

Contemporary bio-anthropology

Where the trailing edge of anthropology meets the leading edge of bioethics

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By the late 18th century the chimpanzee was recognized as overwhelmingly and confusingly similar to the human, even before the existence of genetic data.

The question of how we infer genetic patterns and subsequently interpret them as history has arisen every generation in biological anthropology (Marks 1996), but only with the thorough molecularization of biology, beginning in the 1960s, did it become a central research programme. If the point of contact between biological anthropology and the rest of anthropology is often difficult to identify, that with molecular anthropology – ideally a synthesis of the reductive technology of genetics and the holistic approach of anthropology – is even more obscure. In this essay I discuss the place of molecular biological research in anthropology, with special emphasis on the issues of identity and descent, in which biological data frequently claim an authoritative voice.

Deep molecular bio-history

Since early in the last century, blood analyses have shown that 'the sanguinity of the horse and donkey, which are capable of hybridization, is less close than the kinship of *Homo sapiens* and the anthropoids' (Hussey 1926), a datum inexplicable to anyone committed to the proposition of the zoological uniqueness of humans, which had in any event been under assault since the turn of the 17th century. Biochemical work in the early 1960s found close relations between particular proteins in the blood – human proteins being very similar to the corresponding proteins of the apes – and, by inference, between the genes coding for them (Goodman 1963).

In the ensuing decades that result has been consistently confirmed by diverse methods of genetic analysis, including comparisons of amino acid sequences comprising proteins, and nucleotide sequences comprising DNA: humans are very closely related to the chimpanzee and gorilla – so closely, in fact, that it is difficult to tell just which pair of the three is most closely related. In the 1980s some argued (particularly in the derivative literature) that a molecular consensus had emerged, uniting humans and chimpanzees phylogenetically against gorillas, but there is in fact no dearth of molecular analyses that fail to show that association, and some powerful sets of data that sup-

port the traditional chimpanzee-gorilla association (Livak et al. 1995, Nickerson and Nelson 1998, Barbulescu et al. 2001).

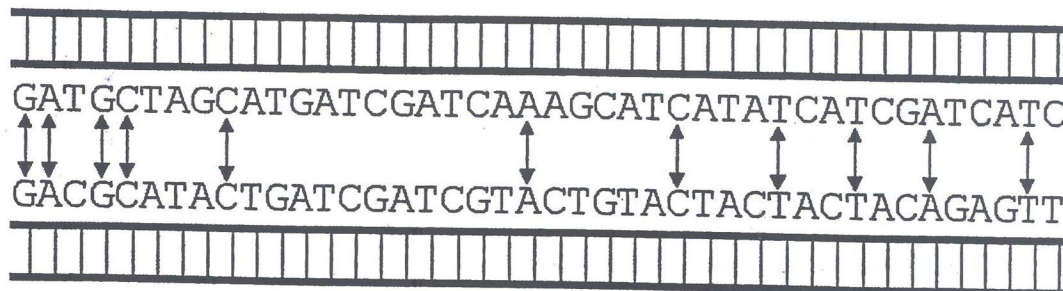
Studies of genetic variation within extant ape species are now well known to show it to be significantly greater in scope than the corresponding variation in humans, in spite of the fact that apes are endangered species, living in small, relict populations (Kaessmann et al. 2001). This, in turn, implies that the ancestral ape-human species was characterized by considerable genetic diversity, and may preclude the possibility of identifying a pair of closest relatives from among its descendants (Ruano et al. 1992).

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This chimpanzee was displayed in London in the late 1730s, and struck viewers as extraordinarily similar to humans, being trained to walk upright and to enjoy an occasional cup of tea.



A comparison of DNA sequences involves tabulating the differences in nucleotide sequences between species. But since there are only four nucleotides (A,G,C,T) the expectation from comparing two DNA sequences purely at random is a 25 per cent match.



1. The quality of a phylogenetic tree is here judged by the number of mutations invoked to unite the DNA sequences into a single array. Molecular evolution is (gratuitously) taken to be parsimonious; i.e. change is assumed to be rare, and thus fewer mutations make for a better tree.

