

CHAPTER 13

“We’re Going to Tell These People Who They Really Are”:
Science and Relatedness

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RELATIVE VALUES

Reconfiguring Kinship Studies

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The title of this essay is derived from the justification given for the Human Genome Diversity Project (HGDP) by a spokesman, to an audience of bioethicists, in an unsuccessful attempt to drum up support for the project at the International Congress of Bioethics in 1996. A Native American activist responded from the audience: “I know who I really am. Shall I tell you who you really are?”

Identity and descent — the constructions of *who* and *what* you are — are traditional foci of anthropological studies of kinship. David Schneider presented as a cultural fact that American beliefs about kinship are strongly rooted in folk-hereditary ideologies, expressed as the proportional sharing of “biogenetic substance” (1968, 23–25). It is not surprising, then, that the development of genetics in the twentieth century would be accompanied by a strong claim of authority by the science of genetics in precisely those contested cultural arenas of identity and descent.

Here, I look at one such claim — that of population genetics — expressed recently in the controversial proposal for the founding of the HGDP, a consortium of population geneticists attempting to establish itself as “big science,” with the goal of retrieving and storing genetic samples from indigenous peoples. The justification for the HGDP resides in the promise of an ultimate microphylogeny of the human species, a goal that is both intractable and anthropologically problematic. Nevertheless, the HGDP successfully managed to represent itself as the locus of authority in population-level studies of relatedness. There are any number of precedents in the last hundred years for bio-genetic studies to cast themselves in opposition to anthropology. Presently situated on the cutting edge of modern ideologies of identity, relatedness, and history, as well as on the cutting edge of modern bioethics, the HGDP

may necessitate rethinking the place of anthropology in the larger academic community.

GENETICS AND ANTHROPOLOGY IN THE EARLY PART OF THIS CENTURY

In 1911, the same year that Franz Boas published *The Mind of Primitive Man* and established the case for the conceptual divorce of biology (i.e., race) and culture (i.e., history), geneticist Charles Davenport published *Heredity in Relation to Eugenics*. Equally paradigmatic, Davenport approached similar questions in different ways, arguing that culture was a direct outcome of the newly discovered Mendelian genes, and that there was a direct translation between superior genes and superior cultures.

Davenport, however, had an advantage. He presented his ideas with the well-financed and well-respected cachet of modern biological science. As the American eugenics movement emerged in the next two decades, it would consciously cast itself as the modern, scientific antidote to the newly emerging field of anthropology. On one level, it was an idealistic expression of the desire to impose some form of rationality on the capricious acts of marriage and reproduction; on another, it carried a racist and elitist appeal to restrict the immigration of populations with bad "germ-plasm," and to sterilize the poor, involuntarily if need be.

It is thus easy to find unsettling appeals in unlikely places. For example, the first edition of a popular genetics textbook by E. W. Sinnott (later the dean of Yale's graduate school) and L. C. Dunn (later an outspoken critic of racist biology) exhorts students to sterilize their neighbors (or worse?) on the basis of their social position:

Even under the most favorable surroundings there would still be a great many individuals who are always on the border line of self-supporting existence and whose contribution to society is so small that the elimination of their stock would be beneficial. (1925, 406)

To oppose eugenics was to oppose modernity, science, and evolution. Although critiques were available—for example, by Boas (1916), Alfred L. Kroeber (1916), and Clarence Darrow (1926)—no biologist published a serious challenge to the ideology and methodology of eugenics until Raymond Pearl's article, "The Biology of Superiority" (1927), which became newsworthy for that very reason.

The eugenics movement ultimately failed not so much because of new data

or the persuasive merits of alternative ideologies but because the Great Depression graphically illustrated the lack of fit between genes and social standing; and its embrace by the Nazis touched off a reciprocal concern for individual rights in the United States that had been lacking a generation before (see Paul and Spencer 1995). For a while, however, the eugenics movement was eminently successful in popularizing its cause as well as influencing public opinion and legislation, largely by virtue of representing itself as a modern, scientific analysis of cultural phenomena—in other words, as an improved alternative to anthropology.

HUMAN GENETICS AS RACIAL HISTORY

It is not terribly difficult to find the same scenario repeated in slightly different contexts throughout the twentieth century. The discernment of the fundamental divisions of the human species, for example, was taken to be the basic task of physical anthropology in the first half of that century. The earliest blood group data, inherited as simple Mendelian factors, were immediately taken to supersede the old-fashioned, anatomically based anthropological data. The fact that these new data created random artificial associations between the Poles and Chinese, and among the peoples of New Guinea, West Africa, and Southeast Asia, did not seem to diminish the geneticists' zeal in the 1920s (see Snyder 1926), nor again a generation later (see Boyd 1947).

These studies incorporated the ABO blood group, the earliest genetic "marker"—that is, a trait passed on perfectly intact, without adulteration either by the circumstances of life or by gross convergence due to common environmental adaptation. It simply marked a bit of heredity. But what good was a genetic marker unless it could reveal the deep aspects of ancestry?

Harvard's Earnest Hooton, the dean of U.S. physical anthropology, had graphically represented the complex ancestry of human populations literally as blood relations, evoking the anastomoses and capillaries of the circulatory system (see figure 13.1). Daunting and value-laden as the depiction of these historical relations seems to be (with Keltic and Nordic representing the top of the main trunk of the species, and an obvious subtext of purity, for example), it nevertheless served to illustrate the ostensible affinities of these groups as subject to the dual forces of growing apart and together.

The exercise proved too daunting for most other physical anthropological treatises. Racial anthropology generally limited itself to maps and classifications, not to branching diagrams representing ancestry. Indeed, Hooton's

over all lineages. Otherwise, one particular rapidly evolving lineage might be closely related to another, but quite dissimilar from it, and therefore the fact of relatedness would be masked.) The most interesting aspect of the tree was that it appeared to juxtapose Oceanic and Asian populations against Eur-African populations, indicating that a fundamental biological division existed in our species, along an east-west axis (see figure 13.2). They noted "a remarkable similarity between the blood group map thus obtained, and the geographical map; this fact is not too surprising, as physical proximity implies, on average, higher rates of gene diffusion" (929–30). In other words, there are two reasons why peoples might be genetically similar: either recent divergence or coming back together, but they only graphically illustrated and considered *divergence*. This point is crucial because the analysis is predicated on taking cultural or political entities as natural units, and inferring historical bifurcations from the patterns of similarity of these units. Neither of these assumptions is valid since the structure of the tree is sensitive to the composition of the populations, their demographic expansions and contractions, the statistical algorithm applied, and the gene systems analyzed (Harpending 1994) — in addition to any ethnohistorical genetic contact among them that may make them inseparable as natural categories. In other words, the inflexibility of the tree metaphor led to the reification and naturalization of units that were not genetically stable, and as we shall see, probably illusory.

