Science as Culture
Vol. 14, No. 2, 161–183, June 2005

Routledge
Taylor & Francis Group

The Mitochondrial Eve of Modern Genetics: Of Peoples and Genomes, or the Routinization of Race

AMADE M'CHAREK

Department of Biology, Department of Political Science, University of Amsterdam, The Netherlands

Introduction: The Diversity Project

In June 2000 the sequence of the complete human genome was presented to the world by science, politics and commerce. Since then, we have learned that the work of the Human Genome Project is not yet complete. Substantial parts of that genome are still being mapped. However, as early as 1981 a complete sequence of another human genome was produced in Cambridge—not a sequence of nuclear DNA, but that of the mitochondrial DNA. Ever since the publication of this sequence, it became the reference genome for geneticists. It is a standardized technology that is known as 'Anderson', referring to the first author of the scientific paper (Anderson *et al.*, 1981). Now it can be downloaded from the Internet, and appears on the computer screen as a text. Anderson plays a central role in studies of genetic diversity—the study of similarities and differences within and between populations—and most notably so in the international endeavour of population genetics known as the Human Genome Diversity Project.

Anderson is a reference genome and thereby a standard to which other human sequences are compared. However, standards can never be neutral. They are always produced somewhere in particular kinds of practices and they involve specific social worlds (Fujimura, 1992, 1995; Star, 1991, 1995). Yet their functioning as standards and their ability to comply with everyday practice, tends to obscure their normative content and to make that inaccessible for interrogation (Star, 1995). So, in the words of Susan Leigh Star, '[w]here does the mess go' (Star, 1995, p. 111)? Her answer to this question is that: 'it doesn't go anywhere; rather, it is the formal representations that attempt to leave it behind' (Star, 1995, p. 111). In this paper I will investigate how the Anderson sequence was produced and how it is applied nowadays in scientific practice. I will draw in some particular 'mess' attached to this reference genome and situate that back in laboratory practice. This is not because I think it should be there all the time, but rather because

Correspondence Address: Amade M'charek, Department of Biology, Department of Political Science, University of Amsterdam, OZ Achterburgwal 237, NL-1012, DL Amsterdam, The Netherlands. Email: a.a.mcharek@uva.nl

0950-5431 Print/1470-1189 Online/05/020161–24
DOI: 10.1080/09505430500110945

I contend that there are stakes involved in its accessibility for geneticists and others. As Helen Verran argues: 'Being messy and seamy, acknowledges the actualities of other times and places, and makes the generalizer's accumulation of power more evident—and, for that reason, less certain' (Verran, 2002, p. 757). Even though it moves smoothly between laboratories, Anderson carries with itself practices from other times and places. I will analyse these practices and argue that the naturalization of this technology in the context of genetic diversity contributes to the erasure of race and sex-differences as embodied parts of the sequence. Before introducing the argument and the organization of this paper, let me first elaborate on the Human Genome Diversity Project (hereafter the Diversity Project).

The Diversity Project was initiated in 1991 by Luigi Luca Cavalli-Sforza (Stanford University) and Allan Wilson (Berkeley University). It is aimed at studying as many as 500 populations in order to map human genetic diversity.[1] Departing from the presupposition that modern humans originated in Africa and that they are members of one genealogical family, one of the goals of this Project is to reconstruct this history. This has included posing questions such as: how did humans migrate out of Africa, to 'colonize' the rest of the world? How do contemporary populations relate to one another? What are the similarities and differences between them? And which populations could be considered older and which younger? In short, geneticists want to learn about genetic diversity and lineage.

Such studies of populations are not new. However, newly introduced technologies within the field of genetics have brought within reach a study of diversity on a much larger scale. Technologies, such as PCR (Polymerase Chain Reaction) which is a DNA copying technology, automated sequencing technologies, huge numbers of genetic markers, and also the Internet and other aspects of information and communication technologies (ICT) that make possible the compilation of databanks, are at the heart of the Diversity Project (HUGO, 1994, pp. 22–28).

However, while this technology is cutting-edge and favourable for the purpose of the Diversity Project, there appeared several problems with the issue of population. 'What is a population?' was not just a question that needed to be tackled in terms of definition. Populations seemed to be disappearing as discrete entities, specifically in the West. Due to admixture their genetic material had become oblique and difficult to analyse. Geneticists in the Diversity Project thus turned to *isolated populations* and *indigenous peoples.* Analysing and comparing the genetic material of various of these populations, geneticists aim at gaining insight into 'genetically complex' populations, i.e. populations that are less isolated, less unique and less easy to categorize and to study (HUGO, 1994, pp. 6–7, 12–13). It seems that those who are not taken to be connected to the global traffic of humans and things, especially those in far-off places, are considered the best sources for understanding how the genetic 'melting pots' must have come about (Lock, 2001; Haraway, 1997). Based on the idea that genetic diversity is better preserved in 'isolated populations' and the idea that all humans belong to one 'genealogical family', these populations are assigned the role of 'origin' and 'resource'. They are thus considered to be more homogeneous and their genetic makeup to be more conserved than those of the western 'melting pot'. Although various different versions of population circulate in the Diversity Project (M'charek, 2005; NRC, 1997), this particular emphasis on 'isolated' or 'indigenous' populations caused problems for the Project.

Haste and Race

The Diversity Project was launched with a rhetoric of preservation, time pressure, and alarm (see also Hayden, 1998). In June 1991 the journal *Science* published an article headed: 'A Genetic Survey of Vanishing Peoples', which opened: 'Racing the clock, two leaders in genetics and evolution are calling for an urgent effort to collect DNA from rapidly disappearing populations' (Roberts, 1991, p. 1614). One of them, the population geneticist Cavalli-Sforza argued that:

> if sampling is too long delayed, some human groups may disappear as discrete populations [. . .]. At a time when we are increasingly concerned with preserving information about the diversity of the many species with which we share the Earth, surely we cannot ignore the diversity of our own species (Cavalli-Sforza, 1993, p. 2).[2]

However, the Diversity Project soon ran into trouble. It was faced with a variety of criticisms, especially from indigenous and environmental organizations. It was soon dubbed 'The Vampire Project', referring on the one hand, to the collecting of blood samples (de Stefano, 1996; Dickson, 1996; Lock, 2001), and on the other, to the implicit notion of a pure and untouched 'other' (Haraway, 1997). Furthermore, this naming suggested that the groups from which samples were taken were ill-informed and misled by geneticists and that the samples were collected for interests other than those of the sampled groups. In the television documentary *The Gene Hunters*, the professor of medical ethics George Annas (MIT) put it as follows:

> We're taking from them their DNA, which we now consider like gold. It's even worse than standard colonialism and exploitation, because we are taking the one thing that *we* value, and after we take that, we have no real interest in whether they live or die.

In that same documentary the spokesperson for the Arhuaco People, Leonora Zalabata, stated:

> Our land, our culture, our subsoil, our ideology, and our traditions have all been exploited. This [the Diversity Project] could be another form of exploitation. Only this time, they are using *us* as raw material.[3]

Now, interestingly enough the Diversity Project was launched as a response to the Human Genome Project. As Cavalli-Sforza has put it:

> [t]he Human Genome Project aims to sequence 'the' human genome with DNA taken mainly from individuals likely to be of European ancestry in North America and Europe. But, like all brothers and sisters, all humans have slightly different genomes (Cavalli-Sforza, 1993, p. 2).