2. National Research Council 1997. *Evaluating human genetic diversity*. Washington, DC: National Academy Press.

3. Opinion by US Magistrate John Jelderks, in *Bonnichsen et al.*, issued 27 June 1997, p. 3.

4. Quite possibly the most widely known scholar formally trained in physical anthropology is the infamous Nazi camp doctor Josef Mengele, who earned a doctorate in physical anthropology under Theodor Mollison and was subsequently apprentice to Otmar Freiherr von Verschuer at the Kaiser Wilhelm Institute.

Anderson, W. 2000. The possession of kuru: Medical science and bioclonial exchange. *Comparative Studies in Society and History*, 42: 713-744.

Anonymous 1932a. Blood groups. *The Lancet*, 7 May: 1024-1025.

- 1932b. Discussion of human blood groups. *Man* 32: 142-143.

Barbulescu, M. et al. 2001. A HERV-K provirus in chimpanzees, bonobos, and gorillas, but not humans. *Current Biology* 11: 779-783.

Begley, S. and Murr, C. 1999. The first Americans. *Newsweek* 26 April 1999: 50-58.

Bonnichsen et al. v. United States of America (Civil No. 96-1481JE).

Boyd, W.C. 1950. *Genetics and the races of man*. Boston: Little Brown and Company.

This has been something of a surprise in the study of molecular evolution generally, where it was once assumed that it would be straightforward to derive a single compelling narrative of bio-historical origins or relationships from molecular genetic data. Actually, the extraction of phylogeny from DNA sequences routinely utilizes statistical packages so arcane that they may well constitute a digital Kabbalah.

In a well-known example, a reanalysis of the original 'mitochondrial Eve' data (Cann et al. 1987) found that the authors had used the computer program PAUP (Phylogenetic Analysis Using Parsimony) naïvely, and had overlooked 10,000 trees 'better' than the one they had actually published (Templeton 1993).¹

It has also come as a bit of a surprise to some observers that it takes no more genes to make a man than to make, say, a grain of rice. This, however, should not be surprising unless one holds that the properties of the cell somehow constitute a microcosm of the properties of the body, the mind, or the society; it is actually simply another demonstration of the adage that genotype (DNA) and phenotype (organism) are phenomenologically distinct. There is no obvious relationship between organic or behavioural complexity on the one hand, and the constituent cell's amount of DNA, number of chromosomes, or the quantity or complexity of its genes, on the other hand (Knight 2002). Rather, a plateau of genomic complexity seems to have been reached fairly early in the emergence of multicellular life, wherein diverse physical, mental, and social adaptations have been produced by the persistent application of a small class of alterations, shufflings, and minor amplifications and reductions to the cell's genes.

My own favourite is the genetic similarity between human and chimpanzee – over 98 per cent – which sounds profound, but only when presented without the context that human DNA is statistically constrained to match banana DNA over 25 per cent of the time. (The constraint is that DNA is a linear series of nucleotides, and there are only 4 nucleotides that can occupy any position; thus a

baseline random similarity must be a 25% match.) Somehow, to aver that we are over one-quarter genetically banana sounds more inane than profound; but it does illustrate the cultural assumptions behind 'natural' similarities. This is not to say that molecular bio-history doesn't work – only that it has its own set of liabilities, which are only gradually coming to light, and commonly in an *ad hoc* fashion. A list of weird phylogenetic results in the published record derived from ordinary analyses of molecular data is easy to compile, and attests to the simple fact that bio-history is just as difficult to infer from genetic as from anatomical data; there is just no substitute for rationation.