But the geneticists went a step further. Extracting data from a classic compendium (Rudolf Martin's *Lehrbuch der Anthropologie in Systematischer Darstellung*), they proceeded to generate a tree from twenty-six anthropometric traits for fifteen matching populations — subsuming classic gross measurements such as stature, chest girth, prognathism, nose height, skin color, and ear length. The tree generated from these characteristics had a fundamentally different branching structure: it appeared to link Europeans and Asians in juxtaposition against Africans — a north-south division (with Oceanics split between them). While critical of their naive selection of anthropological data, William Howells (1973, 1976) generated a concordant tree of his own based on craniometric data for sixteen worldwide populations.

Cavalli-Sforza and Edwards used the dichotomy between their genetic and anthropometric trees to argue for the superiority of the genetic tree as a representation of the ancestry of the human species. The scientific rhetoric quickly recalled an earlier era. For instance, in a popular 1974 article in *Scientific American*, Cavalli-Sforza again juxtaposed the anthropometric tree against his genetic one, explicitly labeled the "evolutionary" tree. Thus, anthropology

was old-fashioned and creationist; genetics would be modern and scientific. "The study of single genes is probably more useful for reconstructing a common ancestry than the study of superficial traits" (1974, 89). Cavalli-Sforza concluded, somewhat self-servingly. (So had, it should be noted, J. B. S. Haldane a generation earlier: "The blood-groups on the other hand, give information of a more fundamental nature on racial structure, just as do the palaeozoic rocks on geological structure" [1940, 477; see also Marks 1996].)

And yet, there were irreconcilable tensions within the genetic analysis itself, which were rendered invisible in the presentation. A different computer algorithm applied to the same class of genetic data by a different group of population geneticists would yield a tree more harmonious with the anthropometric tree than with the original Cavalli-Sforza genetic tree (see Nei and Roychoudhury 1974, 1981). In this genetic tree, the deepest node distinctly separated the African populations from Europeans and Asians (and Oceanics), suggesting a fundamental north-south division in human ancestry — similar to what the anthropometric trees had appeared to yield — if read literally as biohistory (see figure 13.3). Even though these population geneticists were somewhat skeptical of reading the details of such a tree literally, they nonetheless proceeded freely to do so, calculating that "the divergence between the Negroid group and the Caucasoid-Mongoloid group seems to have occurred about 110,000 years ago" (Nei and Roychoudhury 1981, 13). This, it is important to remark, was in considerable contrast to Cavalli-Sforza's calculation for "the oldest separation in the tree [that is, Eur-Africans versus Asians] . . . as being approximately 35,000 to 40,000 years ago" (1974, 89).

While claiming authority for the biological microevolutionary history of our species, the analytic techniques utilized in human population genetics in fact made unrealistic assumptions about human population histories, and rendered those assumptions largely invisible through the representational medium of the evolutionary tree. The evolutionary results were more unstable and more context dependent than was readily apparent, but they nevertheless seemed to generate quantitative, genetic, scientific answers to archaic anthropological questions.

SYSTEMATICS AND THE RACES

The assumptions of numerical taxonomy or "phenetics" (and its subsequent rejection in the 1980s) are worth a digression. The construction of relationships among groups of organisms was an arcane specialty through the 1950s,

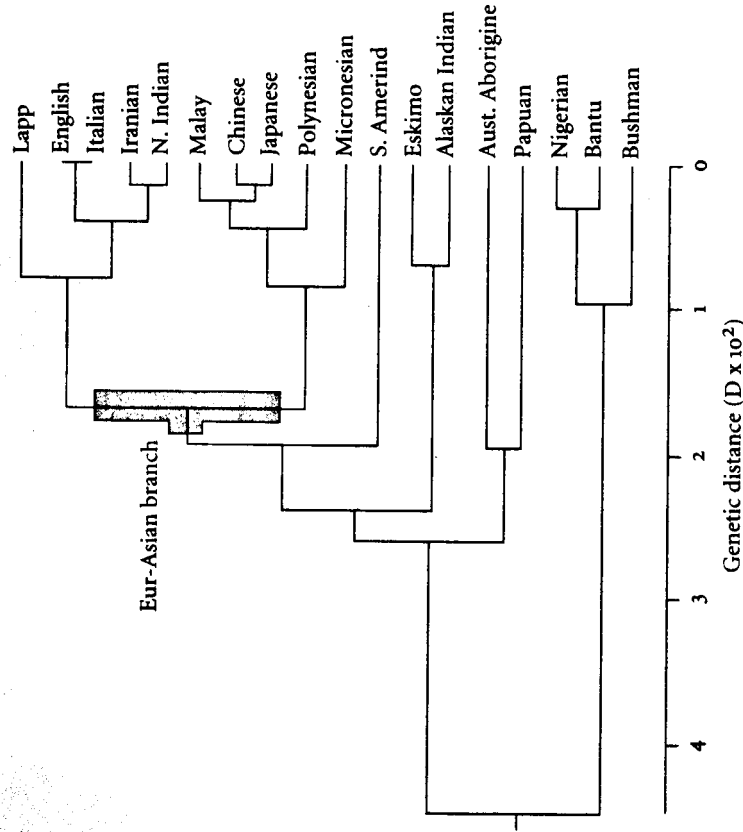


FIG. 13.3 Dendrogram of human genetic relationships, redrawn after Masatoshi Nei, "Human Evolution at the Molecular Level," in *Population Genetics and Molecular Evolution*, ed. Tomoko Ohta and Kenichi Aoki. Berlin: Springer-Verlag, 1985, page 54.

the product of long careers spent in museum basements. A new philosophy arose concurrently with the development of computers and rooted itself in inductive logic. It challenged the pedagogical bias that the best way to classify organisms was to study and become intimately familiar with them, and then to reason out their phylogenetic relationships and devise a suitable taxonomic scheme to describe them (see Gregory 1910; Simpson 1945, 1961). This was insufficiently rigorous for a modern science, argued the advocates of numerical taxonomy (see Sneath and Sokal 1962).