He therefore proposed 'to explore the full range of genome diversity within the human family' by studying a more diverse set of populations (pp. 2–3). Beyond this, population geneticists viewed the Diversity Project as a means to combat racism:

> By leading to a greater understanding of the nature of differences between individuals and between human populations, the HGD Project will help to combat the widespread popular fear and ignorance of human genetics and *will make a significant contribution to the elimination of racism* (HUGO, 1994, p. 1, my emphasis).

The Diversity Project does not only aim at contributing to the elimination of racism but also of sexism. In the evaluation of the Diversity Project by the National Research Council it is suggested that no samples should be collected from women in societies where they are not allowed to give their full consent (NRC, 1997, p. 63). Nevertheless, as my brief account indicates, colonialism and exploitation on the one hand, and knowledge about genetic diversity and the combating of racism (and sexism) on the other, are implicated in the Diversity Project. The question remains whether and how such politics can be disentangled in what comes out of the project as knowledge.

This is the case firstly because, in spite of the promise of amending established ideas about biological difference between races, or populations for that matter, in the debates about the Diversity Project many divides are being reified, such as the melting pot in the West versus the isolate in far off places, and the genetically heterogeneous here versus the genetically pure there. This involves a separation between the world of science and technology and the world of the resourced object of study (Watson-Verran and Turnbull, 1995).[4] In this divide it appears as if (isolated) populations are out there, in nature waiting for geneticists and their technologies to reveal their histories. The idea that human history can be read off from genes is problematic, but so also are questions about what makes a population (M'charek, 2000a) and about what makes some populations into 'isolates' or 'indigenous' and not others.

The Diversity Project has put more than 500 so-called 'isolated populations' on its priority lists. As many anthropologists have shown, the fact that some groups in the world are relatively isolated does not mean that this has always been the case: 'The San peoples of South Africa, for example, at the top of the so called "genetic isolate list", and therefore a pristine example of an uncontaminated population by HGDP standards, embrace three different language groups, suggesting relatively recent formation as a single group. [. . . T]he San became isolated only in the nineteenth century, and their isolation is related directly to colonialism' (Lock, 2001, p. 80). Thus, genetic isolatedness of populations could itself be seen as an effect of the scientific endeavour of the Diversity Project itself, which is based on a rather naïve version of history. Those living in far off places are re-produced as genetically (and culturally) homogeneous and pure, and as having migrated out of the tribe long ago to work their way up to the modernist melting pot.

Secondly, this is the case because the Diversity Project did not start *de novo*, but builds on a history of genetics which is densely intertwined with notions of race and sex-differences (Kevles, 1985). This history did not only materialize in knowledge that can be found in books and papers, but also in the material objects of study (in the form of collections of samples in laboratories) and technologies that are still being applied (M'charek, 2000b). In this paper influenced by post-colonial studies of science and technology, I do not separate beforehand the 'centres' of knowledge production and the

'margins' associated with objectified 'others' (Anderson, 2002). Even though I take the laboratory as my point of departure, I am also interested in the worlds that enter the laboratories, in how these are changed, re-produced, and materialized in such locales. Whereas technology is often represented as autonomous, and knowledge as contained in the object of study, various studies have shown that, in practice, they are interdependent (Latour, 1987; Mol, 2002; Knorr-Cetina, 1995).

Thus in order to *denaturalize* the objects and technologies of science I will view geneticists, their objects of study and their technologies as members of 'a tribe' endowed with culture, norms and values. This is a strategy of location and a crucial move that has been taken in the field of science and technology studies from the late 1970s onwards (Mol, 1990; Mol and Law, 1994; Haraway, 1991b; Anderson, 2002). It is a move through which scientific work is no longer viewed as a machinery through which nature is discovered and through which its functioning is rationally deduced. Rather, science is regarded as practice and culture (Pickering, 1992; Haraway, 1991b). As such, it is an activity that can be *located* somewhere: where nature is enacted in particular ways (see also Watson-Verran and Turnbull, 1995) that cannot be disentangled from how scientific work is done in such a setting. I will therefore direct my attention towards practices of knowledge production and focus on the social worlds that get implicated in technologies and routines. For this purpose I shall enter the laboratory.[5]

I will develop two arguments based on an analysis of a standardized technology, namely the mtDNA reference genome. First, I shall show that, even though it moves smoothly between laboratories where genetic diversity is being studied, this genome was produced somewhere in a particular time and place. I will trace the technologies and tissues that contributed to its sequencing and investigate how race and sex-differences are implicated in it. Secondly, I contend that the reference genome had not only become a standardized but also a naturalized technology. I will examine the practices that contribute to its naturalization and argue that with the help of the universal theory of mitochondrial DNA inheritance, the sequence is performed as a 'natural' origin. To these ends we will first view how Anderson is applied in a laboratory setting and the kind of work it enables there. After this, we go back in time and consider the kind of tissue and technology that was involved in producing the Anderson sequence. The analysis here will focus on the present absence of race and sex-differences. The final part of this paper deals with the naturalization of Anderson. However, since the mtDNA reference genome is embedded in a particular line of research on genetic diversity, I suggest that we begin with a brief look at the different DNA systems applied in such studies.

mtDNA and nDNA in Studies of Lineage

For the purpose of studying genetic lineage, geneticists in the Diversity Project study specifically the non-coding parts of the DNA. These are DNA-fragments that (as far as is known) have no function in the human cell. For such studies geneticists have two DNA systems at their disposal: nuclear DNA (nDNA) and mitochondrial DNA (mtDNA). nDNA is located in the nucleus, whereas mtDNA can be found in the cytoplasm, surrounding the nucleus. The nDNA is a large (3.5 billion base pairs or DNA building blocks) linear genome, stretched out over the 46 chromosomes. The mtDNA is a small (16.6 thousand base pairs) circular genome located on the mitochondria, the energy suppliers of the cell. Each human cell contains one nucleus, but may contain thousands of

mitochondria. Thus, compared to the two copies of nDNA (one stemming from the father and one from the mother), each cell may contain many more copies of mtDNA genomes. This constitutes one of the major advantages of mtDNA. As we will see below, the large number of copies had made it possible to study mtDNA in the early 1980s. Moreover, because of its location in the cytoplasm, mtDNA is passed on only via the mother. Since sperm cells (stemming from the father) consist mainly of a nucleus, only the cytoplasm and mitochondria of the mother become part of a fertilized egg cell.

Now why is this one parental inheritance of mtDNA relevant for studies of genetic lineage? The fact that mtDNA comes from one parent only means that differences that can be found in a genome are the result of one event only, namely mutation. A mutation is a random change in the mtDNA sequence. By contrast, differences in nuclear DNA may be due to both mutation, and recombination (the reshuffling of genes stemming from both parents). Hence the source of differences in the mtDNA is less ambiguous. This one parental (maternal) inheritance of mtDNA allows geneticists to trace back in time the origin of mtDNA and to reconstruct the history of genetic lineage based on straightforward statistical models. This is also the reason for mtEve (also called 'Black Eve'), the mundane and all-human mother who is supposed to have lived in Africa 200,000 years ago (Cann *et al.*, 1987).

The number of mtDNA genomes in one human cell involves a major advantage for geneticists. As will become clear, this is also one of the main reasons that Anderson, a mtDNA genome, could be produced in the early 1980s. But first, let us view how Anderson is employed in scientific practice.

