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The genetic history and diversity of humanity

History, identity and meaning in the Human Genome Diversity Project and the Genographic Project

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Introduction - The genetic history and diversity of humanity

As far back as the written historical record can be traced, and probably well before that, people have invented stories about the origins and ancient history of humans. In modern times, with the emergence of such natural-historical sciences as palaeontology, evolutionary biology, archaeology and anthropology, stories about man's origins and spread across the earth left the realm of the mythic and metaphysical world views, and often contributed to their decline. The new origin stories were the products of the scientific study of bones, fossils, and animal and human morphology. Biblical history made way for evolutionary narratives that stretched the timeline to unprecedented lengths. They were often framed in contrast with their religious precursors, so that in a sense, the dichotomy between the two world views was itself a product of the new evolutionary paradigm.

In the twentieth century, genetics joined the scientific effort to uncover the "deep history" of humanity. Population geneticists started to study patterns in global genetic variation - irregularly distributed genetic differences and similarities, called 'polymorphisms.' By mapping these, geneticists tried to establish the relations between currently living populations. The differences and similarities they found were interpreted in terms of group descent, and used to reconstruct diasporic histories of humanity. In this way, geneticists built humanity's family tree, or rather, lots of tentative versions of it. They interpreted the genetic variation in the present human gene pool as an echo of ancient population movements, splits, bottlenecks and expansions. They produced images, models and narratives. The former include geographic maps depicting the migration of human groups, identified by genetic markers, across the world, and phylogenetic trees.

Phylogenetic analysis reconstructs the history of groups or organisms. Trees depict these groups as branches on a tree. The variation in frequencies of genes found in present populations informs both trees and maps. A high frequency of a specific marker in a specific region of the world ties it to that location. With the help of dating methods, based on average mutation rates, geneticists calculate when the marker first emerged as a mutation in an individual's genome. By mapping the occurrence of markers around the world, associating them with specific regions and with different times of origin, the tree of humanity is constructed. Markers that occur in high frequencies in specific populations are visualised as separate branches on the tree, while similarities between the genetic make ups of groups indicate shared origins.

With such research, genetics contributed to the changing of explanations of variation itself. From the nineteenth century onwards, traditional philosophical and religious explanations of human physical variation were supplanted by biological ones; the sons of Noah were replaced by the great apes. Initially, the focus lay on morphological variation. When Darwinian evolutionary theory was merged with Mendelian genetics in the twentieth century, the level of analysis slowly shifted from physical to genetic variation. Evolutionary theory explained variation in terms of population and migration history, as the result of dynamic and ongoing processes of intermixing and separation. Therefore, any patterning of the human gene pool was seen as a temporary phase in the dynamic, tens of thousands of years long population history of humanity. Nevertheless, on a human timescale, such patterns were medically and anthropologically relevant. The way they had emerged, as a result of the millennia-long history of the species, was visualised in human family trees.

Thus, geneticists studying these phenomena deal with centuries-old questions, the answers to which have traditionally been addressed by and embedded in general world views. That these issues are important carriers of meaning, and, perhaps, pillars of world views, is illustrated by recurrent controversies in research dealing with human origins and diversity, and by the long-lived public impact of many of the themes, metaphors and insights they have produced. Ideas such as the “Out of Africa” theory of human origins, the genetic relations between and historical roots of human populations and ‘races’, and a common genetic ancestor of all humans living today – all of these appeal to the imagination, and maybe to something even more fundamental: not just our need for stories, but our need for origin stories.

Human genetic diversity was studied in many research fields and disciplines. From the mid-twentieth century onwards, the medical sciences sought for population-specific genes for, and genotypes associated with (predispositions to) diseases. Since the 1980s, forensics started to use genetic information to construct ethnic offender profiles. Pharmaceutical companies investigated variation in drug metabolisms to tailor drugs for carriers of specific genetic variants. Genetic research into human history stands somewhat apart from these other lines of inquiry. It is the only line of genetics research that predominantly and explicitly pursues cultural goals. Admittedly, its results sometimes turned out to be useful in forensics. And, in their pursuit of funds and legitimacy, researchers have often referred to possible medical spin-offs. These claims were not groundless, as some disease risks were associated with racial or population identities, so that genetic population histories acquired medical relevance. Sometimes the reconstruction of the migration history of the species in all its diversity turned out to be useful for concrete, practical goals.

But in general, geneticists reconstructing history do not aim at such practical knowledge. They primarily produce narratives. Their adage is that a genetically reconstructed history of humanity can give us more insight in who we are, both as humans – as members of the species - and as members of communities. By uncovering the history of humanity, of its maturation in Africa and its subsequent colonization of the earth, they provide scientific equivalents of origin myths.[1] Tracing patterns of descent and relations between peoples, they provide each of them with specific narratives of origins, migration and kinship; with a specific branch on the family tree of humanity. In short, this research produces identities, in the form of historical narratives, both for specific peoples and for humankind as a whole.

With respect to the argument that science, and biology especially, has replaced traditional "Grand Narratives"[2], a comment is in place. In the case of origins research, 'biology' should be specified and broadened to include 'border' disciplines such as archaeology, paleontology, physical anthropology and linguistics. With this multiplicity of specialised disciplines, and because of the provisional and fragmented nature of scientific knowledge, it remains debatable whether we can speak of "Grand" narratives at all. But however tentative scientific knowledge is, and much as the specific narratives are fragmented along disciplinary, paradigmatic, cultural and societal lines, evolutionary, genetic histories provide origin stori*s* and explanation*s* of human variation and indeed, human nature - or at least provide the raw material for them.

Anthropological genetics, as a research field, interconnects with most of the disciplines that have traditionally dealt with "deep history", such as anthropology and archaeology. All of these produce narratives that not only operate on a cultural, but also

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[1] Sykes: 'Eve's daughters ordinary' yet new version of creation; biological connection fundamental C. Nash, 'Genetic kinship,' *Cultural studies* 18 (2004) 18

[2] Scott Gilbert, quoted in M. S. Lindee et al., 'Anthropology in an age of genetics,' in: M. S. Lindee, et al., eds., *Genetic nature/culture. Anthropology and science beyond the two-culture divide* (Berkeley and Los Angeles, 2003) 15. "The stories that are said to define our culture increasingly involve DNA, cells, organs, animals, plants, and ecosystems, Gilbert has suggested."

on a political level, as scientific legitimisations of slavery and eugenics illustrate. After the Second World War and the horrific extremes of Nazi racial science, a new scientific Grand Narrative was greatly needed; one that could account for human differences while avoiding the pitfalls of scientific racism. There was a need for scientific, 'objective' arguments for its opposite: the idea of the equality of all humans and the unity of humankind. Several disciplines contributed to this redefinition of human variation in evolutionary and historical terms. As is explained in chapter one, these efforts have set the stage for, and defined the objectives and limits of, the post-war scientific investigation of diversity. They have profoundly influenced the way anthropological genetics research has been framed.

Often, there were differences between the discipline-specific histories of man inferred from patterns in, respectively, the distribution of languages, material culture, fossils, geochemicals, genes and physical traits. These sometimes conflicted. Sometimes the feasibility of reconstructing ancient history by these methods was called into question, especially in the case of linguistics.[3] The immigration of genetics into this research shook up existing controversies and consensuses and led to new debates, as it matured, swiftly and sometimes jerkily, into a discipline that is now commonly called 'anthropological genetics'. At the end of the century, genetics had acquired a dominant position, and could boast the settlement of several long-standing scientific debates. As is explored in chapter three, rather than ending the debates, the arena was expanded to include other disciplines - and the public as well, particularly the indigenous populations on which geneticists have focused.

While it contributed significantly to post-war discourses about the nature and social insignificance of human differences, the first global historical narrative that emerged exclusively from this new discipline is that of 'African Eve'. This common ancestor was inferred from patterns in mitochondrial DNA. This part of the genome is transmitted maternally; hence 'Eve', and not' Adam'. The authors of the study calculated her date of birth to be around 200,000 years ago, and presented evidence that she had lived in Africa. She was hailed as a primal mother, as evidence that humanity was one big family, and inspired geneticists to embark on a mission to find evidence for a genetic 'Adam' on Y chromosomes (which are exclusively paternally transmitted).

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[3] e.g. J. Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' *American Anthropologist* 96 (1994)

Several years after the ‘Eve’ study, the first attempt was made to create a genetic database encompassing, or rather, representative of, the whole of humanity. It aspired to organize existing sample collections and to initiate a centrally organised, global sampling effort. In the wake of the Human Genome Project, which aimed to sequence ‘the’ whole human genome (or a representation of it), the Human Genome Diversity Project (1991— 1997[4]) proposed to map variation in ‘the’ global human gene pool (or a representation of it) in order to reconstruct ‘the’ history of humanity. For reasons that will be explored in chapter two, it was not realised as originally conceived, and as a sample effort, did not survive at all.

A decade later, multiple projects attempting to map human genetic variation had emerged. Among them, only the Genographic Project (2005—present), to which chapter four is dedicated, pursues the reconstruction of human history: most of the other projects aim at medical applications. The HGDP and GP are unique in their combination of a global scope with the pursuit of cultural, historiographical goals. The respective initiators, L. Luca Cavalli-Sforza and Spencer Wells, have left a strong mark on the presentation of these projects, and have published extensively for a lay public. It is on these two projects and their leaders that I will focus.

Lucassen et al. argue in their overview of different disciplinary approaches to migration history that there is a role to play for the historian in this increasingly disciplinary field. As a generalist who reads the results of “specialists in genetics and linguistics [focused on ‘deep history’] who prepare the data, conduct the analysis, and interpret the results”, he[5] can “assess their methods, identify the implications of the analyses, and [...] find inconsistencies in the methods or the interpretations of analysts working in different disciplines.”[6] Not migration history, but the *writing* of migration histories by genetic means is the subject of this thesis; and I am not a historian of migration, but I was trained as a historian of science. Nevertheless, I am encouraged by their argument that a historian can say something sensible about this (often quite technical) research.

I focus on the anthropological genetic study of “deep history”, which means that I will include other disciplines’ contributions only when the geneticists that I study do so.

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[4] There is some debate about these dates; while some have argued the project was dealt a deadly blow by the National Research Council in 1997, others have argued that with the continuance of (research conducted on) its database, it has continued to exist until this day. The details of this matter will be discussed in chapters 2 and 3.

[5] Please read for every unspecified ‘he’ the politically correct but stylistically problematic ‘(s/)he’

[6] Jan Lucassen et al., 'Migration history: multidisciplinary approaches,' in: Jan Lucassen, et al., eds., *Migration history in world history* (Leiden, 2010) 20

Rather than looking for inconsistencies between different disciplines, as Lucassen et al. argued, I will examine the ways of doing genetic-historical research that during the past two decades were established as 'normal science', and the historical narratives these produced. I will juxtapose these methods and narratives with the alternatives that were proposed, and the opposition against them, from within and outside of genetics. In so doing, I will investigate what genetic views of the history of humankind, and of its unity and diversity, were proposed; what views dominated; and how they were rooted in methodical and theoretical choices.

In short, I will examine genetic-historical narratives of origins and diversity of the late twentieth and early twenty-first centuries. I will take as representative case studies the HGDP and the GP, which targeted the whole of human genetic diversity, which they conceptualised as common heritage. I will investigate with what intentions these projects were embarked upon; what research strategies shaped them; and how research was presented and interpreted – and criticised. Special attention will be given to the social and cultural meanings attributed to the research, and the ideological messages attached to them.

Thus, this investigation focuses on the HGDP and the GP and the debates about them in the anthropological genetics community. Each of these projects presented a synthetic overview of the insights the discipline has acquired over the years. Both are collectives of specialists, among them the most prominent, and both defined their research goals and their legitimisations broadly. Both have a grand scope, as they intended to establish a global database in order to reconstruct global history. Both project leaders have published extensively for non-scientists. Both have ascribed not just cultural relevance, but also an ideological message to their research.

They operated in a context that was still profoundly shaped by the post-war discourse about the insignificance of human differences, based on ideas about human universals embodied by early modern humans,[7] which received renewed cogency with the end of the Cold War. As Jenny Reardon has demonstrated, this legacy was more complex than the mantra of human equality suggested. That view had never prevented the investigation of differences. On the contrary, it had enabled it, by stripping suspect ideological associations off diversity research. Indeed, scientific statements about the

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[7] "Early Man in Africa [...] was conceived as the prototype of the United Nation's post-World War II universal man, in the ecological conditions of Cold War, global nuclear and urban proliferation, and struggles over decolonization." D. Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* (New York, 1989) 187

equality of all humans *depended on* definitions of differences. However insignificant researchers proclaimed human variation to be, it was that very variation that was the backbone of their research. Research required the subdivision of humanity into more or less delineated entities, now often dubbed ‘populations’ instead of ‘races’. Thus, the conclusion of equality and unity was preceded by these categories. Difference was reintroduced with every attempt to exorcise it.

This tension between similarity and difference pervades the tradition in human biology that begun in the immediate post-war years, and has profoundly influenced anthropological genetics. Geneticists echoed many of the arguments that the post-war reformers had introduced, and added new ones. A shared common human ancestry was presented as evidence for the unity of humankind, and the clinal nature of genetic variation (i.e., the absence of clear genetic boundaries between populations) as proof of the insignificance of group differences. Meanwhile, the population categories with which they organised the human gene pool and human history became powerful and therefore explosive concepts, as genetic knowledge acquired great cultural authority and trickled through to popular discourse.

In this analysis of the HGDP and the GP, special attention will be paid to the ways these tricky issues of unity and difference were dealt with in historical narratives. The perspective I take is that of the student of science, who asks: what is it these scientists claim to do, and why? Who claims and receives the authority to speak? How do models, research strategies, and theories influence the results and what are their alternatives? And finally, how is the research presented, received, and made meaningful? In addition, I will try to examine the research results from the perspective of the student of historiography, or the philosopher of history, who asks: how is history conceptualised by these authors? Who are the protagonists? How is change accounted for and explained? What relationship between present and past is proposed? What universals emerge from these views? What language, metaphors and other narrative structures are used? And what sources are used in what ways? In chapter one, I describe the ‘prehistory’ of anthropological genetics. It explores the way the stage was set for the HGDP and the GP by biologists, anthropologists and geneticists, who from the 1950s onwards developed methods and theories as well as an ideological framework for research into human diversity. Chapter two describes the creation of the HGDP and the work and ideas of its founder, Cavalli-Sforza. In chapter three, I turn to the criticism that was levelled against them, and the alternatives that were proposed. It provides a short overview of the debates that took place in anthropological genetic communities, partially in response to the HGDP, and the way the research field developed. Chapter four is dedicated to the Genographic Project and the work and ideas of its leader, Spencer Wells. In chapter five, I examine the criticism this project received, tentatively comparing this with the reception of the HGDP. In the conclusion, I provide an overview of the ways both projects dealt with the tension between similarity and difference, the narratives they produced, the meanings that were attributed to them, and the way they responded to criticism and to general developments in anthropological developments. I will attempt to place them in a historical context and examine what, if anything, has changed in the two decades which they cover.

The authoritative and dominant position of anthropological genetic histories in science and culture is illustrated by the enthusiasm and opposition it has provoked; by the ubiquity of genetic concepts of descent and identity in popular parlance; and by numerous recent analyses of the "geneticization" of kinship, history, and identity. It is this cultural impact, and the exceptional nature of a science that employs natural scientific, laboratory methods to produce narrative and cultural results, that triggered my curiosity. I hope I can carry this fascination across to the reader of this thesis.

Chapter one - Researching human history and diversity after World War II

The UNESCO statements

After the Second World War, there was a sense of crisis in the biological sciences. A pre-war history of eugenics and the Nazi ideology of 'racial purity' had tainted both the word 'race' and research into human differences. In addition, contemporary racist aggression constituted an image problem for the United States; which also had to deal with Soviet accusations that the US economic success depended on an economic system that exploited colonised peoples: a narrative of unity was needed, and science was called upon to provide it. In the early years following the Second World War a collective attempt was made to correct 'scientific-racist' viewpoints and to separate biology, and especially the study of human diversity, from 'suspect ideologies'. As the Rights of Man were formulated, a need was felt for a scientific basis of the new doctrine of the equality of races.[1] As early as the 1920s, biological scientists had attempted to erect a boundary between the 'science of race' and 'ideological uses of race', in a reaction against the coupling of immigration restrictions with eugenics viewpoints. In the 1940s and 1950s similar attempts were made. This time, it had the backing of the newly erected UNESCO, and a new generation of biologists, who advocated the "new synthesis" in biology, which fused Mendelian genetics with Darwinism. From this sense of necessity to revise biology, and anthropology, a call was made upon UNESCO at its sixth session in 1948, to "disseminat[e] scientific facts designed to bring about the disappearance of that which is commonly called race prejudice".[2] Education in the presumably established scientific truth about racial categories was to prevent the recurrence of "the doctrine of the inequality of men and races" which had made possible the "great and terrible war".[3]

This resulted in two Statements on Race, one in 1950 and a revised one in 1952. The objective of the Statements was to separate 'ideology' from science. However, what

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[1] J. Reardon, 'Decoding race and human difference in a genomic age,' *Differences* 15 (2004) 45

[2] Quoted in UNESCO, "The race question," in *UNESCO and its programmes* (Paris: 1950)

[3] UNESCO constitution (1945-1946), quoted in Ibidem

exactly separated "ideology" and scientific "truth" was the subject of much debate.[4] Moreover, the scientific, 'objective' facts were infused with an ideological message: "biological studies lend support to the ethic of universal brotherhood."[5] An appeal was made on 'rational science' to cure the irrationality that lay at the basis of racist aggression. Although, in the course of the whole endeavour, scientists protested when scientific knowledge was distorted to fit the ideological message, few questioned the authority of science to speak about such issues.

The First Statement was drafted by an interdisciplinary group, headed by the British anthropologist Ashley Montagu. Despite the underrepresentation of biologists – the group members were predominantly social scientists – it was decided that race should be defined biologically. It stated that developments in science indicated that mankind is one, as "all men are probably derived from the same common stock".

> *From the biological standpoint, the species Homo sapiens is made up of a number of populations, each one of which differs from the others in the frequency of one or more genes. Such genes, responsible for the hereditary differences between men, are always few when compared to the whole genetic constitution of man and to the vast number of genes common to all human beings regardless of the population to which they belong. This means that the likenesses among men are far greater than their differences*.[6]

In this vein, theories of polygenism, the idea that contemporary races each had their separate evolutionary origins and lineages, were considered unlikely, although not explicitly rejected; it stated that "Race admixture" had "been going on since the earliest of times".[7]

The debate between monogenists and polygenists goes back to the eighteenth century.[8] The nineteenth-century version of monogenism is the idea that the evolution

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[4] Reardon, 'Decoding race,' 46

[5] It continued: "For man is born with drives towards co-operation, and unless these drives are satisfied, men and nations alike fall ill." UNESCO, "The race concept. Results of an inquiry," (Paris: UNESCO, 1952) 103

[6] Ibidem 98

[7] Ibidem 101

[8] "In de verlichting komt nog een derde aspect van het moderne denken over cultuurverschillen op, namelijk de opvatting dat de mensheid onder te verdelen valt in verschillende 'rassen' met specifieke fysiologische en psychologische kenmerken. Wat de rassentheorieën van de zeventiende en achttiende eeuw met elkaar gemeen hebben, is de – soms expliciete, soms impliciete – hiërarchische ordening van de mensenrassen. Een belangrijk onderscheid is dat tussen polygenetische theorieën, waarin betoogd wordt dat de verschillende rassen niet van dezelfde oorspronkelijke mens afstammen, en monogenetische theorieën, die het meer egalitaire uitgangspunt hebben dat alle rassen deel hebben aan een gemeenschappelijke menselijkheid. De laatste benadering treffen we bijvoorbeeld aan bij Buffon, die raciale verschillen analyseert als effecten van het klimaat en andere omgevingsfactoren." Stuurman's *Uitvinding van de mensheid* summarised by Jacques Bos, 'De universele aantrekkingskracht van het gelijkheidsideaal. Review of Siep Stuurman, *De uitvinding van de mensheid. Korte wereldgeschiedenis van het denken over gelijkheid en cultuurverschil*

of modern humans from archaic members of the *homo* family took place exclusively in Africa, and that they migrated from this continent to populate the world. It is generally summarized as the “Out of Africa” - hypothesis. The idea of African origins has a long history in archaeology, anthropology and other intellectual ancestor disciplines of anthropological genetics. For instance, Africa was already proposed by Darwin as the birthplace of man[9]. Alternatives in biology, generally lumped together as ‘the multiregional hypothesis’, propose that modern humans evolved independently in several places. The modern lineages subsequently developed in parallel, to admix when they expanded their territories. This view can be placed on the polygenist tradition.

The Statement proclaimed that mental differences are not innate; nor are cultural differences between groups the result of inherited genetic differences. Man doesn’t speciate, according to Mayr (1904-2005), as “Man has, so to speak, specialised in despecialisation”, and this has accounted for his evolutionary success.[10] Likewise, the first director of UNESCO, Julian Huxley, defined culture as ‘the’ human adaptation.[11] “The one trait which above all others has been at a premium in the evolution of men’s mental characters has been educability, plasticity. This is a trait which all human beings possess. It is indeed, a species character of Homo sapiens.” This shared “species character” guaranteed that races are mentally equal:[12] culture – such as technology or complex social organization – was an equalising factor, and had shaped human biology, human nature, rather than the other way around. The historical-evolutionary view was that man as a cultural being first appeared as a hunter-gatherer.[13] Thus, in the context of the Cold War, and increasing decolonization,” “Early Man in Africa [was] conceived as the prototype of the United Nation’s post-World War II universal man.”[14]

Because the capacity for culture was universal, race could now be defined as a merely physical, not mental entity: only bodies were different, and these physical differences were the results of geographical isolation. In other words, difference was merely external, the result of coincidental and sometimes random processes, and not

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(2009),' *Krisis* 2 (2010) 73

[9] “In each great region of the world the living mammals are closely related to the extinct species of the same region. It is therefore probable that Africa was formerly inhabited by extinct apes closely allied to the gorilla and chimpanzee; and as these two species are now man's nearest allies, it is somewhat more probable that our early progenitors lived on the African continent than elsewhere.” C. Darwin, *The descent of man and selection in relation to sex* (1871 [cited 15 May 2011]); available from http://darwin-online.org.uk/pdf/1871_Descent_F937.1.pdf 199

[10] Richard G. Delisle, 'Adaptationism versus cladism in human evolution studies,' in: Raymond Corbey and Wil Roebroeks, eds., *Studying human origins* (Amsterdam, 2001) 111

[11] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 214

[12] Ibidem 199

[13] Ibidem 215

[14] Ibidem 187

indicative of differences in mental or cultural potential. Moreover, the idea of 'races' was replaced with 'populations', which were defined as overlapping, statistical entities.[15] Furthermore, these populations were conceived of as dynamic groups, ever-changing under the influences of historical and evolutionary forces. "The biological processes which the classifier [...] embalm[s], as it were, are dynamic, not static."[16] The forces that produce, and continuously change species diversity ensure that any distribution of biological differences is only a temporary, snapshot reality. There was a strong argument against the notion of purity: "There is no evidence for the existence of so-called "pure" races. [...] Race formation itself was the result of "hybridization", which had been going on for a considerable time.[17] Race was "not so much a biological phenomenon as a social myth."[18]

Much as the First Statement was appreciated by the general public, it wasn't by the scientific community. Scientists objected to the misplaced certainty the Statement suggested, such as the rejection of multiregionalism, as if that debate was already settled. They also objected to the designation of race, "and not merely racialism," as a 'myth'; to the presentation of the absence of mental differences between races as an established fact; and to the conflation of biological and social concepts of race. The "most constant target for criticism", however, was the presumption of an inborn human "drive towards co-operation" which was presented in the First Statement as "support for the ethic of universal brotherhood."[19] Such discussions, critics argued, belong "rather to philosophy than to the realm of pure science".[20]

Some objections against the First Statement were framed in terms of a clash between traditional and modern race concepts, or so-called 'typological' versus 'populational' views. [21] With regard to hominid evolution, Mayr characterised the 'outdated' typological definition of species as one that presupposed "a limited number of types in nature". By contrast, a 'modern', "biological definition of species assesses the variability of individuals as flowing from their membership of a reproductive community, an ecological unit, and a genetic unit. Accordingly, typologists would tend to exaggerate the constancy of taxa and the sharpness of the gaps separating them. [...]

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[15] Reardon J. Reardon, *Race to the finish. Identity and governance in an age of genomics* (Princeton, 2005) 28

[16] UNESCO, "The race concept. Results of an inquiry," 99-100

[17] Ibidem 101

[18] Ibidem 101

[19] Ibidem 103

[20] UNESCO, "Working paper meeting of physical anthropologists and geneticists for a definition of the concept of race," (Paris: 1951), Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 201

[21] Delisle, 'Adaptationism versus cladism in human evolution studies,' 109

typologists would be more inclined towards a multilinear scheme and taxonomic inflation, whereas populationists would be more inclined towards a unilinear scheme and taxonomic reduction." Physical anthropology reformed along these lines:

> *'According to one opinion, the core of the controversy is a difference in points of view. The traditional school of anthropology maintained that races exist as rigorously defined, genetically homogenous, and discrete entities. The modern conception is more fluid and dynamic. It is based on "advances in human genetics (which) have served to expand the scope of social biology; (and) a problem focus which seeks to articulate and systematize the manifold inter-relations of human biological and behavioural factors. These advances, as we know, are the result of a shift in biological analysis from taxonomic-descriptive studies to studies of function, process and diversity."'*[22]

While describing fundamental changes in the way evolutionary history was conceptualised - the emergent 'new synthesis' took 'population' as its new object, and emphasized change and process - the typological-population dichotomy was also a useful way of politically distinguishing pre- from post-war views. Mayr (1904-2005) considered typological thinking "the foundation for all racist thought."[23] Similarly, Dobzhansky (1900-1975) proposed the 'population'-approach, with its emphasis on change and variation, as a way to counter racism.[24] "International and nearly simultaneous interest in the synthetic theory of evolution and populational thinking" triggered a change of focus in physical anthropology "from racial classification to [...] processes of change."[25] The "new physical anthropology", of which Washburn was the front man[26], followed in its wake. Thus, in physical anthropology and biology the 'historicisation' of the concept of race, which started in the nineteenth century, came to its completion. As the physical anthropologist Frederick Hulse argued, "races are simply episodes in the evolution of a widespread species."[27]

The criticism of the First led to a revised, Second Statement, this time authored

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[22] UNESCO, "Working paper meeting of physical anthropologists and geneticists for a definition of the concept of race," 4

[23] quoted in Lisa Gannett, 'Racism and human genome diversity research: the ethical limits of "population thinking" ' *Philosophy of science* 68 (2001) S489

[24] Reardon, *Race to the finish. Identity and governance in an age of genomics* 35

[25] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 206-207

[26] Marianne Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' *Journal of the History of Biology* 41 (2008) 481-82

[27] Frederick S. Hulse, 'Race as an evolutionary episode,' *American Anthropologist* 64 (1962) 943

by a group that included biologists and geneticists. It was emphasized that critics "did not reject [the] general spirit [of the First Statement] nor its main conclusions." But the impression that the objections raised represented a "victory for racism and the defeat of a naive humanitarianism" needed to be avoided. Twelve population geneticists and physical anthropologists among the critics were asked to draft a document that "reflect[ed] more accurately the views of scientific circles".[28].

The resulting Second Statement added to the 'common stock' argument that "there is some dispute as to when and how different human groups diverged from this common stock." "Crossing" and specialization (which were partly the results of random processes) "create what we perceive as races" – and these are continuously changing. Admixture was considered a constant factor in human history and necessary for the health of the species. The possibility that mental group differences were biological was now left open, but considered unlikely.[29] Thus, the Second Statement nuanced several statements and kept open possibilities for further research into differences. Furthermore, the "ethic of universal brotherhood" was kept more separated from biological knowledge. It was argued that biological concepts of race have no 'fixed' social meaning – which is different from the view that race is biologically meaningless, as the Statements have been interpreted to proclaim.[30]

The geneticists' and biologists' opposition against the First Statement – their argument that it was as ideology-ridden as the ideas it intended to counter[31] - can be explained as an attempt to secure their freedom to define race. Along this line, Reardon argues that the UNESCO Statements on race were not a closing, but an opening of the debate.[32] According to her, the canonical historiographical view of a 'paradigm shift,' which holds that after the UNESCO Statements race was less and less used as a biological concept, and relegated to the social,[33] is flawed. Dobzhansky didn't believe race is a social construction; he did emphasize the social boundaries between populations, the statistical, quantitative nature of genetic differences between races, and the subjective nature of racial classification systems.[34] Race as a research topic was not abandoned: it was *redefined* in terms of a dynamic concept, as a Mendelian population:

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[28] UNESCO, "The race concept. Results of an inquiry," 7
[29] Ibidem 14
[30] Reardon, *Race to the finish. Identity and governance in an age of genomics* 31
[31] Ibidem 31
[32] Ibidem 24
[33] Ibidem 12-13
[34] Gannett, 'Racism and human genome diversity research: the ethical limits of "population thinking" ' S484-5

"a reproductive community of sexual and cross-fertilizing individuals which share in a common gene pool".[35] In Reardon's view, the population concept was a *tool* to study race (formation), rather than its replacement.[36] The opposition against 'typological' notions of race seemed consensual among the reformers, but the definition of what was to replace it remained an issue to be settled: "the act of deciding what will count as a group [became] a major site of political/scientific struggle". [37]

Moreover, typological thinking continued to exist,[38] both within and outside of science. Two sociopolitical discourses existed in parallel after WWII. On the one hand there was a humanistic vision of unity, and on the other a discourse of difference, which shored up identity politics that "turned race into a resource", and served the reconstruction of the national and global political order of independent nation states.[39]

Genetic knowledge was of central importance in the post-war redefinition of race, as the quote from the First Statement above illustrates – "*genes, responsible for the hereditary differences between men, are always few...".* Genetic data contributed to the discrediting of the typological view.[40] Population genetics had emerged in the first half of the twentieth century, following the discovery of blood group variation, as an alternative to physical anthropology.[41] Several biologists had argued that animal variation below the species level is structured clinally, that is, that variation is gradual as opposed to discrete, and that therefore the term 'race' should be abandoned. Livingstone argued that this also applied to humans. To his much-quoted argument that "There are no races, there are only clines" he added: "this position does not imply that there is no biological variability between the populations of organisms which comprise a species, but just that this variability does not conform to the discrete packages labelled races".[42] This all is not to say that early genetics research could not be used to argue for the opposite. As the anthropologist Jonathan Marks argues, "for such a fundamental and classical question as the basic structure of the human species, geneticists identified races when races were assumed to be there, identified the *absence* of races when they

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[35] Dobzhansky, quoted in Ibidem S484

[36] Reardon, *Race to the finish. Identity and governance in an age of genomics* 66

[37] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 202-3

[38] Ibidem 202

[39] Reardon, *Race to the finish. Identity and governance in an age of genomics* 18

[40] Deborah Bolnick, 'Individual ancestry inference and the reification of race as a biological phenomenon,' in: Barbara A. Koenig, et al., eds., *Revisiting race in a genomic age* (New Brunswick, New Jersey, and London, 2008) 70

[41] Reardon, *Race to the finish. Identity and governance in an age of genomics* 42

[42] Frank B. Livingstone and Theodosius Dobzhansky, 'On the non-existence of human races,' *Current Anthropology* 3 (1962) 279 1962 Clines Brace, CL (1964). "A Non-racial Approach Toward the Understanding of Human Diversity". In Ashley Montagu. *The Concept of Race* J. Marks, 'Ten facts about human variation,' in: M.P. Muehlenbein, ed., *Human evolutionary biology* (Bloomington, 2010) 265-276 267

were assumed *not* to be there."[43] He argues that "a principal role for genetics in anthropology has been as a naturalistic alternative explanation for social inequalities, associated with reactionary conservative politics and anti-democratic discourses—in reference to a timeline that unites the otherwise disparate sciences of the eugenicists, the psychometricians, the segregationists, the sociobiologists, and the evolutionary psychologists." Remarkably, he states that "genetic data were not even recognized as undermining the concept of race until the 1970s." Evidently, genetics could provide arguments for both the relevance and irrelevance of differences.