The advocates of numerical taxonomy began by conceptually divorcing classification from phylogeny. Phylogeny (that is, the genealogical history of species), they contended, could never be known accurately, and therefore was not worthy of study except as a byproduct. One could, however, compare and classify things. The goal, therefore, would be a correct classification. The clas-

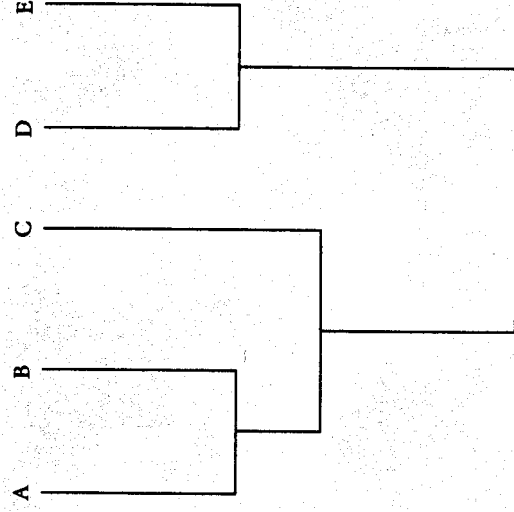


FIG. 13.4 A dendrogram, representing similarity among operational taxonomic units, labeled A, B, C, D, E.

sification would be generated by measuring many characteristics and allowing a computer to sort the organisms ("operational taxonomic units" or OTUs) into groups based simply on their similarity. The product was thus a branching diagram, a dendrogram, which established nested patterns of similarity—resembling a convention of football goalposts—with the vertical axis as an empirical scale of similarity (see figure 13.4). Classifications would be read simply by taking clusters of organisms at particular arbitrary degrees of similarity. Once the proper classificatory tree had been generated, the phylogeny might be read from it.

Phylogeny, however, is crucial to post-Darwinian biology, and patterns of similarity sometime conceal it. A species that has evolved extensively in a short period of time may be closely related to a species to which it is not very similar. (A classic example, of course, is chimpanzees being closely related to humans, yet physically similar to orangutans—a result of the rapid evolution of the human form over the last few million years.) Thus, two taxa may be different either because of distant common ancestry or because one of them diverged from the other rapidly. Numerical taxonomy was not equipped to differentiate between these alternatives, and consequently, focused only on similarity, rather than ancestry (see Hull 1970).

Further, the phenetic method ignored key aspects of modern biology. Species, for example, are conventionally seen as natural units unified by reproductive criteria, not by general similarities; to ignore that fact seemed

unbiological. The problems were even greater operationally. One could not get males and females of sexually dimorphic species to cluster together in a dendrogram without introducing a priori knowledge that they were indeed the same species (see Boyce 1964), which defeated the inductive philosophical assumptions of the method. The goal was ostensibly to feed data to the computer and then let the computer mindlessly decide the relationships of the species; but if one had to introduce decisions about placing males and females together in spite of their appearance, the "objectivity" of the method vanished.

As a result, the 1970s saw the development of a rival systematic philosophy, phylogenetic systematics or "cladistics" (see Hennig 1965; Eldredge and Cracraft 1980). The goal of cladism was quite explicitly the reconstruction of patterns of descent, and it began by discriminating among the kinds of similarity that exist and establishing a lexicon to accommodate them. Similarity due to remote ancestry would be "plesiomorphy"; such similarity could be independently retained in many different lineages and were thus not useful in phylogenetic reconstruction, so they would be ignored in that context. (Imagine the futility of sorting primate relations on the basis of quadrupedalism, a trait possessed by the vast majority of species.) Only shared evolutionary novelty or "synapomorphy" was indicative of common ancestry. (Bipedalism would be a synapomorphy, and all primate species habitually doing it are considered close relatives, hominids. All primates sharing the feature of quadrupedal locomotion, by contrast, are a diverse lot, not necessarily very close relatives.) Hence, a chimpanzee and orangutan are similar to one another, both looking "apish," with long arms, hairy bodies, and large canine teeth; but details of the chimpanzee's upper palate place it as a close relative of the human, not of the orangutan. The new emphasis, then, would be on key particular features rather than on overall similarities. Cladistics thereby reversed the relationship between classification and phylogeny established by numerical phenetics: phylogeny was now the goal, and classification would be derived from it. Cladists redefined the criteria of "difference" and altered the representation of their analytic results.

Importantly, the new innovations in taxonomic philosophy altered the significance of temporality in depictions of relationships. The cladists represented their work with "cladograms," branching diagrams representing patterns of common ancestry, but without a temporal dimension (see figure 13.5). Animals living at different times would be placed together along the top, among their closest relatives. Only afterward would the time dimension be

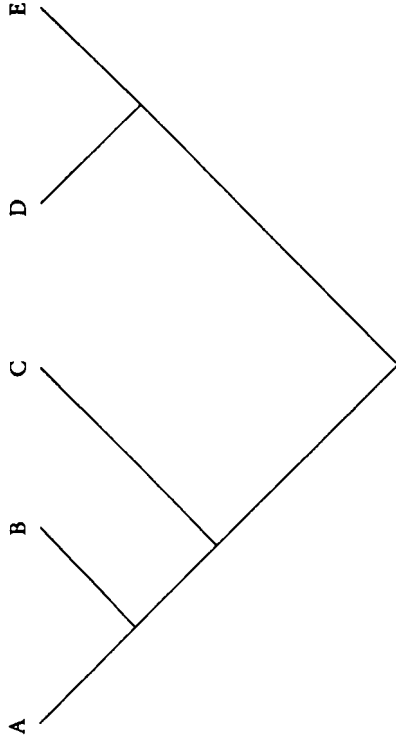


FIG. 13.5 A cladogram, representing shared common ancestry among species, labeled A, B, C, D, E.

added to help infer ancestor-descendant relationships and produce a "phylogenetic tree." Here, the vertical axis represents the relative recency of shared ancestry. Cladism thus focuses on establishing "close relatives" at the expense of literal lineal ancestors, and as such, has been criticized for downplaying biological descent.