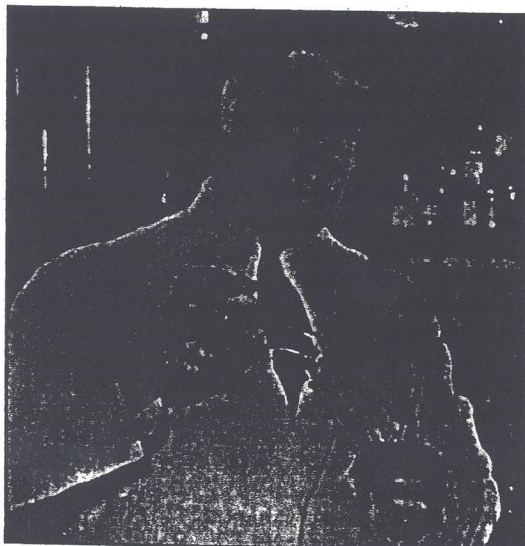
And very likely our models of evolution need to become a bit more sophisticated than the simple bifurcations usually considered. It is easy to envision, for example, an archaic and widely dispersed population of proto-chimpanzees in equatorial Africa, some of whose descendants became gorillas at one end of its range while others became hominids elsewhere, at roughly the same time (Chaline et al. 1991). The result a few millions of years later might well be a pattern of genetic ambiguity very similar to what we in fact find (Deinard 1997).

Human variation

The genetic study of race has a deep history in our field, which it is easy and convenient to forget. For example, the ABO blood group, which is now invoked as *prima facie* evidence supporting our inability to identify discrete large human groupings in genetic data, was used in the opposite way in the 1910s and 1920s, when discrete large genetic groupings were assumed to exist. Thus, Laurence Snyder (1926) could readily identify seven ABO races in the human species. And yet, because the ABO alleles vary within a fairly circumscribed range in human populations, some peoples have ABO frequencies similar to those of distant people, simply at random. Consequently, Snyder was forced to place the Poles and Hunan Chinese in the same ABO race, on the basis of having the same frequencies. The obvious problem is that if there is anything at all to the concept of race, the people of Poland and the people of China were more or less compelled to be in different ones. Consequently the dean of racial studies in America, Harvard's Earnest Hooton, blithely dismissed the utility of genetic/serological research for physical anthropology in his 1931 text, *Up from the ape*.

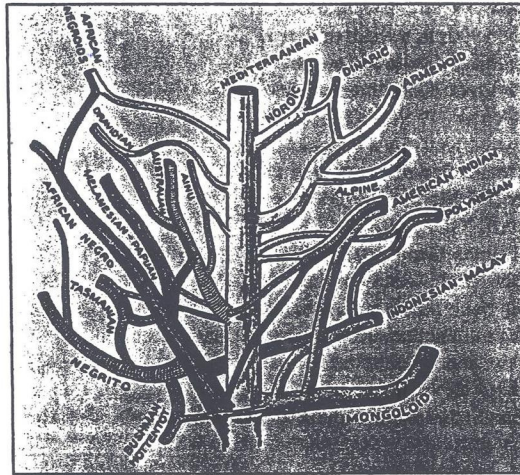
Likewise, the field of racial serology proved vexing for the British anthropology community (Young 1928). When geneticist J.B.S. Haldane gave a paper before the Royal Anthropological Society in 1932 extolling the virtues of blood-group data for racial studies, he was roundly criticized by anatomist Grafton Elliot Smith, who argued that 'anthropologists did not yet know how to fit these tentative new facts into existing ideas of race', and 'it would be rash to try to formulate any comprehensive interpretation at present.' (Anonymous 1932a, b)

Three more decades did little to deflate the balloon of racial serology. In 1962, Frank Livingstone wrote epigrammatically 'there are no races, there are only clines', but a year later serologist William C. Boyd (1963) would



William C. Boyd, serologist and physical anthropologist (ca. 1950); from Boyd 1950.

Ernest Hooton's (1931) depiction of 'Blood streams of the human races' showed them as a complex capillary network, rather than as the simple bifurcating structures regularly shown by contemporary population geneticists.



Boyd, W.C. 1963. Genetics and the human race. *Science* 140: 1057-1065.

Cann, R.L., Stoneking, M. and Wilson, A.C. 1987. Mitochondrial DNA and human evolution. *Nature* 325: 31-36.

Cann, H. M. et al. 2002. A human genome diversity cell line panel. *Science* 296: 261-262.

Cavalli-Sforza, L.L. 1974. The genetics of human populations. *Scientific American* 231(3): 81-89.

Cavalli-Sforza, L.L. and Edwards, A.W.F. 1965. Analysis of human evolution. In S. J. Geerts (ed.) *Genetics today: Proceedings of the XI International Congress of Genetics*, pp. 923-933. Oxford: Pergamon.