Nevertheless, genetics was one of the weapons against what were now considered to be outdated anthropological views of race. The concept of race as a 'Mendelian population' - a reproductive community of individuals that share a common gene pool[44] - defined groups in cultural or behavioural (breeding patterns), as well as biological terms.[45] Genetics shored up the important scientific argument that populations are mere 'statistical entities'[46] that overlap considerably.[47]The 1952 UNESCO Statement read:

> *"Genetics has revolutionized anthropology and these two branches of study are now seeking a way of fusing into a new integrated whole. The Statement published here, and the comments to which it has given rise, reflect this stage, so rich in possibilities for advances in our knowledge of man."*[48]

Revised and more traditional views existed side by side for decades after World War II.[49] In anthropology and genetics, cultural and genetic group definitions were linked, as were discourses of unity and difference. However, slowly, molecular biology genetics changed the meaning of phenotypic differences: these were increasingly considered to be trivial and misleading, not useful for defining groups. They were relegated to the level of "folk accounts", and gave way to genetic definitions of race.[50] This was later reinforced by a focus on those regions of the genome that had no known direct relation to the

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[43] Jonathan Marks, 'Lessons from history,' *International Journal of Cultural Property* 16 (2009) 199
[44] Dobzhansky, quoted in Reardon, 'Decoding race,' 41
[45] Reardon, *Race to the finish. Identity and governance in an age of genomics* 38-39
[46] UNESCO, "The race concept. Results of an inquiry," 26: "The important point, politically, is surely that the group differences are only statistical."
[47] Ibidem 12; Reardon, *Race to the finish. Identity and governance in an age of genomics* 18
[48] UNESCO, "The race concept. Results of an inquiry," 9
[49] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 204; In theorising about hominid evolution, "typological thinking continued to be actively applied." Delisle, 'Adaptationism versus cladism in human evolution studies,' 110
[50] Gísli Pálsson, *Anthropology and the new genetics* (Cambridge, 2007)179

phenotype, or indeed, were known or presumed to be non-coding. This was also because these regions were considered most appropriate for use as ‘molecular clocks’: they were presumably not subjected to natural selection so that their mutation rates were determined only by chance, and not by contingent external factors. “Sequences were seen to store evolutionary history most directly, exactly where they were considered only loosely related to the phenotype. It is in this sense that they most accurately documented evolutionary transmission and stochastic change.”[51]

Cavalli-Sforza’s trees

Although L. L. Cavalli-Sforza (1922) was not directly involved in the post-war attempts to draw the teeth from racism with the use of biological knowledge, he moved in circles and entered research fields that were very much influenced by these endeavours. He turned from the study of bacterial to human genes at the end of the 1950s. Originally trained as a medical scientist, he investigated human genetic history in Parma, using basic information about genealogy, geographic location, blood groups and consanguinity.[52] In the late 1940s he had worked with one of the architects of the evolutionary synthesis, Fisher (1890-1962), in his lab in Cambridge.[53] Although Cavalli was far from politically outspoken, when in the 1960s and 1970s some prominent scientists uttered statements reminiscent of scientific racism and eugenics, Cavalli debated them fiercely. In Stanford, where he started working in 1971,[54] he repeatedly challenged Arthur Jensen (1923), who argued that IQ was hereditary, and differences between blacks and whites innate and unalterable. Cavalli’s decision to direct his attention to “cultural evolution” was informed by Nobel prize winner William Shockley’s plea to financially reward the voluntary sterilisation of women with a low IQ. Cavalli felt “the concept of human cultural learning was a valid weapon against racist arguments that differences between people (for example, different IQ scores among ethnic groups) were due to biologically determined “racial” differences.”[55]

Cavalli argued that culture and genes have coevolved, and humans have shaped their biology by shaping their environment over thousands of years, an argument that

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[51] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 517

[52] L. Stone and P. F. Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* (2005) 62

[53] Ibidem 37

[54] Ibidem 84

[55] Ibidem 86

resembled that of the UNESCO Statements. He tried to develop mathematical models for cultural evolution. These models were adaptations of models used to describe genetic phenomena. For instance, he used Fisher's 'wave of advance' model, which was originally designed for the dissemination of genes, to describe the geographical spread of agriculture, starting about 9,000 years ago.[56] 'Cultural drift' is another example of a genetics concept that Cavalli applied to cultural phenomena.[57] Genetic drift, in his research, is defined as the spread, over several generations, of a polymorphism in a population due to chance effects, so that the population can be identified by a high frequency of this genetic 'marker'. The chance that a polymorphism spreads widely through a small population is bigger than an equivalent spread through a large one. 'Founder effect' is a variant of such genetic drift: it is the loss of genetic diversity when a small part of a group splinters from its group of origin. The migrants carry a selection of the original gene pool, and this selection is visible in its 'offspring population' for long periods of time, however large it grows. Population bottlenecks – the temporary, radical decrease of population size – have the same effect. Cavalli applied this statistical model to cultural phenomena. For instance, he explained contemporary American religiosity as the result as such a cultural 'founder effect': the 'founders' in this case were religious refugees, whose religious ideas were passed on to a large proportion of its descendants (as compared to its European 'ancestor population').[58]

He investigated the existence of other analogies between genes and culture: for instance, he wondered whether variation in archaeological style between ancient cultures (as displayed in the material record) was correlated with genetic variation between the historical peoples who constructed the buildings. Genetic 'echoes' of the civilisations identified by an architectural style presumably could be found in the genomes of contemporary populations living around the archaeological sites. One would only have to investigate whether genetic and archaeological patterns mapped onto each other.[59]

Cavalli tried to model the transmission of ideas, both vertical (between generations) and horizontal (between individuals or cultures). In 1981, he published a book, together with the mathematical biologist Marcus Feldman (1942), which summarized their work

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[56] L. L. Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* (Princeton, 1996) 107; Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 89

[57] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 97

[58] Ibidem 107

[59] Ibidem 80

on this subject as the “gene-culture coevolutionary theory”. Their ideas about “dual transmission” [..] and “gene-culture coevolution” were largely ignored by cultural anthropologists – perhaps, Cavalli’s biographers propose, because it was “too mathematical.” Also, many objected to their “atomic” view of cultural traits as discrete entities.[60]

Notwithstanding the importance of his theoretical excursions into the study of culture and his engagement in debates about racism for the development of his ideas, Cavalli spent most of his time doing empirical research and developing genetic methods and models. He had moved from medicine to bacterial genetics, from bacterial to human genetics, and subsequently helped develop genetic research into human migration history. In the 1960s, Cavalli invited another student of Fisher’s, Anthony Edwards (1935), to Pavia, where Cavalli had started working 1963[61]. Together, they developed methods to study drift and migrations in humans[62] and to construct human evolutionary trees based on genetic diversity[63] (as opposed to more traditional trees depicting species or subspecies morphological diversity). In 1964, Cavalli-Sforza and Edwards were the first to propose a method based on a matrix of distances between all possible pairs of populations sampled. They argued that “trees should represent fissions”.[64] Although they mentioned hybridisation in an article published in 1967 - “the course of evolution (were it but known) could be seen as a tree, whose branches split as populations diverge, unite as they hybridize, and end as they become extinct”[65] – their trees generally showed diverging branches only. They acknowledged the “inability [of their trees] to handle hybridization, convergence, and parallelism (that is, the similar selective response to similar environmental stimuli in different populations)” and the possible “breakdown of the assumption that evolution proceeds independently on each branch of the tree, an assumption that is basic to our model.” But, they argued, “there is reason to believe that, where enough different genes are considered, the effects of truly convergent genes will be swamped by the larger number of genes behaving independently in different populations.”[66] Furthermore, the extent to which any data was suitable for a tree model could be measured. In a paper in 1975, Cavalli and Piazza

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[60] Ibidem 107-09
[61] Ibidem 115, 62
[62] Ibidem 62
[63] Ibidem 115-6
[64] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 25
[65] L. L. Cavalli-Sforza and A. F. Edwards, 'Phylogenetic analysis. Models and estimation procedures,' *American Journal of Human Genetics* 19 (1967) 234
[66] Ibidem 255-6

proposed the term ‘treeness’ for this measure.[67]

They presented the first of such trees at the Intemational Congress of Genetics in 1963.[68] “Many human geneticists were skeptical of their results at that time, but it turned out to be the start of phylogenetic analysis of human populations that fascinated many population geneticists and anthropologists in subsequent years.”[69]

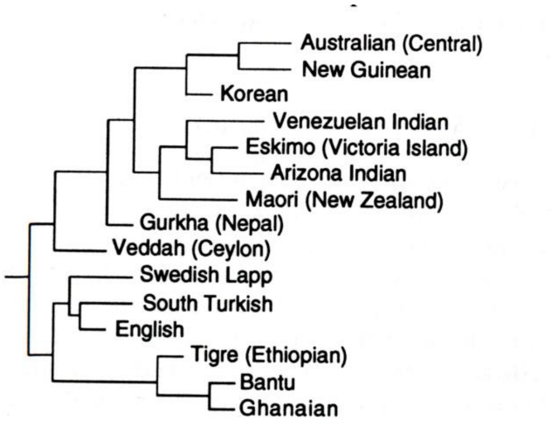

Figure 1 “Tree of 15 populations reconstructed on the basis of 20 alleles”, presented at the 11th international congress of genetics in 1963 by Cavalli-Sforza and Edwards.[70]

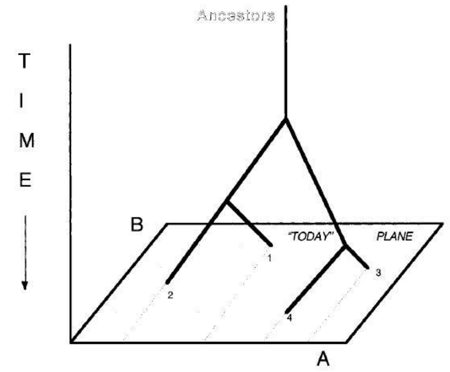

Figure 2. A theoretical example of the tree concept as proposed by L. L. Cavalli-Sforza, I. Barrai, and A. W. F. Edwards 1964. Redrawn in Stone and Lurquin, A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza 73

Initially, the roots of the trees, if they postulated any, were arbitrarily placed in the middle of their diagrams.[71]

Cavalli helped develop several other methods for the assessment of genetic diversity and history. Among them were ‘synthetic maps’, which compounded the information from many genes. For this, he used ‘principal component analysis’. Principal

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[67] L. L. Cavalli-Sforza and A. Piazza, 'Analysis of evolution: Evolutionary rates, independence, and treeness,' *Theoretical Population Biology* 8 (1975) 127-165

[68] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 73

[69] Masatoshi Nei, 'The history and geography of human genes: Book review,' *Trends in Genetics* 11 (1995)

[70] Reproduced from L.L. Cavalli-Sforza and A.W.F. Edwards, ‘Analysis of human evolution’ in *Proceedings of the 11th international congress on genetics* (1964) 2 923-33 in Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 68

[71] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 115

components (PCs) allow the visualisation of the variation of multiple gene frequencies – which without the PC method would require a three-dimensional image, as it deals with many genes at the same time.[72] “The first principal component extracts the most information regarding gene variation from the total information available. The second principal component extracts a little less information (information which is *not* explained by the first principal component, however), the third less still (but information not explained by the first and second principal components), and so forth, until 100 percent of the total information has been extracted from the data. In practice, one rarely goes beyond the seventh principal component because, at that stage, most of the recoverable information needed has been gathered, unless the phenomenon is particularly complex.”[73] In short, PCA chops up the genetic variation of several genes in several populations, into ‘PCs’. These PCs depict the gradual change in gene frequencies over geographic distances – as distinct structures, or several ‘kinds of difference’. Cavalli argued that these gradients of gene frequencies were generated by migrations, “because migration has a linear effect on gene frequencies.”[74] Thus, every PC, every gradient form high to low frequency, reflected a migration path.

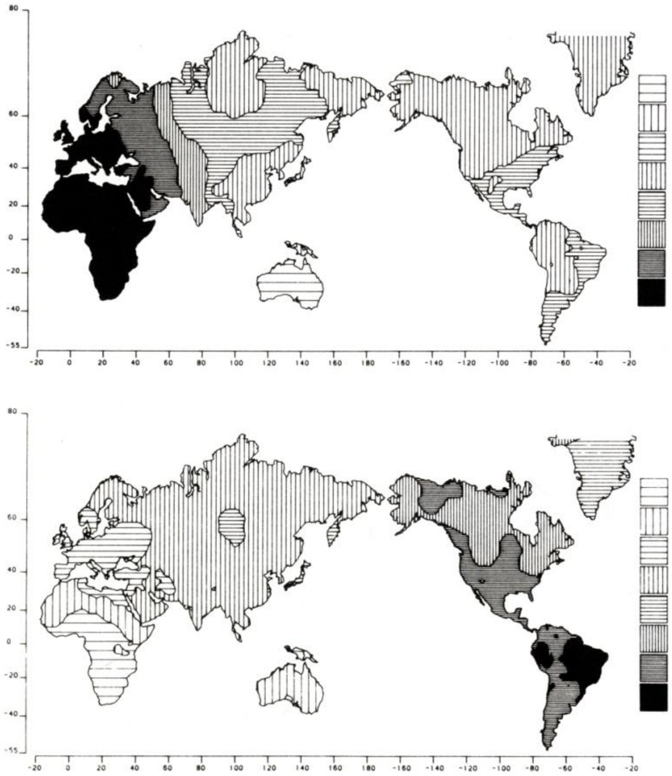

Figure 3 Synthetic maps of the world based on the first and second principal component. The colours indicate gene

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[72] Ibidem 68

[73] Ibidem 69

[74] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 133

frequencies and are ordered, in the legend, from high to low ones. The upper map depicts the first PC, with poles in Africa (where the maximum frequency was found) and Australia (where the minimum was found). The first map was thought to correspond with the first split in the world tree between Africans and non-Africans. "The first PC tends to indicate the expansion from the south and east of Africa, toward the rest of the world, first north and east, then toward Australia and the Americas." However, "PCs can only indicate a static situation, and we add the movement to the picture from external evidence."[75]

The genetic data used to build such trees came from isolated populations, of which the genetic make-up was thought to be the least affected by admixture and therefore the most informative of human history. The 1950s had brought increased attention to indigenous populations, or more specifically, their gene pools, as sources of information about rare genetic diseases.[76] Furthermore, ancient hunter-gatherers had become the icons of a shared humanity, representatives of a phase in the species history shared by all lineages. "Contemporary hunter-gatherers became cultural and biological representatives of our Paleolithic ancestors", especially after the highly influential volume *Man the hunter* was published in 1968.[77] In 1966, Cavalli started sampling Central African Pygmy's DNA because their hunter-gatherer mode of subsistence was "similar to the human species' Palaeolithic adaptation." Their short stature, which he thought might indicate a somewhat separate evolution, was another reason. The Pygmies surprised him by being so "different" and so "nice," and he considered their life in a blissful state a moral example for modern man. Such experiences provided another incentive for Cavalli to study culture. He visited them several times until the mid-1980s.[78]

Thus, in the 1960s and 1970s, by the hands of people like Cavalli, the body of anthropological data, methods and theory expanded. In the 1970s the field transformed from one that "borrowed" genetics methods to one that enhanced these "by an anthropological perspective of using diversity of social and demographical patterns to guide genetic analysis and inference."[79] For the reconstruction of evolutionary history and the building of trees the "molecular clock" hypothesis had been proposed in the 1960s.[80] Degrees of difference and similarity between species could be used to calculate genetic distances and construct trees with a time scale. It rested on the assumption that evolutionary rates are constant, that is, that mutations occur at steady similar intervals. The genetic differences can then be divided by the amount of time known from

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[75] Ibidem 135

[76] Michael H. Crawford, ed., *Anthropological genetics. Theory, methods and applications* (Cambridge, 2007) 6

[77] Pálsson, *Anthropology and the new genetics* 188

[78] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 74-77

[79] Dennis O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' *American Anthropologist* 105 (2003) 102-3

[80] Zuckerkandl E, Pauling L (1962) Molecular disease, evolution, and genic heterogeneity. In: Horizons in Biochemistry (Kasha M, Pullman B, eds), 189–225.

paleology that has passed since the separation of species. The resulting average mutation rates per year can be used to calculate other fissions. The relative age of samples could be calculated, and therewith the moment of fissions of species or (on the subspecies level) populations. In human population genetics, average mutation rates were calculated by comparing human with chimpanzee DNA, or that of another 'close relative.' As the separation times of species and humans were known from fossil records, the former's genome could serve as an Archimedean point, a reference with which the relative genetic distances between populations can be determined. The molecular clock hypothesis allowed the location of splits, the determination of the length of the branches, and thus the addition of a temporal dimension to trees of descent. By focusing on presumably non-coding regions of the genome, the information was separated from the phenotypic level.[81]

Another essential development was that of the cladistic method, which some trace back to the 1950s.[82] It organises species of groups of organisms into clades, which consist of an ancestor and all its descendants. It modelled *phylogeny*: descent, or evolutionary history conceptualised as a family tree. Cavalli has emphasized that the trees he and Edwards proposed in the 1960s were different from most cladistic trees as developed by zoologists and botanists. Those were based on the selection of characters that are useful for the reconstruction of evolution and dealt with greater degrees of differentiation than is discernible between human populations. Cavalli-Sforza and Edwards preferred the name 'phylogenetic tree,' which is based on 'numerical taxonomy' – the calculation of genetic differences.[83] With the help of the molecular clock hypothesis, such numerical taxonomies could be transformed into phylogenetic trees – the major aim of Cavalli and Edwards was not to produce accurate taxonomies, but to build trees of descent.[84] These trees, however, reconstructed descent and organised genetically defined groups in a way similar to cladistic trees, with nested ancestral and descendant groups. They depicted an increasingly large body and variety of data. Cavalli-Sforza was one of those pioneering the study of regional and continental patterns and started to compare linguistic and genetic patterns.[85]

Thus, the human family trees (or parts of it) were analogous to cladistic species

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[81] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 507
[82] Robin O. Andreasen, 'The cladistic race concept: A defense,' *Biology and Philosophy* 19 (2004) 425
[83] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 31
[84] Cavalli-Sforza and Edwards, 'Phylogenetic analysis. Models and estimation procedures,' 234
[85] O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' 102-3

trees, and based on calculations of genetic distances between indigenous populations, which were interpreted in population history terms and dated with the use of the molecular clock hypothesis. At least two alternative historical models to 'the tree way' to model genetic variation existed, reflecting disagreements about the importance of 'hybridisation.' Hulse wrote in 1962 that an ancestral tree is a misleading model for the evolutionary history of humanity. He referred to Weidenreich's "grid or trellis" (figure 4a and 4b) and Hooton's "vine" models, for which Hooton also used the human cardiovascular system as a metaphor (figure 5).

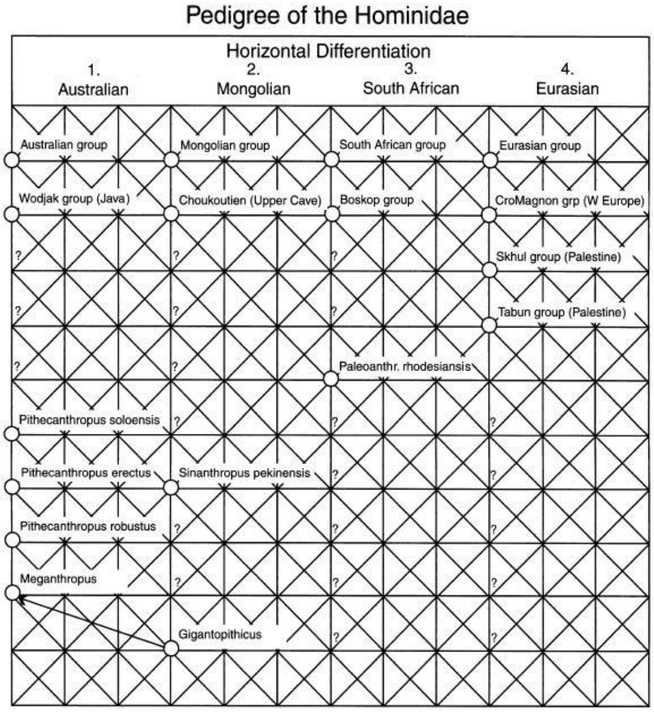

Figure 4a Multiregional 'trellis' model of human evolution, by Weidenreich, reproduced from A. Templeton, 'Genetics and recent human evolution', in *Evolution* 61:7 p1509. "Key fossils and sites known at the time are placed in a trellis, with vertical lines indicating regional descent, and diagonal and horizontal lines representing genetic exchange between regions." Templeton explained that according to this model, "humanity consists of a single evolutionary lineage with no subbranches because humanity's geographically dispersed populations were and are interconnected by gene flow and lines of recent, not ancient, common descent due to this gene flow."

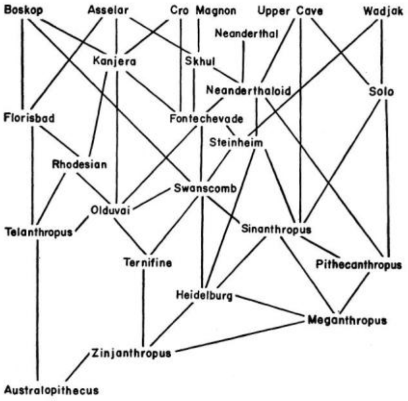

Figure 4b 'Trellis' model, after Weidenreich, from F. Hulse, 'Race as an evolutionary episode' *American Anthropologist* (1962) p931

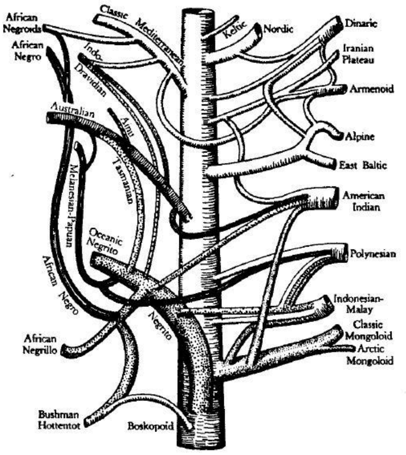

Figure 5 Hooton's model (1946), from J. Marks, '"We're going to tell these people who they really are": Science and relatedness', in Sarah Franklin and Susan McKinnon (eds), *Relative values. Reconfiguring kinship studies* (2001) p358

Such models, Hulse argued, more accurately represented the reality of gene flow between populations, which is downplayed by the branching pattern of trees and their emphasis on fissions. "within a species, genetic continuity exists, and [...] any diagram which does not show this fact is bound to be misleading.[86] On the other hand, others proposed models that emphasized more or less distinct 'racial' lineages, tracing back to multiple human origins. In the 1960s, the appropriation of Carleton Coon's polygenist theories about race by segregationists threw anthropology into a crisis.[87] But the very crisis they caused also reveals that his views were considered outdated by many. Tree building methods were developed further and so where the methods to determine their roots. And although the geographic location of this root remained unclear - Cavalli has

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[86] Hulse, 'Race as an evolutionary episode,' 931-2

[87] *Marks The Two 20th-Century Crises of Racial Anthropology* 198-202

argued for Asian origins[88] - the idea of a common ancestry slowly defeated multiregionalism.

Many continued to advocate a broader variant of the multiregional hypothesis, though, most persistently the leader of the multiple origins school, Milford Wolpoff.[89] Still in 1992, he argued that "there is no single home for modern humanity - humans [that is, archaic humans] originated in Africa and then slowly developed their modern forms in every area of the Old World."[90] Multiregionalists pointed to local resemblances between fossil Homo Erectus skulls and modern skulls, and to the presence of 'intermediate' skulls in several regions.[91] The current genetic diversity, they argued, is the result of 'isolation by distance': the equilibrium between mutation and short distance migration, which leads to a correlation between geographic and genetic distances.[92] Variants of this hypothesis have never been completely discarded, but "Out of Africa" has slowly gained prominence and today has become the dominant view.

One of the arguments for a single origin came from genetics: humans turned out to be genetically very much alike. Cavalli allegedly was the first to show in 1966 "that of the total genetic variation observed in the human species, less than 15 percent accounts for differences between races."[93] His biographers argue that because Cavalli didn't attribute to this finding any implications for the socio-political concept of race, his results did not enter the history books. The calculations made by a more politically outspoken researcher (Cavalli's biographers argue that he "confirmed" Cavalli's observations) six years later did.[94]

Lewontin's measurements

This researcher was Richard Lewontin (1929). His calculations became a landmark in anthropological genetics and have played an important role both within and outside science. For decades, his calculations served as reference points, as well as mantras, in anthropological genetics and beyond.

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[88] Jane Gitschier, 'All about Mitochondrial Eve: An interview with Rebecca Cann,' *PLOS Genetics* 6 (2010) 3-4

[89] J. N. Wilford, 'Critics batter proof of an African Eve,' *Science* (1992)

[90] M. Wolpoff and A. G. Thorne, 'The multiregional evolution of humans,' *Scientific American* (1992) 76

[91] A. Gibbons, 'Eve wounded, but not dead yet,' *Science* 257 (1992) 875

[92] T.D. Weaver and C.R. Roseman, 'New developments in the genetic evidence for modern human origins,' *Evolutionary Anthropology* 17 (2008) 69-80: 69

[93] Jan Klein and Naoyuki Takahata, *Where do we come* from p387, quoted in Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 195

[94] Ibidem 195

While developments in research into genetic variation in animals trickled through to human genetics, the advent of computer technologies enabled the faster analysis of more data. In the late 1960s and early 1970s, Lewontin attempted to calculate the amount of, and ratio between, intra- and within-group diversity. Similar calculations had been made by Lewontin himself and by Harris in 1967 and 1970, respectively.[95] There is a long history of thinking about this issue, Lewontin explained in his 1972 article; but in the absence of rigorous methods to measure diversity, results were contingent upon "socioeconomic relations" – and "even in the present era of Darwinism" opinions on the matter varied.[96] With the development of new technologies, the assessment of variation "directly and objectively", locus by locus, had become possible.[97] And this is what Lewontin did: he analysed variation in blood group systems, serum proteins, and red blood cell enzymes[98] to investigate "How much of human diversity between populations is accounted for by more or less conventional racial classification."