Both schools of thought—cladists and phenetics—focused on specific aspects of biological evolution and represent their results with characteristic diagrams as emblems (both classically utilizing right angles, but differently oriented). Both "work" to some extent *above* the species level, where lineages always diverge. On the other hand, neither of these affords an accurate depiction of the processes of evolution *below* the species level, particularly of human microevolution, where blood lines diverge and remerge. Numerical taxonomy omitted rates of change, indeed it omitted evolution altogether—for the products of evolution are not more or less similar groups of things but more or less recently descended taxa.

The intervening decades since Cavalli-Sforza and Edwards's work have seen the populations and genetic markers increase, but the rise of DNA technology in the 1980s made possible the direct comparison of the hereditary material, rather than merely their weak surrogates, the blood proteins. The breakthrough study of the DNA relationships within the human species was the famous "mitochondrial Eve" analysis of Rebecca Cann, Mark Stoneking, and Allan Wilson (1987). Genetic similarities were sampled across the mitochondrial genome, which has the properties of being small (16,500 bases in-

stead of 3.2 billion in the nucleus), readily isolated, and inherited clonally through the maternal lineage (and thus not subject to the vagaries of Mendelian assortment and recombination). The compactness, simplicity, and unilinearity of mtDNA permitted the possibility of inferring genetic linkages more directly. This newer generation of molecular systematics produced a tree that was neither strictly phenetic (based on similarity) nor cladistic (based on evolutionary novelties) but parsimonious—constructed by minimizing the number of evolutionary events or mutations that must be invoked to link all the taxa into a network. This method entails assumptions about the modes of mutational change and its rarity, which are themselves contested. But for the present purposes, the crucial feature of this work is that the tree was constructed specifically from the 140-odd individuals studied, not from any a priori groupings (see figure 13.6). The computer (a program called PAUP—Phylogenetic Analysis Using Parsimony) generated a tree linking all the mtDNA sequences into the shortest network. Only subsequently was the geographic origin of the samples imposed on the result.

Most aspects of the mtEve study, and the evolutionary model that accompanied it, have been effectively criticized in the last decade, but the basic findings have stood up well: that Africans are more genetically diverse than Europeans and Asians; that they indeed subsume the genetic diversity found in the rest of the world; and that racial clusters are not inherent in genetic comparisons of humans but must be imposed by the investigator.

These conclusions, however, trickled down into the genetics community in curious ways, for they were not readily translated into methodological revisions. Cavalli-Sforza quickly identified in genetic data the African–EurAsian split he had denied decades earlier (Cavalli-Sforza et al. 1988). This new analysis comprised frequencies of 120 nuclear alleles across 42 populations, among which the division between Africans and non-Africans would now be dated to 92,000 years ago, but from essentially the same analysis. (The headline, though, involved the isomorphism between the tree obtained genetically and a classification of world languages, itself anthropologically problematic.)

It must nevertheless be observed that the most direct implication of the Eve work was not the appearance of a deep division between Africans and EurAsians but a deep division *within Africans*, of which one branch included EurAsians. In other words, the Cann, Stoneking, and Wilson (1987) genetic study found Africans to be paraphyletic—incorporating the genetic diversity of non-Africans, and thus not a single separate branch (see figure 13.7a)—while the Cavalli-Sforza genetic study took Africans as monophyletic—a

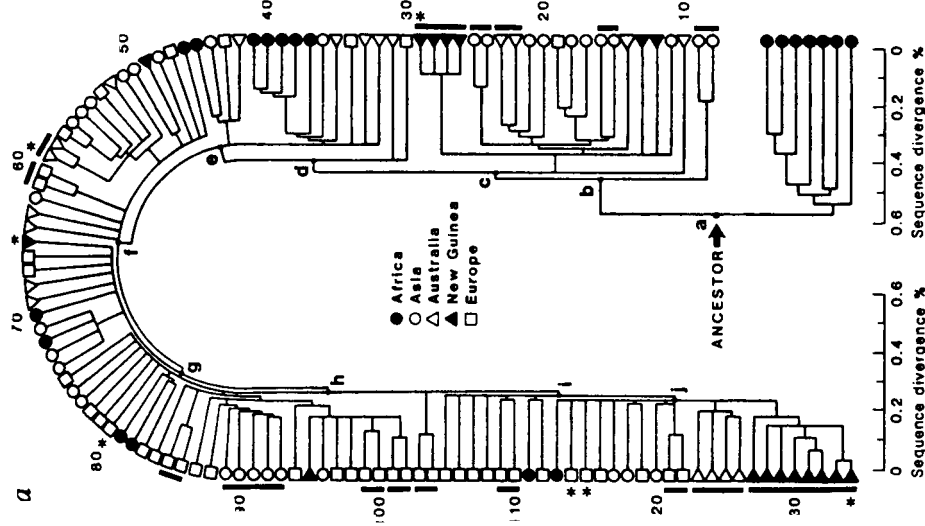
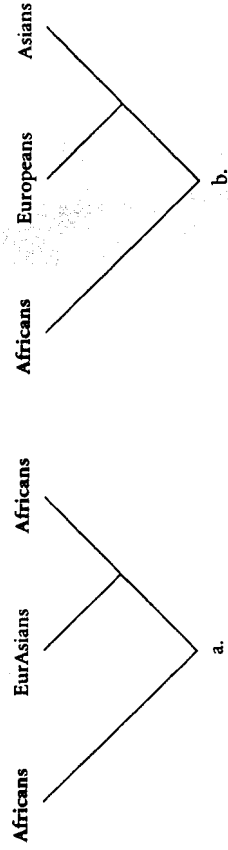


FIG. 13.6 Parsimony tree, the shortest network (that is, the one ostensibly invoking the smallest number of mutational events) linking all the mtDNA sequences, from Rebecca L. Cann, Mark Stoneking, and Allan C. Wilson, "Mitochondrial DNA and Human Evolution," *Nature* 325: 33.

single branch—and still calculated the divergence of that group from others (see figure 13.7b). These two studies, in short, encoded extremely different biohistorical narratives.

Yet with the optimism that more populations and genetic markers could resolve what an earlier generation had called "the racial history of man" (in spite of the history of the research, the unresolved methodological flaws, and epistemological difficulties), and further bolstered by the success of the Human Genome Project and the public interest generated by mitochondrial Eve, population geneticists put a new project before the American public: the Human Genome Diversity Project.