Cavalli-Sforza, L.L. et al. 1989. Reconstruction of human evolution: Bringing together genetic, archaeological, and linguistic data. *Proceedings of the National Academy of Sciences, USA* 85: 6002-6006.

- 1991. Call for a worldwide survey of human genetic diversity: A vanishing opportunity for the Human Genome Project. *Genomics* 11: 490-491.

Chaline, J. et al. 1991. Un modèle chromosomique et paléobiogéographique d'évolution des primates supérieurs. *Geobios* 24(1): 105-110.

Chatters, J. 2001. *Ancient encounters*. New York: Simon and Schuster.

Cunningham, H. 1997. Colonial encounters in post-colonial contexts. *Critique of anthropology* 18: 205-233.

Deinard, A. 1997. 'The evolutionary genetics of the chimpanzees'. PhD dissertation, Department of Anthropology. New Haven: Yale University.

Goodman, M. 1963. Serological analysis of the systematics of recent hominoids. *Human Biology* 35: 377-436.

Harpending, H. 1994. Gene frequencies, DNA frequencies, and human origins. *Perspectives in Biology and Medicine* 37(3): 384-394.

Hulse, F.S. 1962. Race as an evolutionary episode. *American Anthropologist* 64: 929-945.

publish a definitive classification of the human races, based on their blood group data. It is instructive to examine Boyd's 13 races, in light of the claims to objectivity that accompanied them, and the fact that we now say they do not exist at all. Boyd's first five races comprised the European group, consisting of (1) the Basques, (2) the Lapps, (3) northwest Europeans, (4) eastern/central Europeans, and (5) Mediterraneans. His sixth race was Africans, and his seventh was Asians. His eighth and ninth were the Indo-Dravidians and the American Indians. The list was rounded off with his Pacific group – (10) Indonesians, (11) Melanesians, (12) Polynesians, and (13) Australians.

The fact that Boyd could identify only one race on the world's largest landmass, Asia, and no less than five in Europe, speaks eloquently about the cultural nature of the endeavour (likewise, the fact that he could somehow find biological equivalence between the Basques and the Africans!). Julian Huxley (1931:379) had written decades earlier, 'It is a commonplace of anthropology that many single territories of tropical Africa, such as Nigeria or Kenya, contain a much greater diversity of racial type than all Europe.' But somehow that issue wasn't raised against the genetic work in the 1960s.

When genetic data were expected to yield races, they did so readily; now they routinely do the opposite. With genetic data, it seems, one could find entities that did not really exist, or impose cultural assumptions on the data and mistake them for patterns inherent in the data, yet still cloak oneself unimpeachably in the mantle of modern science.

At about the same time, in the early 1960s, the renowned population geneticist L.L. Cavalli-Sforza was beginning to apply newly developed multivariate statistical techniques to the interpretation of the blood-group data and isozymes (variant forms of enzymes detectable in blood) – not for the classification of races, but for the more intricate study of the history of human populations. When programmed to do so, a computer could digest a complex array of data on several populations, and transform those populations into a simple bifurcating structure that resembled a phylogenetic tree. The resemblance was merely superficial, since the real biological history of human populations involved lines that branched and merged, like the anastomoses of a capillary system, which is precisely the way Hooton had depicted them in *Up from the ape* (Marks 2002b: Figure 2). Hooton's former student Frederick Hulse (1962) asked whether 'the standard design of the ancestral tree, so useful in representing the descent of different species [which are always divergent], has misled us. Is such a design appropriate as a representation of sub-specific diversification?' – and answered in the negative.

Technology, however, prevailed over such minor reali-

ties, and the new work depicted bifurcating *trees* of human populations and represented them as bifurcating *histories*. The *dénouement*, however, was a contrast between such trees generated from genetic data and from anthropometric data, and reverted directly to a racial question: of Europeans, Africans, and Asians, which two were closest relatives?