He explained the difficulties with determining what this classification should look like: "I have tried to include what would appear to be *a priori* representatives of the range of human diversity. But how does one do that?" Who to include, how to weigh, and how to determine the boundaries between 'races' – these were complicated issues.[99] The use of external criteria (linguistic, historical, morphological, etc) for classification would decrease the calculated diversity between races, as it would lump together groups that are genetically divergent; to use internal evidence only would produce the difficulty that "the procedure would have no end. The between-race component would be maximized if every population would be made a separate race!" Eventually, Lewontin chose a "conservative approach", and used a "classical racial grouping" with a few adjustments based on "obvious total genetic divergence." He distinguished seven races, some of which were defined exclusively geographically (e.g. "Oceanians" and "Australian aborigines"), some were more hybrid, referring to morphological ("Caucasians", "Mongoloids") and linguistic entities.[100] This research strategy produced the famous results:

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[95] Ibidem 382

[96] R.C. Lewontin, 'The apportionment of human diversity,' in: T. Dobzhansky, et al., eds., *Evolutionary Biology* (New York, 1972) 381–398 381

[97] Ibidem 382

[98] Ibidem 383

[99] Ibidem 384-5

[100] Ibidem 386-7

> *"The mean proportion of the total species diversity that is contained within populations is 85,4% [..]. Less than 15% of all human genetic diversity is accounted for by differences between human groups! Moreover, the differences between populations within a race accounts for an additional 8,3% so that only 6,3% is accounted for by racial classification."*[101]

Several factors influenced the result, he explained. Overrepresentation of '"primitive"' peoples meant that their within-population diversity was heavily counted, and that total human diversity was inflated because "these groups tend to have gene frequencies that deviate from the large races."[102] His *a priori* racial classification on the one hand also added much weight to diversity between races, because "aborigines and Oceanians" were "overrepresented"; while on the other hand, the lumping together of populations in racial categories underestimated differences between races.[103] He explained that if he would have abstained from organizing the data altogether, and had assigned samples to racial categories based on gene frequencies alone, this would have increased the racial component. "But if this were carried out objectively it would lump certain Africans with Lapps!" Therefore, "if we want to assess the meaning of racial classification in genetic terms, we must concern ourselves with the usual racial divisions." This approach resulted in the 6,3% of total diversity that accounted for differences between races; a number which he estimated to be "about right or slightly overestimated."[104]

He concluded that

> *"our perception of relatively large differences between human races and subgroups, as compared to the variation within these groups, is indeed a biased perception [...;] human races and populations are remarkably similar to each other, with the largest part by far of human variation is being accounted for by the differences between individuals. Human racial classification is of no social value and positively destructive of social and human relations. Since such racial classification is now seen to be of virtually no genetic or taxonomic significance*

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[101] Ibidem 396

[102] Ibidem 396-7

[103] Ibidem 397

[104] Ibidem 397

> *either, no justification can be offered for its continuance."*[105]

Lewontin has since written extensively on the subject. In 1982 he published *Human diversity*, a long argument against behaviourism and genetic determinism. In it, he argued that there are no 'pure' groups, that admixture and the absence of perfectly isolated groups[106] guarantee that there are no discrete human groups, only clines[107]. This argument has later also been made by Cavalli.[108] Also, the human species is young, so differences are relatively recent (and, by implication, superficial);[109] a very small amount of migration is sufficient for the prevention of differentiation of groups by genetic drift - in short, the ""unifying forces of migration and common selection" explain why "categorisation efforts fell under their own weight".[110]

Lewontin's findings were foreshadowed by research in the preceding two decades – even if Cavalli's biographers exaggerate when they state that the apportionment of diversity was already 'discovered' by Cavalli, in the UNESCO Statements it was already stated that "Some biological differences between human beings within a single race may be as great as, or greater than, the same biological differences between races."[111]

Methods and technologies

From the beginning of the 1970s, attempts were made to synthesize methods and theories in anthropological genetics, a term which (according to the author, Crawford) was coined in *Methods and theories of anthropological genetics* in 1973.[112] In the late 1970s and 1980s, new technologies accelerated developments in this emerging discipline. Until then, human genetic variation had been investigated by the analysis of blood groups and proteins, later dubbed 'classical' polymorphisms. The former had been studied since their discovery in the early twentieth century. In the 1950s, technological

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[105] Ibidem 397

[106] R. Lewontin, *Human diversity* (San Francisco, 1982) 113

[107] Ibidem 116

[108] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 19

[109] Lewontin, *Human diversity* 162

[110] Ibidem 111-113

[111] UNESCO, "The race concept. Results of an inquiry," 14

[112] Crawford, ed., *Anthropological genetics. Theory, methods and applications* 10; he makes the reservation that D.F Roberts had referred to anthropological genetics in a lecture in 1965. It is difficult to establish when the field was 'founded', as it "built on the research and formulations of many disciplines and theoretical approaches to human evolution." Crawford, ed., *Anthropological genetics. Theory, methods and applications* 8

developments made the study of protein variation possible. In retrospect, a recently published anthropological textbook states, these proteins provided only a "glimpse into the genetic variation contained within the human genome": looking at "primary gene products", proteins, i.e., by secondary phenomena, was as close as one could get to the level of DNA[113]. This level was unlocked in the 1980s. Roughly between 1975 and 1985, new methods were described and developed, sequencing methods, restriction fragment length polymorphism (RFLP), and polymerase chain reaction (PCR) methods among them. In 1981 the first human mtDNA genome was sequenced.[114] Because the majority of DNA doesn't code for proteins, the direct access to DNA that these technologies provided can be considered revolutionary.[115] The flowering of computational and other technologies produced previously unknown amounts of data, as large quantities of specific DNA segments for analysis could be generated (by PCR), sequencing could be automatised, and classical markers were replaced with their new, high-technological successors such as single nucleotide polymorphisms (SNPs) and restriction site polymorphisms (STRs, or sequences of nucleotides). In 1984-5, the first of Cavalli's Pygmy cell lines were produced.[116] And in 1984, Centre d'Etude du Polymorphisme Humain (CEPH) was created, the future host of the HGDP database. This "laboratory [...] coordinated the first international genome mapping collaboration by making available DNA from 40 large reference families (later 61) to researchers throughout the world." And it "provided the foundation for the International Genome Project, the physical mapping of the human genome (largely initiated at CEPH), which in turn led to determination of the DNA sequence."[117] All of these technological developments in turn led to new analytical and statistical methods to tackle the ubiquitous data with.[118]

With computer technologies, anthropological genetics acquired an even greater air of objectivity and quantification, and was now hardly comparable to traditional morphological approaches to human diversity. Indeed, from 1975 onwards, molecular anthropology was contrasted with traditional physical anthropology and paleoanthropology, which were "subjective and ideology-ridden", while molecular anthropology "was seen as characterized by rigorous mathematical logic and

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[113] Crawford, ed., *Anthropological genetics. Theory, methods and applications* 5
[114] Ibidem 3
[115] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 136
[116] Ibidem 164
[117] *Centre d'Etude du Polymorphisme Humain (CEPH) - Fondation Jean Dausset*, ([cited 10 June 2011]); available from http://www.cephb.fr/en/index.php
[118] O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' 103

technology-driven quantitative approaches". "The supposed value neutrality and objectivity of molecular anthropology were also associated with the fundamental nature of the anthropological gene and genome itself. Correspondingly, the techniques that promised the most direct approach to the most basic level of analysis had gained the highest authority among the molecular methods. Amino acid sequencing dominated, and even the unmediated study of DNA had come within reach. This meant direct access to the molecule that documented our evolutionary history. The prospect was linked to the hope that molecular anthropology would be able to tackle intra-human phylogeny." [119]

Computer programmes were developed to calculate the structure of trees and the locations of their roots. Looking back, Crawford argues that since the early years of the 'molecular revolution' in the 1980s, anthropological genetics' research emphasis has moved from the study of population structure to the study of human origins and diasporas. The sequencing and analysis of mtDNA and Y chromosome polymorphisms made this possible: these regions of the genome were found to be highly informative, and do not recombine, so that they allowed the building of molecular clocks and the reconstruction of migration from a female and a male perspectives, respectively.[120] Phylogenetic trees had become the model of choice for the depiction of human population history.

African Eve

The 'African Eve' study, published in 1987, was the product of these technological developments, especially of the computer program PAUP. The conclusion that 'Eve' lived in Africa was based on both the high variation in African mtDNA, the large differences between African and other samples, and the fact that the computer program that was used to build trees positioned the primary branches exclusively in African mtDNA samples.[121] The researchers estimated that she lived 200,000 years ago.[122] She was presented as an ancestor common to all humans living today: a mutation that occurred in her mitochondrial DNA was shared by "all humans currently alive" (as represented by

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[119] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 478

[120] Crawford, ed., *Anthropological genetics. Theory, methods and applications* 11

[121] R. L. Cann et al., 'Mitochondrial DNA and human evolution,' *Nature* 325 (1987) 33

[122] or more precisely, between 140,000 and 290,000 years ago Ibidem 34

the 147 samples from five continents). The mtDNA of Eve's contemporaries was lost in the contingencies of sexual reproduction of subsequent generations, making her the earliest common ancestor.

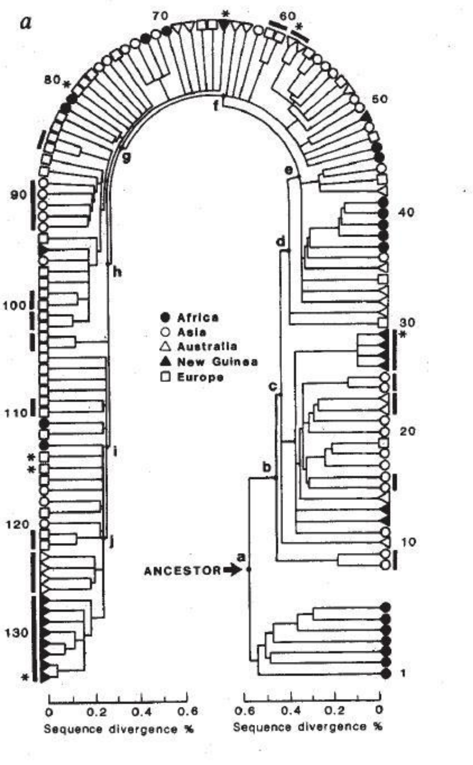

Figure 6 Genealogical tree for 134 types of human mtDNA, R. L. Cann et al., 'Mitochondrial DNA and human evolution', ***Nature*** **325 (1987) p.34**

'Mitochondrial Eve' marked not only the beginning of the strong decline of the multiregionalist scenarios, but also the ascent of anthropological genetics' Grand Narratives. Eve's relatively recent year of birth confirmed equally recent datings of the dispersion of modern humans across the globe. This meant that human differences, thought to result from natural selection in different environments and random effects of population splits on gene pools, had also emerged recently and could be considered 'superficial'. Thus, the 'Eve' study carried a double message of unity: sharing a mother and most of its history, humanity was one.

The location of the "cradle of humanity" and a shared common ancestor appealed to the imagination and was widely picked up by the press. In a Newsweek cover story, titled 'The search for Adam and Eve', Stephen Jay Gould was quoted to say that

> *If [the idea of one single centre of origin is] correct, and I'd put money on it, this idea is tremendously important. It makes us realize that all human beings, despite differences in external appearance, are really members of a single entity that's had a very recent origin in one place. There is a kind of biological brotherhood that's much more profound than we ever realized."*[123]

Thus, at the end of the 1980s, anthropological genetics was established as a field of research which, although fragmented into medical and evolutionary biological branches, had its own methods, research groups and narratives. Swept along by the molecular revolution, it flowered, with an increasing number of researchers dealing with large quantities of data which were analysed with increasingly sophisticated technologies. What is more, with a scientific scoop that was picked up by the press and produced powerful popular images, it had acquired the cultural authority to speak about human diversity and origins. While views about such matters often echoed the ideology of post-war antiracist science, the population concept had evolved since the 1950s. Anthropological genetics had co-developed and further defined it in terms of evolutionary and migration history, anthropologically and geographically ordered genetic markers, and positioned them as branches on the genetic human family tree.

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[123] J. Tierney, 'The search for Adam and Eve,' *Newsweek* (1988)

Chapter two - Cavalli-Sforza and the Human Genome Diversity Project: vanishing opportunities

The Human Genome Diversity Project

It has been argued that with the end of the Cold War a “market for humanitarianism” emerged[1] -in which “human similarities, not racial and ethnic differences, gained political currency.” The attempt of the Human Genome Project to map ‘the’ human genome, begun formally in 1990,[2] can be seen in this light[3]– notwithstanding the importance of economic, medical and other motivations. However, some anthropological geneticists felt that the HGP threatened to produce a one-sided and Eurocentric view of the human gene pool. The sequencing of only a few donors’ DNA would not be representative of human genetic diversity, they argued. The HGP focus on existing Eurocentric DNA databases in order to map ‘the’ human genome would have serious “historical and medical implications”.[4] In other words, they questioned the unifying claims of the HGP and proposed an alternative view of human genetic unity that included and accommodated human difference. Their criticism informed plans for a second project that would document the diversity of the human gene pool. In 1991, Cavalli-Sforza, A. C. Wilson, C. R. Cantor, R. M. Cook-Deecan, and M.-C. King called for a worldwide survey of human genetic diversity.[5] They were prominent human geneticists: Alan Wilson had been the leader of the team responsible for the ‘Eve’ study, and the human geneticist Mary-Claire King had become famous for calculating that human and chimpanzee DNA is 99% identical.[6] Their call, published in the journal *Genomics*, stated that

> *“Human genomes that exist today have been determined by historical population structure and dynamics [...]. Hence, information from nuclear and*

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[1] Reardon, *Race to the finish. Identity and governance in an age of genomics* 45, quoting Rabinow and Pálsson, unpublished
[2] HGP website http://www.ornl.gov/sci/techresources/Human_Genome/project/timeline.shtml
[3] Reardon, *Race to the finish. Identity and governance in an age of genomics* 45
[4] HGD Project North American Committee, *Human Genome Diversity Project: Frequently asked questions* (Stanford University, 1993-1994 [cited 03-12-2010); available from http://www.stanford.edu/group/morrinst/hgdp/faq.html
[5] L.L. Cavalli-Sforza et al., 'Call for a worldwide survey of human genetic diversity: a vanishing opportunity for the Human Genome Project,' *Genomics* 11 (1991)
[6] Mary-Claire King and A. C. Wilson, 'Evolution at two levels in humans and chimpanzees,' *Science* 188 (1975) 108

> *mitochondrial genes from present-day populations worldwide can document prehistoric migrations, natural selection, the social structure of populations, and the frequency and types of mutations our species has experienced [...]. The novel perspective of genetics can supplement and strengthen findings from archeology, linguistics, and history.*[7]

Such an endeavour would equal the Human Genome Project in importance:

> *The potential medical gains from the Human Genome Project are immense, and the benefits these will bring are enormous. The potential intellectual benefits of understanding human diversity and its origins are equally striking. By an intense scrutiny of human diversity, we will make enormous leaps in our grasp of human origins, evolution, prehistory, and potential.*[8]

HUGO, the organisation coordinating international human genetics, whose vice president was an acquaintance of Cavalli, suggested Cavalli request an *ad hoc* HUGO committee to investigate the possibilities to set up such research. So it happened, and several planning workshops took place. After the final workshop in Sardinia in 1993, the Human Genome Diversity Project was officially proclaimed. During this meeting, the goals and organisational details had been defined. They were outlined in a "summary document," written on behalf of the Human Genome Diversity Committee of HUGO, of which Cavalli was appointed the chairman.[9] It stated that the "overall goal of the project" was "to arrive at a much more precise definition of the origins of different world populations by integrating genetic knowledge, derived by applying the new techniques for studying genes, with knowledge of history, anthropology and language." The HGDP would "create a resource […] that represents the genetic variation in human populations worldwide."

The project was presented with promises of cultural, biomedical, disciplinary and societal benefits. While, according to its initiators, the main value of the HGDP lay in "its enormous potential for illuminating our understanding of human history and

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[7] Cavalli-Sforza et al., 'Call for a worldwide survey of human genetic diversity: a vanishing opportunity for the Human Genome Project,' 490

[8] Ibidem 491

[9] Committee members were Dr Julia Bodmer, Dr Walter Bodmer, Dr Marc Feldman, Dr Takashi Gojobori, Dr Ken Kidd, Dr Mary-Claire King, Dr Partha Majumder, Dr Onesmo ole-MoiYoi, Dr Alberto Piazza, Dr Svante Pääbo, Dr Marcello Siniscalco, Dr Ken Weiss.

identity," it would also "provide valuable information on the role played by genetic factors in the predisposition or resistance to disease." Furthermore, the project would "link" the work of geneticists "in an unprecedented way with that of anthropologists, archaeologists, biologists, linguists and historians, creating a unique bridge between science and the humanities." Moreover, "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."[10] It was officially adopted by HUGO in January 1994.[11]

That same year, it more or less collapsed. Looking back in 2001, Greely argued that after a relatively fast start, "the HGDP spent the succeeding seven years stuck largely at the planning stage."[12] This was to a great extent the result of criticism from its intended research objects. The HGDP planners had a special interest in "isolates", populations that were considered to be genetically, linguistically, culturally and otherwise distinct units – in other words, in indigenous peoples. "The populations that can tell us the most about our evolutionary past are those that have been isolated for some time, are likely to be linguistically and culturally distinct, and are often surrounded by geographic barriers." In 1993, these indigenous groups that the project aspired to sample started to oppose the Project. One of the earliest protests came from the Rural Advancement Foundation International (RAFI) an organization occupied with issues of biodiversity, intellectual property rights, and indigenous identity, that occupied itself with protests against the patenting of indigenous knowledge.[13] It considered the taking of indigenous blood to be just another chapter in the history of exploitation: they saw "parallels between the taking of Plant Germ Plasm and Human Germ Plasm." Its objections were mostly related to issues of ownership, access and profit.[14]

Many other non-governmental organisations followed.[15] One of the most

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[10] Human Genome Diversity Committee, "Human Genome Diversity Project: Summary document," (Porto Conte, Sardinia: HUGO, 1993)

[11] H.T. Greely, 'Human genome diversity: what about the other human genome project?,' *Nature Reviews Genetics* 2 (2001)224

[12] Ibidem 224

[13] Ibidem 223; *ETC group*, ([cited 07-03 2011]); available from http://www.etcgroup.org/en; J. Reardon, 'The human genome diversity project: A case study in coproduction,' *Social studies of science* 31 (2001) 369

[14] RAFI, "Patents, indigenous people, and human genetic diversity," (1993)

[15] The 1995 UNESCO report lists declarations against the HGDP: Karioca Declaration (June, 1992, Brazil); Mataatua Declaration (June 1983, Aotearoa New Zealand); UN-Working Group on Indigenous Populations, 10th Session (July 1993, Geneva); Maori Congress (1993, Aotearoa New Zealand); National Congress of American Indians (3 December 1993, Resolution NV-93-118); Maori Congress Indigenous Peoples Roundtable (June 1994); Guaymi General Congress (1994, Panama); Geneva IPR Workshop (August 1994); Latin and South American Consultation on Indigenous Peoples Knowledge, Santa Cruz de la Sierra, Bolivia (September 1994); Asian Consultation on the Protection and Conservation of Indigenous Peoples Knowledge, Sabbah, Malaysia (February 1995), Pan American Health Organisation Resolution (15 April 1995); Pacific Consultation on the Protection and Conservation of Indigenous

persistent was the Indigenous Peoples Council on Biocolonialism (IPCB) that was a product of the opposition against the HGDP.[16] The HGDP was soon dubbed the 'vampire project',[17] referring to the taking of blood samples to obtain DNA. At the First International Conference on the Cultural & Intellectual Property Rights of Indigenous Peoples in 1993, a call was made “for an immediate halt to the ongoing 'Human Genome Diversity Project' (HUGO) until its moral, ethical, socio-economic, physical and political implications have been thoroughly discussed, understood and approved by indigenous peoples.”[18] Many other indigenous groups voiced similar demands. Greely, the HGDP head of ethics, met representatives of the World Council of Indigenous Peoples in 1993. This was, apparently, to no avail: afterwards the WCIP issued a statement which stated that “we resolve to categorically reject and condemn the human genome diversity project as it applies to our rights, lives and dignity.”[19] According to Rodrigo Contreras, the executive director of the WCIP, they were "not opposed to progress. For centuries indigenous people have contributed to science and medicine, contributions that are not recognized. What upsets us is the behavior of colonization.”[20]

In 1995, the UNESCO International Bioethics Committee discussed the many objections against the HGDP. While judging the scientific goals to be “generally valid”, it urged the Project’s ethical committee to address the objections, to develop mechanisms for the protection of intellectual property rights, and to involve indigenous people in ethical oversight. Calls to halt the project were not granted: “it would seem to be impossible to stop the general progress of this project, and it is not within the mandate of UNESCO to call for a moratorium on such a project or on population genetics research. The response of UNESCO has been to ask other groups to join in the regulation of population genetics, and the HGDP. Invitations to join the ethical oversight committee of the HGDP should be formally extended to indigenous communities who could select

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Peoples Knowledge, Suva Statement (May 1995). "Subcommittee on bioethics and population genetics", "Bioethics and human population genetics research," (Paris: UNESCO 1995) 24

[16] “The IPCB [is] an Indigenous organization that addresses issues of biopiracy [that] began its work in 1993 to oppose the Human Genome Diversity Project (HGDP)”. IPCB, *Press release: Indigenous Peoples Oppose National Geographic & IBM Genetic Research Project that Seeks Indigenous Peoples’ DNA* (June 26 2005 [cited 15 May 2011]); available from http://www.ipcb.org/issues/human_genetics/htmls/geno_pr.html

[17] The WCIP has been mentioned as the inventor of the term, but others have also been mentioned. For instance, according to Rimmer, this term is an invention of the Central Australian Aboriginal Congress. Matthew Rimmer, 'The Genographic Project: Traditional Knowledge and Population Genetics,' *Australian Indigenous Law Review* 11 (2007) 37

[18] Commission on Human Rights Working Group on Indigenous Populations, Sub-Commission of Prevention of Discrimination and Protection of Minorities, "The Mataatua declaration on cultural and intellectual property rights of indigenous peoples," (Whakatane: 1993)

[19] The council’s resolution is quoted in Joanne Barker, 'The human genome diversity project,' *Cultural studies* 18 (2004) 593-94

[20] Patricia Kahn, 'Genetic diversity project tries again,' *Science* 266 (1994)

their own representatives.”[21] The HGDP responded to criticism by developing a Model Ethical Protocol, developed by bioethicist Greely.[22]

The fuss had attracted the attention of the media and the scientific community. The indigenous protests were followed by academic criticism, which was voiced most audibly in anthropology departments. One year earlier, the National Institutes of Health, the Department of Energy, and the National Science Foundation, financiers of the planning stage, asked the National Research Council to evaluate the proposal in response to the criticism. In the three years which it took the NRC to evaluate the HGDP, between 1994 and 1997, only the Chinese Regional Committee and the Southwest Asian Regional Committee collected samples, starting in 1996. NSF funds were awarded for a ‘pilot project’ in that same year, but these were not to be used for the collection of samples.[23] Finally, the NRC committee reported in 1997, the seventh year of the project’s planning stage, that it found ‘[...] no sharply defined proposal that it could evaluate’.[24] Instead, it evaluated issues that might be posed by such a global survey of human genetic variation, and formulated general guidelines.

Different interpretations of the NRC report circulate. Many thought it meant the end of the project,[25] but Cavalli-Sforza interpreted it, at least retrospectively, as a green light.[26] However, the Project didn’t succeed in the raising of funds, and after 1997 it more or less disappeared from view. In 2001, samples from the Asian committees and some cell lines that were donated were stored the Centre for the Study of Human Polymorphism (CEPH) at the Fondation Jean Dausset in Paris, where it was made publicly available in 2002.[27].[28] Greely stated that ‘This collection, at CEPH, could be the kernel for the international repository and database that make up so much of the HGDP’s plan. But the problem of collecting samples remains. Without samples, the repository is meaningless.’[29]

When in 2003, in a *Nature* news feature, the HGDP was said to never have gotten

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[21] UNESCO International bioethics committee, "Bioethics and human population genetics research," (Paris: UNESCO 1995) 21

[22] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 174

[23] Greely, 'Human genome diversity: what about the other human genome project?,' 223

[24] "NRC Committee on human genome diversity", "Evaluating human genetic diversity," (Washington: NRC Commission on life sciences 1997) viii

[25] J. Marks, '”We’re going to tell these people who they really are”: science and relatedness,' in: S. Franklin and S. McKinnon, eds., *Relative values. Reconfiguring kinship studies* (2001) 374

[26] “The recommendation of the NAS-NRC committee, made public at the end of 1997, was that the HGDP could proceed,with particular attention being paid to informed consent and related ethical issues.” L.L. Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,' Nature Reviews Genetics 6 (2005) 333-340 334

[27] “The recommendation of the NAS-NRC committee, made public at the end of 1997, was that the HGDP could proceed, with particular attention being paid to informed consent and related ethical issues.” Ibidem 334

[28] L.L. Cavalli-Sforza, 'Diversity project takes time but leaps rewards,' *Nature* 428 (2004) 467

[29] Greely, 'Human genome diversity: what about the other human genome project?,' 227

off the ground,[30] Cavalli-Sforza sent a letter to report that, on the contrary, the project was alive and well. For instance, the HGDP database, he stated, had facilitated a renowned study of human genetic diversity, published in 2002.[31] In 2005, Cavalli presented an overview of the "past, present and future" of the HGDP, in which he listed several other influential studies that were conducted on the HGDP database.[32] These had, for instance, provided evidence for "the hypothesis that [genetic] divergence is mostly due to chance (random genetic drift)" and "confirmed that genetic differences between populations are extremely small"; also, research on the database had led to methodical insights into the use of markers, and addressed "general questions about sampling strategies and analysis of human genetic diversity."[33] He made a case for continued support, and again referred to both medical and cultural relevance. "Studies of human population genetics and evolution have generated the strongest proof that there is no scientific basis for racism. [....The HGDP's] potential uses in medicine, science and social problems such as racism are sufficiently important that the project should be continued and expanded."[34]

While the HGDP continues to exist as a database, it has never collected samples outside Asia.[35] Most of the samples from other continents it contains were donated. The suggestion in Greely's article that as a sampling effort, it was non-existent, seems correct. Cavalli-Sforza admitted in 2005 that as a result of this lack of new samples and a coordination of global sampling, the HGDP database was not representative of global diversity: "India and Polynesia are not represented at all, and Europe, northern Asia, the Americas and Oceania have limited representation."[36] When Cavalli-Sforza discussed the future enlargement of the database, he only mentioned the donation of cell lines, not the renewed sampling of populations. He also again mentioned lack of funding.[37]

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[30] Carina Dennis, 'The rough guide to the genome,' *Nature* 2003 758

[31] Cavalli-Sforza, 'Diversity project takes time but leaps rewards,' 467; also mentioned in Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,' ; N.A. Rosenberg et al., 'Genetic Structure of Human Populations,' *Science* 298 (2002) 2381-2385

[32] Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,' (Among them: Zhivotovsky, L. A.,Rosenberg, N. A. & Feldman, M. W. Features of evolution and expansion of modern humans, inferred from genome-wide microsatellite markers. *Am. J. Hum. Genet.* 72, 1171–1186 (2003); Ramachandran, S., Rosenberg, N. A., Zhivotovsky, L. A. & Feldman, M. W. 'On the robustness of the inference of human population structure', *Hum. Genomics* 1, 87–97(2004); Shi, M., Caprau, D., Romitti, P., Christensen, K. &Murray, J. C. 'Genotype frequencies and linkage disequilibrium in the CEPH Human Diversity Panel for variants in folate pathway genes *MTHFR, MTHFD*,*MTRR*, *RFLI* and *GCP2*', *Birth Defects Res. A* 67,545–549 (2003); Bersaglieri, T. *et al.* 'Genetic signatures of strong recent positive selection at the lactase gene', *Am. J. Hum. Genet.* 74, 1111–1120 (2004); and Macpherson, M. J., Ramachandran, S., Diamond, L. & Feldman, M. W. 'Demographic estimates from Y-chromosome microsatellite polymorphisms: analysis of a worldwide sample', *Hum. Genomics* 1, 345–354 (2004).)

[33] Ibidem 335

[34] Ibidem : 340

[35] Greely, 'Human genome diversity: what about the other human genome project?,' 224, 227

[36] Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,' 339

[37] Ibidem 340

Cavalli-Sforza

As co-initiator and director of the project, Cavalli-Sforza has left a deep mark on the HGDP. Anthropological geneticists in the early nineties built on the work he had done in the preceding decades, used the methods and models he had helped develop. He has been called the "father of genetic geography"[38]. He worked at the forefront of such research and was connected to influential people, HUGO's Walter Bodmer among them. The HGDP was considered Cavalli's 'brainchild'.[39] Although the planning workshops involved many scientists, his ideas and ways of doing research resonate in the HGDP proposals and language.

This is especially the case with the choice of the sampling strategy. Admittedly, this was partly the result of circumstances. In the early months, a fundamental debate took place between the HGDP's two most prominent geneticists, Allan Wilson and Cavalli-Sforza, about the selection of sample donors. Wilson, responsible for the "African Eve" study, wanted to focus on sampling individuals, and to let go of all presumptions about what a population is. He argued for a grid approach: the sampling of indigenous people at even geographic intervals. In this way, he argued, the research would be properly empirical. The scientists should "abandon previous concepts of what populations are and go by geography. We need to be explorers, finding out what is there, rather than presuming we know what a population is."[40] Cavalli-Sforza objected that this would give chaotic results, and argued for the sampling of isolated populations that "represent ancestral populations", as a *Science* reporter put it.[41] Wilson died in 1991, but the debate continued during the first HGDP meeting in 1991, shortly after his death. Mark Stoneking declared that he was "very troubled" by the list of criteria for populations to be sampled – these groups had to be "aboriginal" and "well-defined, either by language, geography, or endogamy". "It just focuses on well-defined ethnic and linguistic groups. And when you are done with your survey you will find the human species is made up of well-defined ethnic and linguistic groups. By sampling that way

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[38] http://www.stanfordalumni.org/news/magazine/1999/mayjun/articles/cavalli_sforza.html, accessed Dec 14 2010

[39] Kahn, 'Genetic diversity project tries again,' 720

[40] L. Roberts, 'A genetic survey of vanishing peoples,' *Science* 252 (1991) 1615

[41] L. Roberts, 'How to sample the world's genetic diversity,' *Science* 257 (1992) 1204-12051204

you bias the results."[42] Eventually, Cavalli's population approach became dominant.[43] *Science* reported that in the 1991 meeting a compromise was reached: the sampling of 25 individuals from 400 populations and the collection of a large number of non-immortalized samples (meaning these would not be used to produce cell lines) from individuals.[44] However, the HGDP texts favoured the sampling of populations rather than individuals.[45]

In the HGDP document reporting on the planning workshop held in Sardinia in September 1993, the populations to be sampled were defined in terms of the historical and anthropological questions their genetic information may help answer. Thus, the HGDP targeted "Populations that can answer specific questions concerning the processes that have had a major impact on the genetic composition of contemporary 'ethnic groups,' language groups and cultures" and "Populations that are anthropologically unique" and so "may help resolve local anthropological and archaeological questions".[46] Practical issues also determined which populations would be sampled: those that had "anthropologists or other experts working among them" were more likely to be singled out than those that did not. The reasons why these populations were considered interesting included "unusual language, culture, or history; an indication of susceptibility or immunity from particular diseases; or a possible relationship to another interesting population."[47] Another criterion was a presumed autonomous evolutionary history. Criteria for selecting populations were 'linguistic isolation' or 'anthropological uniqueness' (which could also be defined linguistically). Populations considered to be in danger of losing their 'identity as genetic units' were of particular interest;[48] these should be sampled while it was still possible.