FIGS. 13-7A-B Alternative genetic relationships of the "races": a. Africans subsume Europeans and Asians, as per Cann, Stoneking, and Wilson 1987; and b. Africans contrast with Europeans and Asians, as per Cavalli-Sforza et al. 1988.

GENETICS AND IDENTITY POLITICS

I first heard about the HGDP from Leslie Roberts, a journalist for *Science* magazine who was researching a story about it. A few months earlier in 1991, a small group of geneticists, led by Cavalli-Sforza, had formally proposed the large-scale collection of DNA from indigenous populations in the journal *Genomics*. Now, an argument had erupted over the strategy such a project should adopt. Cavalli-Sforza expected that samples would be collected according to ethnic grouping: Yanomamo, Hopi, Chukchi, and so forth — which of course would be ideal for the kinds of studies he had been doing since the 1960s. Allan Wilson, senior author of the Eve study, maintained that since named groups did not map onto genetic diversity particularly well, a more objective sampling strategy should be sought — namely, simple geography. Lay a grid over the world, asserted Wilson, and sample our species by transect. I sympathized with Wilson's approach over the phone (but I ended up on the cutting room floor when the article appeared) and then ran out to read the *Genomics* proposal.

What the HGDP represented was the culmination of the previous three decades in neo-racial history studies: it held out the extraordinary promise of revealing the ultimate biological history of our species, very much in line with similar attempts over the course of the twentieth century, although this time on a grander scale and with the highest level of genetic resolution. At the same time, however, its own rhetoric was decidedly antiquated. As if the lessons of racial anthropology had never been learned, its Web site presently highlights the collection of these data specifically "to see if, for example, the Irish are more closely related to the Spaniards or to the Swedes." Answers to such odd questions would become available through the collection of DNA samples, which would be retrieved and stored for the use of geneticists. The Irish, Span-

ish, and Swedish, however, were not their principal targets; their targets were remote, exotic peoples, presumably on the verge of disappearance.

The populations that can tell us the most about our evolutionary past are those which have been isolated for some time, are likely to be linguistically and culturally distinct, and are often surrounded by geographical barriers. . . . Isolated human populations contain much more informative genetic records than more recent, urban ones. Such human populations are being rapidly merged with their neighbors, however, destroying irrevocably the information needed to reconstruct our evolutionary history. (Cavalli-Sforza et al. 1991, 490)

The appeal to "salvage" research was a familiar one to anthropologists (see Gruber 1970), but less so to geneticists. But even though it was addressed to geneticists, the proposal was notably lacking in epistemological detail. For example, it glaringly failed to make clear exactly whose evolutionary past was to be illuminated by the study of, say, the !Kung San's genes, or how one could reliably extract any evolutionary history from these data given the failures of the science to do so thus far.

Nonetheless, the implication was clearly that "our evolutionary past" was that of the "recent, urban" populations reading the article, and it was to be illuminated by other people's genes. Contemporary bioanthropological knowledge, of course, holds it to be exceedingly unlikely that the genes of any specific socially constructed group of people are going to shed any light onto anybody's evolutionary history but their own. The idea that the genes of indigenous peoples are somehow more representatively primitive than those of "recent, urban" peoples is a holdover from an earlier era, which anthropologists remember with regret. Yet according to its first major publicity in *Science*, the San, Pygmies, Basques, and Yanomamo offer (quoting one of the HGDP's principal spokesmen) "a window into the past," and even more explicitly, "a unique glimpse into the gene pool of our ancestors who lived thousands of years ago" (Roberts 1991a, 1614).

As the proposal came out, research on the genetic history of human populations was still proceeding, as it had been for thirty years. Cavalli-Sforza's research group published a paper the same year in the prestigious *Proceedings of the National Academy of Sciences*, for example, that examined the DNA of two groups of African pygmies, native-born Chinese living in San Francisco, and a heterogeneous European sample, and concluded that "ancestral Europeans are estimated to be an admixture of 65 percent ancestral Chinese

and 35 percent ancestral Africans" (Bowcock et al. 1991, 840). And these findings were eagerly consumed by the popular science press: as *Time* magazine duly reported in promoting the research and the project, "All Europeans are thought to be a hybrid population, with 65 percent Asian and 35 percent African genes" (Subramanian 1995, 55).

The paradox that became the signature theme of the HGDP was the celebration of modern techno-science applied within the framework of archaic racist language and thought, clearly loaded with astonishingly archaic assumptions of primordial division and purity of certain large segments of the human species — assumptions that were not being acknowledged. Particularly noteworthy was its acceptance as authoritative information in the derivative literature — capitalizing, as the genetics of earlier eras did, on the combination of technology and modernity associated with the field, and engendering little, if any, criticism.

One striking example of the broad insensitivity of human population genetic studies to the complexities of identity construction and of ethnohistory, and of the general absence of effective critique, involved a recent study of two sites on the Y chromosome, passed on from father to son (the opposite of mtDNA). Here, 54 percent of self-designated Hebrew priests (Cohanim), many of whom have the surname Cohen, had the same configuration of two genes on the Y chromosome, as opposed to only 33 percent of Jews who did not think they were priests (Skorecki et al. 1997). The authors inferred that this particular configuration was the bona fide genetic constitution of the Jewish priestly line, inherited directly from biblical Aaron and, by implication, reflecting the genetic makeup of his brother, the lawgiver himself.

Of course, men with the same last names are going to be more closely related than those with different last names, reflecting recent common shared ancestry. Anthropologists call this "isonymy" and have used it effectively as a crude measure of local inbreeding (see Lasker 1985). In the absence of information on the distribution of Y chromosome haplotypes of a sample of Horowitzes or Steinbergs, however, the inference that the one simply represented at 54 percent rather than 33 percent must be authentic and primordial for the ancient lineage of "Cohanim" is highly dubious. (Not to mention the fact that it assumes that the origin myth recorded in the book of Exodus is literally true.)

More important, the authors of that report quickly found themselves in the middle of an identity controversy, as people wanted to know authoritatively if they were "really" Hebrew priests or not (see Grady 1997). Since there

is no Temple or priesthood, nobody's a Hebrew priest, although apparently a lot of people would like to be.