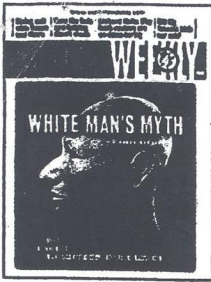
What Cavalli-Sforza and his colleagues found was that a tree derived from anthropometric data grouped EurAsians against Africans, implying a primordial North-South division of peoples of the Old World; but a tree derived from genetic data grouped EurAfricans against Asians, implying a primordial East-West division. His interpretation was nothing if not self-serving: 'This suggests that anthropometric characteristics are more affected by climate than genes are, so that the relations [they show] are due more to similar environments than to similar descents' (Cavalli-Sforza 1974:87). Cavalli-Sforza also calculated a divergence time for the split between the EurAfricans and Asians, estimating that it occurred 35,000-40,000 years ago.

But with a different analytical method applied to the same class of genetic data, Nei and Roychoudhury (1974) obtained an entirely different result. The earliest split was between Africans and EurAsians (as the anthropometric data had indicated), and it was about three times earlier than the date Cavalli-Sforza had suggested. This tree was derived most strongly with enzyme and protein data, rather than with classical blood-groups, but was ultimately acknowledged as the correct one by Cavalli-Sforza in 1988.

It is now commonsensical that such tree construction is sensitive to the demographic histories of populations – especially contact and expansion, the populations chosen, the genetic systems chosen, the evolutionary processes operating, and the clustering technique used (Harpending 1994, Relethford 2001, Rogers 2002). Indeed, the most robust result of the 'mitochondrial Eve' work seems to be the discovery that Africans subsume the genetic diversity found in the rest of the human species. This, in turn, would imply that Africans cannot be contrasted genetically with Europeans and Asians, any more than the category Mammalia, which subsumes Carnivora (e.g. cats) and Cetacea (e.g. whales), could meaningfully be contrasted against Carnivora and Cetacea. Which two of Mammalia, Carnivora, and Cetacea are most closely related? Any tree obtained – and of course, you can always get a tree! – would depend first and foremost upon what you chose to represent Mammalia.

Likewise, if Africans genetically subsume Europeans and Asians, then the three are not comparable units, and a comparison among them is not bio-historically meaningful. They do, of course, constitute comparable 'racial' units in a cultural or folk-taxonomic sense – which is obviously the basis on which the question was framed. Thus, once again, behind a veneer of modernity, science, and objectivity lay a research question structured culturally and rendered sensible only in the context of the social categories of race.

Widely publicized recent results, such as the age and number of waves of immigration into prehistoric America, or the identity of a group of indigenous South Africans as crypto-Jews (Thomas et al. 2000), are still frequently predicated on uninterrogated interpretations of patterns of modern genetic diversity, often with strikingly essentialist assumptions. They frequently casually elide 'haplotypes' (a configuration of specific genetic variations adjacent to one another) and 'founders', or 'haplogroups' (a cluster of similar haplotypes in a population), and 'migrations'. I suspect we have every reason to be at least as sceptical of their conclusions as we can be in retrospect of similar pronouncements in earlier generations.



Top: The reconstructed skull of Kennewick man on the front cover of Seattle Weekly.

Right: 'Hurrah! We've come to rescue your DNA' exclaimed the title of this story sarcastically in the Dutch news magazine Elsevier.

Hussey, L.M. 1926. The blood of the primates. *American Mercury* 9: 319-321.

Huxley, J. 1931. *Africa view*. London: Chatto and Windus.

Kaessmann, H., Wiebe, V. and Paabo, S. 2001. Great ape DNA sequences reveal a reduced diversity and an expansion in humans. *Nature Genetics* 27: 155-156.

Knight, J. 2002. All genomes great and small. *Nature* 417:374-376.

Livak, K.J., Rogers, Jeffrey and Lichter, J.B. 1995. Variability of dopamine D4 receptor (DRD4) gene sequence within and among nonhuman primate species. *Proceedings of the National Academy of Sciences, USA* 92: 427-431.

Livingstone, F.B. 1962. On the non-existence of human races. *Current Anthropology* 3: 279-281.

Marks, J. 1996. The legacy of serological studies in American physical anthropology. *History and Philosophy of the Life Sciences* 18: 345-362.

-2002a. *What it means to be 98% chimpanzee*. Berkeley: University of California Press.

-2002b. 'We're going to tell those people who they really are': Science and relatedness. In S. Franklin and S. McKinnon (eds) *Relative values: Reconfiguring kinship studies*, pp. 355-383. Chapel Hill, NC: Duke University Press.