Cavalli's ideas about the proper methods, models, and the relevance of anthropological genetics and those expressed in HGDP overlap considerably, if not coincide. Cavalli's *The history and geography of human genes* (authored with his Italian colleagues, P. Menozzi and A. Piazza) provides an overview of his ideas. The HGDP has been called a translation of this work into a research proposal. Therefore, an integral

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[42] Ibidem 1205

[43] A. M'Charek, 'Een kwestie van technieken. Over de buitensporigheid van de genetica en de onbestendigheid van ras,' *Krisis* (2004) 31

[44] Roberts, 'How to sample the world's genetic diversity,'

[45] Reardon, 'The human genome diversity project: A case study in coproduction,' 364

[46] Committee, "Human Genome Diversity Project: Summary document,"

[47] Committee, *Human Genome Diversity Project: Frequently asked questions* ([cited)

[48] "Human Genome Diversity Committee", "Human Genome Diversity Project: Summary document," (Porto Conte, Sardinia: HUGO, 1993)

discussion of Cavalli's work and the HGDP seems appropriate. Published in 1994, the book provided the interdisciplinary field with a synthetic overview of anthropological genetic investigation of human history and diversity. It presented methods, theories and insights, as well as information from other disciplines that was used in the genetic reconstruction of history. Sometimes, it presented archaeological and paleontological information to fill in where genetics leaves blanks, and sometimes such evidence was ignored or debated.[49] Although reviewers were critical of some of the authors' assumptions and viewpoints pervading the book (especially the linking of language and genetic trees) they generally hailed it as an important overview.[50]

Cavalli-Sforza attributed both practical and "intellectual" relevance to the genetic reconstruction of history. He argued that most aspects of human life are determined by cultural and biological history, and can be better understood if we take our heritage, in a broad sense, into account. Genetic history provides the key to our biological and cultural identity as a species, and reconstructing it would "help us understand ourselves". This argument also holds on the individual level: "to develop our personality harmoniously, we need to study and respect [...] individual variation."[51] For him, historical knowledge is a way to gain insight into human nature, and can provide moral education in the ways to deal with this nature. The problems humanity faces – illness, violence, intolerance, unhappiness - are unsolvable without knowledge of history:

> *We all recognize the importance of knowing the past, because history holds the key to phenomena and expressions of human life that would otherwise appear incomprehensible. The biological history of humankind is that of its evolution, and cultural history is an integral part that has both influenced it and been influenced by it. The two must become inseparable if we wish to avoid our heartrending ocean of suffering. The animal part of our natures, often lacking in restraint, is responsible for many of these excesses, but our cultural history should teach us how to avoid them.*[52]

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[49] E.g. the *sapiens sapiens* fossils in China. These were estimated to be older than 60,000 years, but Cavalli-Sforza remarks that the dating is uncertain. L. L. Cavalli-Sforza and F. Cavalli-Sforza, *The great human diasporas* (1995; Italian original 1993)56

[50] Dennis H. O'Rourke, 'Patterns of peopling: Review of The history and geography of human genes,' *Science* 267 (1995); Nei, 'The history and geography of human genes: Book review,'

[51] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 261; L. L. Cavalli-Sforza et al., *The history and geography of human genes* (Princeton, 1994) 157

[52] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 265

Cavalli-Sforza framed his research as an attempt to contribute to this educational goal. Among the 'excesses' he mentioned, racism received special attention, and he considered his research a powerful tool to fight this "chronic disease".[53] In *Genes, peoples and languages* (2001) he explained that the subject of the book "has significant implications for important social problems. It explains, among other things, why racism is fallacious".[54] The HGD Project would "help emphasize the importance both of human diversity and of the extraordinarily close relationship of the human family."[55] The occasional medical arguments for the HGDP also had a political edge to them. "Not knowing enough about the genetics of [aboriginal] populations may also have medical ramifications. What is going on now is ethnic exploitation by neglect."[56] Therefore, "even populations that do not seek scientific explanations for their origins may reap long-term benefits from the discovery of useful medical information about their susceptibility to, or treatments for, disease."[57] However, the HGDP has not aimed specifically at medical applications, and neither has Cavalli-Sforza in previous or other research; history was his main target. It has been argued that reference to medical benefits only served to 'sell' the science of the HGDP. It has even been argued that these research goals were added later, probably to attract funds and sympathy for the HGDP.[58] However, this view can be countered with Cavalli's remark that "Uncertainties concerning such issues as strategies for collecting samples in a way that would facilitate anthropological or medical research, and the choice of the populations, were obviated by the sources of the cell lines, which were donated by researchers working on human evolution. [...] it became clear that orientation of the collection towards anthropological interests also offered excellent chances of aiding medical research."[59]

Overall, in Cavalli's research, polymorphisms are embodied historical sources. The human gene pool, and isolated populations especially, is a living archive. But, he argued, late modern man is on the brink of a new period: a radical shuffling and smoothing of these patterns, as a result of increased mobility and admixture, was taking place. Thus, "we are now at a crossroads in the genetic analysis of human populations."[60]

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[53] Ibidem 244

[54] L. L. Cavalli-Sforza, *Genes, peoples and languages* (London, 2001) viii

[55] Committee, *Human Genome Diversity Project: Frequently asked questions* ([cited)

[56] Ibidem([cited)

[57] Ibidem([cited)

[58] Reardon, *Race to the finish. Identity and governance in an age of genomics* 141; It is also claimed that historical goals require different sampling strategies – that a search for diversity that provides insight into history would not yield the results necessary to find out about disease susceptibility. Roberts, 'How to sample the world's genetic diversity,'

[59] Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,'

[60] Cavalli-Sforza et al., *The history and geography of human genes* 377

There is great haste to secure the information in the DNA of indigenous peoples, who have yet been least affected by 'genetic mobility' but whose identities are quickly disappearing (as are many of the populations themselves):

> *The number of populations that can enlighten us on the past history [sic] of humanity is shrinking continuously. Only perhaps one or two decades remain in which we still have access to these populations. From the point of view of genetic history, we are an endangered species, and it is essential to avoid delay before taking the necessary steps to preserve this important knowledge about ourselves.*[61]

If current genetic patterns provide a snapshot of a dynamic genetic process, this picture is rapidly fading. This sense of urgency was a central argument in the case for the HGDP. The isolated populations targeted by the HGDP "are being rapidly merged with their neighbours [...] destroying irrevocably the information needed to reconstruct our evolutionary history. Population growth, famine, war, and improvements in transportation and communication are *encroaching on once stable populations*." At the very historical moment the 'biological tools' to study human variation had become available, the patterns in this variation threatened to be lost in the blender of a globalising world. Therefore, "a systematic, international effort to select populations of special interest throughout the world, to obtain samples, to analyze DNA with current technologies, and to preserve samples for analysis in the future"[62] was needed. "We must act now to preserve our common heritage."[63]

View of history

In other words, in Cavalli's view of history, there is a significant caesura between premodern and modern times. The voyages of discovery and the colonization of the Americas marked an abrupt change in tens of thousands years old migration patterns. This process was accelerated by the industrial and transport revolutions. Cavalli-

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[61] Ibidem 157

[62] Cavalli-Sforza et al., 'Call for a worldwide survey of human genetic diversity: a vanishing opportunity for the Human Genome Project,' 490

[63] Ibidem 490

Sforza's view of the history of humanity before this breach is summarised in *The History and geography of human genes*. It includes an abundance of visual material illustrating this history, as well as an introduction to the methods and models to reconstruct it: genetic distance matrices, world maps and world family trees. From this extensive, nuanced and technical work, the following narrative of human history emerges.

According to Cavalli, humans very probably originated in Africa. While there are "passionate debates" and "little consensus" between (paleo-) anthropologists adhering to, respectively, the "polycentric" (multiregional) and African hypothesis[64], "From a geneticist's point of view, a single origin followed by expansion is the more credible of the two hypotheses."[65] While *Erectus* had left the continent to populate Eurasia, modern humans stayed in Africa for tens of thousands of years. Cavalli-Sforza estimated that they started to expand from there and move into the Middle East around 100,000 years ago[66]. However, for a long time, modern humans did not migrate any further, until around 60,000 years ago, when "the real expansion began." The period between hundred and sixty thousand years ago is a 'blank' in the archaeological record. Presumably, during this time, a "cultural maturation"[67] took place, as reflected in the archaeological styles, which after 60,000 years ago start to vary locally. This diversity may indicate the development of complex languages. Cavalli-Sforza quotes paleoanthropologist R.G. Klein to describe this shift as a development from "modern physical form", that is, anatomically modern humans, to "fully modern behavior".[68] Complex culture indicated "an intensively active population that [was] expanding to the whole world."[69]

Small bands of such anatomically and culturally modern humans split off from the African population, and left Africa, following the footsteps of archaic humans. As humans originated in parts of Africa that were close to Asia, contact may have been possible. Two routes out of Africa are mentioned in *History and geography*, one through North Africa and one through Ethiopia. In Asia, humans underwent "demographic developments" that favoured their migration into the rest of the world. Genetic traces of a southern route from Africa into Asia can be found in Southeast Asia and possibly India,

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[64] Cavalli-Sforza et al., *The history and geography of human genes* 66; Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 49-50

[65] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 49-50

[66] Cavalli-Sforza et al., *The history and geography of human genes* 154

[67] Ibidem 155

[68] Ibidem 64

[69] Ibidem 64

but only there.[70] South Asians are genetically quite different from other Asian populations, which made it “tempting” to hypothesize that they are genetic connections between the African ancestral and Australian populations. The large differences between Australians and southern Asians that apparently undermine this theory are countered with the argument that such a genetic relation between Africans and Australians would be ancient, and is therefore possibly obscured by more recent mixing. Archaeological evidence shoring up the theory of a southern route may be found in areas that are now under water, as the coast lines have moved with the rising sea level.[71]

West Asia may have been the seat of an important phase in human evolution, possibly even the location where human “cultural maturation” took place, between 100,000 and 50,000 years ago. This may have occurred after the possible first expansion to Australia. After this crucial West Asian phase in human development, and as a result of it, man expanded into the whole of Asia and Europe, possibly mingling with other, more ancient human populations already living there.[72] From West Asia, humans also expanded into Europe, around 30,000 years ago. Small populations survived the peak of the glaciation period, around 18,000 years ago, in the southern parts of the continent. This was a situation that favoured drift, both genetic and linguistic. This may explain the peculiarities associated with, for instance, the Basques. This population has high frequencies of specific genes, and a language that is quite different from neighbouring tongues.[73] The last continent to be colonised was America. East Asians crossed the Bering Strait between 35,000 and 15,000 years ago and spread swiftly all the way to southern South America.[74]

In this period of migration – approximately between 60,000 and 10,000 years ago - the patterns in the human gene pool were created. Genetic patterns emerged as a result of the isolation of small groups of people splitting off to migrate into new territories, and of natural selection as humans adapted to new environments.[75] (Cavalli stated somewhat dramatically that “natural selection can also be called necessity or destiny.[76]) Group isolation, resulting in genetic diversification, should be interpreted broadly: even when there is no “clear-cut geographic discontinuity” providing evident

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[70] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 252
[71] Ibidem 252
[72] Ibidem 253
[73] Ibidem 300
[74] Ibidem 320
[75] Cavalli-Sforza et al., *The history and geography of human genes* 156; Cavalli-Sforza, *Genes, peoples and languages* 51
[76] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 102

boundaries between peoples, isolation and migration act on gene pools.[77]

Then another major caesura took place, around 10,000 years ago, when agriculture was developed in several regions independently. This allowed for a "quantum jump in potential population density."[78] Sedentary lifestyles and population growth acted as a "freezer" on the genetic diversity. Of course, after they became agriculturalists, people continued to migrate. But, Cavalli-Sforza argues, the time of colonization over long distances by very small human populations was over. During all of history, at least until the mass relocations of the past five centuries, genetic patterns reflecting the earliest movements were preserved, despite a limited blurring due to modest gene flow. The expansions of farmers and nomads did change genetic patterns and created new ones, but much of the original local diversity remained, especially in "refugia".[79] Underneath the new genetic structures that resulted from slower and small-distance gene flow, the imprint of the earliest movements was preserved. This could be distinguished from newer structures by principal component analysis, the first PC indicating the oldest pattern.

One of the central questions in history is how to account for change. What are the catalysts of history? And, in the case of Cavalli's research: why did people move (and groups split)? Derived questions involve the social configurations, the pace of migratory movement, the size of these groups, and their relationship with other groups. In order to capture history in a model, Cavalli-Sforza formulates generalizing answers to these questions. Indeed, he almost cannot escape generalization, given the time scales involved – any remark about human behaviour in the context of his research carries the weight of the tens of thousands of years it covers. Because of the large periods of time he describes, his assumptions easily take the shape of (tentative) ideas about historical and anthropological constants.

One of the central factors in Cavalli's history is technological innovation, including linguistic, material and social innovation, as well as the domestication of animals, the development of agriculture, means of transport, and military innovations.[80] Overpopulation, resulting from innovations in subsistence methods,[81] was one of the catalysts for expansion and migration. The earliest and most fundamental 'technical

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[77] Ibidem 202

[78] Cavalli-Sforza et al., *The history and geography of human genes* 67

[79] Ibidem 1

[80] E.g. Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 158, 139; Cavalli-Sforza, *Genes, peoples and languages* 29; Cavalli-Sforza et al., *The history and geography of human genes* 16

[81] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 157 139

innovation' was language: "the expansion of modern humans must have been strongly influenced by the possession of greater skills in communication [...] favoring exploration and travel into unknown lands."[82] Modern man emerges from his narrative as an exploring being, defined by technology and communication.

Cavalli modelled this cultural-demographic process as a "genesis of demic expansions" in a scheme that depicted innovation and migration feedback cycles.[83] Apart from technological innovation, climate and other environmental changes are important factors,[84] such as desertification, or the migration of the animals that were an essential part of their diet, which forced people to follow them. Next to the "push" of these motivations, he also mentions the "pull" of new niches opening up and increasing carrying capacity of the surrounding land.[85] Interestingly, these factors – climate, overpopulation and technological innovation – were also the sources of his worries about the future of humanity.

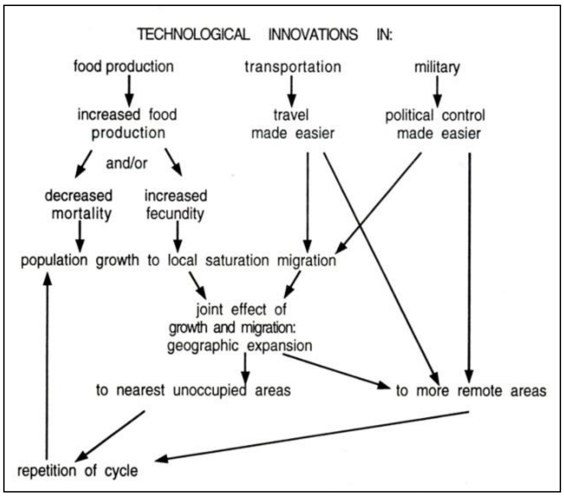

Figure 7 "A model for the genesis of demic expansions", Cavalli-Sforza, 1986.[86]

Unity

Cavalli-Sforza was uncomfortable with the biblical connotations of the term

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[82] Cavalli-Sforza et al., *The history and geography of human genes* 155; L. L. Cavalli-Sforza et al., 'Reconstruction of human evolution: bringing together genetic, archaeological, and linguistic data,' *PNAS* 85 (1988) 6002

[83] Cavalli-Sforza et al., *The history and geography of human genes* 111 Fig. 2.7.5

[84] Ibidem 54

[85] Ibidem 106

[86] From L. L. Cavalli-Sforza, 'Population structure' in H. Gershowitz, D.L. Rucknagel, R.E. Tashian (eds.) *Evolutionary perspectives and the new genetics* (New York 1986) 13-30, reproduced in Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 111

'Eve'.[87] However, he has used similar terms, most notably when he proclaimed he hoped to one day find "a Y-chromosome Adam"[88] In 1994, Cavalli-Sforza and his colleagues reported the discovery of a Y-chromosome polymorphism that would provide insight into human origins.[89] Cavalli-Sforza describes in *Genes, peoples and languages* how, in his laboratory, the Y-chromosome Adam was indeed inferred from these data. 'Adam' was estimated to have lived about 144,000 years ago, roughly in the same place as the female common ancestor: Adam was as African as Eve.[90]

Whether defined in imaginative terms or not, Cavalli was a proponent of the idea that the human tree has a single root, and objected to the multiregional hypothesis. In *History and geography*, he discussed a "narrow" version of the multiregional theory, which assumed parallel evolution with limited exchange between the continents. "If we first disregard genetic exchange (gene flow) and its possible influence on the process, we must justify the acquisition of a very similar external appearance (phenotype) by all modern humans, by independent evolutionary processes." This he considered unlikely – but the assumption that genetic exchange should be ruled out is a very strong one, which most multiregionalists had already rejected. Cavalli-Sforza considered a multiregional scenario including gene flow more likely, but presented several arguments against it. Firstly, he mentioned the shortness of the timescale. The use of molecular clocks indicated that modern humans were a recent phenomenon. Genetic similarities, he thought, were better explained by a common origin than with admixture of distinct lineages, which could not have produced the genetic similarities in such a short time. Furthermore, the multiregional hypothesis did not account for the "cascade of expansions" that had taken place. Also, the multiregionalists view of humanity as one single lineage was indefensible, because of physical and cultural barriers preventing one single global gene exchange network.[91]

His fundamental argument was that the genetic differences between people from all over the world are too small. Even in cases where the same selective pressure acts on different populations, for instance, in different malaria regions, the way they adapt differs from continent to continent. If the same selective pressure can have such different outcomes, he argued, imagine what the effect of long periods of parallel

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[87] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 73

[88] Ibidem 73

[89] Mark T. Seielstad et al., 'Construction of human Y-chromosomal haplotypes using a new polymorphic A to G transition,' *Human Molecular Genetitcs* 3 (1994) 2159

[90] Cavalli-Sforza, *Genes, peoples and languages* 81

[91] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 62-67

evolution, in different environments, from different archaic ancestral populations would be.[92] The little amount of genetic difference found in the current human gene pool does not seem likely in this scenario. Cavalli-Sforza's argued that any model that ignores the *'dynamics of history'*, the "massive movements of populations" in the last 50,000 years, is not acceptable.[93]

Thus, humanity has a single root and this root most probably is located in Africa. An important argument for this came from the methods for building population trees. These make use of internal and external evidence. An example of the former is the average linkage method. It chooses the population pair with the greatest distance between the members and places them at the lowest split in the tree.[94] As the largest differences were found between Africans and non-Africans, these were the two lowest branches. The credits for this 'discovery', based not on DNA evidence but on more 'classical' blood group data, go to Masatoshi Nei;[95] in 1988 Cavalli-Sforza et al. confirmed this 'deepest split' with research on existing, classical polymorphisms.[96] In *The history and geography*, he argues that the most important conclusion of recent research is the split between Africa and the rest, and the accompanying conclusion about African origins. He makes the reservation that it depends on the assumption of "reasonably constant" evolutionary rates[97] - i.e., on the evolutionary clock hypothesis. Added to the tree evidence is the fact that the African gene pool is the most heterogenous of all, indicating great ancientness.

External evidence for an African root includes alleles shared with non-human primates, which he designates as "ancestral forms [of] gene[s]". Africans carry such an allele, while all non-Africans share a gene that Africans have not, indicating and reinforcing the special status of the African gene pool and the likelihood that the root of the primate tree should be placed there.[98] This also served as an argument that, so to speak, we are all Africans: all non-African peoples carried genetic evidence of an African past. Archaeology and palaeontology provided external evidence as well,[99] but most of the important arguments were 'internal', genetic and statistical in nature. All in all, the process of finding the root was a complicated endeavour. Cavalli-Sforza was still

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[92] Cavalli-Sforza et al., *The history and geography of human genes* 66
[93] Ibidem 67; italics mine
[94] Ibidem 31-32
[95] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 119
[96] Cavalli-Sforza et al., 'Reconstruction of human evolution: bringing together genetic, archaeological, and linguistic data,' 6002
[97] Cavalli-Sforza et al., *The history and geography of human genes* 154
[98] Ibidem 33
[99] Ibidem 33-34, 119

cautious in 1994: "*If* modern humans originated in Africa…".[100]

The emphasis on the genetic similarity of humans, their short shared history, the great likelihood of a single origin and, especially, human family trees – all these provided scientific arguments to regard humanity as a unity. Notwithstanding the basic message, Cavalli's relatively short and 'dynamic' history of modern humans is defined by population splitting. The greatest – epic – part of the story emphasizes separations and specialization. This created the risk of reification of the population categories in his research, as he was well aware. Cavalli nuanced such concepts. He showed how every level of clustering of genetic data allowed for the creation of different partitions.[101] He emphasized that variation is continuous, and that variation within groups was bigger than between them[102]- the two famous antiracist arguments of the clinal nature and individual level of genetic variation. Genetic essentialism was explicitly rejected both in HGDP texts and in Cavalli-Sforza's own research. "As far as scientists know, no particular genes make a person Irish or Chinese or Zulu or Navajo. These are cultural labels, not genetic ones. People in those populations are more likely to have some alleles in common, but no allele will be found in all members of one population and in no members of any other. (There may, however, exist rare variations that are found only in some populations). This cannot be very surprising, he argued, in light of "the vast extent of intermarriage among human populations, now and throughout history and prehistory."[103]

Cavalli had researched classical polymorphisms – regions of the genome that were known to code for phenotypic phenomena - rather, it was these phenotypic expressions themselves, such as blood groups, that were the subject of his enquiries. When direct access to genotypes became possible, loci in non-coding regions were added to the number of markers that were studied. In Cavalli's work, he focused on both. Still, many references to phenotypes were made in *The history and geography of human genes*. For instance, the authors remarked about the pastoral nomads of the Sahara that "Their typical 'elongated' phenotype makes it tempting to search for a common

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[100] Ibidem 192; emphasis mine

[101] Ibidem 19

[102] "What is the point in talking about the 'purity' of a race, when every group of people, no matter how small, is variable? […] every microcosm […] tends to reflect the macrocosm [of the whole human gene pool]". Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 238

[103] *Genographic Project: Frequently Asked Questions*, ([cited 05 April 2011]); available from https://genographic.nationalgeographic.com/genographic/lan/en/faqs_about.html#Q9

origin."[104] And the HGDP summary document proposed as one of the research questions: "What special phenotypes, such as diseases, characterise certain populations, and are these correlated with genes or genotypes?"[105]

Trees

The unity of Cavalli's human family, as in most families, accommodated great diversity. Cavalli-Sforza's preferred visual representations of humanity's diversity and history are synthetic maps and population trees. Although Cavalli-Sforza admits that "the history of the world is not made solely of fissions of peoples",[106] fission trees are his models of choice for migratory history: they are "invaluable for summarizing extensive bodies of data" and "the only way to infer evolutionary histories." Nevertheless, they are "fallible friends".[107] They simplify matrices of distances between populations, and this simplification means loss of information. An advantage of the model, he thought, was that it provided insight into visually less informative matrices.[108] Therefore, this oversimplication was "beautiful", because it helped describe "chaotic data."[109]

But trees "do not easily take into account the existence of cross-connections between branches."[110] Such cross-connections – admixture – had a blurring effect on trees.[111] He explained that there is still no satisfactory method of analysis for "networks", or trees that are "complicated [sic] by interconnections between branches". He called such processes "reticulate evolution." "Methods to recognize cross-connections and to introduce them into evolutionary models are in their infancy."[112] "There has probably been enough intermingling of the clusters that a network representation (i.e., a tree with interconnections between the branches) would be highly desirable."[113] But no such 'network representation' can be found in his books, and these processes do not feature in his models and visualizations.

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[104] Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 194
[105] Committee, "Human Genome Diversity Project: Summary document,"
[106] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 202
[107] Cavalli-Sforza et al., *The history and geography of human genes* 30
[108] Ibidem 38
[109] Cavalli-Sforza, *Genes, peoples and languages* 86
[110] Cavalli-Sforza et al., *The history and geography of human genes* 28
[111] Ibidem 92
[112] Ibidem 28; check sec 2.4
[113] Ibidem 81

This is because these are not the kind of processes that results in the colonization of new continents. The splitting of populations, and their subsequent independent evolution, are considered the primary creators of genetic diversity.[114] These processes characterize the phase of the first migrations and have created the most basic genetic patterns:

> *The generation of diversity among modern humans is the result of a large number of separations of splinter groups that migrated to other territories. The separation need not have been abrupt every time: simple demographic expansion beyond the range usually covered in matrimonial migration, which is usually less than 100 km in a settled population, is sufficient to increase diversity.*[115]

Cavalli's subtle argument in favour of trees is therefore that they describe not all genetic processes that have taken place in the history of humanity, but focus only on those that have created the patterns of variation. In other words, the emphasis of trees on fissions does not allow a picture of all of human history, but only on the episodes and processes relevant for the study of genetic diversity. The apparently 'dramatic' separations of splinter groups and long-distance migration need in his view not be swift nor cover long distances;[116] and neither are they the rule. Individual migration takes place constantly (on a small scale) and leads up to continuous intermixing. This admixture generally does not have dramatic effects, save for occasionally blurring the picture.

This effect of admixture on trees could be predicted and detected in matrices, so that 'admixed' data could be excluded. The assumptions that populations split and evolve separately, and that admixture never takes place to such an extent that it blurs the structures in genetic data that are described by trees [that there is "no selective convergence and divergence"] "may be flawed in some cases." Because of continuous gene exchange between neighbours, the use of trees for geographically close

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[114] Ibidem 15

[115] Ibidem 54. Also: "Fissions, followed by independent evolution in the two branches formed after each fission, must have had an important part in shaping the genetic history of humans," even though in many cases the branches admixed with their new neighbours. Cavalli-Sforza et al., *The history and geography of human genes* 28

[116] Cavalli-Sforza et al., *The history and geography of human genes* 54

populations is less desirable.[117] For instance, it is difficult to decide whether the African Berber population falls in a Eurasian cluster because there was gene flow between the two continents, or because the Berbers' North African ancestors settled Europe – or both. In other words, the question remains whether the Eurasian-African connection is ancestral (temporal) or geographical.[118] Occasional admixture of branches is likely to have occurred[119] and two people admixing often creates a new, probably unique population, intermediate between the two original ones. 500 years were probably sufficient to erase traces of original population when gene flow is 10% - only fairly rigidly endogamous groups' origins can be retraced.[120] Thus, he considered trees useful mainly for the big picture.

Another important argument in favour of trees was that they clearly represent hypotheses about evolutionary developments of gene pools. Thus, the method of 'average linkage', "corresponds to a specific evolutionary model that assumes the independence of branches [..] with a constant evolutionary rate." The advantage is that that made the assumption testable – a 'scientifically correct' method.[121] The hypotheses and assumptions were, in a way, built into the tree model.[122] "The validity of a tree depends on exchanges being small"[123] and on "populations splitting cleanly", and this could be verified.[124] From this perspective, large scale exchanges between neighbouring peoples are considered "anomalies".[125]

"A tree with a large number of populations can hardly be without errors." Cavalli considered the methods that were developed to evaluate the extent to which trees 'fit' the data used, such as the 'bootstrap method' an excellent way to acquire the "necessary degree of humility".[126] The extent to which trees accurately describe the data was referred to as the statistical analysis of the 'treeness' of the data.[127] Cavalli also mentioned another explanation of variation patterns, "isolation by distance." This is the tendency of populations to admix with neighbouring populations so that genetic difference and similarity are correlated with geographic distance.[128]

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[117] Ibidem

[118] Cavalli-Sforza, *Genes, peoples and languages* 88

[119] Cavalli-Sforza et al., *The history and geography of human genes* 19

[120] Ibidem 55

[121] Ibidem 374

[122] Ibidem 70

[123] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 190

[124] Cavalli-Sforza, *Genes, peoples and languages* 36

[125] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 120

[126] Cavalli-Sforza et al., *The history and geography of human genes* 37

[127] Ibidem 36; "a "good" matrix, with good treeness (no admixtures, no large discrepancies in evolutionary rates)…" 375

[128] Ibidem 52

All in all, what level of realism Cavalli-Sforza attributed to his trees remained somewhat unclear. They should be distinguished from more descriptive, classificatory ones that focus on shared traits. The kind of trees he built was specifically designed to reconstruct a specific phase in history. In response to criticism of the fact that the "clusters" in his world tree - that is, the branches that represent several sampled populations clustered together - differ in homogeneity, he argued that this would only be a problem if taxonomy would be the goal of the endeavour. This is not the case: "the hope of producing a good taxonomy is a lost cause – a minor scientific loss – that of reconstructing evolutionary history retains full strength and has the advantage that hypotheses can be tested on the basis of other, independent sources of data."[129] In other words, what he's after is not an encyclopaedia of current diversity but history itself. The population categories serve as tools.

Nevertheless, his discourse and graphic representations suggested that the populations are 'real', whether or not this was intended or just resulted from the use of convenient shorthand concepts. Cavalli-Sforza described the migrations that he reconstructed in rather epic terms. The first migration out of Africa was often dubbed the "great exodus". Journey metaphors have the effect of personifying these groups, making them characters in a story.[130] This narrative feature does not necessarily bend or stretch the scientific conclusions: it fits the focus on fissions and population splitting, on the hypothesis of small migrant groups colonizing the continents in a short time.

His shorthand population concepts were often defined with reference to linguistic groups. Therewith, these linguistic identities were extended to include past, presumably ancestral populations. Thus, ethnic definitions with strong linguistic connotations, such as "Bantu", were used for populations presumed to have lived several tens of thousands of years ago.[131]

Linguistics itself had a long tradition of building family trees depicting the relations between languages, and their descent from primal 'superlanguages' such as Indo-European. Cavalli found similarities between genetic and linguistic trees. He has investigated this match extensively and explored possibilities to integrate them. Cavalli argued that "the linguistic criterion often gives similar results to a geographic one or

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[129] Ibidem 19

[130] In Lakoff's theory of metaphor, travel metaphors are ubiquitous in thought and language. G. Lakoff, 'The contemporary theory of metaphor,' in: A. Ortony, ed., *Metaphor and Thought* (Cambridge, 1992)

[131] Moore objected to such views, which emphasize that "the biological population or deme and the linguistic community are one and the same", and dubbed them 'synthetic'. Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 925

that deduced from physical and cultural similarities." These matches were not coincidental: "we have [...] demonstrated that the chances of the similarity between the genetic tree and linguistic classification being due to chance are negligible."[132] He published about matching biological and linguistic world trees in an article in *PNAS* in 1988.[133] The surprisingly similar structures of such trees, he argued, is explained by the fact that languages and genes are subject to similar processes of isolation and drift,[134] so that "languages provide a powerful ethnic guidebook".[135] Cavalli's analogies between cultural and genetic transmission, exchange, and dissemination applied in particular to linguistic processes. The matching of language and gene trees provided an extra argument to use linguistic data for defining and selecting populations, as the HGDP proposed to do.