But the Jewish priest study was not a central focus of the HGDP, which was to be principally directed at exotic, "isolated" peoples. Scholars interested in, say, the gene pool of African Americans were not greeted warmly by the HGDP — as a "hybrid" population it was of little interest, given the HGDP's assumptions about the genetic purity of indigenous peoples. For example, this purity was argued to be manifested in the IKung San, who were featured in most of the early write-ups of the HGDP, in strong counterpoint to their ethnohistory.

What these populations have in common is that each has been isolated and has only rarely — if ever — intermixed with its neighbors. (Roberts 1991a, 1614)

Such populations, isolated for hundreds or thousands of years, contain in their genes clues to human evolution, migration, and diversity. (Roberts 1991b, 517)

This assumption of isolation is what permits the reticulating evolutionary tree drawn by Hooton (see figure 13.1) to be simplified into the bifurcating evolutionary tree of Cavalli-Sforza and Edwards (see figure 13.2), which is now firmly planted in the soil of modern genetic essentialism. The underlying genetic fallacy is not new, and was pointed out explicitly a generation earlier to geneticists studying the blood groups of the Navajo and identifying them as pure, when Clyde Kluckhohn could readily produce ethnohistoric evidence that they were not such at all (Kluckhohn and Griffith 1950).

It should be noted that the new generation of geneticists working in "racial history" comes with a liberal political bent, acknowledging the equality of the so-called races, while even at the same time often reifying them. The HGDP, for example, alleges that the results of the project are expected to undermine the popular belief that there are clearly defined races, to contribute to the elimination of racism as well as to make a major contribution to the understanding of the nature of differences between individuals and between human populations. Yet their flagship literature presented color-coded maps of the world in which "four major ethnic regions are shown. Africans are yellow, Australians red, [Mongoloids blue], and Caucasoids green" (Cavalli-Sforza, Menozzi, and Piazza 1995, unnumbered page, color plate 1; see also Subramanian 1995; Piazza 1997).

It was precisely this inability to reconcile folk ideologies, liberal politics, and science that has led the HGDP into its greatest difficulties, and to its ultimate failure. At the bioethics conference that produced the exchange at the beginning of this essay, a German bioethicist, Benno Müller-Hill, posed a question to the HGDP's spokesman, Marcus Feldman. Expressing his discomfort with what he had heard from anthropologists and representatives of indigenous groups about the HGDP, the bioethicist posed a simple problem. "Someday," he said, "we will find some gene that influences some aspect of intelligence. Further, we're going to find that it's not perfectly equally distributed among all populations. As custodian and spokesperson for the genetic diversity of our species, how will you handle that?"

The HGDP geneticist stammered through an answer that simply denied the premise of the question — he didn't think there would be any gene that might influence intelligence, so the scenario would never arise. The bioethicists resoundingly found it unsatisfactory, simply another example of the project's inability to think through its political and ethical implications, while simultaneously asserting scientific hegemony over the study of human population history.

PRESENT STATUS OF THE HGDP

The HGDP's decline began with an issue that was not actually its fault. On 14 March 1995, a patent was awarded to the National Institutes of Health to cover a cell line derived from a man from a Papua New Guinean population known as the Hagahai. Although in this case a deal had actually been negotiated in the Hagahai's interests by a medical anthropologist, whereby the tribe would receive a significant proportion of any profits, there was nothing compelling the scientific interests to do so, and it could just as easily not have been the case. This was troubling to some.

The Hagahai problem for the HGDP was twofold. First, its elder sibling, the Human Genome Project, had successfully used a campaign of purple prose to drum up public support for its multi-billion-dollar cause. The human genome was routinely represented as "the holy grail," "book of life," "essence of humanity," or something along those lines. Suddenly, that rhetoric of its elder sibling could be flung in the face of the HGDP, for if DNA was the essence of life, then the Hagahai man no longer owned his own essence — it was now the legal possession of a branch of the U.S. government. This, of course, conjured an image of the West economically exploiting the very

bodies and cells of indigenes on the scale promoted by the HGDP. The second problem was more directly related to the HGDP: the project had steadfastly maintained the economic neutrality, and financial disinterest, of the HGDP program. Anyone who raised that concern, or more broadly the possibility of classic economic exploitation of indigenous people, was dismissed as overly suspicious and unrealistic. A catechism from its Web site, dated 6 October 1994, acknowledged the need to protect indigenous peoples from financial exploitation by genetics, but emphasized that the HGDP "does not intend to patent the samples or any products made from them. The Project is not a commercial enterprise. It seeks knowledge, not profit." After all, "it is not clear whether any commercial products are likely to emerge from its samples or data" (<http://www.stanford.edu/group/morrinst/hgdp/faq.html>). As the HGDP's bioethicist, Hank Greely, stated in *Discover* magazine in November 1994, "There's no commercial money in the project. No pharmaceutical-industry backing. This is pure science" (cited in Gutin 1994, 75).

Clearly, however, there was indeed a great deal of financial interest; the purity of the science was as illusory as the purity of the people the researchers wanted to study. Although the HGDP was not itself involved in the Hagahai case, the case showed in high relief that as official custodians of the human gene pool, either the HGDP spokesmen were lying, or they were extraordinarily naive and not sufficiently attuned to the implications of their proposed research to be entrusted with it. Presented with an opportunity to take a strong ethical stand, the HGDP demurred. It took a beating from a nongovernmental organization called RAFI (Rural Advancement Foundation International, see Christie 1996).

On 21 October 1997, a panel convened by the National Research Council (NRC) on behalf of the National Academy of Sciences released its summary report evaluating the merits of the HGDP. In an extraordinary gesture, the panel found the project too nebulous even to evaluate. As the committee's fact-finding progressed, it became apparent that the precise nature of the proposed HGDP was elusive; different participants in the formation of the "consensus" document had quite different perceptions of the intent of the project and even its organizational structure. Accordingly, because there was no sharply defined proposal that the committee could evaluate, it chose to examine the scientific merit and value of research on human genetic variation as well as the organizational, policy, and ethical issues that such research poses in a more general context.