Anderson: A Reference Genome

Anderson is a standardized technology. It is a sequenced genome that can be retrieved from the Internet for usage in numerous laboratories. How is this reference genome applied in laboratories where genetic lineage is being studied?

First of all, it helps geneticists to *locate other sequences* that they are studying. Since geneticists would only study a small fragment of such sequences, Anderson helps to identify the beginning and the end of a target DNA fragment within its larger sequence. Aligning Anderson to such fragments, geneticists search for the highest match between the nucleotides (the DNA building blocks) of the reference genome and of the target sequence. Secondly, it allows geneticists to *trace differences* between Anderson and the sequences studied. These differences (mutations) are the pieces of information that geneticists are after. Comparing the sequences of interest to Anderson allows them to reconstruct genetic lineage based on proximity and distance. Shared mutations are read as lineage and non-shared mutations as divergence between populations. Thirdly, Anderson provides geneticists with a *nomenclature* and a system of how to refer to differences between sequences within a scientific community. It provides a template for the numbering of mutation sites according to the reference sequence. Anderson therefore functions as a communications technology. This is exemplified by the fact that geneticists do not have to present the sequence fragment of the individual studied; they just mention the mutations they find and the locations of these mutations.

But as we know, communication technologies are not neutral media. They always come with a message. While facilitating communication, technologies also structure the nature of that communication. So let us take a look at one of the messages conveyed by Anderson,

and at how it interferes with the sequences that are being studied in laboratories. Despite its high-tech, automated, and roboticized features, sequencing DNA may still produce ambiguities and involve decision making. For example, next to the familiar nucleotides (A,T,C,G), sequences may contain positions addressed as 'M' or 'N'. Such letters indicate that the sequencing and visualizing technology could not decide which of the nucleotides it had to be. It is at these moments that Anderson comes in handy. It helps in the *editing* of sequences, which contain such ambiguities. In laboratories such sequences are usually corrected *towards* Anderson. In doing so geneticists rely on earlier experience and established ideas in genetics concerning the sites that are likely to vary from Anderson.

However a statistician, who had been involved in the compiling of the mtDNA databank, articulated her puzzlement with this particular role of Anderson. She reflected:

> I was wondering, because it seemed to me as if the Anderson sequence [i.e. sequences that are similar to Anderson] is found more often than other sequences, and I can imagine no reason why this should be the case. But of course, I first of all have to quantify this guesswork.[6]

In research reports and scientific publications, these kinds of practical decisions and the contingencies of sequencing are usually obscured.[7] However, and ironically enough, in the paper in which the Anderson sequence was published in 1981, it was stated that: '[n]ucleotides 10, 934–5, 14,272 and 14,365 were ambiguous and their identity *assumed to be the same* as in the bovine mtDNA sequence' (Anderson *et al.*, 1981, p. 458, my emphasis). Thus, the Anderson sequence itself was corrected towards another sequence, namely the sequence of a cow which was available in the Cambridge laboratory. Now this aspect of Anderson shows that a reference genome does not enter the research after the production of other sequences, but during such sequences. Anderson is not merely a reference, but it helps produce the sequences. It is therefore implicated in such sequences and codetermines what they look like. This practical handling of sequences shows that in order to study differences, similarities have to be established via the work of editing. None of this is external to Anderson's role as a communication technology.

There is some debate among scientists about the self-evident nature of reference sequences (Lewontin, 1993). In an interview with the head of the Laboratory for Evolutionary and Human Genetics in Munich (hereafter the Munich Lab), I asked him about the reference sequence and about his ironic allusion to the Neanderthal being more neutral than Anderson.[8] When I was in that laboratory in 1997 it had just produced the first ever Neanderthal sequence (Krings *et al.*, 1997). In response to my request that he tell me a little bit more about Anderson and how it was proposed to the scientific community, Professor Pääbo provided the following account:

> It wasn't proposed. It was determined. Now, that's a difference between constructionists and geneticists. [laughter] I mean to say it was the sequence that was sequenced, right. [laughter] It was the first complete human sequence that was ever determined. It was done in Cambridge. And the first author's name on that paper is Anderson. [laughter] This was in 1981. It is a composite though, because different parts of that 16.5 kb [kilo base-pair] count for different individuals. It's not even from one person! *But the control region is from one person.* It had come

> to be the reference. Because when people determined sequence number two, they had, of course, compared that to the first one since it was already there. And now four thousand sequences later, we still compare to that [first] one. It is, of course, totally arbitrary. We could take any other sequence as the reference. Anderson is just a *convenient convention.* Because everybody knows the sequence that you're referring to. But it is of course a *British sequence.* Or, certainly European, but probably British, because it was done in England.

The allusion to the difference between 'constructionists and geneticists' mentioned above underlines that to become a standard, Anderson did not require a 'central actor' (Timmermans and Berg, 1997, p. 275). That is, its standardization is not so much the result of a co-ordinated effort from an alleged centre, but rather an effect of its availability and application in various different practices. Anderson became available and turned out to be convenient. Once published as a scientific paper it started to move between laboratories and to establish its standardized quality in various different places in the world. It thus became a convenient convention.

Referring to the implications of its Britishness, Pääbo explained that:

> One should of course keep in mind that Anderson is not a golden standard. But if we were to take the Neanderthal sequence, now that would be the perfect reference. It is not a Eurocentric one. And from the analysis we are doing now, it is equally far away from all humans. But it would also be a kind of political correctness, I guess. Kind of purist. Because one avoids the 'optical bias' of Anderson. But it wouldn't be practical. In comparison to the Neanderthal, all people would have many shared mutations. These shared mutations are not informative, they would just tell you that people are different from the Neanderthal. They don't tell you how people relate to each other.

Thus, despite the Eurocentricity or Britishness of Anderson, replacing it would not be practical for the kind of work that geneticists do. The Neanderthal sequence would be a 'perfect reference', but, as such it is viewed merely as a 'politically correct' technology. This underlines geneticists' preoccupation with difference. Taking this into account suggests that Anderson is not just a matter of *reference*, but especially *difference*. It also indicates that the differences that result from comparisons with Anderson are theoretically invested. In this sense Anderson helps to produce the *right* kind of information with which geneticists may compare and analyse data.

As the interview excerpt above indicates, compared to the Neanderthal, Anderson is less 'politically correct'. Let us take a further look at the kind of politics it contains.[9] Sensitized by discussions about race and racism in the Diversity Project, the head of the laboratory referred in the interview to the ethnic bias of Anderson, namely its Eurocentricity. On another occasion he stated that people tend to *naturalize* it and take it for granted. 'They would speak of mutations *from* Anderson, but one could also reason the other way around', he argued.[10]

In the analysis below I take seriously both the problem of Eurocentricity and that of naturalization. What is naturalization about? How is it established? And to what effect? These will be my leading questions. I set out to investigate Anderson as a piece of technology that was produced at a particular time, in a particular place and through a particular

practice. As such it can be seen as a 'frozen moment' of various constituent parts (Haraway, 1991a). To investigate its Eurocentricity in conjunction with its naturalization, I will consider both sides of the coin called naturalization. First, we will have a look at the kind of nature 'brought home' in the sequence (Knorr-Cetina, 1995; Latour, 1987)[11]—the kinds of practices, technologies, and tissues that enabled its sequencing, and how this relates to race. Second, we will address the question of how it is that such a locally crafted object can become a technology, travelling so smoothly between laboratories to become a *naturalized* tool. For this purpose let me take you back to the early 1980s, to the era in which Anderson was produced.