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[132] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 197-8

[133] L. L. Cavalli-Sforza et al., 'Reconstruction of human evolution: bringing together genetic, archaeological, and linguistic data,' *PNAS* 85 (1988)

[134] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 202

[135] Cavalli-Sforza et al., *The history and geography of human genes* 23

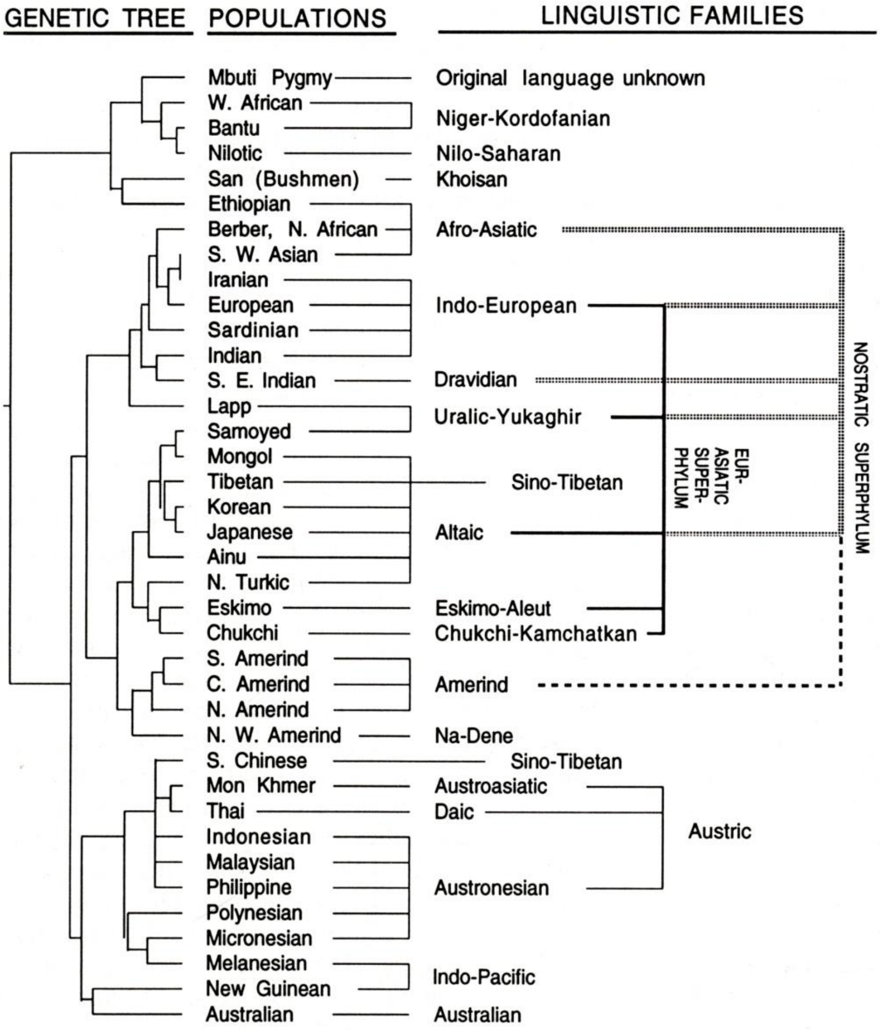

Figure 8 A comparison of a genetic and a linguistic tree, published by Cavalli-Sforza et al. in *PNAS* in 1988.[136]

It is therefore unsurprising that Cavalli-Sforza was an enthusiast for an increasingly “quantitative approach”[137] to the comparison of “anatomical features”[138] of languages.[139] Similarities of words and sounds in different languages served as measures of relatedness between languages, described in terms of shared origins. Linguists even reconstructed the ‘root’ or ancestral forms of words, for instance, ‘tik’ for ‘finger’.[140] There was much debate about the feasibility of this approach; Cavalli chose the side of linguists like Ruhlen and Greenberg who became controversial (but influential) for such research. Cavalli explained: “Most linguists are convinced that

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[136] Reproduced from L.L. Cavalli-Sforza, A. Piazza, P. Menozzi and J. Mountain, ‘ ‘Reconstruction of human evolution; bringing together genetic, archaeological, and linguistic data’ in *Proceedings of the National Academy of Sciences USA* 85 (1988) 6002-6 in Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 99

[137] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 183

[138] P. Underhill et al., "Y chromosome variation and human evolution," in *ISFH Hakone symposium on DNA polymorphisms*, ed. Toyoshoten (Hakone: 1996) 25

[139] Cavalli-Sforza uses a classificatory system and accompanying trees built by the linguist Greenberg, who has been controversial but influential in linguist circles.

[140] Cavalli-Sforza et al., *The history and geography of human genes* 96

languages evolve too fast to allow recognition of relationships of [great] time depth. Recent preliminary results, however, [...] suggest that this scepticism is unjustified."[141] Nevertheless, Cavalli argued that linguistic data should be used with reserve, as it is less clear-cut than genetics because languages evolve much faster. "Dates indicated [...] for the origin of linguistic families are suggestions that should be taken with a ton of salt."[142]

Maps

Next to trees, maps were another way in which Cavalli represented global genetic variation – and, interestingly, global history. The geographic study of genetic variation is very different from that based on trees. If the latter inadequately presuppose abrupt colonization, maps can add to the picture, Cavalli argued.[143] In *The history and geography,* more than 550 pages are dedicated to genetic maps. Cavalli-Sforza was one of the geneticists who introduced the method of making 'synthetic maps', which depict the frequencies of several genes. Several, because "[n]o single gene provides a clear record of the changes brought about by later migrations on the original differences, but a combination of the information from a large number of genes allows such reconstructions." The "optimized linear functions of all available gene frequencies", the principal component values discussed before, are indicated by isopleths, similar to altitude lines on geographic maps.[144] Genetic maps depict the mountainous genetic landscape with peaks where a specific (combination of) marker exists in high frequencies and valleys where they are low.

To recuperate, principal components analysis "discovers trends, patterns and latent structures which are probably dictated by historical structures, in large amounts of data." PC's essentially divide genetic diversity into several distinct patterns, which are depicted as colours fading into each other (Figure 3 in Chapter one). As each pattern depicting the geographic variation of the frequency of genetic markers is interpreted as a historical trace of a population movement, the "latent structures" created by early migrations (the 'first' PC) can be found 'beneath' the genetic structures created by later

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[141] Ibidem 300

[142] Ibidem 104

[143] Cavalli-Sforza, *Genes, peoples and languages* 55

[144] L. L. Cavalli-Sforza et al., 'Demic expansions and human evolution,' *Science* 259 (1993) 640

movements or expansions (second, third etc PC).[145]

Therefore, these maps were not purely geographical; a temporal (if not narrative) element was added. A "downhill" gradient of the genetic 'altitude lines' was thought to be indicative of the direction of migration.[146] The idea was that the oldest split in the world tree often corresponded with the isopleth of the first PC (accounting for the greatest percentage of genetic difference in the data), because the oldest migrations create the greatest variation.[147] Other PCs represent differences that emerged more recently, as the result of later migrations, or expansions, such as those associated with agriculture. These "[e]xpansions tend to add detectable patterns of nearly circular genetic gradients around their areas of origin and can extend to large regions in a few thousand years"[148] – like ripples in a pond. The original population presumably lived in the geographic area where the highest point in the genetic landscape is located. Yet "population expansions, centrifugal, and centripetal migrations are hard to distinguish"[149] and subsequent migrations could have blurred the picture.[150] Cavalli-Sforza used these methods for his famous study of the spread of agriculture in Europe, asking whether it was the agriculturalists themselves, or agricultural practices that spread. He concluded that farmers spread and took their agricultural knowledge with them – or in more epic terms: "the great trek of the cultivators."[151]

With the PCs corresponding to splits, and isopleths to branches, maps and trees were connected. Cavalli-Sforza proceeded to literally merge them: he projected trees onto a world map, therewith adding a geographical dimension to the branches, as he added historical meaning to the maps. The lines that represented branches or lineages of descent now became the migratory routes taken by these successive generations.

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[145] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 147

[146] Ibidem 147, 160

[147] Ibidem 153; Cavalli-Sforza et al., *The history and geography of human genes* 41

[148] Cavalli-Sforza et al., 'Demic expansions and human evolution,' 639

[149] Cavalli-Sforza et al., *The history and geography of human genes* 51

[150] Cavalli-Sforza et al., 'Demic expansions and human evolution,' 639-41

[151] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 126

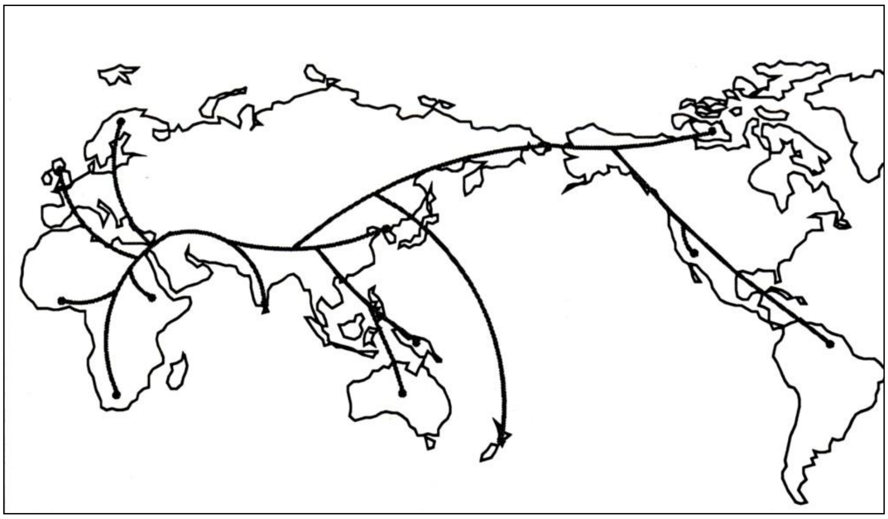

Figure 9 "An unrooted tree [...] adjusted for display on the geographic world map" by Edwards and Cavalli-Sforza, 1964, using the same data as used for the genetic tree in Fig 1 chapter 1.[152]

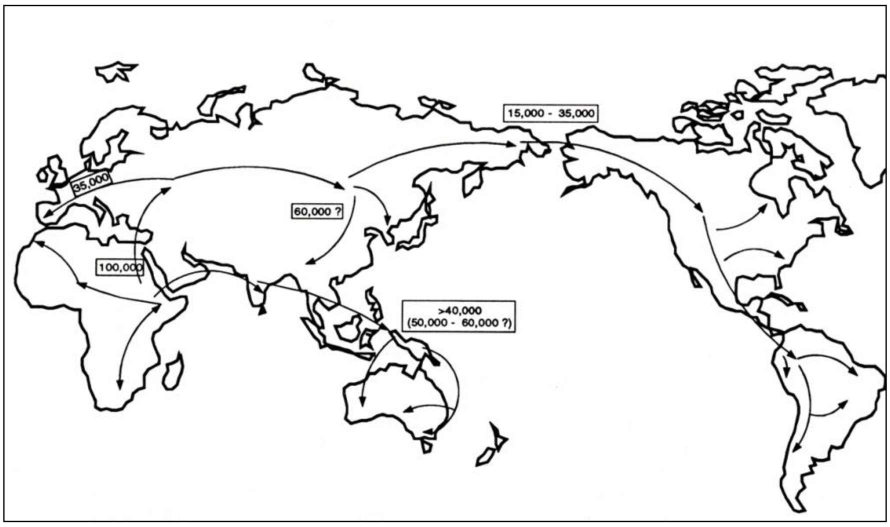

Figure 10 A similar merged map and tree, depicting the "Possible history and routes of expansion of modern humans in the last 100 ky [100,000 years]". [153]

Cavalli's view of history was based on decades of research, and on his explicit hypotheses. The latter include an emphasis on fissions, albeit with the disclaimer that this emphasis results from the assumption that population splits and migrations have most profoundly shaped the human gene pool, and not from the idea that admixture is an unimportant factor in history. Current genetic differences were interpreted as the result of a history of such population dynamics, and therefore, current populations could be connected through lineages with ancestor groups. Trees, maps and narrative

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[152] Reproduced from L.L. Cavalli-Sforza and A.W.F. Edwards, 'Analysis of human evolution' in *Proceedings of the 11th international congress on genetics* (1964) 2 923-33 in Cavalli-Sforza et al., *The history and geography of human genes, paperback edition* 69

[153] Ibidem 156

structures were merged. This complex, in turn, was infused with a moral message that racism is groundless. A shared origin, an almost identical genetic make-up, the shortness of the period in which humans separated – such information was valuable for solving technical issues of locating the root of the tree, but at the same time, it was used as an argument against racism and for a 'family' view of humanity. Such a view was reinforced by his use of tree models. These are analogous not only to biological species trees (and their prescientific precursor, the 'great chain of being'), but most importantly, to genealogical family trees.

In other words, representations, research methods, and moral message were closely knit. These also particularly lend themselves for narrativization. This is especially striking if we compare Cavalli's preference for the 'out of Africa' theory, tree images and narratives of migration, with the multiregional scenario. The latter offers an alternative vision of continuous hybridisation and much messier migration processes, and is less suitable for the construction of heroic narratives.

The tree view also brought with it a view of historical populations as relatively well-discernible entities, of which the identities are continuous and traceable through historical time. This was to a great extent the result of Cavalli's assumption, or inference, that in the historical period he studied, populations were small and isolated, and this isolation created relatively clear patterns. Because of this assumption of isolation and bottlenecks, the populations could be identified as genetic and linguistic groups: in evolutionary isolation they acquired distinct identities. They are the colonizers of continents, 'vessels' of polymorphisms and ancestral languages that can be traced like breadcrumbs in the gene pools of currently living populations.

Notwithstanding Cavalli's influence on the way anthropological research was done, his ideas triggered much debate. Initially this debate took place within the emerging community of anthropological geneticists and was rather technical. When the HGDP entered the stage and met with ferocious lay opposition, discussion transcended disciplinary boundaries, while fuelling debates within the discipline. It is these debates that are the subject of the next chapter.

Chapter three - Criticism and controversy

The numerous and intertwined debates in and about anthropological genetics in the 1990s revolved around two general themes, both of which connect to the epistemological status of categories, and the ethics of diversity research. Firstly, the question of (dis)continuity in genetic variation was subject of debate in all genetic sciences, medical, biological and anthropological. Secondly, criticism of anthropological research into human history focused on the cladistic method and tree models, and the underlying views of history. The HGP and the HGDP had brought these issues to the surface, and especially Cavalli's ideas and models became targets of criticism, most notably from anthropologists. Objections were raised against his definition of genetic group differences and their identification with genetic markers – both of currently existing populations and inferred ancestral ones. Because medical group categories were also defined in terms of the history of such groups, debates in medical and anthropological research blended into each other.

The opposition ranged from pleas for a cautious and nuanced treatment of such concepts to a general rejection of categories. Historical, anthropological and genetic arguments were used. The clinal nature and the complexity of the human gene pool were used as arguments for the insignificance of differences. Alternative views of the migratory history of the species informed opposition against Cavalli's 'fission-centred' narrative. An extra urgency was added to these already heated scientific exchanges by the public appropriation of scientific views, the antiracist claims based on genetic research, and general fears of genetic essentialism and a return of racism.

Modelling history

From the 1990s onwards, criticism of the HGDP, of Cavalli-Sforza's work, and of tree models in general was led by Jonathan Marks, an anthropologist with an M.S. degree in genetics. His main argument against the use of trees was that they do not accurately reflect the realities of human admixture. Admixture, he argues, is a constant factor in human history. The discreteness of populations suggested by their depiction as branches on human ‘family trees’ cannot be found in reality; it is the product of research strategies. He emphasizes the clinal nature of genetic patterns, that is, the gradual variation of polymorphisms that is correlated with geographic distance. This clinal pattern, he argued, results not necessarily from migration, but from gradual environmental variation (and thus of the adaptations to them), as well as from continuous genetic contact.[1]

The continuity of gene flow and admixture in human history is a central argument in the critique of the tree model of history. The latter required the assumption that current admixture is a modern phenomenon, or in other words, it rejected ‘uniformitarianism’. Indeed, Cavalli-Sforza considers 1492 as a watershed in this regard. The HGDP planning document states that “Human populations have probably always been in flux but there is widespread interest in being able to reconstruct the dynamics of human populations in the time prior to known or written history ('prehistory'), particularly in the time before the dislocations caused by the large-scale transoceanic/continental migrations of recent millennia.[2]

The geneticist Alan Templeton has argued that “the major human populations have been interconnected by gene flow (recurrent at least on a time scale on the order of ten thousand years or less) during at least the last six hundred thousand years, with 95 percent statistical confidence. Hence, [...] the existence of multiple evolutionary lineages of humans, [..] the idea that Eurasians split form Africans one hundred thousand years ago, and [...] the idea that “pure races” existed in the past” are rejected by genetic research.[3] Anthropologist John Moore held a similar view and pointed out that by neglecting this, cladism presents an erroneous view of history. “Only by maintaining that the processes of change recently observed among tribal peoples are new and unprecedented can it be alleged that in the past, before there were ethnographers, things were different.[4] Marks argued that to approach the issue as if population contact suddenly began in 1492 or later, and to project a pseudo-history onto population biology, “are unlikely to be optimal intellectual strategies for studying the genetic

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[1] Jonathan Marks, *Human biodiversity* (New Brunswick, 1995) 185

[2] Committee", "Human Genome Diversity Project: Summary document,"

[3] Alan Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' in: A.H. Goodman, et al., eds., *Genetic nature/culture. Anthropology and science beyond the two-culture divide* (Berkeley, Los Angeles and London, 2003) 248

[4] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 937

variation in our species”.[5] Gene flow is “a pervasive feature of human history.”[6] He thought human culture may be an explanation for the degree of admixture that guarantees that the human species is one single evolutionary lineage, instead of a branching tree. Cultural variation has replaced biological variation and group identity.[7] “The fairly small proportion of human diversity that is not cultural and can be separately analyzed as biological or genetic variation, is structured principally as polymorphism” – by which he meant that the markers are present in all populations, but with different frequencies.[8]

Moore too pointed to ethnographers’ and linguistic field-workers’ objections. He argued that they knew from experience that there is admixture between apparently distinct communities, and saw no reason to believe it was different in the past.[9] Moore himself studied intermarriage between Native American tribes and found that “any mutation appearing in a tribe would be transmitted within a few generations to neighboring groups and completely across the continent within a few hundred years”.[10] To illustrate the ambiguous nature of kinship, the anthropologist Gisli Pálsson quoted an (Alaskan) Inupiat who, he reports, said “He used to be my relative” about a community co-member. He also pointed to the fact that in that same community, adoption is very common, which he argued undermines a biological notion of kinship.[11] Many indigenous objected against the reduction of the histories of populations to biological ancestry, “prioritizing genetic homogeneity over linguistic, cultural and social interaction and heterogeneity”.[12]

Alternatives for tree models attempted to accommodate the idea of gene flow as the rule and population splits as exceptions. Templeton’s preferred model of human history was based on the view that the human species evolved as one, and that groups fragment and realign constantly. He dubbed this alternative (or addition) to tree models the ethnogenetic or “trellis” model.[13] Groups do not descend only from one common

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[5] Marks, *Human biodiversity* 178

[6] Marks, 'Ten facts about human variation,' 268

[7] Marks, *Human biodiversity* 200

[8] Jonathan Marks, 'What is the viewpoint of hemoglobin, and does it matter?,' *History and philosophy of the life sciences* 31 (2009) 253,“Even markers that do allow differentiation of disparate groups exhibit clines of differing intensities within those groups “ J. Marks, 'Ten facts about human variation,' in: M.P. Muehlenbein, ed., *Human evolutionary biology* (Bloomington, 2010) 267-8

[9] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 927

[10] Ibidem 934

[1111] Pálsson, *Anthropology and the new genetics* 197

[12] M.W. Foster and R.R. Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' *Genome Research* 12 (2002) 844-850 846

[13] Alan R. Templeton, 'Out of Africa again and again,' *Nature* 416 (2002) 45. According to this model, “genetic contact between African and non-African Homo erectus populations was maintained although restricted by isolation by distance. Isolation by distance allowed local populations to become differentiated from one another, but gene flow prevented long-term independent

ancestral population, but can also emerge from different root populations in a process called 'ethnogenesis'.[14] Pálsson pointed to archaeologists' evidence that 'the' Inuit have intermixed and regrouped throughout history.[15]A similar argument came from Marks, who spoke of "a continual pruning of the evolutionary tree."

Thus, a main argument against Cavalli's model was that his trees incorrectly emphasized vertical modes of genetic transmission at the cost of horizontal ones. Marks also proposed modes of representation resembling trellis, rhizomes or capillary systems.[16] "If we really must use tree metaphors, perhaps the Banyan tree would be a "more accurate and compelling metaphor", Pálsson argues[17] - as these trees' aerial roots grow back into the ground, they appear to have several trunks.

Marks argued that due to a long history of gene exchange there are "no obvious genetic clusters corresponding to what we would identify as a race"[18]. He accused Cavalli-Sforza, who acknowledged this clinal nature of human genetic diversity, of not aligning his research practice with this insight. He found a parallel between this ambiguity in Cavalli-Sforza's research with Blumenbach's, who said that "One variety of mankind does so sensibly pass into the other, that you cannot mark out the limits between them" – to which Marks adds that "[Blumenbach] nevertheless proceeded to do just that."[19] He accused Cavalli of the same ambiguity.

Although they argued that the differences are not 'obvious', these critics had alternative explanations for genetic variation between populations. They considered it the result of a "dynamic balance of gene flow and drift,"[20] or "isolation by distance," in a genetic continuum. Already in 1969, this process was described as follows: "differentiation arises from the balance between local fixation by inbreeding and swamping effect of dispersion."[21] Another explanation was the development of locally adaptive traits. – an explanation which did not contradict the idea of continuous gene flow between populations throughout history, Templeton emphasized.[22] Marks summed up the possible historical explanations for differences between 'gene pools': these could be the result of length of separation time, isolation, natural selection and/or drift – and

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evolution such that humanity evolved into modernity as a single evolutionary lineage."

[14] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 925

[15] Pálsson, *Anthropology and the new genetics* 191

[16] J. Marks, 'Ten facts about human variation,' in: M.P. Muehlenbein, ed., *Human evolutionary biology* (Bloomington, 2010) 268

[17] Pálsson, *Anthropology and the new genetics* 85

[18] Marks, *Human biodiversity* 167

[19] J. Marks, 'Ten facts about human variation,' in: M.P. Muehlenbein, ed., *Human evolutionary biology* (Bloomington, 2010) 267

[20] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,'   242

[21] Wright, quoted by Pálsson, *Anthropology and the new genetics* 180

[22] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,'   252

why, he asked rhetorically, take only the first as an explanation, as do most phylogenetic trees.[23] Templeton argued that statistical techniques that separate the influences of historical events (such as population range expansions) from recurrent events (such as gene flow when a population is isolated by distance), techniques which did not regard these two forces as “mutually exclusive alternatives”, in most cases pointed to a combination of both.[24] The ‘travelling’ of a marker could therefore not necessarily be interpreted as reflecting a population’s journey.

The ‘trellis’ model fitted the multiregional view of *homo* history: it held that gene flow took place between Africa and the rest of the world throughout history, with *Erectus* travelling back and forth.[25] According to this view, modern humans could have emerged anywhere, to subsequently spread across the continents. The model is reminiscent of Hooton’s ‘circulatory system view’ of human ancestry, or races (1946), with groups growing apart and together, which was approvingly quoted by Marks.[26] Pointing out this resemblance also served to illustrate that the debate goes back far into the history of anthropology.

The paleoanthropologist Milford Wolpoff is considered to be the leader of the multiregional view. He argued in 1992 that “there is no single home for modern humanity—humans originated in Africa and then slowly developed their modern forms in every area of the Old World.”[27] In the same year, Templeton argued in *Science* that ‘Out of Africa’ was not the only viable theory of human origins.[28] The original version of multiregionalism, which proposed that parallel evolution on different continents could account for current variation, was by that time left behind, in favour of a ‘one lineage’ view. Wolpoff et al. defended the theory against Cavalli-Sforza’s accusations of promoting this traditional ‘polycentric’ view in 1993: “Our working hypothesis is that […] complex morphological patters reflect underlying genetic phenomena that also were complex, involving amounts and patterns not only of gene flow but also of mutation, drift, and selection operating over hundreds of thousands of years.”[29] Expansions out of Africa – an increasing number of multiregionalists agreed that modern traits evolved on this continent - did not result in the replacement of Eurasian populations, but in

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[23] Marks, *Human biodiversity* 178

[24] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 247

[25] Ibidem 241

[26] Marks, '”We’re going to tell these people who they really are”: science and relatedness,' 357- 8. See chapter 1.

[27] Alan G. Thorne and Milford H. Wolpoff, “The Multiregional Evolution of Humans,” Scientific American, 266 (April 1992), 76 Quoted in P. Wald, 'Future Perfect: grammar, genes, and geography,' *New Literary History,* 31 (2000) 701

[28] Human Origins and Analysis of Mitochondrial DNA Sequences *Science* 1992

[29] R. B. Eckhardt et al., 'Multiregional evolution,' *Science* (1993) 974

admixture, it was argued.[30] Templeton argued that continuous interbreeding resulted in the emergence of "only one kind of modern human."[31] He was critical of the mtEve study, and argued that the data did not support the rooting of the tree in Africa.

"Eve" was the subject of much scientific debate and controversy. For instance, scientists objected that Africa was represented in the sample collection by Afro-Americans' DNA.[32] The Wilson group had legitimized this with the argument that white admixture in Afro-American groups was 'male material' that had not influenced mtDNA lineages.[33] More fundamentally, both the tree building method, which placed the root in Africa, and the method to detect mutations were criticized as inferior. Several of the Eve researchers confirmed the Eve study in 1991.[34] But again it was criticized: the most basic split in word tree divided an African population known to be closely related. Critical scientists found that more than one tree can be made, and non-African roots were equally likely. Worse still, it was shown that the order of entering data into computers influences the end result. One of the Eve scientists, Matt Stoneking, admitted the error in *Science*.[35] Cavalli-Sforza mentioned in 1993 that the statistical re-analyses weakened the Eve hypothesis as a possible support for "Out of Africa". But, as Rebecca Cann emphasized, this did not diminish the importance of the other mtDNA argument: that of greater African mtDNA heterogeneity.[36] A study by Cavalli-Sforza, Kidd and Kidd confirmed this for nuclear DNA.[37]

Proponents of the general conclusions of the Eve study, Cann and Cavalli-Sforza among them, acknowledged that there had been some flaws in the study[38], but that the inference of an African root was not invalidated by them; the large variation in the African gene pool buttressed this claim.[39] The doubt about mass replacement, however, fuelled multiregionalist arguments.[40]

In short, multiregionalists explained local differentiation between populations

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[30] Templeton, 'Out of Africa again and again,' ; John Relethford, 'Genetics of modern human origins and diversity,' *Annual review of Anthropology* 27 (1998)2-3

[31] Gibbons, 'Eve wounded, but not dead yet,'

[32] Ibidem 873

[33] Cann et al., 'Mitochondrial DNA and human evolution,' 32

[34] Linda Vigilant et al., 'African populations and the evolution of human mitochondrial DNA
' *Science* 253 (1991)

[35] Gibbons, 'Eve wounded, but not dead yet,' 873-4

[36] Cavalli-Sforza et al., 'Demic expansions and human evolution,' 639; Gibbons, 'Eve wounded, but not dead yet,'

[37] Gibbons, 'Eve wounded, but not dead yet,' 874; *DNA Markers and Genetic Variation in the Human Species* L.L. Cavalli-Sforza, J.R. Kidd, K.K. Kidd, C. Bucci, A.M. Bowcock, B.S. Hewlett, and J.S. Friedlaender

[38] Ibidem

[39] Stoneking responded to Templeton with the accusation that the latter's methods and data were "questionable" and "inappropriate": "while at present the genetic data are insufficient to statistically reject the multiregional evolution hypothesis, they do raise serious questions for supporters of this hypothesis." M. Stoneking, 'In defense of "Eve" - A response to Templeton's critique,' *American Anthropologist* 96 (1994) 131

[40]Wilford, 'Critics batter proof of an African Eve,' ; Gibbons, *Eve wounded* (1992)

with isolation by distance, but pointed to continuous gene flow between populations that prevented truly independent evolution. Humanity evolved "into modernity" as a single evolutionary lineage. More recent range expansions expanded modern humans' geographical range, but all territories were interlinked by gene flow[41] – with the exception of the New World. Gene flow was only barred by the natural boundary between Old and the New world, but as migrations into the Americas were either numerous or massive, there are many shared polymorphisms at both sides of the boundary, and isolation was relatively brief.[42]

According to the anthropologist Dennis O'Rourke, the testing of the two theories of human origins was problematic: at the time, mtDNA was "the only useful marker" [sic], "but [...] its robusticity for inferring demographic events may be questioned." It was hard to decide between alternative explanations for genetic phenomena, he argues. Instead of population expansion and greater ancestry, the greater size of a population may also serve as an explanation of African heterogeneity, "weakening the inference of a recent African origin".[43] Nuclear DNA did not produce unambiguous results. "It is difficult to distinguish effects of selective sweep from population expansion without selection." "Anthropological genetics cannot decide between two models, let alone settle more subtle questions regarding this possible combination." Nevertheless, Out of Africa gained dominance over the years.[44] Indeed, Science reported in 1998 that while nuclear DNA studies are not all consistent, Out of Africa was "generally accepted."[45]

Although the multiregionalist scenario slowly lost ground, the debate continued for years, in genetics and other disciplines, such as archaeology, physical anthropology and paleontology. Templeton, anthropologist John Relethford and Wolpoff[46] were among the few who continued to criticize the consensus that started to emerge in favour of the Out of Africa theory.[47] They continued to argue that "Although the genetic data do provide support for the recent African origin model, they also are compatible with the multiregional model. Numerous genetics papers indicate the genetic data come down firmly in favor of an African replacement model - most often, however, the data can be

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[41] Templeton, 'Out of Africa again and again,' 45

[42] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 248

[43] O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' 105 See also L. B. Jorde et al., 'The distribution of human genetic diversity: A comparison of mitochondrial, autosomal, and Y-chromosome data,' *American Journal of Human Genetics* 66 (2000)

[44] O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' 105

[45] Science *'DNA studies...'* (1998) 655

[46] Templeton, 'Out of Africa again and again,'

[47] Ibidem 02

interpreted in several ways."[48] Templeton argued in 2003 that the replacement version of Out of Africa was falsified because many DNA regions that he analysed turned out to have evolutionary history that was longer than 100,000 years. Such markers should have been wiped out according to the replacement scenario.[49]

Each model provided explicit ways of accounting for differences and similarities, with different ideas about what humans share and what divides them. The ways in which unity was conceptualized – common roots versus continuous genetic contact, or: vertical continuity versus horizontal continuity – were coupled with a specific view of population differences: an isolation by distance versus a lineage view. Trees embody the Out of Africa view, while the multiregionalist theory has no equivalent model.

Pálsson accused geneticists of not being aware of the subjectivity and historically contingent nature of their models. He referred to Bouquet's argument that the mere 'family resemblance' of "pedigree thinking" in several disciplines, including linguistics and evolutionary biology, and even literature studies, is a strong indication of the historicity of the trope. The 'genealogical view' provides a "purified vision of languages and organisms as timeless artifacts with parallel roots and histories," emphasizing divergence.[50] Bouquet argued that the tree model derives its "visual and moral clout" from its biblical and secular ancestors. These were the sacred trees that facilitated the study of biblical texts, tracing the Messiah's ancestry back to Adam, and nineteenth century scientific "appropriations" of them by Haeckel, among others.[51] Bouquet asked rhetorically whether users of tree images are conscious of these precursors, and whether they "scrutinize their own arborification of knowledge." "Could it be that trees differentiate and create identities"?[52] The value of anthropology is, Pálsson argued, that it can offer geneticists such mirror images of themselves, as well as point to alternative (indigenous) ideas about relatedness and descent that challenge the "implicit practices of genealogical imaging and tacit assumptions about [...] the "nature" of kinship" that pervade [Western] science."[53] Many geneticists agreed with Cavalli that trees were

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[48] Relethford, 'Genetics of modern human origins and diversity,' 1-2. Templeton argued in 2003 that while recent literature supported Out of Africa, the data that it was based upon supported the trellis model too. The only thing it rejected, he argued, was the "candelabra model," of separate lineages, and without replacement. Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 239-241

[49] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 247

[50] Pálsson, *Anthropology and the new genetics* 63

[51] Mary Bouquet, 'Family trees and their affinities: the visual imperative of the genealogical diagram,' *The Journal of the Royal Anthropological Institute* 2 (1996) 59

[52] Mary Bouquet, 'Family trees and their affinities: the visual imperative of the genealogical diagram,' *The Journal of the Royal Anthropological Institute* 2 (1996) 60-62

[53] Pálsson, *Anthropology and the new genetics* 67

convenient models, as long as one kept in mind that the branches represent 'statistical sampling units.' Nevertheless, many accused them of reifying them as biologically real.[54] More ardent critics bluntly stated that trees do not adequately represent biological and historical reality.[55]

The idea that the tree model is a metaphor rather than a realistic explanatory model of genetic patterns connected with other critiques that emphasize the metaphorical nature of the concepts used in anthropological genetics. Nash argued that the metaphors such as "family of man", the "idiom of kinship" and the "gendering of narratives of reproduction and descent" served to naturalise genetic markers as links to other people and to historical populations.[56] The truth of genetics' claims about these relationships and about history not only derived from the status of science as 'objective', but also depends on the use of "narrative, analogy, metaphor and imagination" in communication within and beyond laboratories.[57] These could be traced back to century-old models of 'families of man', both national and universal, which were naturalised by means of an analogy with the 'natural' family, and infused with "racial-hierarchical evolutionary views".[58] Often, these models reflected imperial hierarchies, she argued. By contrast, Greely, then head of ethics for the HGDP, argued that the HGDP provided a necessary counterweight to the West-centred and "parochial" Human Genome Project: "We'll show that humanity is an extended family", he proclaimed.[59] Nash argued that attempts to create a sense of 'global paternal fraternity' and 'universal brotherhood' through constructing a Y-chromosome genealogy "elide[...] the implications of using genetics as a measure of similarities and differences."[60] In this view, the emphasis on the trunk, the common ancestor so enthusiastically picked up by the press, served to downplay the centrality of divergence and the discreteness of the branches.