Agreeing that the study of diversity in the human gene pool was a valid

scientific goal, the report went on to describe how the panel felt it ought to be done, in effect jettisoning the work of the HGDP itself over the last eight years. Part of the reason they had such difficulty was that the goals of the project had begun to change when it quickly became clear that human microphylogeny — or the clumsy representations of it adduced by the HGDP — did not resonate with the public. So they had begun to emphasize other goals, especially biomedical (see Kidd, Kidd, and Weiss 1993; Weiss, Kidd, and Kidd 1992). But since the project was planning to collect genotypes, and not medical histories to associate with the genotypes, there was actually relatively little chance of deriving biomedical benefits (see Marks 1995b). Thus, as the press release issued in October of 1997 summarized: "Following an exhaustive examination, the committee found the proposal does not clearly explain the purpose of the project or provide the necessary safeguards for protecting participants" (compare National Research Council 1997).

It may be difficult to imagine the leading population geneticists in the United States, after seven years of brainstorming, half-a-million dollars of National Science Foundation money, publicly and privately funded seed money and meetings, unable even to explain *the purpose of the project* adequately to a review panel. Nevertheless, that was the panel's judgment. A brief attempt at "spinning" the NRC report (see Cavalli-Sforza, Bodmer, and Dausset 1997; Merriwether 1997) was aided by conflicting accounts in the leading journals. *Nature* stated that the report recommended dumping the HGDP (MacLiwain 1997), while *Science* noted that the project had been given a thumbs-up (Pennisi 1997). Ultimately, NRC committee members themselves were obliged to clarify the record: "Nowhere in the report does our committee endorse the HGDP," wrote Virginia Dominguez (1998; see also Schull 1998).

At the time of this writing (mid-1999), the HGDP still has money allotted, but is undergoing a major reorganization. Desperately trying to salvage an image, it has gone so far as to claim credit for discovering the absence of biological races in our species (see Marshall 1998) — despite decades of anthropological research and teaching of that very point (see Marks 1995a). The American Anthropological Association's statement on race not only makes that point, but details the long-standing institutional commitment of anthropology to the position that biological races, equivalent to zoological subspecies, do not exist in *Homo sapiens*.

BIOLOGICAL ANTHROPOLOGY AS A FORUM FOR THE UNIFICATION OF GENETICS AND ANTHROPOLOGY

Perhaps the most tragic aspect of the Human Genome Diversity Project lay in its relationship to biological anthropology. In principle, the project might have benefited immensely from this field, in areas such as the critique of the relationship between named populations and natural categories, or from the collection of anthropological and medical data to correlate with the genotypes in order to expand the questions the project could address. In practice, however, the HGDP managed to attract a tragically sycophantic biological anthropology: the geneticists organizing it saw no need for anthropological input until the major decisions had already been made, and the biological anthropologists were grateful to be included in such a big project. Its major anthropologists have now dropped out.

The role of anthropology in the HGDP is best encapsulated in an exchange from the *Anthropology Newsletter*, in which HGDP insider Ken Kidd (1996), of Yale's genetics department, wrote an indignant letter contesting the point that anthropologists were not involved in the planning of the project. According to Kidd, "By any objective criteria — publications, academic appointments, training of students, society memberships — most people would agree that Luca Cavalli-Sforza, Mary[-]Clair[e] King and I are anthropologists" (2). Actually, they probably wouldn't. But more important, to this geneticist, there is no body of scholarship or expertise that might differentiate a geneticist interested in humans from an anthropologist interested in human genetics. This may sound like a trivial bit of turf patrolling, but it reflects a serious issue in biological anthropology that stretches back to the modern origins of the field.

When the science of human genetics was the science of eugenics, few anthropologists could be counted among its advocates (a notable exception was Yale's Clark Wissler). But the two leading American *physical* anthropologists, Earnest Hooton and Aleš Hrdlička, were both members of the advisory council of the American Eugenics Society (along with many American geneticists and other intellectuals). As the representatives of the biological/scientific arm of anthropology, they chose to follow the "real" scientists in claiming to approach anthropological issues scientifically, rather than lead the nonanthropologists to a better grasp of the relevant anthropology. A similar phenomenon was at work with respect to the HGDP, as some prominent biological

anthropologists chose to follow the intellectual course charted by the geneticists, as if human population genetics itself could exist in a timeless bubble of cultural purity and isolation.

And as in the 1920s, contemporary genetics successfully managed to portray itself as a modern alternative to anthropology. *Nature*, the leading science journal in the world, editorialized that

with physical anthropology under a cloud for its habit of using measurable skeletal indices as proxies for less tangible attributes (cranial capacity as a measure of intelligence, for example), it would be better to invest what goodwill there is in some quite different field. The Human Genome Diversity Project is already battling to win the consent of distinctive racial groups to schemes for collecting and analysing DNA. (Bias-Free 1995, 184)

Where *Nature* could have gotten such an archaic view of anthropology is a good question, for it is precisely the juxtaposition of scientific and humanistic issues that is the greatest intellectual strength of contemporary anthropology. As the HGDP succeeded in representing itself as a scientific program, but founded humanistically, it would seem to have been an ideal forum for the establishment of a *truly* biological anthropology—a program that acknowledges the cultural dimensions of all human activities, including science; that casts an analytic humanistic eye on the construction of genetic facts; and that mediates the genetic and anthropological realms, “biogenetic substance,” and notions of identity and descent.

Budding geneticists learn to think technologically. It is the current generation that is being forced to think about responsibilities and obligations to their subjects as well as accountability. A significant shift can be seen in contemporary science—from “designing a research project” to “designing a research project so that you don’t harm, victimize, or stigmatize anybody, because you will be held accountable if you do.”

That is, of course, a central problem with the HGDP. Should there be a research museum or warehouse of genetic material on the diversity of the human species? The question is *how* it should be established; and the problem is quite simply that technology was considered to be the central issue and responsibility to be something that would be dealt with at some vague time in the future. It is not simply that, as Alan Swedlund said at a 1993 Wenner-Gren conference on the HGDP, it is twenty-first-century technology put to the service of nineteenth-century ideas (compare Lewin 1993). These well-intentioned geneticists went to bed with the idea of a genetic repository of

the human species—a nice idea, and one that has been proceeding on a small scale for decades—and they woke up on the cutting edge of anthropological ethics and bioethics—having to account publicly for the apparent exploitation of the bodies of indigenous peoples in an ostensibly postcolonial world—and were unfortunately entirely unprepared for it.