Anderson: The Tissue

Anderson was presented in a *Nature* publication co-authored by 14 scientists. This article tells us that Anderson is a composite. That is, its sequencing was based on cell material from two individuals—placental tissue and HeLa-cells (Anderson *et al.*, 1981).[12]

Within the context of genetics, 1981 was a pre-PCR era. Polymerase Chain Reaction (PCR) is the DNA copying technology of the late 1980s which made it possible to study DNA with very little biological material. In order to understand DNA work in the early 1980s I will present an account offered by the population geneticist Mark Stoneking. Although he was not involved in the making of Anderson, his account indicates how cell material was retrieved, handled and analysed. Stoneking conducted research on mtDNA in the early 1980s. At that time he was working with Allan Wilson and Rebecca Cann at Berkeley University. Together they published a famous paper on mitochondrial DNA, the so called 'Mitochondrial Eve Paper' (Cann *et al.*, 1987).

During 1997 Mark Stoneking was on sabbatical leave and decided to spend a year in the Munich Lab. I interviewed him about mtEve and about working with mtDNA in the 1980s in general. Referring to his PhD project in the Wilson Lab he stated:

> Initially I wanted to do Australia, because earlier work indicated that Australian mtDNA is somewhat divergent. But it proved to be impossible to get the samples that we needed from Australia back in the United States. You know in the 1980s, just before PCR, so to do mitochondrial DNA studies we had to purify the mtDNA to its homogeneity.[13] And to do that, we couldn't do that from a blood sample, because you don't get enough mtDNA from blood. So, we have these tissue samples, sort of a placental tissue. So that puts a lot of constraint on what sorts of population you want to get samples from. And it was just impossible to get Australian Aboriginal placentas. But our contact in Australia was a trained student who got to New Guinea to do fieldwork. He ended to be an extremely valuable colleague. Because even though he was in the Highlands of New Guinea, he was able, over the course of two or three years, to arrange a collection of almost a hundred and fifty placentas from different parts of New Guinea; to ship them out to us in California and keep them frozen. So they arrived in excellent condition.[14]

To sequence DNA in the 1980s was not an easy task. Geneticists' work had been under a number of constraints. Before the introduction of PCR-based methods, retrieving enough DNA from blood so as to study it appeared to be difficult.[15] Although cloning technologies, such as the recombinant DNA technology, which served as a technique to

produce many copies of DNA, were already established in the 1970s, the tissue was crucial to the success of sequencing.[16] Large amounts of DNA were needed. Unlike blood, placenta is rich in DNA and was considered most *convenient* for (a DNA-based) human genetics.[17] To relate this back to Anderson, its Britishness and the tissue used for its sequencing, it has become clear that, given the technical possibilities for cloning and sequencing of DNA, such tissue was indispensable for its success. Mark Stoneking's account highlights problems in retrieving placentas. In particular, obtaining the placentas of people in 'far-out' places was not easy. It was a matter of having the appropriate networks (Clarke, 1995, p. 186; Anderson, 2000). People from New Guinea, for example, may prefer the ritual of burying placentas to other rituals, such as those of doing science.[18]

In addition, as his remark indicates, to 'bring home' the placenta in a condition in which it could be worked with, was not an easy process. It involved putting the tissue on ice within a limited amount of time, keeping it frozen, and shipping it to the laboratory for preparation (Clarke, 1995, pp. 195–198). It could therefore be said that the crucial role of placentas in DNA studies in the 1980s and the difficulties involved in collecting them from all over the world are also involved in Anderson. Whereas placentas from other parts of the world were difficult to collect and ship, collecting British placentas might be simply a matter of going to the next hospital.[19] Children are born and placentas are at scientists' disposal, so to speak. Even though, as we will see below, the latter requires work as well, it does not call for a transnational organization and co-ordination of activities. From this perspective, it could be said that the sequencing of Anderson was itself based on 'a convenient convention', namely the convention of working with placentas because they are DNA-rich, and the convenience of using tissue at hand, that was easy to retrieve 'locally'.

What does an emphasis on technology and tissue mean for the questions raised above about the bias and 'Eurocentricity' of Anderson? The nature 'homed in' for Anderson in the early 1980s involved a particular technical handling of DNA. We have seen that the DNA cloning technology co-determined which tissue could be considered for sequencing. The organization of scientific work, in terms of having access to hospitals and clinics to collect the placentas, or knowing someone who does fieldwork in other parts of the world, puts constraints on and opens up possibilities regarding whose tissue is to be studied. Taking these practices into account highlights that 'Eurocentrism' and the bias of Anderson is an effect of technology. Race is here practised in the form of how DNA was handled in a pre-PCR era. In such practices, geographic proximity and distance, the work involved in acquiring good tissue, and using the technology and tissue that is at hand become integral parts of scientific routines and codetermine how the sequencing is done and whose tissue it involves. In this particular case, race is an activity of inclusion and exclusion firmly embedded in the routines of genetics and dependent on the technologies of cloning and sequencing DNA. However, this is not the only way race is implicated in the sequence. We will first consider sex-differences to then have a further look at the issue of race.

The Ir/relevance of Sex Differences

As stated above Anderson was based on cell material of two human individuals: placenta and HeLa cells. Trying to find out what HeLa cells are on MedLine, I hit upon hundreds

and thousands of references to journal articles. However the abstracts held no more promise of information than the Anderson paper itself. It was in my *Penguin Dictionary of Biology* (Thain and Hickman, 1996, p. 294) that I found out what it was: 'Hela cell: Cell from human cell line widely used in study of cancer. Original source was Helen Lane, a carcinoma patient, in 1952'. So HeLa is an acronym for Helen Lane and it refers to her immortalized cells, which have become the HeLa cell line. Just like the placenta, HeLa cells seem to be a convenient source for DNA, for they come in large numbers. But the specific combination of cell materials used for Anderson, namely placental and HeLa cells, indicates that Anderson is not just a composite. It is not just based on two persons' cell material, but on material stemming from two women. How, then, should we understand this specific combination of tissue? How does the sex of tissues matter with regard to Anderson?

In the interview with Mark Stoneking I asked him about the problems of retrieving DNA from blood:

> AM: Does this mean that before PCR you could only look at tissue from women?
> MS: Right. We did only placental tissue. It turns out that the placenta, I mean, strictly speaking the placenta is a foetal organ. If the foetus is a male, strictly speaking, it's a male tissue. But right, if I'm looking at the mtDNA, it's the mtDNA of the mother.

What does it mean to state that: 'if I'm looking at mtDNA, it's the mtDNA of the mother', even if the tissue is male? This hints at theoretical aspects of mitochondrial inheritance. As stated above, this DNA is inherited via the mother only. Males *do* inherit mtDNA, but cannot pass it on to their offspring. Thus, in population genetics, mtDNA is of 'woman made', revealing maternal lineages (e.g. von Haeseler *et al.*, 1996). As the quote indicates placentas may be male, but mtDNA's not male. Consequently, the mitochondria of a male foetus and its mother are interchangeable and similar. To put this another way, the sex of the tissue is not an issue for geneticists studying mtDNA: males as well as females inherit and thus have mtDNA. This makes the combination of tissue in Anderson—placenta and HeLa—even more striking. Based on this one could say that this combination of tissue seems to suggest a *fit* between the theory of mtDNA inheritance (revealing maternal lineage) and the tissue (derived from women's bodies).