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[54] Kittles and Weiss quoted in Ibidem 204. "While most population getenicists readily acknowledge that the clusters are statistical reifications, it is not too difficult to find them naïvely interpreted as cladogenetic events." Marks, 'Ten facts about human variation,' 268

[55] Pálsson, *Anthropology and the new genetics* 220. It is interesting that in 1998 it was argued that the tree may not be an accurate model for life itself in W. F. Doolittle, 'Phylogenetic classification and the universal tree,' *Science* 286 (1998)

[56] Nash, 'Genetic kinship,' 25

[57] Ibidem 3

[58] Ibidem 3

[59] Reardon, *Race to the finish. Identity and governance in an age of genomics* 110

[60] Nash, 'Genetic kinship,' 14

Essentialism

In the 1990s several popular scientific publications on the 'reality of race' were published, some of which explicitly used genetics insights.[61] They were read by large audiences, and caused severe criticism and indignation both from within and outside of the scientific community. *The Bell curve* (1994), by the psychologist Richard Herrnstein and political scientist Charles Murray, dealt with variation in IQ and the presumed genetic basis. It evoked a big controversy in scientific circles and beyond. Cavalli-Sforza criticized it extensively in *The great human diasporas* (1995), in which he dedicated several pages to explain why the science behind it was fallacious.[62] Another example is *Race. The reality of human differences* by the anthropologist Vincent Sarich and journalist Frank Miele, published in in 2005.[63] Such work triggered debate and fears about genetic essentialism. Ironically, these fears also concerned Cavalli's work.

Moore, and most other critics, objected to the naturalization of the branches as if they were real populations. "It is clear that the biological process itself is cladistic and that cladograms constitute the most appropriate presentation of results". But according to him these models depict the history of markers. "In no case do the ancestral nodes necessarily represent real populations [..] that is, the nodes are not demes."[64] Cavalli's discourse and graphic representations however suggested that the populations are 'real'.[65] Templeton agreed: gene trees could represent the evolutionary history of genes, provided no recombination had occurred. Even then, other blurring effects were also possible. The "mutational differences" that define the branches in tree models can be misleading: a mutation may have occurred more than once. Likewise, he argued, population trees are only realistic representations of history when no admixture has taken place between the populations under investigation.[66] In general, trees "reflect only the evolutionary history of specific DNAsegment under study; they are not necessarily evolutionary trees of species or subspecies." Moreover, it is possible to force a tree model on admixed data: "suppose a species is and always has been completely randomly

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[61] E.g. R.J. Herrnstein and C. Murray, *The bell curve: intelligence and class structure in American life* (New York, 1994); V. Sarich and F. Miele, *Race. The reality of human differences* (Boulder, 2005)

[62] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* postscript 268

[63] Sarich and Miele, *Race. The reality of human differences*

[64] bidem 934

[65] The style of discourse, as well as the graphic representation of results, also explicitly indicates that anthropological geneticists are concerned with real antecedent populations, not hypothetical [phenetic] constructs. Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 928

[66] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 641

mating as a single population and therefore has no subpopulation evolutionary history at all; yet that same randomly mating species will have […] trees for all homologous DNA regions that show little or no recombination."[67] Many critics objected to a confusion of markers with populations. Marianne Sommer pointed out that by calling their 1987 tree a "human family tree", Cann et al. identified groups with their mtDNA.[68] This confusion, and the vocabulary surrounding tree models, creates the impression that the tree deals with the evolution of real populations, critics felt. Although "No responsible geneticist would say that there exists [...] the marker for an ethnic racial group,"[69] populations were often implicitly equalled with DNA material used to study them. Moore argued that "The style of discourse, as well as the graphic results presented by Cavalli-Sforza et al. [...] indicate that anthropological geneticists are concerned with real antecedent populations, not hypothetical constructs.[70]

For Marks the 'tidiness' of the mtDNA tree rendered it by definition incompatible with the chaotic reality of actual genetic relationships and group dynamics.[71] And Nash argued that the emphasis on paternal and maternal relationships that resulted from Y chromosome and mtDNA studies downplayed the importance of recombination. "The Y-chromosome makes up about 2 percent of genotype, but by emphasizing its significance as a marker of genetic similarity and diversity it seems to stand for all that is inherited."[72] Many pointed out that such analyses reconstructed only one of many lines of descent[73] - the farther back in history and the more generations included in the reconstruction, the more ancestors and lineages were ignored. Medical anthropologist Paul Brodwin explained: "If you had 1 European ancestor [five generations back], and the rest of your male (and female) ancestors were African, then you would be 1/32 European, but phenotypically black, and of course culturally black in the USA. But if that European man happened to be your father's father's father's father's father, then Y-chromosome typing would place your ancestry entirely in Europe."[74] Nash quoted the geneticist Mark Jobling: 'people sharing a most recent common ancestor a mere ten generations ago are only expected to share around a millionth of their DNA by direct

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[67] Ibidem 246

[68] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 510

[69] P. Brodwin, 'Genetics, identity, and the anthropology of essentialism,' *Anthropological Quarterly* (2002) 328

[70] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 928

[71] Marks, *Human biodiversity* 170

[72] Nash, 'Genetic kinship,' 20, 11

[73] Brodwin, 'Genetics, identity, and the anthropology of essentialism,' 328; K. Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' *Journal of Law, Medicine & Ethics* (2007) 414

[74] Brodwin, 'Genetics, identity, and the anthropology of essentialism,' 328

descent, and there's no telling which millionth that might be'.'[75]

As such research entered discourses about identity and kinship, critics warned against the narrowing down of ethnic identities to genetic ones. Medical research especially was accused of contributed to this view, as it connected disease risks to certain genetic populations. In 1995 UNESCO warned against reductionist views resulting from medical diversity research: "Individuals have been categorised according to specific markers of inherited susceptibilities. Whatever the theoretical and scientific benefits of such categorisations, research scientists must always have regard to a more holistic appreciation of human beings, considered both as individuals with an inherent dignity, and as communities living in a given environment and culture."[76]

Morris Foster and Richard Sharp, an anthropologist and a bioethicist, located such genetic essentialising in the sphere of popularisation and public interpretation, rather than in scientific models and practices. They argued that when "genetic linkage studies emphasize one particular lineage that donors share and ignore all lineages that they don't, a genomic feature may be perceived by the public as defining a social population."[77] Scientists should be aware of the loss of nuances that takes place in popularisations, they argued, since "Public perceptions of genetic information tend to collapse distinctions and categories that scientists use to maintain distance between social and genetic definitions of populations, and genetic information has greater public authority than social information."[78] Others located the reductionism even more firmly in the realm of the public. Brodwin argued that "the scholarly (and left-liberal) opposition to "genetic essentialism" is not really a reaction to contemporary genetics, but rather to its reception. The essentializing occurs at the level of popular reconstructions of genetic science.'[79] People "regard genes as "more stable over time than more putatively accidental aspects of identity" (such as nationality, citizenship, religion, etc.)."[80]

While Brodwin concluded that "professional anti-essentialist interventions" should be directed at the level of "popular reconstruction", he, interestingly, left room for exceptions. If "misunderstandings of genetics have a positive effect", such as "increased pride in one's heritage", it may be wise to pursue a "strategic essentialism," by not giving

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[75] Nash, 'Genetic kinship,' 11
[76] committee, "Bioethics and human population genetics research," 17
[77] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 848
[78] Ibidem 848
[79] Brodwin, 'Genetics, identity, and the anthropology of essentialism,'
[80] Ibidem

out “otherwise salutary warning[s] against genetic essentialism”. Such issues, he thought, “cry out for anthropological expertise.”[81] Foster and Sharp, on the other hand, regarded reification and “unintended genetic essentialism” as an inherent (and “the greatest”) risk of population-specific research into genomes itself, for example, in legal cases and forensic DNA profiling, where geno- and phenotypic characteristics are now listed.[82]

Most critics did not separate popular and scientific discourse. They pointed out that the way categories are constructed and conceptualised has also problematic consequences for the research results themselves. As could be expected, especially those who emphasized the non-existence of self-evident and “genetically stable” clusters objected to the “inflexibility” of the tree metaphor, which in their view led to the naturalisation of categories.[83] Thus, the anthropologist Alan Fix, in his review of Cavalli’s *The great human diasporas,* pointed to an ambiguity in this work, that in his opinion resulted from the combination of an antiracist agenda with a “persistent use of dendrograms for displaying differences among human populations and his use of “separation times” for human continental groups”. He concluded that the section titled ““When did the races of humanity separate?” might be answered, “They haven’t””.[84]

To produce anthropological genetics categories much work had to be done: the selection of markers and populations, the development of algorithms and computer programs to analyse abundant resources of data. This length of the chain of operations and decisions provided room for criticism along social constructionist lines. For instance, bioethicist Troy Duster argued that “It is possible to make arbitrary groupings of populations [...] and still find statistically significant allelic variations between those groupings”, at some loci. “When researchers claim to be able to assign people to groups based on allele frequency at a certain number of loci, they have chosen loci that show differences between the groups they are trying to distinguish.” He pointed to studies that suggest that “only about 10 percent of sites in DNA are useful for making distinctions.”[85]

The computer programs used for the construction of trees were based on the

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[81] Ibidem 329

[82] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 848

[83] Marks, '”We’re going to tell these people who they really are”: science and relatedness,' 360

[84] Alan Fix, 'Review: The great human diasporas,' *American Journal of Physical Anthropology* 101 (1996) p549

[85] T. Duster, 'Buried alive. The concept of race in science,' in: A.H. Goodman, et al., eds., *Genetic Nature/culture. Anthropology and science beyond the two-culture divide*
(Berkely, 2003) 258-277 265

assumption that the data they analysed ‘had treeness’, that is, that the differences found are the result of group separations and founder effect rather than isolation by distance or natural selection.[86] Critics argued that the reliance on only one model for differences made the trees dependent on research strategies: their “grossly oversimplif[ying]” nature rendered them “unstable and [...] sensitive to the statistics used, the genes analysed, the particular populations chosen and the demographic history of the groups.[87] “They felt that the assumptions about human population histories that pervade the research were “rendered invisible through representational medium of evolutionary tree.” [88]

Anthropologist of science Kimberly Tallbear objected to the elimination from genetic databases of populations that were considered ‘admixed’, which in her view overemphasized differences and rendered the selection not representative of the human gene pool.[89] Nash argued that “Reports on new findings in population genetics do not reflect on the way in which the process of sampling to test the degree of genetic similarity […] involves screening out those whose bodies suggest their origins are elsewhere.”[90] The main argument against Cavalli’s work concerned his criteria for sampling populations. These were selected to not have been subjected too much gene flow; there should be no exogamous matings, nor too much acculturation; the populations should not be too small (to exclude those subjected to genetic drift); and urban populations should be excluded.[91]

Marks argued that statistical cluster analyses are “sensitive to the population samples chosen, the individual people representing them, the demographic history of the populations, the assumptions of the particular algorithm, and the patterns of contact among the populations. In other words, “the species still doesn’t come pre-packaged for you; you still have to decide, given the fact of difference, how much and what kind is meaningful and how much and what kind is not.”[92] He considered decisions about what genetic data are used to be of great influence: every choice could result in a different

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[86] Pálsson, *Anthropology and the new genetics* 183; “The computer programs used to generate "trees" from genetic distance data will do so regardless of what evolutionary factors generated the distances. It is therefore the obligation of the users of such programs to ensure that the genetic distance data have the properties of treeness before presenting their data as a tree” A. Templeton, 'Human races: a genetic and evolutionary perspective,' *American Anthropologist* 100 (1999) 639

[87] Jonathan Marks, "Human genome diversity studies: Impact on indigenous communities," in *Encyclopedia of life sciences*, ed. John Wiley and sons (Chichester: 2008)

[88] Marks, '"We’re going to tell these people who they really are”: science and relatedness,' 360-1

[89] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 416

[90] Nash, 'Genetic kinship,' 15

[91] A. Bowcock and L. L. Cavalli-Sforza, 'The study of variation in the human genome,' *Genomics* 11 (1991) 496

[92] J. Marks, "The realities of races," in *Is race "real"?*, ed. Social science research council (2006)

tree.[93] And the interpretation of results is also subject to bias, anthropologist Deborah Bolnick argued: studies “both reflect and reinforce traditional racial views.[94] Templeton concluded that one can make a race out of everything: “genetic surveys usually reveal so much variation that some combination of characters distinguishes virtually every population from all others”.[95]

Amade M’Charek has described, in an anthropological study of scientific laboratory work, how difference was “produced” with the use of a reference genome against which all samples are examined. This reference sequence for mtDNA was produced in the 1980s by Anderson et al. In everyday laboratory language, the sequence was referred to as “Anderson”, a practice that (she argued) reflected its naturalisation, and hid the work that was done to produce it. In a sense it (‘he’) even took the place of a common ancestor, as the samples’ divergences from it were conceived of as ‘mutations’. “Often, Anderson is naturalised and presented as an individual on a genealogical tree”.[96]

Sampling practices especially, critics argued, determine the input into such ‘black boxes’. Obviously, “Sampling cannot possibly take place without a subjective judgment about how to proceed.”[97] As already discussed, the HGDP itself started off with dispute about the way to sample global diversity. In several of his publications, Marks cited a 1991 study that he considered to be an especially striking example of the effect that the selection of samples can have on the outcomes of research. Analysis of “64 samples of Chinese ... living in the San Francisco Bay Area’, 94 samples from ‘two groups of African pygmies’, and 110 samples from ‘individuals of European origin” led to the conclusion that “ancestral Europeans are estimated to be an admixture of 65% ancestral Chinese and 35% ancestral Africans.’[98]

So what should the selection of samples be based on, according to these critics? Foster and Sharp explained that there were no self-evident biological criteria to capture human genetic diversity in genomics resources, so that social categories were needed as proxies, to make sure the whole of human variation is represented. There was no other way: “These social categories may correspond more or less precisely with biological variation of interest to geneticists” and so “they are critical for assembling diverse

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[93] Marks, *Human biodiversity* 178-9

[94] Bolnick, 'Individual ancestry inference and the reification of race as a biological phenomenon,' 81-82

[95] Templeton, 'Human races in the context of recent human evolution: A molecular genetic perspective,' 237

[96] A. M'Charek, 'De onzichtbare (f)actor. Standaardisatie, ras en genetische diversiteit,' *Medische antropologie* 14 (2002)

[97] Pálsson, *Anthropology and the new genetics* 204

[98] J. Marks, 'Book review: Stone and Lurquin, A genetic and cultural odyssey: the life and work of L. Luca Cavalli-Sforza,' *Journal of the Royal Anthropological Institute* 12 (2006)1002, quoting A. M. Bowcock et al., 'Drift, admixture, and selection in human evolution: A study with DNA polymorphisms,' *Proceedings of the National Academy of Sciences of the United States of America* 88 (1991)

resources" - but the disadvantage is that they "indicate biological significance to racial or ethnic class that they don't necessarily possess."[99] They did not object to the use of "Categories like race and ethnicity [...] as heuristic *starting points* for variation research.[100] These were more than just organising tools: "Social categorizations [...]create real barriers to reproduction, interaction, and migration". They thus define boundaries of haplogroups, which share disease susceptibilities, specific drug metabolisms and environmental responses. However, "The biological significance of social categories for one purpose may dissolve when they're used for other biological questions.[101]

Pálsson argued that "It may be tempting to conclude that the issue of sampling in human genetic research [...] is hopelessly trapped in social constructions, body politics and ideological discourse" – but that would be an "overstatement."[102] Nevertheless, he objected to the 'insular view' of genetic diversity, to the assumption that populations are more or less distinct islands, which in his opinion risked circularity of research. This could "lead to sampling from the extremes of the continental landmasses, which [...] generates results that reify the cultural notions about essences and boundaries assumed at the outset."[103]

Many objected to sampling strategies that were based on a 'commonsense logic,'[104] against using everyday, non-genetic categories to describe genetic units. In the same vein, Duster analyses a study of genetic diversity in 2005 and concludes that "Classification is the starting point, not the end result," which results in a "Scientific Catch-22." Using pre-existing categories based on phenotype, "differences that emerge are likely to be racialized."[105]

Linguistic information was, as we have seen, often used as an organizing tool; it was an important basis for Cavalli-Sforza's approach, which served as the basis of the HGDP design. Cavalli-Sforza's models for cultural phenomena triggered much criticism, as did proposals to integrate linguistic and genetic evolution. For instance, Moore pointed out that a study conducted along these lines used "political boundaries of sedentary, industrial, and dense modern societies - products of long ideological

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[99] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 845
[100] Ibidem 849
[101] Ibidem 846-7
[102] Pálsson, *Anthropology and the new genetics* 183
[103] Ibidem 176
[104] Nash, 'Genetic kinship,' 16
[105] T. Duster, 'Lessons from history: Why race and ethnicity have played a major role in biomedical research,' *Journal of Law, Medicine & Ethics* (2006) 488

struggles to promote linguistic and cultural unity - to construct an ethnographic analogy for early Indo-Europeans whose cultural and environmental context was entirely different." In his view, the complexities of linguistic evolution cannot be equalled with genetic history: "I would assert that present linguistic processes in Europe are almost irrelevant to reconstructing the events of 8,000 years ago." [106] Ilhan Ilkilic summed up the arguments against the "ethnically and linguistically defined population concept and that of race": these are "derived from 19th century."[107] Marks argued that "The confusion of biological with cultural diversity is the most broad and persistent problem in the study of humans."[108] "To consider [groups "defined by non-biological criteria", such as political - national ones] as biological groups with a phylogeny to be discerned is to impose biological transcendence on historically ephemeral units."[109]

Pálsson objected against the conflation of the evolutionary history of genes, language and culture: "the data [fails] to reflect the constraints of treeness" and the "models of islands and clades" are flawed. An alternative model that would assume more or less permanent "hybridity and creolization" would make more sense.[110] Moore too pointed to the fact that "Such attempts require the premise, usually implicit, that human societies have always been bounded or discrete to some extent, so that each society's language, physical type, and culture have coevolved." The equation of a biological population or deme with a linguistic community was considered simplistic: ethnohistorical and anthropological expertise showed that language, culture, and physical type changed independently through time.[111] Critics regarded similarities between these types as merely apparent, the result of cladistic graphic techniques to model different kinds of data.[112] Congruence of language, physique and culture due to environmental circumstances was not ruled out, but the conclusion that the traits are connected was rejected.[113] Tallbear concluded: "Scientists wade through an uncategorizable swamp of biogenetic and cultural inputs. Despite acknowledging that biology is not culture, narrow scientific questions lead to methods that conflate the two."[114]

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[106] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 931-2

[107] Irhan Ilkilic and Norbert W. Paul, 'Ethical aspects of genome diversity research: genome research into cultural diversity or cultural diversity in genome research?,' *Medical health care and philosophy* 12 (2009) 27

[108] Marks, *Human biodiversity* 46

[109] Ibidem 179

[110] Pálsson, *Anthropology and the new genetics* 218

[111] Moore, 'Putting anthropology back together again: the ethnogenetic critique of cladistic theory,' 925, 935

[112] Ibidem 939

[113] Ibidem 931

[114] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 416

Duster explained the dilemma of sampling and naming the samples: “When they use already categorized samples, molecular geneticists are buying into a taxonomic system that has little to do with a molecular geneticist’s professional training or expertise. But if they strip such categories they don’t know how widely they sampled or if it’s a representative collection.”[115] As “social identities overlap”, their use in science builds in inaccuracy, “which might reduce the value of their association with specific genetic findings.”[116] Foster and Sharp emphasized the necessity of providing contextual information with each sample: “The initial social labelling of samples in commonly used genomic resources is crucial; that’s where scientific limitations should be framed explicitly. Self-ID of the sampled should be included in such contextual background, as well as historically contingent definitions of the population under study, so that a dynamic population identity concept emerges.”[117] More non-genetic information, not less, would ensure less rigid categorisations.

Apparently, around the turn of the century there was a perceived lack of coordination of the way samples were labelled: Nature published an editorial in 2000 urging for the “equal, consistent and informative description of human populations and ethnic groups.”[...] An interesting case is the attempt by the NIH in 1998 to create a database to study inherited diseases. Initially, they used census categories to organize the samples, which turned out to be unworkable for geneticists. Subsequently, they decided not to provide the ethnicities of the sampled at all. Kidd, a prominent geneticist, stated that “that means the database is useless.”[118] In the same year, the AAA urged the government to do away with census categories and let people choose their own ethnicity.[119] The confusion about population categories was not restricted to science.

Critics warned that despite the good intentions of the scientists (and because of their naiveté), population categories threatened to live a life of their own, outside the laboratory where they were conceived. Reardon argued that there is no neutral space when it comes to these issues; that labelling was connected to discourses of race. This was not only because scientists presented research as evidence against racist notions, therewith placing it firmly in a social and ideological discussion about race. Also and especially because antiracist claims “creat[e] the very racial concepts they claim to

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[115] Duster, 'Lessons from history: Why race and ethnicity have played a major role in biomedical research,' 488

[116] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 847

[117] Ibidem 848-9

[118] Eliot Marshall, 'DNA studies challenge the meaning of race,' *Science* 282 (1998) 655

[119] Ibidem

deny." Evidence that "we are all one human species depend[s] upon first dividing us into racial and ethnic groups and studying our differences.[120] "Genetics, most geneticists argue, refutes 'race', yet their work often reinvigorates and appears to sanction a return to questions of bodily difference and biological relatedness". They named and mapped human groups "even as the existence of pure, isolated, genetically distinct groups is denied."[121] In short, criticism targeted the ambiguity between human similarity and differences that anthropological genetics carried within it, and that had haunted and complicated diversity research for decades.

The authority with which genetics was endowed in the popular imagination rendered such research culturally explosive, critics argued. They accused geneticists of being careless. When human ancestry was reduced to genetic relationships and classification to phylogenetics, this amounted to a return of the concept of race as a natural category, Marks argued.[122] The privileging of a genetics perspective – the "viewpoint of hemoglobin" - over other views of human diversity because the former was more objective, was problematic precisely because "hemoglobin has no comprehension of human rights or of political injustice, yet these are integral to the act of classifying people".[123] In this view, the alleged objectivity of genetics on which the antiracist discourse of anthropological genetics was based, could become self-destructive. "The very conviction that genetics can refute the logic of racism is an assumption about the authority of genetics to establish definitive terms of relatedness." This view increases the danger that the "concerted efforts to refute racism might well reproduce it." While genetics research had not provided the last word on the subject, it does "unsettle terms like population."[124]

Others also pointed to the role this research has in identity formation processes, to the extent that perceptions of genetic difference in medical research into genetic variation could lead to the emergence and construction of new social categories. Cavalli-Sforza was accused of being irresponsible because he did not acknowledge that his population categories were influenced by, and influenced sociocultural group definitions, rather than being 'discovered' by him and his peers.[125] The critical argument

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[120] Reardon, *Race to the finish. Identity and governance in an age of genomics* 163; *decoding race and human difference,* in 'differences' 41

[121] Nash, 'Genetic kinship,' 4

[122] Marks, 'What is the viewpoint of hemoglobin, and does it matter?,' 241

[123] Ibidem 254

[124] Wald, 'Future Perfect: grammar, genes, and geography,' 704

[125] Ibidem 697

was that he would do better to acknowledge his own subjectivity. To illustrate the situatedness and historicity of interpretations of genetic diversity, Marks invokes a historical analogy with the history of ABO blood groups: continental patterns in ABO variation were 'discovered' in the years following the First World War, but are now undetectable. Indeed, "the ABO genetic system is taken as paradigmatic of a genetic system in which discrete boundaries among populations or clusters of populations cannot be discerned."[126] In short, they pointed out that genetics research is subject to historically changing and cultural-specific ideas. And in turn, M'Charek argued in her study of research in a HGDP lab, "race is a by-product of [it]."[127]

There was a difference between studies of genetic diversity per se, on which many of these arguments focused, and those that tried to reconstruct history. The latter based their sampling strategies on the assumption that indigenous peoples are the only 'remnants' of a past orderliness of the human gene pool. On the other hand, both kinds of research often shared this assumption that information about 'ancestral' or 'founder' populations was relevant and accessible through indigenous populations. Medical and other studies of genetic patterns that did not focus on the reconstruction of history also assumed that differences between groups should be conceptualised as lineages. "Recruiting individuals with shared social identities increases likelihood of capturing common demographic history (e.g. founder effect) which may be useful in finding disease-related genomic structures"."[128]

The indigenous

The focus on comparatively isolated populations may have been a reaction against the difficulty of defining human populations, O'Rourke suggested.[129] It may not only have reinforced the tradition of 'insular thinking' in genetics, but also determined the composition of genetic databases. Critics questioned the relevance of such data – can inferences from small, isolated communities produce insights that are relevant for the human gene pool as a whole?[130] As we have seen, indigenous populations were central to the HGDP. The idea that the indigenous gene pools were especially informative of

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[126] Marks, *Human biodiversity* 127

[127] M'Charek, 'De onzichtbare (f)actor. Standaardisatie, ras en genetische diversiteit,' 70

[128] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 846

[129] O'Rourke, 'Anthropological genetics in the genomic era:a look back and ahead,' 104

[130] Pálsson, *Anthropology and the new genetics* 55

historical patterns of the human gene pool was based on a contrast between ‘admixed’ and ‘unadmixed’. Anthropologists especially have objected to this view, and referred to what they thought were similar ‘mistakes’ in the history of their discipline.