The face of civilized Europe conceals a prehistoric past. An australopithecine with a human mask from the exhibition The Human Story: Commonwealth Institute, 21 November 1985-23 February 1986.

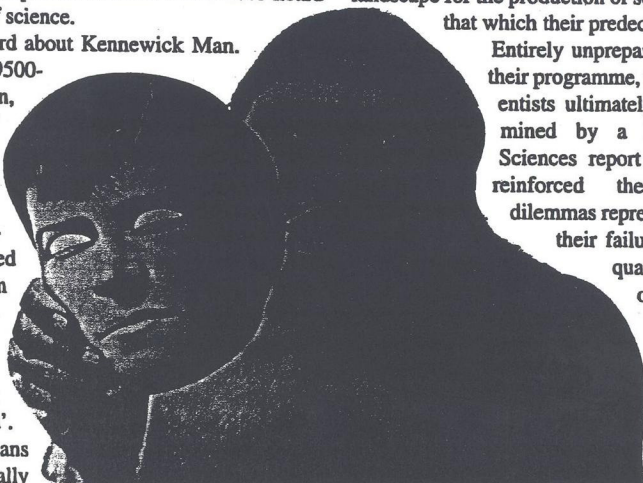
Human rights

A related issue arose initially in the 1990s as a result of the efforts of human population geneticists to drink at the trough of the Human Genome Project. Conceived as a medical programme, the Human Genome Project's goal of sequencing 'the' human genome was effectively a Platonic throwback, casting a blind eye to the bio-diversity that characterizes real species (Walsh and Marks 1986). The Human Genome Diversity Project (HGDP), proposed in 1991 as an augmentation to the Human Genome Project, would study the biodiversity in the human species (Cavalli-Sforza et al. 1991). But their aim was not to describe the human gene pool at the millennium, but rather to collect and catalogue the DNA of indigenous, 'endangered' people (Roberts 1991), with the goal of reconstructing an imaginary pre-colonial human species of centuries earlier.

Anthropologists had, of course, been retrieving blood from the field for decades on a small scale, and effectively flying under the bioethical radar. Coming just a year after the passage of the Native American Graves Protection and Repatriation Act (NAGPRA), which was intended in part to return biological remains of sacred value to their rightful proprietors in the US, the HGDP suddenly shone a bright light on the collection and disposition of indigenous peoples' blood. After all, it was a commodity that made academic careers, forged scientific alliances (Anderson 2000), and in most cases gave virtually nothing back to the original communities, much less to the original blood 'donors'. Moreover, recent legal precedents supported the financial interests of researchers working with bio-genetic materials over the financial interests of the people who were the original sources of those materials. The blood of indigenous peoples might well thus constitute a motherlode of patentable genetic gold. This was not lost on activists, who began to protest against 'bio-colonialism' (Cunningham 1997, Reardon 2001).

The HGDP, however, denied any economic interest in the cells they sought. They professed to be interested only in the pursuit of scientific goals. Participating in a HGDP symposium at a bioethics conference in 1996, I was struck by the justification given for the project by one of its advocates: 'We're going to tell these people who they really are.' And he didn't mean it in a New-Age sense, either. He meant it *literally*! They wanted the blood of indigenous peoples in order to de-legitimize these peoples' own senses of identity and history. And if the 'samples' he sought were rapidly becoming a valuable global commodity, he was not interested in talking about it. Over and above all the reservations I already harboured about the Human Genome Diversity Project, what kept reverberating in my mind was that this was undoubtedly the most thoughtless and presumptuous twaddle I had ever heard uttered in the name of science.

That is, until I heard about Kennewick Man. Kennewick Man is a 9500-year-old skeleton, found in the state of Washington on 28 July 1996. A study of his cranial morphology led to the discovery that he looked rather different from the expected appearance of American Indian skulls, and to the bizarre claim that he was 'Caucasoid'. That ancient Americans were more skeletally



'Hoera, we komen uw DNA redden'

HET CONFLICT OVER HET MENSELIJK DIVERSITEITS PROJECT

Het leek zo mooi. Amerikaanse onderzoekers wilden het DNA van uitstervende inboorlingen vastleggen voor het te laat was. Actiegroepen vonden dat maar niets. Inboorlingen zijn geen fruitvliegen! En dus is het 'Human Genome Diversity Project' dat volgend jaar officieel van start zou moeten gaan, in allerlei problemen terecht gekomen.