Mark Stoneking's 'sexing' of the placenta points to a different reading. His statement that the placenta is a foetal organ—its sex is dependent on that of the foetus—emphasizes the triviality of sex for mtDNA studies. Both males and females have mtDNA and so does the placental tissue. mtDNA does not make a sex-difference. This means that the tissue used for Anderson might just as well have been a liver (which is also known to be DNA rich), and its source might just as well have been a male. Yet the availability of placentas for scientists to work with cannot be disentangled from a long history of medicalization of the female body, of birth-giving in western medical practice, and of reproductive technologies (Martin, 1987; Oudshoorn, 1994; Ginsburg and Rapp, 1995; de Ras and Grace, 1997; Pasveer and Akrich, 1998; Franklin and Ragoné, 1998). Whereas organs of humans tend to be difficult to retrieve in general, a placenta and a cell line (as we will see below) have become institutionalized through such practices and may literally function as a *resource* for scientific studies.[20]

The circulation of such 'resources' accounts for their convenience in a laboratory setting. The authors of the Anderson paper in fact thank a colleague for 'a gift of HeLa cell mtDNA' (Anderson *et al.*, 1981, p. 464). But also the placenta used for the sequencing of Anderson was already available in the laboratory. It was cloned and studied for another purpose by Jacques Drouin, a colleague and co-author of the Anderson paper, who was based in the same laboratory. The placenta was 'described' in a paper written by Drouin, and although the paper does not include details about the 'origin' of this placenta, it is clear that it was retrieved from a hospital or a clinic. In the paper it is stated that: 'Human placentae were obtained at term from normal or caesarean section deliveries and put on ice within 30 min'. It is also indicated that one of these placentae had been the source for Anderson: 'A collection of recombinant clones has thus been obtained using mtDNA isolated from a single placenta and is now being used to obtain a complete nucleotide sequence of human mtDNA' (Drouin, 1980, pp. 15–16).[21] Thus, both the placenta—in the form of mtDNA clones—and the HeLa cells—in the form of mtDNA—have become available through an exchange within an organized scientific practice.[22]

Scientists are practical reasoners who rely on established ways of doing things, and laboratory work is primarily about practical solutions rather than ideological ones. However, this does not mean that practices are not normative or that they may not have an ideological effect. For raising the question about a possible fit between a 'gendered' theory of mtDNA inheritance and that of the tissue applied demonstrates that practicality is normatively charged. It builds on power relations—in this case gender relations—which exist outside of the laboratory. Even though the sex of the tissue was made irrelevant and was not actively performed,[23] the practices that existed outside the Cambridge Laboratory did matter. Even more, one could say that these practices have become, what Donna Haraway has called 'frozen moments' built into the reference sequence. They may not be relevant now, but this may change. Thus, in addition to race, sex is also involved in Anderson. In the next section I will examine further how race and sex are made irrelevant and how this is connected to a process of naturalization.

Anderson: The Cell Line

My search for information about HeLa did not stop at the *Penguin Dictionary of Biology.* From a colleague I received an e-mail in which he suggested that Helen Lane had been a black woman from the USA.[24] He had seen a television documentary about a black woman whose cell material had been immortalized in the early 1950s. Spurred by this information, I started to ask various geneticists what or who HeLa was, but without success. In a telephone conversation Allan Bankier, the second author of the Anderson paper, told me that he did not exactly recall either the origin of the placenta or of HeLa. But he did remember that they had materials of 'black' individuals in their laboratory and he stated: 'At that time these issues were not so much addressed and we were not after an individualized sequence. Our aim was a consensus sequence that everybody could work with'.[25]

I received some information about HeLa from the Dutch Cancer Institute in Amsterdam, indicating that 'Helen Lane' may be one of the many synonyms for the woman whose cell material had become the cell line.[26] This information included a paper by Howard Jones, a physician who examined Helen Lane (alias Henrietta Lacks). His paper, 'Record of the first physician to see Henrietta Lacks at the Johns Hopkins

Hospital: History of the beginning of the HeLa cell line', indicates how difficult it was to grow a cell line successfully in the early 1950s. 'The project [of making a cell line] appeared to be a failure until Henrietta Lacks walked onto the stage' (Jones, 1997, p. 227). She had a specific cancer of the cervix which grew fast enough to facilitate the cell line, as Jones explains. Although the paper gives information about the age of 'Helen Lane', the number of children she had and a clinical diagnosis, there is no reference to her colour. The paper explains that: 'She died six months after diagnosis' and '[i]n terms of Mrs. Lack's birth date, the tumor is some 75 years of age and probably immortal' (Jones, 1997, p. 228).

It was in a paper dealing with population genetics that I found the HeLa cell line addressed in terms of colour and origin. The paper, written by Rebecca Cann, Mark Stoneking and Allan Wilson on the subject of mitochondrial Eve, describes the HeLa cell line as 'derived from a Black American'. In this study 148 samples from different geographical regions were compared and Anderson was used as one of the compared sequences. Whereas Anderson remains rather indeterminate—it is without further specification taken to be of European descent—'Helen Lane' and 17 other black Americans were not only labelled as black Americans, but were also regarded as 'a reliable source of African mtDNA' (Cann *et al.*, 1987, p. 32).

The Ir/relevance of Race

This story about HeLa suggests that the answers to questions about race and the Britishness of Anderson are not straightforward. The HeLa mtDNAs had travelled from the Johns Hopkins Hospital in the United States to Cambridge UK, where Anderson was sequenced. Although it is not clear where the placenta came from, one part of the sequence was based on HeLa and points to Anderson's multiple origin in the DNA. This underlines that the *Britishness* of Anderson is not so much in the DNA, but rather in where and how it was produced.

In the attempts to locate HeLa the simultaneous presence and absence of 'Helen Lane's' racial descent is striking. My search took place in 1998 in a European context. This is relevant because, whereas at that time in the United States an extended debate was going on about HeLa and its value for scientific research, about the fate of Henriette Lacks and her children who were actually not informed about the origin of the cell line, this information was virtually absent in the European context. The ongoing US debate makes clear that the cell line is thickly entwined with race, class, gender and sexual reproduction (Landecker, 2001).

The absence, or rather, the inaccessability of this history in the quest described above is instructive regarding the relevance and irrelevance of race in genetics. For most geneticists 'Helen Lane' has lost her racial identity through becoming a cell line. Her value for genetic research lies in her rapidly reproducing cancer cells.[27] Also the producers of Anderson did not mention her racial identity (nor that of the placenta) in their paper, testifying to the irrelevance of race for the reference sequence. As one of the authors, Alan Bankier, has stated, the makers of Anderson were not after an individualized sequence. Instead, their aim was to present the scientific community with a 'consensus sequence'. However in other contexts, as was the case in the population study by Cann and her colleagues, 'Helen Lane's' colour was seen as highly significant, allowing geneticists to regard her mtDNA as African.