As they attempt to construct an authoritative (possibly accurate, but *decidedly* authoritative) approach to social/historical identity based on DNA, the HGDP replays some of the major themes of contemporary issues in kinship study: Who owns the body? On what criteria is racial membership based? How are social groups constructed and constituted through time? What is the role of heredity in establishing self-identity, both in the organic and social realms? Of what significance is genealogy to cultural understandings of “who we really are”?

MRS. BURNHAM'S BABY

I will end this essay, as I began it, with a flashback to the 1920s. In January 1928 eugenics was a household word and the educated classes took it for granted that good germ-plasm was the secret to a healthy nation. Long before Dan Quayle and Murphy Brown, long before Dolly the cloned ewe, there was Mrs. Burnham. Grace Mailhouse Burnham was a wealthy thirty-seven- (or forty-one-) year-old social worker and widow who decided she wanted a child more than another husband. So she selected a consort, one with good genes, and on 10 January 1928, had a baby, whom she named Vera. For the father's name in the birth registry, she signed “Karl Graham,” the last name as a contraction of her own, and the first name after a well-known social theorist she admired. Then she told friends that she had borne the first “eugenic baby.”

Immediately, Mrs. Burnham became a cause célèbre in New York and, indeed, around the nation. Newspapers presented readers with the opinions of Clarence Darrow (“Mrs. Burnham's venture is her own personal business”); Valentino's widow, Natacha Rambova (“If she's poor, it's all quite different”); Nan Britton, who claimed to have borne Warren Harding's child (“How is it possible for a woman to want the child of a man she does not love?”); actress Olga Petrova (“Woman has the right to conceive children any way she pleases”); as well as judges, writers, ministers, and advice columnists. A photo of the understandably reclusive Mrs. Burnham was finally obtained from the passport office to adorn the stories (see figure 13.8), and her baby became the focal point for a public referendum on the American family, “companionate



FIG. 13.8 Mrs. Burnham, halfpence originally published in the *New York Mirror*, 25 January 1928; taken from a photo on file at the United States Passport Bureau.

marriage,” sex, marriage, illegitimacy, and reproduction. More than that, the public clamored to know, “Who is the baby’s father?”

When a photographer from the *New York Mirror* actually managed to get a shot of baby Vera, it was front-page news on 6 February. Indeed, the story was widely enough known that when Eugene O’Neill’s play *Strange Interlude* opened a week later, nearly every review related the motherhood of O’Neill’s character Nina (whose husband comes from a line of mentally ill folk, so she secretly has his best friend sire their child) to that of Mrs. Burnham. Walter Winchell’s review punned on O’Neill’s name, calling the play (which would go on to win the Pulitzer Prize for drama) “Another Eugenic O’Neill Baby.”

“Eugenic” had subtly become a euphemism for “illegitimate, wealthy” — bastardy legitimized by science. Spokespeople for the American Eugenics Society quickly assured the public that they were really in favor of traditional family values — home, hearth, and two parents of different sexes — although their writings had previously only mentioned good genes. And in April of that year, England received its own eugenic baby, suffragette Sylvia Pankhurst’s son Richard — greeted with international headlines.

It is obviously no coincidence that a similar class of questions about repro-

duction and kinship is being raised in public in the era of the Human Genome Project as in the era of eugenics. If, as David Schneider observed of American culture, new facts of biology are new facts of kinship (1968:23), it is hardly surprising that the genetic discoveries occurring on a nearly weekly basis must be seen to produce new cultural forms, too. I would venture to guess that these social questions were not resolved in the 1920s because of the depression and world war, and the subsequent disfavor into which human genetics fell as a result of the Nazis’ enthusiasm for it.

The importance of heredity in cultural and biological life is the heart of the matter. As folk notions of “who you are and what you are” are reinforced by extravagant scientific claims, a prior scientific generation’s mistakes loom larger. While the HGDP is free of the taint of genetic determinism, it is not immune from the ethical questions produced by global inequalities of wealth and status. Consequently, even as they were promoting the study of “declining human populations” (Diamond 1991) and “ethnic groups on the verge of extinction” (Lewin 1993), the HGDP scientists were obliged to endure criticism for their apparent insensitivity to the real problems faced by the indigenous peoples they were targeting. The project was represented in a Dutch magazine by a photo of a geneticist visiting a presumably isolated people, sarcastically captioned, “Hooray, we’ve come to save your DNA!” (Rozendaal 1995). Was their DNA indeed the most important thing to preserve?

The HGDP promised to study the closest molecular facsimile of the folk “biogenetic substance” all over the world — a promise that resonated in crucial ways with modern contested sites of descent and identity. Are the descendants of Sally Hemings, for example, also those of Thomas Jefferson? Perhaps their DNA would tell. And indeed, some of her descendants “really are” Jeffersons, and others “really aren’t” — although those conclusions do not alter the material conditions of American slavery and its legacy, which were certainly more prominent in determining the life courses of the intervening generations.

Is “Kennewick Man” an ancestral Native American or an ancient Caucoid? Perhaps its DNA would tell. Literally, of course, he was very possibly ancestral to no one — there is no reason to think he was a *genitor*; so his role as ancestor would be in all cases symbolic, the relationship of “his” people to modern people. But having situated these remains in the midst of a highly racialized discourse makes it very difficult to imagine that there might exist a “pure,” “isolated” scientific value of such a find (see Marks 1998).

More tragically, these human remains have been invoked to challenge the identity of Native American "scientifically," an ignominious political role for science at best, although not without precedent. Obviously Kennewick Man is "native" (he is the earliest known inhabitant of the continent) and equally obviously he is "American" (that is, indeed, the landmass on which he was found). His relationship to contemporary populations might be a valid scientific issue, but perhaps not at the cost of cavalierly humiliating and disorienting the indigenous groups that claim him.

It's not that the Indians don't know who they really are and the geneticists do, or vice versa. It's that people's own notions of who and what they are, are important to them and cannot be taken lightly; and that scientific notions are themselves cultural products. When the science is loaded with specious and archaic assumptions about the composition of populations, the ontology of races, and the relationships of ancient and modern peoples, it is of no great benefit either to science or to society. A truly biological anthropology, at once biological and anthropological, might assume a central place in public discourse over these issues. Situated on the boundary between the classically juxtaposed culture and nature, fictive and blood relations, science and humanities—such a field would seem ideally suited for such work. The structure of the discipline is such, however, that we are unlikely to see that—until modern biological anthropology becomes more self-consciously aware of its anthropology.

NOTES

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