Tallbear argues that the theme of the “vanishing indigene” goes back at least to the 17th century, and contradicts indigenous self-perceptions as still vital.[131] Other objections were raised against this ‘fossil view’ of indigenous groups: it placed them outside of history and attributed a lifeless, historyless identity to them. When Cavalli-Sforza proclaimed that “Humans are an endangered species from the point of view of genetic history,”[132] he equalled the ‘vanishing’ of indigenous identities and groups with the historical identity of the human species. The HGDP designation of indigenous as “isolates of historical interest” was critically interpreted as ‘curiosities’. (The HGDP later acknowledged this as a ‘naive error’).[133] There are “no valid grounds for regarding the genetic lineages of hunter-gatherers as more ancient than those of any other population”, Pálsson stated.[134]

Marks remarked that the “Genetic fallacy of assumption of isolation of indigenous and bifurcating trees is not new.”[135] He accused geneticists of a lack of awareness of anthropological insights. He gave the example of how, already in the 1940ies, a Native American group was proclaimed ‘pure’ by a geneticist (based on his genetic data) while cultural anthropologists knew that they had history of admixture.[136] Geneticists, he argued, practice ‘old-fashioned science.’ The idea of the indigenous as representative of primitive times, he argued, is a “holdover” of the past.[137] One of the many investigators of the San or !Kung (who are often posited at the roots of the human tree and are therefore a of particular interest to the anthropological geneticists), felt it was needed to emphasize that they “occupy the same time zone as we do.” What is more, decade-long anthropological and genetic investigations have changed them dramatically, Haraway argued. The view of the !Kung as “natural savages” persisted and even acquired a political function, as it legitimized constructing the remaining lands [of the San] into a new game reserve in Namibia, on which the !Kung will not be permitted to engage in

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[131] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 415

[132] Bowcock and Cavalli-Sforza, 'The study of variation in the human genome,' 495

[133] Reardon, *Race to the finish. Identity and governance in an age of genomics* 68

[134] Pálsson, *Anthropology and the new genetics* 189

[135] Marks, 'Ten facts about human variation,' 269

[136] Ibidem 269

[137] Marks, '”We’re going to tell these people who they really are”: science and relatedness,' 369

modern economic activities."[138]

The United Nations definition of the term 'indigenous' also hinted at a historical definition of indigenous peoples, estimated to count around 370 million people in 70 countries: "According to a common definition they are descendants of those who inhabited a country or a geographical region at the time when people of different cultures or ethnic origins arrived. The new arrivals later became dominant through conquest, occupation, settlement or other means." The UN did not adopt an official definition; instead, it aimed "to identify rather than define." Criteria other than the historical were included, such as social, cultural, economic, and political characteristics; self-identification, group acceptance, a link to the territories they occupy, a "non-dominant" position, and a resolve to maintain and reproduce ancestral environments and systems as distinctive.[139]

The acquisition of the label 'indigenous' was often beneficial for the group in case; the perception was that land claims and funds could depend on it. It was increasingly often connected to historical-biological criteria for kinship. The US, for instance, required Native Americans to produce certificates with a 'Degree of Indian Blood' to qualify for entitlements.[140] So when scientists started to issue statements about the indigenousness and ancientness of groups, they entered a political sphere: such identities had become a resource.[141] The political sensitivity of the definition of indigenousness meshed with historical sensitivities that resulted from past 'colonial scientific' exploitation.[142] The objection that geneticists regarded indigenous bodies as "storage for genetic miners" is telling.[143]

A lack of influence on the research, and the feeling that the authority to define origins and identities lay exclusively with the geneticists, fuelled fears that scientific results would inform political decisions. The statement by a HGDP spokesman in 1996 that anthropological genetics can tell people "who they really are"[144] has been quoted

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[138] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 194

[139] United Nations, *Who are indigenous peoples?* (2006 [cited June 26 2011]); available from http://www.un.org/esa/socdev/unpfii/documents/5session_factsheet1.pdf

[140] Duster, 'Buried alive. The concept of race in science,' 267

[141] Reardon, *Race to the finish. Identity and governance in an age of genomics* 103

[142] "It has been recently revealed that biomedical experiments were performed on more than 23,000 persons in about 1,400 different US Defence Department projects for over 30 years after the Second World War, and in which the requirements of informed consent were neither sought nor met. The selection of target populations included soldiers, prisoners, those considered to be mentally defective (both children and adults), hospital patients with terminal illnesses, and pregnant women. Despite the fact that these were all vulnerable persons whose involvement in research needed special ethical scrutiny, informed consent was generally not sought at all or not given" (Estling, 1995), committee, "Bioethics and human population genetics research," 7

[143] Tallbear *Narratives* 422

[144] As the title indicates, the remark and the underlying assumptions were discussed extensively by Marks in Marks, '"We're going to tell these people who they really are": science and relatedness,'

extensively as an example of the hubris that provoked the indigenous and their advocates into protest. The perception was that the indigenous right to determine group membership was threatened by HGDP:[145] Debra Harry of the IPCB proclaimed that "If we have genetic scientists saying their research suggests that certain Indigenous peoples really are recent immigrants from somewhere else, this denies those peoples' claim to their own indigeneity."[146] Not only should one not take lightly "people's own notions of who they are", said Marks; scientists should also abandon the contrasting of 'objective' scientific narratives with 'subjective' indigenous ones. "Scientific notions are themselves cultural products: when loaded with specious and archaic assumptions about composition of populations, ontology of races, relationships of ancient with modern peoples, it is not very useful. A truly biological anthropology would address such issues in public discourse."[147] Reardon recounts how critics were depicted as irrational and politically motivated, while supporters of the project were considered rational and apolitical.[148] Indigenous demanded to be involved in the research and have a right of veto.[149]

Not always did the debates revolve around group objections against research. Reardon noticed a tendency towards "affirmative action in science", a reaction to medical research into variation. Afro-Americans for instance were afraid they would "miss the genetics boat." in 1994, Afro-American social and biological scientists drafted a manifesto on Genomic studies among Afro-Americans.[150] Foster and Sharp's argument that distributing (medical) benefits of research depends on naming socially defined populations, despite the ethical risks involved, was based on similar arguments.[151]

As the HGDP suddenly found itself immersed in the politics of identity, it failed to see, Reardon argued, that the very categories it worked with were themselves problematic. The organizers reacted to protests by departing from their initial focus on sampling the indigenous to include all of humanity,[152] by inviting population members

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[145] Reardon, *Race to the finish. Identity and governance in an age of genomics* 122

[146] Decoding Implications of the Genographic Project for Archaeology and Cultural Heritage, Transcript of A Panel Discussion Held at the Chacmool Conference "Decolonizing Archaeology" University of Calgary, Alberta, Canada, November 2006 International Journal of Cultural Property (2009) 16

[147] Marks, '"We're going to tell these people who they really are": science and relatedness,' 380

[148] Reardon, *Race to the finish. Identity and governance in an age of genomics* 160-1

[149] Ilkilic and Paul, 'Ethical aspects of genome diversity research: genome research into cultural diversity or cultural diversity in genome research?,' 27; RAFI, "Patents, indigenous people, and human genetic diversity,"

[150] Reardon, *Race to the finish. Identity and governance in an age of genomics* 151

[151] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 847

[152] "the HGDP is now moving away from both the idea of central control to regional control and from the focus on indigenous populations, to *include all populations*" and 'in fact the HGDP included all populations, not only indigenous populations" committee, "Bioethics and human population genetics research," 4; 8

to “co-design research”, by including organizers from ethnic groups,[153] and re-evaluating their ethical framework for research into indigenous gene pools, especially their consent procedure. But they should have realized, she states, that these measures were preceded by the definition of a group, and the assumption that this definition unproblematically reflects a social reality.[154] Similarly, Foster and Sharp pointed to the ethical risks involved in this process of ‘naming’, which could not be solved by individual consent procedures, as research results have effect on these whole populations.[155] If only a few individuals agree to collaborate, results still apply to the whole group. Reardon concluded that this was one of the reasons why the HGDP failed to enrol critics. As a result, the ethical framework didn't suffice and was designed to accommodate science only, she argued.[156]

In addition, HGDP organizers thought the solution lay in ‘better education’ about the research. They assumed that the conflicts arose from a lack of understanding, and that more informed consent would be sufficient. This proposal was judged ill-considered: “the HGDP ignores the practical problems regarding educating research subjects”: the high demands it places on interpreters, the large amounts of time necessary, and translation problems.[157]

These translation problems point to a fundamental problem for anthropological geneticists: the conflict between indigenous and scientific cosmologies.[158] This is reflected in some critics’ standpoints. Marks argues that there is a basic asymmetry to the research: “Others”’ (indigenous’) genes serve to illuminate “our” (recent urban population’s) past.[159] In this view, the ‘people without a past’ parasitize on those who still have stories and origin myths. What reason would the latter have to cooperate? Likewise, Tallbear argues that “’Who we are’ is not a compelling research outcome for people who already know who they are, who define this identity by other historical or mythological narratives. Furthermore, “the ‘we are all related’ story”, said Tallbear, is based on a view of relatedness that is culturally specific, favouring maternal and paternal lines to unnamed genetic ancestors over other forms of kinship.[160] Pálsson

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[153] “The objective should be to have the individual participants and the entire community become partners in the scientific effort.” Committee, "Human Genome Diversity Project: Summary document,"

[154] Reardon, *Race to the finish. Identity and governance in an age of genomics* 100, 160, 161.

[155] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 847

[156] Reardon, *Race to the finish. Identity and governance in an age of genomics* 160-1

[157] Ilkilic and Paul, 'Ethical aspects of genome diversity research: genome research into cultural diversity or cultural diversity in genome research?,' 32

[158] Ibidem 32

[159] Marks, '”We’re going to tell these people who they really are”: science and relatedness,' 369

[160] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 416

agreed that anthropological genetics overstretched its cultural aims: “It is one thing [...] to explore genetic histories and quite another to tell people ‘who they really are.’”[161]

Scientific statements about the real identities and origins of peoples were not only considered irrelevant, but also threatening. A UNESCO report on bioethics observed that “Some representatives of indigenous populations […] have expressed concern that they do not want to know the results of scientific studies that challenge their local understanding of history.” “Why participate in research that will contradict your own histories?”[162] “If genetic reductionism derives from a misunderstanding of science and is suggestive of discrimination against a "genetic underclass", it also represents a threat to those mythologies or cosmogonies which are different from the dominant world cultures.”[163]

This mismatch of world views could explain opposition against research practices. For instance, the taking of bodily substances sometimes conflicted with beliefs.[164] And Ilkilic observed that “it is contrary to Maori traditions to objectify a gene”. Interestingly, the example illustrates how indigenous protest often led to the adoption of the vocabulary of the science they opposed;[165] opposition against such research projects seems to have transformed the indigenous cosmologies themselves.

Concerns that the benefits of research would not be shared with the indigenous involved also intersected with such views of the handling of blood and other substances. Since the 1980s, when the patenting of human genetic material had first entered legal discussions, the handling of biological material and information had been subject of debate. By 2005, 20% of human genes had been patented worldwide.[166] And during the same period, attempts were made to have indigenous traditional knowledge fall under intellectual property right,[167] with reference to a history of colonial scientific exploitation. In line with this view, Debra Harry argued that “If you consider genes to be a cultural right, then no individual can really give consent to alienate those things”.[168] UNESCO judged in 1995 that the sharing of benefits from patents was not considered

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[161] Pálsson, *Anthropology and the new genetics* 196

[162] Marks, "Human genome diversity studies: Impact on indigenous communities," 3

[163] committee, "Bioethics and human population genetics research," 18

[164] Ilkilic and Paul, 'Ethical aspects of genome diversity research: genome research into cultural diversity or cultural diversity in genome research?,' 30

[165] Ibidem 28

[166] Boyle, *Shamans, Software, and Spleens*, 97–107. Julie Hollowell and George Nicholas, 'Decoding implications of the Genographic Project for archaeology and cultural Heritage: Transcript of a panel discussion held at the Chacmool conference “Decolonizing archaeology” University of Calgary, Alberta, Canada, November 2006,' *International Journal of Cultural Property* 16 (2009) 16

[167] By WIPO, the World Intellectual Property Organization, http://www.wipo.int/tk/en/; Ibidem

[168] Ibidem

sufficient: such a solution would still incorporate indigenous peoples "into a system that views living organisms and community knowledge as commodities which can be patented, "owned", and traded."[169]

Challenging Lewontin

A second phase, or thread, of the debate about group categories revolves around Lewontin's famous calculations of inter- and intra-group differences and started at the end of the 1990s. Lewontin's research had created a consensus that had lasted for several decades. It was criticized from the very beginning, but with significant intervals, and until the turn of the century, without much effect. Mitton argued in 1978 that "multivariate analyses may provide resolution of groups that is not apparent in a sequence of single-locus analyses".[170] Smouse wrote in 1982 that "Human gene pools in different parts of the world occupy largely non-overlapping portions of the multidimensional genetic space available, in spite of the fact that most of the variation at single loci can be found within any one population."[171] In other words, Lewontin's findings would hold only when one looked only at single locus differences.

But these arguments did not find a large audience, and Lewontin's results were generally accepted as evidence that racial categories had "virtually no genetic or taxonomic significance."[172] The HGP message that 'we are essentially the same' was in that sense "nothing new": Lewontin's result was generally accepted as evidence against races.[173] Throughout the 1990s, the idea that genetics had provided evidence that racial categories are scientifically meaningless was held widely. In anthropological histories of the species, the emphasis lay on the root of the tree model, not on the branches. In a time when the unreality of racial categories was proclaimed, the popular imagination focused on narratives about shared African origins. Cavalli-Sforza's address to UNESCO to call an abandonment of the term 'race' and use 'population' instead stood in a long tradition that can be traced back to the 1950s. In his 1994 book he called the concept of

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[169] committee, "Bioethics and human population genetics research," 18

[170] Jeffrey B. Mitton, 'Measurement of differentiation: Reply to Lewontin, Powell, and Taylor,' *The American Naturalist* 112 (1978)1143

[171] Peter E. Smouse et al., 'Multiple-locus allocation of individuals to groups as a function of the genetic variation within and differences among human populations,' *The American Naturalist* 119 (1982) 459

[172] Lewontin (1972) quoted in Ibidem

[173] Barbara A. Koenig et al., 'Introduction: Race and genetics in a genomic age,' in: Barbara A. Koenig, et al., eds., *Revisiting race in a genomic age* (New Brunswick, New Jersey, and London, 2008) 1

human races a “scientific failure”.[174] In 1995, a UNESCO report on bioethics stated that “Population studies in the past have shown that most of the diversity within the genes studied is to be found in every race or population and, if this is true, then this information could be used to combat racism. Since current population studies show that the typological classification of humans into different 'races' is scientifically invalid, we should avoid the use of the term "race".[175] This trend culminated – as was hoped[176] - in the presentation of the sequenced human genome in 2000 “as evidence of impossibility to distinguish ethnicities”.[177]

The idea that race was history spread widely. The AAA urged the US government in 1998 to do away with census categories and let people choose their own ethnicity.[178] The American Anthropological Association issued a statement on race in 1998, stating that “it has become clear that human populations are not unambiguous, clearly demarcated, biologically distinct groups”, referring to to the ‘Lewontin consensus’.[179] A Nature editorial quoted it in 2000: “The AAA statement also calls for research to determine what terms best capture human variability in ways understood by the American people, and argues that “probably the clearest data on human variation come from genetic studies. Genetic data do show differences between groups, and these can potentially trace an individual’s likely geographic origin. Nevertheless, these data also show that any two individuals within a particular population are as different genetically as any two people selected from any two populations in the world.”[180]

Genetics had indeed contributed to this view by separating two levels of diversity: it was argued that variance in physical appearance did not map onto genetic diversity patterns. Originally, Lewontin had argued that there was no genetic equivalent at all to social, economical and cultural categories of race.[181] When others argued there were, they could still render such patterns harmless with the argument that these patterns did not coincide with everyday categories. Geneticists argued in 1999: “The possibility that human history has been characterized by genetically relatively homogeneous groups (“races”), distinguished by major biological differences, is not

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[174] Reardon, *Race to the finish. Identity and governance in an age of genomics* 153-154
[175] committee, "Bioethics and human population genetics research," 14
[176] It was hoped by some that the sequencing if the human genome would show that racial and ethnic classifications had no biological significance, Foster/Sharp *Race ethnicity and genomics* 844
[177] Reardon, 'Decoding race,' 38-40
[178] Marshall, 'DNA studies challenge the meaning of race,'
[179] *AAA statement on "race"*, (1998 [cited June 26 2011]); available from http://www.aaanet.org/stmts/racepp.htm
[180] Editorial, 'Census, race and science,' *Nature genetics* 24 (2000) 97-8
[181] Armand M. Leroi, 'A family tree in every gene,' *The New York Times*, March 14 1995

consistent with genetic evidence. How, then, does genetics explain the stereotypic features of "races": skin color, hair color and texture, and facial traits? These traits are quite literally superficial, in that they affect exposed surfaces of the body."[182] Scientists had the capacity to look beyond this everyday level of inconsiderate prejudice, at the more fundamental level, "beneath the skin".[183] What Marks called the Linnean tradition in anthropology, which emphasizes taxonomies and classification, was considered "not only empirically wrong (as there is no consensus about categories) but also pointless in the context of democratisation and equal rights – there was no need for categories anymore.[184]

However, at the end of the century, many felt that the race concept had returned.[185] This was to a great extent the result of diversity research in biomedicine. Possibly, potential clinical applications helped pave the way for the revalidation of such a controversial concept – if it helped save lives, perhaps racial classification was to be accepted. Foster and Sharp's argument should be seen in this light. They argued in 2002 that although there are significant risks involved with the labelling of populations, "the distribution of benefits resulting from genomic resources may depend on identifying populations from which study participants are recruited."[186] And in another article published in the same year, a geneticist argued that given the reality of differences and the possibility of tailoring treatments, "Identical treatment is not equal treatment".[187] In contrast with the general argument that racial thinking risked racism, now the neglect of differences was presented as damaging for the minorities that would be denied access to lifesaving treatments.

But the critics of cladistics and tree models pointed out that there had been more continuity in the preceding decades than the idea of a "revival of race" suggests. They argued that population categories and cladistic concepts simply had taken the place of race, and some argued the new terms functioned as euphemisms. The reason for the sense that racial categories returned lay with a breakdown of the consensus based on Lewontin's research, and explicit arguments for the reality of genetic clusters coinciding

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[182] Kelly Owens and Mary-Claire King, 'Genomic views of human history,' *Science* 286 (1989) 453

[183] Reardon, *Race to the finish. Identity and governance in an age of genomics* 54

[184] Marks, *Human biodiversity* 58. What is more, "*Racialised biomedicine puts actual lives at risk by ignoring natural patterns of variation and mistaking the confabulations of social history for authoritative knowledge about the world*." Jonathan Marks, 'Race. Past, present and future,' in: Barbara A. Koenig, et al., eds., *Revisting race in a genomic age* (New Brunswick, New Jersey and London, 2008) 34

[185] Marks, 'Race. Past, present and future,' 34; American health agencies use race concepts, often to protest of scientists, Leroi, 'A family tree in every gene,'

[186] Foster and Sharp, 'Race, ethnicity, and genomics: social classifications as proxies of biological heterogeneity,' 847

[187] N. Risch et al., 'Categorization of humans in biomedical research: genes, race and disease,' *Genome Biology* 3 (2002) 1-12 11

with ‘racial’ taxonomies.

In 1995, Marks had still argued that “the more genes you look at, the more differences you find among populations” – “the problem of infinite regress”.[188] And in 1997, Barbujani et al. (including Cavalli-Sforza) had recalculated Lewontin’s findings, examining several loci, to conclude that differences between members of the same population account for 84.4% of the total, and continental differences accounted for only 1/10 of the total - almost the same result as Lewontin’s. “If loci showing a discontinuous distribution across continents exist, they have not been observed in this study, and so the burden of the proof is now on the supporters of a biological basis for human racial classification.”[189] They added that “Probably any two populations compared at a sufficient number of loci may be shown to differ, as suggested by the fact that several variances among populations, although low in relative terms, are statistically significant in this study. However, this has little to do with the subdivision of the human population into a small number of clearly distinct, racial or continental, groups. The existence of such broad groups is not supported by the present analysis of DNA.[190] Jorde et al. analysed autosomal, mitochondrial, and Y-chromosome polymorphisms and confirmed the results.[191] NE Journal of Medicine editorial: ethnic clusters are insufficient and inaccurate.

But then Seielstadt et al. (again including Cavalli-Sforza) found that Ychromosome analysis produced a different result: almost 53% variation accounts for differences between continents.[192] They argued that “A higher female than male migration rate (*via* patrilocality) explains most of this discrepancy.” Subsequently, Risch et al. published an article in 2002 that came to be known as a “pivotal event.”[193] They found that “The greatest genetic structure that exists in the human population occurs at the racial level.” “Two Caucasians are more similar than one Caucasian and one Asian.” [194] While “genetic cluster analysis is only powerful to distinguish people whose ancestors separated millennia ago,” closely related groups may be distinguishable by analyzing hundreds of markers, they argued.[195] Focusing on medical research, they

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[188] Marks, *Human biodiversity* 132

[189] Guido Barbujani et al., 'An apportionment of human DNA diversity,' *Proceedings of the National Academy of Sciences of the United States of America* 94 (1997) 4517

[190] Ibidem 4518

[191] Jorde et al., 'The distribution of human genetic diversity: A comparison of mitochondrial, autosomal, and Y-chromosome data,'

[192] Crawford, ed., *Anthropological genetics. Theory, methods and applications* 8; Mark T. Seielstad et al., 'Genetic evidence for a higher female migration rate in humans,' *Nature* (1998)

[193] Koenig et al., 'Introduction: Race and genetics in a genomic age,' 3

[194] Risch et al., 'Categorization of humans in biomedical research: genes, race and disease,' 4, 5

[195] Ibidem 7

stated that the results implied that “Identical treatment is not equal treatment.” “Identifying genetic differences between groups is scientifically appropriate; attaching value systems to these categorizations is not. Ignoring our differences will disadvantage minorities.”[196]

Rosenberg et al., focusing on methods in genetic reconstruction of history, came to a similar conclusion in 2002. They used the HGDP cell line collection. Although they found that 93-5% of genetic variation accounted for within-population differences, and 3-5% between populations (the estimate was higher than other studies, possibly due to different sampling schemes), they identified six clusters “without prior information,” “5 of which correspond to geographic regions.” They found that “Genetic clusters often corresponded closely to predefined regional population or to collections of geographically or linguistically similar groups.”[197]

They admitted that “The program likely produced more distinctive groups than random worldwide sampling would have,” because sampling was population-based. But this was exactly what they were looking for: “The challenge of genetic studies of human history is to use the small amount of genetic differentiation among populations to infer the history of human migrations. Because most alleles are widespread, genetic differences among human populations derive mainly from gradations in allele frequencies […]. Indeed, it was only in the accumulation of small allele-frequency differences across many loci that population structure was identified.” These patterns were mostly appropriate for the reconstruction of history.[198] Notwithstanding these reservations, the research was received as an argument against Lewontin and for the existence of races. These were now definable in geographic and genetic terms, and disconnected from the sociocultural realm to which they were banned during preceding decades:

> *The identification of racial origins is not a search for purity. The human species is irredeemably promiscuous. We have always seduced or coerced our neighbors even when they have a foreign look about them and we don't understand a word. Even homogenous groups like native Swedes bear the genetic imprint of successive nameless migrations. Some critics believe that*

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[196] Ibidem 11

[197] Rosenberg et al., 'Genetic Structure of Human Populations,' 2381

[198] Ibidem 2384

> *these ambiguities render the very notion of race worthless. I disagree. Race is merely a shorthand that enables us to speak sensibly, though with no great precision, about genetic rather than cultural or political differences.*[199]

Bamshad et al. too found in 2003 that "substantial genetic structure" exists and that the geographic origin of individual samples, stripped of identifying information, could be assigned with a moderate level of accuracy, even from an admixed population. Also, "ethnic and cultural [..] proxies associated with the samples used in this analysis were sometimes, though not always, sufficient representations of the inferred genetic clusters, reflecting the complex and interwoven history of the human species."[200] "Importantly, the inclusion of [intermixed] samples demonstrates geographic continuity in the distribution of genetic variation and thus undermines traditional concepts of race."[201]

These studies led Edwards in 2003 to publish an article under the title "Lewontin's fallacy". This fallacy, he argued, had been the locus-by-locus analysis: "The 'taxonomic significance' that Lewontin denies the differences, arises from correlations amongst different loci." Lewontin had ignored hidden patterns like Cavalli-Sforza's 'treeness', and a contrasting analysis by C-SF and Edwards in 1963.[202] Moreover, Lewontin should not have attached a moral message to his results: "It is a dangerous mistake to premise the moral equality of human beings on biological similarity because dissimilarity, once revealed, then becomes an argument for moral inequality."[203]

Such findings triggered criticism. Serre and Paabo compared continuous and discontinuous (based on what critics dubbed the 'island model') sampling strategies in 2004. They found that geographic discontinuous sampling reinforced a 'clustered' view of the human gene pool. They reanalyzed the HGDP collection (used by Rosenberg et al.), focusing on diversity within subsamples, which produced results that suggested the human gene pool was not composed of discrete clusters."[204] This result led Cavalli-Sforza to state that the "article invites rethinking" of the HGDP approach, "whether the

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[199] Leroi, 'A family tree in every gene,'

[200] Michael J. Bamshad et al., 'Human population genetic structure and inference of group membership,' *American Journal of Human Genetics* 72 (2003) 579

[201] Ibidem 587

[202] A.W.F. Edwards, 'Human genetic diversity: Lewontin's fallacy,' *BioEssays* 25 (2003) 798-801 799. He argued that statements like 'two random individuals in a group are as different as any two random individuals from all over the world', 'people are different because they are individuals not because they belong to different races', and 'you can't predict someone's race by their genes' are false; they would only be true if all characters studied are independent, and they're not - frequencies are correlated. Edwards, 'Human genetic diversity: Lewontin's fallacy,' 801

[203] Edwards, 'Human genetic diversity: Lewontin's fallacy,' 801

[204] Pálsson, *Anthropology and the new genetics* 182

HGDP should focus in the future on individuals as the unit of sampling, or whether the emphasis should remain on sampling populations".[205] But he did not seem to have lost belief in the basic assumptions: the "narrow geographical range of most individual migration means that the similarity of geographically close populations is strong, so it is reasonable to continue sampling small, well-defined populations of obvious anthropological or medical interest – to proceed in the direction followed so far by the HGDP."[206]

In a reaction to Serre and Paabo, Rosenberg et al. reported that they had studied the influence of study design in the clustering of genetic data. They found that several factors had effect on clustering: the number of loci, the sample size and dispersion, the number of clusters the program was asked to make, and assumptions about allele frequency correlation. However, contrary to what Serre and Paabo had argued, a more random dispersion did not lead to reduced clusteredness.[207] They argued that research results supported both a clinal and a clustered view of the data: "small discontinuous jumps help STRUCTURE find clusters that correspond to geography."[208] They too added a disclaimer that states "Our evidence for clustering should not be taken as evidence of our support of any particular concept of "biological race." The findings should be used for research into human evolutionary history and the identification of medically important genotypes. Both clines and clusters can be useful in this regard. The issue of race, they concluded, has nothing to do with science. [209]

Bolnick has examined the research methods of those who found evidence for 'genetic races' in detail. Rosenberg et al. focused on multilocus genotype data with the use of a computer program called STRUCTURE, which allocates samples to a predefined number of clusters (K). Several values for K were examined, and the program was designed to find the most appropriate value for K – the most appropriate number of clusters to divide the data in. The problem with this method, Bolnick explains, is that it is computationally difficult to estimate this probability; it can only be defined as an approximation. Furthermore, different runs may provide different results, especially if there is a large number of genetic clusters or if there are several highly probable possibilities – which multiregionalists would argue is always the case. Also, the model is

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[205] Cavalli-Sforza quoted by Ibidem 183

[206] Cavalli-Sforza, 'The Human Genome Diversity Project: past, present and future,' 339

[207] Noah A. Rosenberg et al., 'Clines, clusters, and the effect of study design on the inference of human population structure,' *PLOS Genetics* 1 (2005) 664, 667

[208] Ibidem 668

[209] Ibidem 668-9

not suited for data shaped by restricted gene flow with isolation by distance; she quotes two geneticists who argue that in such sets, K "can be rather arbitrary."[210] Rosenberg et al. only published the results for K=2-6; for lager values the results were "not robust", that is, subsequent runs produced both very high and very low probabilities. The probability for K=6 was higher than for lower values 2-5, but not as high as some replicates of larger values of K. Bolnick concludes that this "study does not challenge our current understanding of human genetic structure as much as some have suggested", but is consistent with clinal view.[211] "Nevertheless, both scientific and popular media have emphasized K=5 or 6. She "would suggest that these particular results have been emphasized simply because they fit the general notion in our society that continental groupings are biologically significant."[212]

Bolnick also evaluated the study by Bamshad et al. that identified continental clusters. She reported that they found that K=1 was a very appropriate value for K when an "intermediate population" (an Indian sample set) was included. As the researchers themselves pointed out, if geographic intermediate samples were included, traditional race concepts were undermined. However, they did not include them, and the authors chose K=3 with reference to "proxy information", that is, the fact that the samples came from what the researchers assumed were distinct populations. Bolnick argues that this reliance on "proxy information", and the ungrounded assumption that continental groupings were important, influenced the analysis. STRUCTURE was asked to assign individuals to clusters; these allocations were judged 'correct' if cluster with greatest proportion of ancestry was the same as the continent of origin of the sample. This means that the research has a circular nature. "The 99% correct score does not necessarily mean that there is substantial genetic difference between continents, but only among population samples: may just indicate geographic distance, as samples were obtained from widely separated regions.[213] She concludes that the researchers "misrepresent and obscure these issues."[214]

Lewontin himself dismissed the arguments for the reality of races in 2006. He acknowledged that populations could be clustered along continental boundaries. But, he argued, the markers used are "not typical of genes", but have been chosen *because* they

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[210] Bolnick, 'Individual ancestry inference and the reification of race as a biological phenomenon,' 75; Pritchard and Wen, quoted by Bolnick, 'Individual ancestry inference and the reification of race as a biological phenomenon,' 75

[211] Bolnick, 'Individual ancestry inference and the reification of race as a biological phenomenon,' 77s

[212] Ibidem 77

[213] Ibidem 78

[214] Ibidem 80

are useful to detect group differences. “Thus, they tell us what we already knew about the differences between populations of the classical "races" from skin color, face shape, and hair form.”[215]

Thus, a new consensus seemed to emerge: if a large number of the right markers are chosen, continental clustering is possible. Lao et al. argued that with these techniques, it is possible to assign an individual to a continent of origin.[216] Cavalli-Sforza interpreted the consensus as follows: there is “more genetic variation within than between groups; yet the patterns of variation are far from random. Genetic variation and geographic distribution correlate; especially in the case of indigenous populations, less so for populations with high degree of interaction with neighbours.[217] Marks concluded in 2008 that race is now “a very careful look at the most divergent qualities of the most geographically separated peoples, so as to maximise detectable differences between groups. Race has become quantitative assessment of similarity to gene pools of most divergent peoples. Studies of what were called ‘Ancestry Information Markers,’ a few markers, selected to be maximally different from other cell lines, were analyses of residuals of human genetic variation once its major features are dismissed, Marks argued.[218] Lewontin’s original research had helped dismantle the view that race is synonymous with population, but “left a small window remaining open [..] for yet another shift in the conceptualization of race[...;] one could direct one’s focus very closely to the small amount of localized variation, essentially contrasting the most extreme members.”[219] But “geographical correlations are weaker hypothesis than genetically discrete races. The former obviously exist; the fact that we can find groups to be different and allot people to them is trivial. Race theory held that there are groups that are homogenous within and heterogenous between,” and the new results did not support this.[220] So “subtly race was yet again redefined, to effectively a very careful look at the very small amount of genetic variation that has a major geographical component.”[221]

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[215] R. Lewontin, *Confusions about human races* (2006 [cited June 26 2011])

[216] See also Oscar Lao et al., 'Proportioning whole-genome single-nucleotide–polymorphism diversity for the identification of geographic population structure and genetic
ancestry,' *The American Journal of Human Genetics* 78 (2006)

[217] Sandra Soo-Jin Lee et al., 'The ethics of characterizing difference: guiding principles on using racial categories in human genetics,' *Genome Biology* 9 (2008)

[218] Marks, 'Race. Past, present and future, 25

[219] Marks, 'Race. Past, present and future, 24

[220] Marks, 'Ten facts about human variation,' 270

[221] Marks, "The realities of races,"

Commercial ancestry testing

The method to allocate individuals to continents held a promise for forensics.[222] But meanwhile, another application of genetics had gained ground. At the end of the 20th century, commercial testing emerged. Companies started to offer people an analysis of their ancestral region. Ancestry and genealogical research became an increasingly popular hobby; Haraway observed in 1997 that "Epistemophilia, the lusty search for knowledge of origins, is everywhere.[223] It was called "America's latest obsession in 2003;[224] Nash observed that "Magic [is] for sale.[225] She argued that the "Discourses of family relatedness provide a grammar for translating the complexities of new genetics in to public culture; genealogical idiom provides tangible physical and temporal scales.[226] The popularity of genealogical ancestry testing may be explained by several famous cases in anthropological genetics that received broad coverage in the popular media. For instance, in 1998 scientists revealed that Thomas Jefferson, or one of his male relatives, had fathered offspring with his slave, Sally Hemmings. And in 2000, a study showed that the southern African Lemba share ancestry with "Jewish priests."[227]

Since 2000, testing companies multiplied; an overview in 2010 listed 38 testing companies.[228] Some of these provided lineage-based tests (mtDNA and Y chromosome analysis; which the majority of the companies study) and a minority used autosomal DNA tests.[229] Companies' selling strategies could be divided into three reasons to test: to determine one's origins, to find relatives, and to discover genetic links with other users:[230] some offer the possibility to match the results with other users and to contact them.[231] Unlike genetic tests that provide medical information, which were also marketed, ancestry tests generally looked at "non-coding regions of DNA (or 'junk DNA') from which no medically-relevant information can be derived."[232]

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[222] Duster recalls how in the early nineties, DNA tests were presented for the first time that provided ethnic information in unsolved crime cases. Duster, 'Buried alive. The concept of race in science,' 266
[223] Quoted in Nash, 'Genetic kinship,' 2
[224] Margot Hornblower, 'Roots mania,' *Time* (2003)
[225] Nash, 'Genetic kinship,' 20
[226] Ibidem
[227] Mark D. Shriver and Rick A. Kittles, 'Genetic ancestry and the search for personalized genetic histories,' *Nature Reviews Genetics* 5 (2004); Nicholas Wade, 'DNA backs a tribe's tradition of early descent from the jews,' *The New York Times*, May 9 1999
[228] Charmaine D. Royal et al., 'Inferring genetic ancestry: opportunities, challenges, and implications,' *The American Journal of Human Genetics* 86 (2010); An overview of companies, their methods, and the costs of a test is provided by Henry T. Greely, 'Genetic genealogy. Genetics meets the marketplace,' in: Barbara A. Koenig and Sandra Soo-Jin Lee, eds., *Sarah S. Richardson* (New Brunswick, New Jersey, and London, 2008) 218
[229] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 202
[230] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 220
[231] Ibidem 221
[232] Richard Tutton, 'They want to know where they came from": population genetics, identity, and family genealogy,' *New Genetics*