Racial identity is therefore important for some scientists and irrelevant to others. But as part of Anderson, 'Helen Lane' has lost this identity, not only for the producers of Anderson but also in the localizing work of Cann *et al.* In the latter, Anderson was taken to be an individual sequence with a European (British?) origin. In this paper it does not only function as the reference for determining other sequences, but it also appears on a genealogical tree as one of the sequences analysed. The legend that accompanies the genealogical tree and the table containing the information found, states: 'The numbers refer to mtDNA types, no. 1 being from the aboriginal South African (!Kung) cell line (GM3043), no. 45 being from the Hela cell line and no. 110 being the published human sequence' (Cann *et al.*, 1987, p. 34). Number 45 is placed next to a black square indicating African origin, while number 110 (despite its 'hybrid nature') sits next to a square, indicating European decent. Paradoxically, this treatment of Anderson, namely as an individual, gives hints about how it operates as a technology. It gives hints about how it has become a *naturalized* technology in studies of genetic lineage. I will argue that also in this capacity, i.e. as a reference genome, Anderson, like HeLa or any other sequence, is treated as if it derived from one individual. This suggests a procedure through which local practices, technologies and 'homed in' nature were deleted once Anderson started to move from one place to another.

Naturalization: Or How a Lot May Become One

As I stated above, population geneticists studying genetic lineage have specifically the non-coding DNA as their object of research. The non-coding part of the mtDNA genome is called the *control region.* During my research I learned that very few geneticists were aware of the fact that the Anderson sequence was a composite, based on the DNA of two (and if we take the bovine DNA into account, in fact, three) individuals. However, the head of the Laboratory in Munich was aware of that as is clear from the interview above. But he was also quick to say that the control region was based on DNA stemming from one individual. By contrast to this, in the Anderson paper, the situation looks rather ambiguous. That paper suggests that, contrary to the rest of the sequence, specifically what is now called the 'control region' is a composite. It describes one part of the control region, the so-called D-loop, on the basis of the HeLa cell DNA, whereas other parts of the control region (a fragment containing small conserved genes: signals of control and promotors) are described in relation to the placental cells. Moreover, in the Anderson paper, there is no such category as the *control region.*

This hints at the existence of different scientific practices between those of the makers of Anderson and those of population geneticists. This can be characterized as a difference between the practice of *coding* and of *non-coding* DNA. The makers of Anderson were specifically interested in the coding of DNA, in the functions of the genome and the genes involved in those functions. For them, the fragment constituting the 'control region' contains different further specified categories, such as the D-loop, promotors, and signals of control. In contrast, population geneticists study the non-coding DNA parts of mtDNA in order to understand differences that occur in terms of population history and lineage. In such a practice the control region and D-loop are used interchangeably, even though the control region contains more than the D-loop. For them, this is all undifferentiated, non-coding DNA (except for some very small genes: promotors and signals of control). As one geneticist put it to me: 'to ask what the control region is, is

an academic question. You just make sure that you *are* in the control region'. So, one could say that the reason that the control region is self-evidently taken to stem from one individual is due to the fact that population geneticists take their own practices too seriously, in the sense that they forget that there exists a variety of different practices within the field of genetics and that these might involve different kinds of objects and different kinds of categories.

A second explanation for why it is that the control region is taken to stem from one individual has to do with the theory of mtDNA inheritance. As stated above, mtDNA is inherited from the mother. However, there is an ongoing controversy about this presupposition. I came across this controversy in the Munich Laboratory. I noticed in their publications that they would describe mtDNA inheritance as '*almost* exclusively passed on from mother to child'. Almost? What does that mean and what about maternal inheritance? The cautious description in the published papers refer to a debate about so-called bi-parental inheritance of mtDNA. The central question in this debate is whether the mitochondria of sperm cells (which are located between the head and the tail of the sperm) enter the egg cell and participate in the fertilization, or not. The standard view is that it does not. But if it does, does male mtDNA become part of the mtDNA genomes of the offspring? Some studies in mussels and in mice suggested cases of this *bi-parental* inheritance (e.g. Thorne and Wolpoff, 1992; Zouros, 1994; Kaneda, 1995; Wills, 1996). As I learned from discussions on this topic during laboratory meetings, the effect of bi-parental inheritance in humans would have a large consequence for a mtDNA based population genetics.[28] So, what is at stake?

The elegance of mtDNA for the purpose of diversity studies lays not only in the fact that it is a small genome which contains a large amount of information (in terms of diversity), but especially in terms of its maternal inheritance. In this respect, a case of bi-parental inheritance would affect the whole interpretative scheme of population genetics. It would mean that diversity is not just the effect of mutation, but also of recombination. Even a small percentage of recombination would have a large effect over a period of say, 100,000 years. For example, this would mean that estimations of mtEve's dating should not be 200,000 years but much more recent (Gyllensten *et al.*, 1991, p. 256). Also, bi-parental inheritance would have a profound effect on how lineage is established. The whole concept of mtEve would become problematic. It would then be more appropriate to speak of EveAdam or AdamEve, but it would then lose its value for studies of genetic lineage. Since there is little evidence of bi-parental inheritance in humans,[29] models for interpreting genetic differences have not changed and human mtDNA comes from one parent, namely the mother and ultimately from the 'all human mother' mtEve. However, the controversy is relevant for the analyses of naturalization.

To bring this debate back to why it is that the control region of Anderson is taken to be derived from one person, one could say that the very presupposition about the origin of mtDNA—as stemming from one individual—is doing the work of naturalization for Anderson as well. Both Anderson and mtEve are products of theory and practice. Unlike Anderson, however, the sequence of mtEve does not exist. It is a 'concept' which is dependent on a theory of inheritance and on standardized practices of comparing sequences. It is dependent on standardized methods of analysing differences and on the universalization of results, in such a way as to establish lineages that lead back to that single origin.[30] This very standardized and universalized approach to genetic diversity and lineage has the naturalization of Anderson as its effect. Above I have shown that,

in the work of Cann *et al.*, Anderson appeared on the genealogical tree, not as a composite sequence (a technology) of mtDNA of a number of individuals, but as that of a singular unified person. By contrast, in medical practices where genealogy and the concept of Eve are not that relevant, scientists have reported extensively on mistakes in Anderson. They have, in this sense, *denaturalized* the reference sequence, because it was not in line with their medical findings (Howell *et al.*, 1992). In 1999 this denaturalization lead to the resequencing of Anderson (Andrews *et al.*, 1999).

Thus, in population genetics in the absence of Eve from which all humans descended, and her sequence from which all humans diverged through the accumulation of mutations, Anderson is performed both as a tool to establish mutations and as an origin from which all other human sequences diverted. The very concept of mutation in this practice establishes Anderson as the origin. To be sure, this origin quality is not to be understood in a genealogical sense. Rather, it is a practical effect of working with the reference sequence on a routine basis, a procedure which is constitutive of Anderson's 'naturalness' in laboratories. It had become what Michael Flower and Deborah Heath (referring to the nuclear human genome) have called 'the generic signifier of the species' (Flower and Heath, 1993, p. 29). The way the practices of the makers of Anderson were taken for granted and the control region was taken to stem from one individual is based on Anderson's investment in the concept of a single origin. Thus, with the help of a universal theory of mtDNA inheritance, Anderson had become the original sequence from which all other sequences descended—'the mitochondrial Eve of modern genetics'.

Discussion

In the first part of this paper I have drawn on debates about the Diversity Project and indicated that its initiators aim to eliminate racism. By producing better knowledge about diversity and lineage their aim is to combat racism, by showing that there is no scientific basis for racial differences. As Margaret Lock (2001) and others have argued, this is rather naïve. The belief that the facts of science will do the work of anti-racism does not take into account the variety of ways in which race is done in society (Barker, 1982) and the persistence of biological ideas about, and techniques for doing race and other differences. Moreover, it defines the problem of race and racism in terms of knowledge, or rather a knowledge-deficit.

