatellite (DYS19). (An allele frequency of a microsatellite refers to the number of times a given triad of nucleotides (say, A-C-G) is repeated at a given locus on a chromosome.
- 6 The Cohen modal haplotype (CMH) is composed of six binary polymorphisms and specific numbers of repeats at six microsatellites. See Thomas and Skorecki 1998.
- 7 I do not deal with the question of the uncertainty of the mutation rate in this paper as it now stands, but will in later drafts. In short, the uncertainty in the mutation rate is crucial to understanding the problem of “dating” in genetic archaeology: confidence intervals can end up stretching over many a thousand year periods.
- 8 Gene flow or admixture refers to the genes introduced into a population from a second population, via reproduction, of course.
- 9 For more on this question, see Ernst Mayr.
- 10 In June 2001, a session titled “The Lost Tribes of Israel” was held at the American Museum of Natural History in New York City as part of public educational programs organized during the genomics exhibition being displayed in the museum. After screening a NOVA video of that name, Karl Skorecki and Tudor Parfitt (two of the primary researchers on the study) were on a panel to discuss the film and their work. (I moderated the session.) All quotations are taken from a tape-recorded transcript.

- 11 Genes are those nucleotide sequences of the human genome that code for proteins: thus, "junk-DNA" are not, technically, genes.
- 12 The conference was held in New York City, August 8-13, 1999. All quotations are taken from tape recordings of the sessions.
- 13 I am working on thinking about how this concept of the gene structures what "a population" is understood to be, and what "its history" thereby is, within the practice of genetic anthropology.
- 14 FamilyTree DNA is a private testing company that offers a test for the presence or absence of the CMH. Mark Hammer is a consultant to the company, and his laboratory at the University of Arizona, Phoenix (the Center for Genetic Anthropology) does the genetic analysis for the company.
- 15 The complexity of these statistical facts and what they actually tell us about the history of a given "population" is one aspect of this research that I am currently focusing on. In addition, the translation of statistical facts based upon an analysis of a given population in order to test the descent lines of a particular individual is highly problematic. When the question becomes individuals wanting to learn something about their "cultural identities," the translation becomes even more fraught.
- 16 This is one debate I intend to pursue further. Rabbinic authorities made statements on the irrelevance of the CMH to the question of who is a Cohen after its announcement in the *New York Times*. Yeshiva University in New York City sponsored a whole public forum on the matter. Nevertheless, many men are testing themselves to find out if they carry the polymorphism. That is a tension between explicit theological doctrine and practice that I intend to explore.
- 17 There is some debate about whether or not one can derive directionality from the genetic evidence in these studies: in other words, absencing Lemba oral traditions and biblical stories, we cannot conclude that this haplotype originated in the ancient near east and moved to southern Africa. The general theory is that a given haplotype originates in the region in which it is found at its highest frequency. Of course, as Boas pointed out long ago, one might want to be careful about assuming that the source of a "diffusionary" cultural event is to be found in the place where that cultural trait is found in its highest frequency today. If one did, one would assume, for example, that Christianity originated in Europe, as he wrote.
- 18 Tudor Parfitt is conducting research on precisely the question of how the results of genetic anthropological studies such as these are affecting how communities, such as the Lemba, understand their own histories and identities.
- 19 Kulanu means "all of us" in Hebrew.
- 20 It is worth remembering that the word "race" initially indicated lines of ancestry (Stevens 1999:179; see also Banton 1998).

- 21 There have been reports in the *New York Times*, various journals and newspapers of the Jewish Press in the United States, *Ha'aretz*, for example.
- 22 Bonne-Tamir and her colleagues emphasized that once converted, Ethiopian Jews no longer married "foreigners:" "Generations of marriages within the community" generated genetic differences between them and non-Jewish Ethiopians.
- 23 This issue also came up in the question and answer period.
- 24 For example, if one assumes that the founding ancestor had two sons, and in each subsequent generation each male descendant had two sons who survived, by generation 14 (the current generation) these two men would be related to 8190 other men ($2^{14}-1$ assuming the founding father is generation #1).

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