Niet alleen vindingen en ontdekkingen... Het is 1998... In 1998 stond er een plebisiet... Het is 1998... In 1998 stond er een plebisiet... Het is 1998... In 1998 stond er een plebisiet...

diverse than contemporary Native Americans is well known - Earnest Hooton identified crania resembling those of Africans, Australians, and Europeans in the pre-contact remains from Pecos Pueblo, Colorado in 1930. In this case, however, Kennewick Man's presumptively Caucasoid features became a fulcrum for unbalancing NAGPRA. If he were Caucasoid, then the 'Mongoloid' Americans could not claim descent from him, which in turn implied that the New World was settled first by Europeans, as could be seen by presumptive similarities between Upper Palaeolithic Solutrean tools and (several millennia later) American Clovis points. That this sounds like a bad undergraduate thesis from the 1890s did little to mitigate the vigour with which anti-NAGPRA scientists popularized this scenario in the media (Preston 1997, Petit 1998, Begley and Murr 1999).

What linked the Diversity Project to Kennewick Man is the cavalier fashion with which scientists - and in both cases, self-righteous, self-interested, self-proclaimed and slightly paranoid spokesmen for science - could rewrite origin narratives and identities of other peoples on the basis of partial, ambiguous, or dubiously interpreted evidence. In both cases, skeletal and genetic anthropology, the current generation faces a different social and political landscape for the production of scientific knowledge from that which their predecessors knew.

Entirely unprepared for the opposition to their programme, the genome diversity scientists ultimately saw their plan undermined by a National Academy of Sciences report issued in 1997, which reinforced the modern bioethical dilemmas represented by the HGDP and their failure to address them adequately.² Nevertheless, some of its enthusiasts maintain the HGDP was 'almost completely derailed by political opportunists' (Henry Harpending in the *American Journal of Physical Anthropology*).

Nei, M. and Roychoudhury, A.K. 1974. Genic variation within and between the three major races of man, Caucasoids, Negroids, and Mongoloids. *American Journal of Human Genetics* 26: 421-443.

Nickerson, E., and Nelson, D.L. 1998. Molecular definition of pericentric inversion breakpoints occurring during the evolution of humans and chimpanzees. *Genomics* 50: 368-372.

Preston, D. 1997. The lost man. *The New Yorker* 16 June: 70-78, 80-81.

Petit, C.W. 1998. Rediscovering America. *U.S. News and World Report* 12 October: 56-64.

Reardon, J. 2001. The Human Genome Diversity Project: A case study in coproduction. *Social Studies of Science* 31: 357-388.

Relethford, J.H. 2001. *Genetics and the search for modern human origins*. New York: Wiley-Liss.

Risch, N. et al. 2002. Categorization of humans in biomedical research: Genes, race and disease. *Genome Biology*, 3: 2007.1-2007.12.

Roberts, L. 1991. A genetic survey of vanishing peoples. *Science* 252: 1614-1617.

Rogers, A.R. 2001. Order emerging from chaos in human evolutionary genetics. *Proceedings of the National Academy of Sciences, USA* 98: 779-780.

Ruano, G. et al. 1992. DNA sequence polymorphism within hominoid species exceeds the number of phylogenetically informative characters for a HOX2 locus. *Molecular Biology and Evolution* 9(4): 575-586.

Snyder, L. 1926. Human blood groups: Their inheritance and racial significance. *American Journal of Physical Anthropology* 9: 233-263.

Templeton, A.R. 1993. The 'Eve' hypothesis: A genetic critique and reanalysis. *American Anthropologist* 95: 51-72.

Thomas, M.G. et al. 2000. Y chromosomes traveling south: The Cohen modal haplotype and the origins of the Lemba - the 'Black Jews of Southern Africa'. *American Journal of Human Genetics* 66: 674-686.

Walsh, J. and Marks, J. 1986. Sequencing the human genome. *Nature* 322: 590.