However, this is just one part of the story. Another way of looking at the issue of race is by addressing how it materializes in practices, from architecture and city planning to the design of medical protocols and techniques. Focusing on practices, race cannot be viewed as a layer that can be removed surgically. It is rather firmly embedded in routines and technologies. Given the history of genetics, which includes colonialism, racism and eugenics (Kevles, 1985) there are good reasons to take race as well as sex-differences as built-in components of genetic practice. The Diversity Project did not start *de novo* but it is, in a very material sense, entangled with these histories and the objects, with the technologies and practices that they have brought forward (Rabinow, 1993, p. 103). Without ignoring the epistemic change that has taken place due to large scale sequencing efforts and the particular understanding of genes as information systems (Kay, 2000), and without ignoring the current emphasis in genetics on the 'human race' as one biological category (Cavalli-Sforza, 1993), my aim in this paper was to focus on how previous practices have materialized in the form of a technology. My prime example has been

a standardized sequencing technology and associated practices.[31] In my analysis of the Anderson sequence I have shown that race and sex differences are part and parcel of the scientific practices that helped produce it and that they are implicated in this reference genome. However, in daily laboratory work, where the reference genome appears as a formal text, this normative content goes unnoticed. The sequence functions as an unmarked piece of technology, a convenient convention. It has thus become part of routines that seem benign to geneticists (and to the world outside?).

However, to reduce the problem of race to a matter of knowledge about genetic diversity, as does the Diversity Project, takes away the possibility of investigating how race materializes such human/non-human interactions. It takes away the possibility of investigating how it has become routinized in daily practices, where nothing strange seems to be going on. It seems to me that now that we have started to question and examine unmarked categories, such as masculinity and whiteness, it is time to redirect our attention to the 'invisible' routines of science, which order the categories that we live in.[32]

As I have briefly outlined in the introduction, the Diversity Project was met by voiced criticism emphasizing its (neo)colonial character. Various indigenous and other organizations have objected to its endeavour to resource large numbers of populations, appropriate their cell material and to reinvent their histories and cultures according to the logic of western science, or at least, one version of that. Adding to this critique, my aim in this paper was to locate and open up the scientific practices of the Diversity Project for interrogation. I have investigated only one standardized technology, but laboratories are populated by many others, to show that the 'in-hereness' of western science and the 'out-thereness' of its non-western objects have long been intertwined, giving way to postcolonial readings of such practices (Anderson, 2000, 2002; Castañeda, 1999; Thomas, 1991).

In genetics, objects and technologies are often interchangeable (Rheinberger, 1997, 1999). Anderson is a sequence based on the DNA of two individuals, and as such it was an object of study for geneticists at different moments in time. Yet, transported to different places and times it has become a technology, a formal text. This double quality has stayed put across these movements. For example, as recently as 1999, Anderson became once more an object of research when physicians decided to re-sequence it because their medical practice suggested that it contained some mistakes (Andrews *et al.*, 1999). In my analyses of Anderson I looked at both aspects of the reference sequence (as an object of research in the 1980s and a technology in other practices). These aspects cannot be treated in isolation. The practices that helped to produce the reference sequence and the normativity they contain have an effect on the knowledge and the data produced through Anderson. They establish genetic similarities and differences and thus co-determine what is near and what is distant in terms of genetic lineage.

In addition, producing Anderson was dependent on specific technologies of cloning and sequencing DNA, on a particular organization of scientific conduct in which racialized and sexualized tissue and data were being exchanged, and on the alignment of tissue at hand to the available technologies. Who will be made into an object of science is therefore a matter of such complex organizations of scientific work. This is by no means a neutral matter. But also what will be made into an object or a technology may not be conclusive, for this may change over time. This, in fact, makes the need for postcolonial studies of scientific practice even more urgent. In addition to studies of power relations between different groups, the politics of *who* as Annemarie Mol has termed this, it is important

to take a politics of *what* into account, that is, the materialization of power in technologies and practices (Mol, 2002).

The reason why Anderson can seem to escape the 'burdens' of locality that helped produce it, to move smoothly between laboratories, and to become a naturalized technology had to do with the double quality described here. The Anderson sequence is naturalized and presented as an individual sequence on genealogical trees, even though it is a composite based on two individuals. Moreover, the examination of the theory of mtDNA inheritance suggests that the naturalization of Anderson is further enabled by the stable and universal character of that theory. It allows the reference sequence to move easily between laboratories, where it could be performed as both a tool for establishing differences between other sequences, and as the origin from which those sequences descend.

The problem of naturalization is not only that it tends to obscure the normative content of technology, but also that it helps to essentialize the differences produced by it. For example, nobody carries mutations by her/himself: this is not an essential feature of an individual. It is only in relation to such a standard that individuals can be compared in terms of differences (Lewontin, 1993). Furthermore, as I have shown, in a laboratory setting, target sequences and Anderson become intertwined, and similarities have to be established actively when ambiguous sequences have to be 'corrected'. However, naturalization tends to obscure the technologies and routines involved, and to foreground differences (or similarities) as characteristics contained in individuals and populations. Given the fact that genetics nowadays is producing objects and differences in excess, there is a significance in *locating* these in scientific routines. And here is the importance of the 'strategy of location', as proposed by Donna Haraway, Annemarie Mol and others (Mol, 1990; Mol and Law, 1994; Haraway, 1991b). In order to prevent the essentialization of differences we need to take account of the technologies and practices involved—to *denature* the objects they help to produce.

Acknowledgements

The author would like to thank the members of the Laboratory for Human Genetics and Evolution in Munich for allowing her to look in their kitchen and to try out some of the recipes herself. Annemarie Mol, Hans-Jörg Rheinberger, Gert-Jan van Ommen, Olaf Posselt and Paul Wouters are thanked for helpful comments and generous suggestions. The author is also grateful to the participants of the 'Between Science, Technology and the Postcolonial Workshop' held at Lancaster University where this paper was presented, especially Maureen McNeil, Claudia Castañeda and Sara Ahmed. Mike Lynch and a second reviewer for *Science as Culture* as well as Les Levidow supplied valuable comments for this final version. Finally, thanks go to the Deutscher Akademisher Austauschdienst (DAAD) and the Netherlands Organization for Scientific Research (NWO) who kindly supported the research in Munich.

Notes

[1]In different documents about the Diversity Project the number of populations to be studied varies between 500 and 700.

[2]Cavalli-Sforza (1993) can also be retrieved on the Internet at http://www.stanford.edu/group/morrinst/HGDP-FAQ. The author of the Internet copy had become a collective, namely, 'The Project's North American Committee'. This copy is a revised version of the copy I received in 1995 from Professor Cavalli-Sforza. Here I refer to the early version of the paper. Moreover, notice that, according to the quote, what is to be preserved is information about genetic diversity and not diversity itself.

[3]Luke Holland (producer), *The Gene Hunters* (Zef Productions, 1995). This documentary was broadcast in June 1995 on Dutch television.

[4]See also Star (1995) who makes a strong argument against what she calls the great divide between science and technology, between nature and culture, between social sciences and natural sciences and the like.

[5]The material presented in this paper is part of a larger study of the Diversity Project. In this study I conducted a participant observation in two laboratories, in the Netherlands and Germany. The results, which are organized around the issues of naturalization, standardization and diversity, are part of my PhD thesis (M'charek, 2000b). A revised version of this study has been published by Cambridge University Press (M'charek, 2005). On laboratory space or 'locales' and on how they are implicated in objects of visualization, see Lynch (1995). For an elegant examination of laboratory routines, see Jordan and Lynch (1998); and on how local and 'global' social worlds of scientific practice are managed via standards, see Fujimura (1992, 1995).