Young, M. 1928. The problem of the racial significance of the blood groups. *Man* 28: 153-159, 171-176.

116:177, 2001) - still unable to confront either the political nature of its own proposal, or its own failure to respond effectively to the global social issues it had raised. Licking their wounds, its advocates continue working on samples collected *ad hoc*, and have recently regrouped in France (Cann et al. 2002).

No clear explanation has yet been given as to why one must seek permission to do research on Yanomamo genetics from researchers at Penn State, rather than from Yanomamo - much less whether there is any understanding on the part of the Yanomamo of the careers and perhaps even fortunes to be made through the study of their blood, or its derivative product DNA, in the perpetual custody of others. Meanwhile, some prominent population geneticists are busy, even now, reifying races for biomedical use (Risch et al. 2002), writing from an unselfconscious 'objective scientific perspective' - which could well jeopardize health care to large numbers of people.

The anti-NAGPRA skeletal scientists, however, having been denied access to the ancient remains of an American ancestor, opted to institute legal action in the belief that they had the right to perform their science over the objections of the local people ('The... plaintiffs filed suit... to enforce what they contend is a legal right to study the remains').

This is the issue on which the HGDP and Kennewick Man converged for me: Do scientists have the right to study whatever they want, without regard to the wishes or sensibilities of the relevant people? That question has, of course, been answered for all time in the wake of World War II. They do not.

The advancement of science is a great thing, but it must be weighed against the encroachment upon basic human rights. And today there is a fundamental human right under constant threat: the right *not* to be a scientist. Science is among the most ruthlessly ethnocentric and intolerant ideologies in the modern world, many of whose most prominent representatives believe they have a Victorian destiny to supplant religion. Please do not misunderstand me - I am a scientist, I teach science, and I was debating against creationists in graduate school long before it became fashionable. But being a scientist, or doing science, does not necessarily entail evangelism for science. After all, teaching or doing art history does not involve intellectually cloning art historians; it simply involves instilling an appreciation for what art historians have done and for how they think.

Neither the Human Genome Diversity Project nor the Kennewick Man battle casts science in a particularly favourable light. Both reveal scientists who believe they have a right - perhaps even a duty! - to de-legitimize other people's ideas about who they are and where they came from.

This is not to say that science should not be interested in such things. Bio-history is a patently approachable question scientifically, and an entirely legitimate venue of scientific inquiry. The pragmatic question is, how, then, do you honestly secure the participation of the very people whose ancestors, relics, relations or blood you wish to study, when your research agenda is constructed to undermine their beliefs? Who would want to participate in such a study, if its purpose were as candidly disclosed to them as it was to the scholarly audience - telling these people who they 'really' are? I certainly can't blame the Native American groups who wished to bury Kennewick Man without letting science study him, when the scientists' initial plans were to transport him to the Smithsonian without permission so that he could be studied in comfort and repatriated only with difficulty (Chatters 2001: 71ff.). The many anthropologists who work in an atmosphere of respect and amity with indigenous groups have been given



As the authoritative voice on identity and descent, science's track record is hardly blemish-free. Pre-Darwinian images like this (from Julien-Joseph Virey's 1824 *Histoire naturelle du genre humain*), which placed non-white peoples in between Europeans and apes, were readily transformed into evolutionary narratives, telling other peoples 'who they really are'.

a black eye by the arrogance and belligerence of the few who recreate exploitative or insensitive relations with local communities. Unlike chemists, who have the leisure to study boron without having to worry what boron thinks of them, anthropologists work at the mercy of other people's thoughts and attitudes about them.

As of this writing, the American Association of Physical Anthropologists is one of the few - perhaps the only - major professional anthropological society to lack a code of ethics. For a field that began as little more than simple grave-robbing, this is perhaps not unexpected. But an anthropology that treats people contemptuously - as represented by the high-profile HGDP and the Kennewick Man combatants - will make it hard for the rest of the field to survive well into the current century. ●

On 21 and 22 September 2002, the Society for the Study of Human Biology will sponsor a symposium entitled 'Diversity, difference, and deviance: Ethics in human biology', organized by George Ellison and Alan Goodman