[6]Communication with author at the Laboratory for Evolution and Human Genetics (Munich), and via e-mail.

[7]Also recently an extended debate has ensued over mistakes in mtDNA data and its consequences for analyses and conclusions about human genealogy, history and evolution. Most notably in this debate is a study that showed that if mtDNA data were studied more carefully, the Icelandic people are far less homogeneous as was presupposed and that their genetic diversity is amongst the highest in Europe (Arnason, 2003; Forster, 2003, see also Dennis, 2003).

[8]The interviews were taped. For the sake of clarity and readability, the transcripts presented here do not contain utterances such as 'ehh' or information about pauses. Also half sentences or sentences stretched out are rephrased in the transcript to make them more comprehensible. For the purposes of the analyses I conduct here, this extra information is not considered important. The interview with Professor Svante Pääbo was conducted on 4 February 1997 in the Laboratory for Evolution and Human Genetics in Munich.

[9]The kind of politics that I aim at here is based on enactments in practices rather than on qualities integral to a technology. In her book *The Body Multiple*, Annemarie Mol has coined this 'a politics of what', as opposed to 'a politics of who' (Mol, 2002).

[10]This was at a conference we both attended in Berlin—*Postgenomics? Historical, Techno-Epistemic and Cultural Aspects of Genome Projects* (Max Planck Institute for the History of Science, 8–11 July 1998, Berlin).

[11]Knorr-Cetina argues that 'laboratories allow for some kind of "homing in" of natural processes; the processes are "brought home" and made subject only to local conditions of the social order' (1995, p. 146).

[12]HeLa cells are derived from a cell line produced in the 1950s. For a critical history, see Landecker (2001).

[13]The determination of the presence, constancy (stability) and number of DNA.

[14]Interview with author, held on 11 March 1997 in The Laboratory for Evolution and Human Genetics in Munich.

[15]Blood was at that time collected on a global basis to determine blood types and protein variations. 'By the mid-1960s, a large number of clear cut biochemical variations were known, including more than a dozen inborn errors of metabolism arising from probable enzyme deficiencies, and so were numerous haemoglobin and blood-serum protein variants' (Kevles, 1992, p. 15).

[16]Anderson was sequenced according to such a technology. It was cloned with the help of the bacteria *Escherichia coli* (*E. coli*) (see Drouin, 1980, p. 15). Moreover Drouin conducted the work for this paper in the laboratory of F. Sanger (at Cambridge), a co-author of the Anderson paper and whose name is especially connected to the development of sequencing techniques but also to the development of recombinant DNA in the early 1970s (Sanger and Coulson, 1975; Sanger *et al.*, 1977).

[17]The so-called blood type genetics, i.e. looking at blood groups in studies of genetic diversity, admixture and migration history was already introduced during the First World War by Ludwig and Honika Hirszfeld in Poland. Blood was widely researched throughout this century not only for reconstructing genetic lineages but also in the context of family diseases (Kevles, 1985, pp. 202–204). A nice representation of the enormous impact that PCR has had on the number of mtDNA sequences (i.e. of parts of the control region) that were determined, is offered in a paper published by members of the Laboratory in Munich (Handt *et al.*,

1998, pp. 126–127). In this paper, a diagram entitled 'Accumulation of HVRI and HVRII (Hypervariable region I and II) sequences during the last 15 years', shows that until 1990, thus until PCR, approximately 100 sequences had been determined, and that from that year on more than 4,000 sequences became available for HVRI (which is part of the non-coding DNA of the mitochondrial genome). In this paper a map of the world is also given, indicating from which parts of the world the current collection of sequences come, i.e. which populations are represented.

[18]About rituals of burying placentas in New Guinea, see Strathern (1992, p. 128); on rituals in science, see Jordan and Lynch (1992).

[19]For an example, see Cann *et al.* (1987, p. 32). For their study Cann and her colleagues received 98 placentas from US hospitals for their research.

[20]The case is different in animal genetic research. Organs of animals, such as rat livers and beef hearts, were studied by Anderson and his colleagues (Anderson *et al.*, 1981, p. 458). In a study of bovines, for example, liver and brain tissue where used as a source for mtDNA (Olivo *et al.*, 1983, p. 401), and to yield large amounts of mtDNA, liver, heart and kidney were studied on the basis of PCR in mice (Gyllensten *et al.*, 1991, p. 256).

[21]I thank the second author of the Anderson paper, Dr Allan Bankier (MRC Laboratory of Molecular Biology, Cambridge), for pointing out to me that they had received the mtDNA clones from Dr Jacques Drouin, and for providing other information about the sequencing of Anderson.

[22]See also Warwick Anderson's study of Kuru brains as objects of exchange among scientists, and on how the Kuru brains oscillated between a gift and a commodity status (Anderson, 2000).

[23]Similarly Marilyn Strathern has argued the following about the gender of the gift: 'However, one cannot read such gender ascriptions off in advance, not even when women appear to be the very items gifted. It does not follow that "women" only carry with them a "female" identity. The basis for classification does not inhere in the objects themselves but in how they are transacted and to what ends. The action is the gendered activity' (1988, p. xi). See also Hirschauer and Mol (1995) who argue that gender may become mute and requires to be performed actively and M'charek (2005) who investigates how the sex of samples is irrelevant in particular practices, and is performed in others due to the application of new technologies.

[24]I thank Ruud Hendriks for his attentive reading of a previous version of this article and for bringing the point to my attention. I also thank his students in the tutorial 'Oorsprong: De Natuur als Spiegel' (held at the end of 1998 at the University of Maastricht) for their feedback on an earlier version of this paper.

[25]Dr Allan Bankier, telephone conversation with author on 17 November 1998.

[26]I thank Professor Piet Borst and Suzanne Bakker of the Dutch Cancer Institute (Antoni van Leeuwenhoek Ziekenhuis) for providing me with this information.

[27]On how this quality had become a problem, see the elegant article by Landacker (2001). The HeLa cells are apparently growing sufficiently fast so as to contaminate other cell cultures and, in fact, complete laboratory spaces. I thank Richard Tutton (York University) for forwarding this manuscript to me.

[28]For a more detailed account of this controversy, and on how it came to play a role in the Laboratory in Munich, see M'charek (2005, pp. 102–105).

[29]For example a recent and extraordinary study reports about a case in which the patient carries not only the mtDNA of his mother (in blood, hair and skin), but also those of his father in the muscles (Bromham *et al.*, 2003).

[30]Essential to such standardized analyses of genetic differences is the concept of the *molecular clock.* The idea is of a clock ticking equally fast in all individuals and which helps geneticists to estimate the time for mutations to occur. For an elaboration, see M'charek (2005, pp. 92–94).

[31]One striking example of how race 'is done' in contemporary genetics can be found in Jeffreys, Turner and Debenham, who state that: '[t]he only preselection of data for this study was that of ethnicity [Caucasian], which was determined on the basis of photographic evidence' (1991, p. 825).

[32]On (the invisibility of) scientific routines and their effect on the object of research, there exists a large body of literature within science and technology studies. I have referred to some of that here. On issues of normativity see especially Star (1991) and Cussins (1998).

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