The advertisement vocabulary was riddled with family and tribal metaphors. Oxford ancestors linked people to “clans” by means of mtDNA analysis. GeoGene provided info about user’s “Geomother” or Geofather.”[233] Some offered tests to determine Native American ancestry. A “Cohanim chromosome test” looked for Y chromosome markers that are associated with the last name Cohen or Cohn. Other examples include a Hindu test and a test to determine whether an individual is descended from Genghis Kahn. The latter determined whether one is a carrier of a Y chromosome marker that is found in high percentages among Central Asians and is thought to have originated about 1000 years ago - a date close to the date of Genghis Kahn’s death in 1227.[234]

Most companies used lineage-based tests, which detect mtDNA and Y chromosome markers. A minority provided tests of autosomal DNA, which was screened for “Ancestry Information Markers” (AIMS).[235] Of the 16 companies analysed by Greely in 2006, 15 provided lineage tests and only one autosomal ones. The number of Y chromosome markers tested by the companies ranged from 9 to 46 – a relatively small number, compared to scientific studies. The tests cost between 100 and 300 dollar.[236]

Although many scientists were affiliated in one way or another with these companies[237], scepticism of the commercialization of genetic ancestry research abounded. The companies failed to communicate the complexities of testing, many argued. Kittles and Shriver pointed to the fact that the tests are, as applications of population genetics, “very statistical”, involving much uncertainty. Many objected that the accuracy of the tests depended on several factors that were not explained on the websites,[238] such as sampling methods, the size of the databases used, the number of markers analysed, and the “level of genetic differentiation” of the sampled populations. Many of the databases lacked samples from specific regions[239] and, Greely added, their sample size was never very large.[240] Tallbear too expressed concern about the insufficient sampling of Native Americans.[241] In an ideal situation, critics argued, the

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and Society 23 (2004) 114

[233] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 220

[234] Ibidem 221, 226 228

[235] Mark D. Shriver and Rick A. Kittles, 'Genetic ancestry and the search for personalized genetic histories,' in: Barbara A. Koenig, et al., eds., *Revisiting race in a genomic age* (New Brunswick, New Jersey, and London, 2008) 202

[236] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 216-7

[237] Ibidem 216

[238] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 207

[239] Ibidem 203

[240] “The number of ethnic groups sampled and the number of individuals sampled [...] varies from company to company; in no case does it appear to be very large.” Greely, 'Genetic genealogy. Genetics meets the marketplace,' 226

[241] Kimberly Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' in: Barbara S. Koenig, et al., eds.,

companies would share databases and a standard set of markers would be defined, so that comparisons are possible, but this was found not to be the case.[242]

A general objection was that lineage-based models provided information about just one lineage, which “Many users do not understand [...] doesn’t represent their genetic makeup.”[243] None of the companies emphasized this, but instead obscured the meaning of such lineages. Often, they referred to them as “direct” or “pure” lines, Greely observed.[244] He pointed out that there is no evidence that mtDNA and Ychromosome lineages are unique to specific groups; these can be distinguished only by frequencies differences.[245] Nevertheless, test advertisements claimed that there are markers that are unique to Native Americans.[246] Marks stated that companies “link clients to particular indigenous peoples”,[247] (rather than to ancestral populations) therewith ridiculing and problematising the equalling of these peoples with historical populations. He stated that the finding of multiple matches (that is, with populations from different continental origins) is not always communicated - let alone the possible matches with other populations that were not sampled, or “the thousands of other lineal ancestors you had in the same generation [...] but are invisible to this analysis.[248] The Genghis Kahn research was used by Greely as an example of the complexities involved in testing and obscured by advertising rhetoric: no one has any genetic material from Genghis Kahn remains, so the claim that users may be his ‘descendants’ was considered ill-founded. The Y chromosome marker attributed to him might have originated in his “stable boy”, or already have been common in the area before the Great Kahn’s time.[249] Markers, Tallbear argues, offer only “weak evidence” for issues of Native American identity. “That is, unless we invest DNA markers with a symbolic power to indicate ethnic and racial identity.” In that case, she states, with reference to Haraway’s term, we make a “fetish” of a genetic link to ancestors “who may or may not be seen (by themselves or by society) as Native American.”[250]

Shriver and Kittles also argued that the use of these categories risked their conflation with racial divisions, despite disclaimers about the continuity of variation and

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Revisiting race in a genomic age (New Brunswick, New Jersey, and London, 2008) 243-4

[242] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 207

[243] Ibidem 208

[244] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 224-5

[245] Ibidem 226

[246] Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' 243-4

[247] Marks, ‘Human Genome Diversity Studies: Impact on Indigenous Communities’ in *Encyclopedia of Life Sciences* 4

[248] Marks, 'What is the viewpoint of hemoglobin, and does it matter?,' 257

[249] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 228

[250] Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' 242

the arbitrariness of groups. They considered this to be the result of “genetic determinism among public and scientists.”[251] Greely argued that the continental definitions of ancestry, and lineage tests that define origin in broad geographical terms, resembles traditional racial categories. Especially those tests that focus on the whole genome are therefore in a sense a test for race.[252] Tallbear pointed to explicit use of racial terms and categories by the company DNAprint, which states that its “test measures the biological or genetic component of race.” Moreover, the juxtaposition of “individuals of relatively pure BioGeographical Ancestry” with “recently admixed peoples” introduces a vocabulary of ‘purity.’ “Mixture is predicated on purity.”[253]

The reintroduction of race was, according to Marks, also the result of medical commercial developments – “we are witnessing the creation of racial niche markets for the pharmaceutical industry, which must be accompanied by the reification or naturalization of race itself.” But ancestry testing services contributed to this development too: “race is being actively reified with the emergence of new privatized services in what is often called biosociality – the construction of identities and networks of kin from presumptively scientific data.”[254] Greely also reserved a prominent role for medical research in the association of genetics with race, and stated that genealogy had more impact on concepts of ethnicity. The conflation of cultural and genetic categories that this impact provoked was considered problematic. Not only because it was not considered accurate (as cultural and genetic categories do not coincide), but also because it might reinforce ideas about behavioural differences between ‘races’, which might be perceived as rooted in the genome.[255] Kittles and Shriver are more prone to clearing science’s record in this regard: “Controversies about genetic ancestry testing have more to do with complex history of race discrimination injustice than with science behind it.”[256] Their position may be explained by their involvement in commercial ancestry testing: Shriver is scientific advisor at DNAprint genomics[257] and has applied for a patent on specific SNPs that serve as AIMs.[258] Kittles is scientific director at African Ancestry.[259] He plays a prominent role in its advertising efforts. Greely found “at least

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[251] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 209
[252] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 223-4
[253] Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' 241
[254] Marks, 'What is the viewpoint of hemoglobin, and does it matter?,'
[255] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 224
[256] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 202
[257] http://www.dnaprint.com/welcome/corporate/scienctificadvisors/
[258] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 222
[259] http://www.africanancestry.com/management.html

thirteen newspaper stories" about Kittles' visit to the Hausa people in Nigeria, to which he traced back his female line of descent, and quotes his statement in one of them that this "gave me a sense about who I am. It grounded me."[260] The scientists' affiliation with these companies contrasts remarkably with their criticism.

Greely argues that the involvement of scientists, and the "selling [of] the imprimatur of science" that the companies' services come down to, promotes false perceptions of science. The greatest risk in his view therefore is not that consumer's self-perceptions are false – "If the consumer feels better "knowing" that he's Mende [a population from Sierra Leone], what's the problem?"[261] – but that false perceptions of science as producing unambiguous results and truths can backfire and result in disillusionment. Science's "professional ethics of honesty, candor, and acknowledgement of limitations" are all violated by advertisement logic.[262] The basic problem is the tension between the morals of the marketplace and the ethics of science.[263]

Others critics would not agree that only science's image is at stake. The tests are central to processes of "self-making",[264] argued Nash, who directed attention to the autonomy and creativity of the consumers to determine the meaning of the tests.[265] Political uses provide an example of this. A company called Genelex explicitly marketed its tests to people attempting to acquire Native American rights.[266] Tallbear pointed out that despite the furious indigenous protests, some tribes use parentage testing for the acquisition of tribal membership. She speculated about the use of DNA testing in such cases, which would upset current power configurations in tribal governance and land rights, a possible application to which she highly objects.[267] Affirmative action qualifications and the assessment of Native American tribal membership sometimes depended on genetic history.[268] New, genetics-based views of kinship were appropriated and inserted into existing views: genes were becoming a substitute for blood, which had been a criteria for determining group membership for a century and is a "locus for Native identity". Scholars disagreed whether blood-based definitions of kinship existed in Native culture before the introduction of this policy. Tallbear suggested that the

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[260] Greely, 'Genetic genealogy. Genetics meets the marketplace,'
[261] Ibidem 230
[262] Ibidem 230-1
[263] Ibidem 216
[264] Nash, 'Genetic kinship,' 22
[265] Ibidem 27
[266] Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' 243
[267] Ibidem 245-246
[268] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 201

substitution of blood for genes can provoke a shift of emphasis from group, or social kinship to individual 'racial' identity due to lineage testing, which reflects a "descendancy understanding of kinship".[269]

African-American people were another lucrative market for ancestry testing companies. They used tests to cross the genealogical information barrier between the Americas and their (alleged) African regions of origin that the slave trade, with its lack of documentation, has created. Also, testing services were used to reclaim non-African ancestry.[270] Marks objected to the use of indigenous peoples as representatives of ancestral populations: the companies did not state "whether Africans were actually asked whether they would like to donate a genetic sample so that the company could market it to wealthy African Americans who could then pretend to be their kinsman.[271] The issue is, he stated, what the similarities between users' genomes and those of the sampled indigenous mean; "in particular, whether our place in the natural order is to be understood in terms of our own existence, or that of our ancestors."[272] Greely argued that the companies are not guilty of consumer fraud, not even dishonest, but neither completely honest. The problem lies, he argued, with the fact that "lack of disclosure" is the moral of the marketplace. Also, for individuals, the results can be psychologically upsetting: "5% of false paternity in each generation" not only ensures that "genetic ancestry is not likely to match official ancestry", but also creates a "Potential to harm people and break family bonds as well as strengthen them."[273]

Shriver and Kittles concluded their article with a call for a code of ethical conduct and accreditation procedures.[274] In 2007, a group of scientists and scholars published a critical article in Science, arguing for a better communication of the complexities involved in the testing of ancestry.[275] The American Society of Human Genetics' Ancestry and Ancestry Testing Task Force has recently responded to this and similar criticism with a white paper on genetic ancestry testing. They explained that the reason for doing so was informed by a sense of the ambiguity of the concept of ancestry:

> *The very concept of "ancestry" is subject to misunderstanding in both the*

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[269] Tallbear, 'Native-American-DNA.com: in search of Native American race and tribe,' 238
[270] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 209
[271] Marks, 'What is the viewpoint of hemoglobin, and does it matter?,' 258
[272] Ibidem 245
[273] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 229-30
[274] Shriver and Kittles, 'Genetic ancestry and the search for personalized genetic histories,' 210
[275] Deborah A. Bolnick et al., 'The science and business of genetic ancestry testing,' *Science* 318 (2007)

> *general and scientific communities. What do we mean by ancestry? How exactly is ancestry measured? How far back can such ancestry be defined and by which genetic tools? How do we validate inferences about ancestry in genetic research? What are the data that demonstrate our ability to do this correctly? What can we say and what can we not say from our research findings and the test results that we generate?* [276]

In the white paper, the task force argued for "develop[ment of] mechanisms for promoting thoughtful and rigorous use of genetic ancestry estimation in academic research", and for "a national roundtable discussion of DTC [direct-to-consumer] genetic ancestry testing" to discuss, among other things, accuracy, "the reporting of statistical confidence", the "communication of limitations and potential consequences", and " mechanisms for accountability."[277] They objected to, among other things, the fact that the ''ancestral populations'' are not directly observed" and that present day populations used as proxies for them were not well chosen.[278] Also, they argued that the application of programs such as STRUCTURE to databases that are 'incomplete' (with "some ancestral populations [...] missing altogether from the analyses") would produce skewed results.[279]

In conclusion, the field of anthropological genetics changed remarkably between the start of the HGDP and that of the Genographic Project. Criticism of tree models had triggered fierce debates. However, this had not led to their demise. Out of Africa had become dominant, and narratives emphasizing equality and unity of humanity now existed next to geneticised definitions of populations and group identities. Databases had grown larger and more numerous, while the analysis of multiple markers had become possible. Indigenous peoples had continued to protest against the HGDP and similar research, but also started to make use of the views of history and group definitions it produced. Criticism and memories of the 'failed' HGDP urged anthropological geneticists to tread more carefully on the politicised ground of indigenous identity, but racial categories had been partially reintroduced, if not rehabilitated with the reinterpretation of Lewontin's study. Reference to group identity

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[276] Royal et al., 'Inferring genetic ancestry: opportunities, challenges, and implications,' 661

[277] Ibidem 671

[278] "For example, present-day Yoruba are the most frequently used proxy for inferring African American ancestry, despite the fact that most African Americans derive their ancestry from diverse West African (and other African) populations that existed over a span of several centuries and that might not all be well represented by present-day proxy populations." Ibidem

[279] Ibidem 667

and ancestry in genetic terms increasingly featured in popularisations and the public imagination. The idea of the unity of humanity was still rooted firmly in a historical narrative, but these very narratives had reinforced and redefined group identities. These were perceived as lineages and tightly linked to an increasing number of markers; and the identities of these groups were sold in an emerging market for ancestral identities.

Chapter four - Spencer Wells and the Genographic: songlines for humanity

The Genographic Project

The Genographic Project was shaped profoundly by the developments of anthropological genetics in the 1990s. Scientists involved in it distanced the Project from the HGDP and continued to emphasize that genetics could put an end to racist ideas. It responded to an increased demand for 'genetic identity', while promoting a view of humanity as one big family. It celebrated human unity-in-diversity and encouraged the tracing of individuals' and groups' "deep ancestry". Anthropological genetics in the new millennium offered both arguments in favour of a unified view of humanity, and newly defined group identities.

The GP leader, Spencer Wells, was trained by the prominent in anthropological and population genetics. He pursued a Ph.D. in population genetics under the tutelage of Richard Lewontin.[1] Wells subsequently worked as a postdoctoral research fellow by Cavalli-Sforza at Stanford University, where, according to his National Geographic biography, he "became committed to studying genetic diversity in indigenous populations and unravelling age-old mysteries about early human migration."[2] He then became director of the Population Genetics Research Group of the Wellcome Trust Centre for Human Genetics at Oxford. In 2001, he decided "to focus on communicating scientific discovery through books and documentary films", and left academia.[3] He wrote his first popular book, *The journey of man: a genetic odyssey* in 2002, and made a documentary film of the same name. The film was broadcasted internationally by National Geographic Channel and, according to the NG website, "laid the groundwork for the Genographic Project".[4] This large scale project, with a 40 million dollar budget and planned to take five years, is a co-operation between National Geographic and IBM, and

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[1] http://www.geographical.co.uk/Magazine/People/Spencer_Wells_-_Sep_10.html

[2] *Explorer-in-residence Spencer Wells*, ([cited 05 April 2011]); available from http://www.nationalgeographic.com/field/explorers/spencer-wells.html

[3] Ibidem, ([cited)

[4] Ibidem, ([cited)

was launched in 2005. Although the objective of collecting 100,000 samples[5] was planned to take five year, it has continued until the present (summer 2011).

The book and film were followed by several popularizing books and documentaries. In 2005, *The search for Adam* appeared on National Geographic Channel; Wells' book *Deep ancestry. Inside the Genographic project* appeared in 2007; and in 2009 National geographic Channel aired *The human family tree*, another documentary about Wells' work and the Genographic. In addition to these popular works, a sophisticated Genographic website, a public participation branch, Genographic public events, and Wells' numerous appearances on television shows all contribute to a high public visibility. The first scientific article by a Genographic investigator that listed "The Genographic consortium" among its authors, on human mitochondrial DNA, appeared in June 2007 in *PLoS Genetics*.[6] The GP press release stated that "[t]he paper establishes Genographic as a leading repository for anthropological genetic information. Included is anonymous data from 78,590 public participants and important insights into modern human genetic diversity."[7] Since that time, about seven articles have appeared in renowned scientific journals. However, in comparison with Cavalli's scientific output, Wells' is modest. This may result not just from the popular nature of the GP, but also from the shorter length of Wells' scientific career. No synthetic overview of his work and views, such as the one Cavalli published in 1994, has yet appeared.

Like the HGDP, the GP is a collaborative project, with 11 participating institutions, mostly universities, from all over the world.[8] The sampling and analysis are organized and conducted regionally by the collaborating scientists in these institutions, but international coordination guarantees a general framework: "[a]n international advisory board oversees the selection of indigenous and traditional populations for testing as well as adherence to strict sampling and ethical research protocols."[9] This board is chaired by Luca Cavalli-Sforza. In addition to the field research, one of the 'Genographic investigators' at the University of Adelaide focuses on analyzing fossil DNA. Next to the fieldwork, a second section of the project consists of the public

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[5] *Genographic Project: Frequently Asked Questions*, ([cited)

[6] M. Behar et al., 'The Genographic Project public participation mitochondrial DNA database,' *PLOS Genetics* 3 (2007)

[7] News release 28-06-2007, *The Genographic press room*, ([cited 08 April 2011); available from https://genographic.nationalgeographic.com/genographic/pressroom.html

[8] The website lists ten research centres around the world, in Australia (covering Australia/Pacific), Brazil (South America), China (East/Southeast Asia), France (Western/Central Europe), India, Lebanon (Middle East/North Africa), Russia (North Eurasia), South Africa (Sub-Saharan Africa), Spain (Western/Central Europe), and the United States (North America). *Genographic Project: Frequently Asked Questions*, ([cited)

[9] Ibidem, ([cited)

participation branch, which "allows [participants] to learn about their own migratory history, as well as, if they wish, contribute to the overall progress of the project".[10] As Wells put it on the Today Show: "it's a chance to be part of a real-time scientific effort."[11] The database with the data that was "donated" by participants is an open source research database.[12] Lastly, there is the Genographic Legacy Fund, aiming at education, and cultural and language preservation among "participating and other indigenous and traditional groups."[13]

Despite its many links with and resemblance to HGDP, the GP distances itself explicitly from the HGDP. The 'frequently asked questions' section of its website addresses the differences between the projects explicitly. The HGDP "for the most part [...] closed shop in late 1990s, killed by opposition to its many flaws,"[14] according to Wells. He explains this opposition in terms of the "zeitgeist of the nineties," with its fears about the negative potential of genetics.[15] The GP presents itself as "completely different" from the HGDP: its approach is anthropological, nonmedical, non-political, nongovernmental, nonprofit; it aims to "enable indigenous rather than take from them." It is transparent, "in compliance with all local and international ethical and legal regulations," participants contribute voluntarily; and consent is free, prior and informed.[16] Furthermore, the GP does not focus on regions of genome that have known medical relevance, will not create cell lines, and doesn't allow the patenting of genetic data, as this is considered part of the "common heritage of our species."[17] The GP FAQ states that

> *when the HGDP was first discussed over a decade ago, the language of DNA and genetic anthropology was foreign to all but a few scientists. Discussion and third party review was less open and frank. Today that language is more familiar to many of us, and many of the ethical and privacy issues are more clearly understood by the global community. Our methodologies and protocols are open for review and we welcome further suggestions for improvement and*

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[10] Ibidem, ([cited)

[11] "Family tree project helps trace deep history," in *Today Show* (2005)

[12] Doron M. Behar et al., 'The Genographic Project public participation mitochondrial DNA database,' *PLOS Genetics* 3 (2007)104

[13] *Genographic Project: Frequently Asked Questions*, ([cited)

[14] Spencer Wells, *Deep ancestry. Inside the Genographic project* (2007)170

[15] Ibidem 170

[16] Ibidem 171

[17] *Genographic Project: Frequently Asked Questions*, ([cited); Wells, *Deep ancestry. Inside the Genographic project* 172

best practices.[18]

Wells recounts in *Deep ancestry* how the project was conceived in 2002 out of a sense of necessity to collect more samples - an urgent one, as people "are being subsumed into the cultural melting pot:" "we're racing against the clock".[19] "This would be the first time, he said, that this work had been carried out using the same technologies, in the same timeframes, using the same ethical methodologies. It was a chance to do the science right."[20] IBM's "computational biology team" was involved, the Waitt Family Foundation agreed to co-fund the field research, and on April 13, 2005, the project was launched. For its public participation branch the GP cooperates with a commercial testing company, Family tree DNA, founded in 2000. The GP was intended as a five-year project, but its website announced that field work and analysis would continue in 2011, while publications usingGP data "will continue for several years into the future." Also, in response to public enthusiasm, its public participation component will be continued as well.[21]

In *Deep ancestry*, Wells explains the aims of the project: "our goal is to assemble the most comprehensive database of human genetic variation that has ever existed."[22] The benefits of reconstructing history by means of genetics are explained in sweeping vocabulary throughout Wells' work. The attempt to "understand [...] ourselves" genetics can help take "incredible leaps forward."[23] Like Cavalli-Sforza, Wells emphasizes the closing of this window of opportunity to elucidate the history of humanity due to global admixture: we have to "to capture a genetic snapshot of our species before great melting takes place".[24] Once the information is lost, "it is lost forever." With the technical possibility to collect it comes the responsibility to do so, which we "ignore at our own peril", as Wells concludes the book *Journey of man* ominously, without giving much further detail about the nature of these risks.[25]

More bluntly than his Italian mentor, Wells repeatedly emphasizes "uniting the world's people while respecting the incredible diversity that defines us as a species":

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[18] *Genographic Project: Frequently Asked Questions*, ([cited)
[19] Wells, *Deep ancestry. Inside the Genographic project* 4-6
[20] Ibidem 7
[21] *Genographic Project: Frequently Asked Questions*, ([cited)
[22] Wells, *Deep ancestry. Inside the Genographic project* 25
[23] Ibidem 2
[24] Ibidem 5
[25] S. Wells, *The journey of man. A genetic odyssey* (Princeton, 2002) 196

indeed, the success of the project is dependent on it.[26] "Ultimately, the goal is to connect people from around the world into one family."[27] "I wanted to draw people together. To make people realize that we're all part of an extended family and that our DNA connects all of us into a very tight-knit group."[28] He refers to Bruce Chatwin's study of Australian aboriginal songlines.[29] These songlines describe a path taken by a certain clan's ancestors, or gods, and refer to both geographical and historical coordinates; every geographical location is associated with a particular part of the song, which describes the ancestor's acts and adventures on that spot. Wells explains that "these songlines reflect the actual journey taken by their ancestors", and that

> *in a sense, this is precisely what we are trying to do with our studies of DNA today - resurrect a global songline for everyone alive today, describing how they reached their current location and what their journey was like. As secular Westerners we have lost our traditional songlines to a greater extent than other peoples around the world, so it is perhaps appropriate that Western science has developed methods for rediscovering them.*[30]

It may be clear from these examples that Wells explicitly attributes cultural meaning to the research. This is also attempted at the level of communities and individuals: GP aims to "enrich" groups and individuals' sense of their own histories,[31] under the umbrella of a unifying songline for humanity.

Like the aboriginal songlines, travel (or migration) is the main plot of this narrative. In the introduction of the documentary *The Journey of Man*, Wells explains that it tells the story of the "greatest journey" ever made, as reconstructed by Y chromosome analysis.[32] This story raises "more questions than answers", Wells explains. Research suggests that the earth was populated in only 50,000 years. This, he gasps, seems "impossible"; the "speed and resilience" necessary for the execution of such an endeavour "def[y] belief".[33] Thus, he leaves the lab and sets out to trace this 'journey'

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[26] Wells, *Deep ancestry. Inside the Genographic project* 161
[27] Ibidem 174
[28] Genographic presentation video at the National geographic website, http://video.nationalgeographic.com/video/player/specials/in-the-field-specials/grand-central-genographic.html accessed 28 March 2011
[29] Bruce Chatwin, *De gezongen aarde* (Amsterdam, 1993) (*The songlines*, 1987)
[30] Wells, *The journey of man. A genetic odyssey* xvi
[31] Wells, *Deep ancestry. Inside the Genographic project* 174
[32] Clive Maltby, "The journey of man," (USA: CPB, 2003) [pt1]
[33] Ibidem [pt1]

across the globe, to find out more about why, how and by whom it was made. This documentary sums up the broad outlines of the history of humankind that Wells presents in most GP popularizations. A short rendering of its plot may therefore serve as an introductory synopsis of the general GP 'songline'.

The journey of man

Wells travels to the San Bushmen in Namibia, the presumed descendants of a shared common human ancestor; then to Australia, the first place where modern humans "appeared next"; and from Australia to India. In India, Wells looks for evidence for a migration, 60,000 years ago, from Africa to Australia, along what was then the south Asian coast. He states that due to the rise of sea levels this coast is now under water, which may explain the lack of archaeological evidence for this hypothesis. The camera witnesses a 'discovery' of what is by now dubbed the 'coastal marker': a mutation associated with Australian aboriginals in an Indian sample –"the missing link", a confirmation of the coastal route hypothesis.[34] The film then moves on to a "second wave of migration" from Africa to Asia and Europe, and the question when and from where the first Europeans arrived. "We discovered," Wells explains, "that the first Europeans didn't come directly from the Middle East".[35] Instead, when mankind left its "cradle", Africa, it stayed in a "central Asian nursery" for a while, before moving on into Asia and Europe. So-called "central Asian markers" are found "all over the world":[36] evidence that a Central Asian history unites all non-Africans.

Wells then visits the presumed ancestors of the ancient humans who migrated into Asia during the second wave, the Chukchi people in the Russian Arctic. Their rough living conditions serve to illustrate the hardships the Asian migrants faced as they "travelled through the Ice Age" to Beringia and the Americas. Finally, these "pretty tough people" arrived in the Americas about 13,000 years ago in what Wells calls the "land of plenty:" "they hit the jackpot". Their numbers swelled, and in "only 800 years" they peopled the continent.[37] As he comes to the end of the journey of man, and to his own, Wells takes stock of his insights:

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[34] Ibidem [pt5]
[35] Ibidem [pt8]
[36] Ibidem [pt8]
[37] Ibidem [pt11]

> *'What have I learned? I've witnessed the powerful combination of intelligence and human spirit. I learned that the years in our lab weren't wasted: the stories are true. One lesson stands out: we're all African under the skin. Brothers and sisters separated by a mere 2000 generations. Old-fashioned concepts of race are not only socially divisive, but scientifically wrong. Only when we realize this the journey is complete.'*[38]

Because he studies the Y chromosome, Wells explains in his book *Journey of man*, this is "literally" a journey of men. The Y chromosome is a convenient object of study: it provides the clearest genetic-geographic "'fingerprints'", because men from the same region tend to share recent common ancestors. And so, it "provides us with the cleanest distillation of human migrational history."[39]

In *Narratives of human evolution* (1991), Misia Landau analyzed theories about human evolution –Darwin's, Huxley's, Haeckel's, and Elliot Smith's, among others - as versions of the universal, folkloric and mythological hero tale.[40] She showed that nineteenth and twentieth century theories about the origins of modern humans share basic narrative elements. These elements can be regarded as narrative building blocks, as standard phases and elements in fairy tales: the hero, change, the departure, the test, the donor, the transformation, and triumph.[41] The specific nature of these stages differs from one theory to another: 'change' can refer to the shift from hominid arboreality to terrestriality, or to human "encephalization", depending on what came first according to the theorist in question. Thus, "encephalization" can also be the 'transformation' stage, while in other theories this phase is characterised by the ascent of civilization.

Wells' story seems suitable for a similar analysis. Indeed, the recurrence of narrative building blocks, reminiscent of Landau's concepts, in several of his works and public performances suggest the story is consciously constructed in that way. The sound bites make up a story suitable for an uninformed audience and for audiovisual media. Like in Landau's examples, humankind features as a heroic protagonist – but when human groups split and disperse themselves around the world, a second narrative line is added, which relates the story of 'the human family', rather than that of 'man' as a

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[38] Ibidem [pt13]

[39] Wells, *The journey of man. A genetic odyssey* 71

[40] Misia Landau, *Narratives of human evolution* (New Haven and London, 1991)

[41] For a schematic overview see Ibidem 8

singular hero. The ‘family members’, human populations that branched off the stem, are the protagonists of the subplots, which describe the multiple legs of the journey across the world. Humanity is often personified into ‘man’, while groups are often referred to as “family members” and are generally designated “clans.” On the whole, Wells’ story agrees with Cavalli’s. The differences between the two views of human history, which are separated by a decade, relate to dating. Also, with regard to some theories Cavalli had to keep several alternative options open, about which Wells could present evidence in favour of one of them.

The story starts in Africa: "Genetics, I think, resoundingly has answered the question of where we ultimately came from, we came out of Africa. And we came out quite recently, within the last 50 or 60 thousand years."[42] In an article published in 2000, co-authored by Wells and Cavalli-Sforza, it was reported that Y chromosome analysis, like mtDNA, indicated human origins are located in Africa.[43] Humanity, Wells explains in *Journey of man*, has its “cradle” in the grasslands of Africa, and more specifically, in the Rift valley, where the “deepest lineages” are found.[44] In *Journey of Man*, Wells reports that “the final nail in the coffin of multiregionalism”[45] was placed when the sequencing of Neanderthal DNA in 1997 proved that Neanderthals were a separate species, and that no admixture with “moderns” could be detected. Thus, modern man has a single birthplace and a clear lineage. For tens of thousands of years ‘he’ dwelled in Africa, occasionally foraying into the Middle East from 110,000 years ago onwards, but not travelling further than that.

Then, a “climatic catastrophe” (between 80,000 and 50,000 years ago[46]) almost wiped out the species.[47] The reason it survived this ‘test’ was a “quantum leap in thinking”:[48] modern man started to think and act modern. Such at least is the way archaeologists and palaeontologists, quoted by Wells, interpret the archaeological data. Diverse, more sophisticated and efficient tools, and the first appearance of art are interpreted as indicators of ‘modern behaviour’, such as the efficient exploitation of resources, the development of complex social networks. As we have seen, Cavalli-

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[42] Wells, quoted in Marsha Walton, "Finding the roots of modern humans. DNA study may reveal who we are, where we came from," (CNN, 2005)

[43] Peter Underhill et al., 'Y chromosome sequence variation and the history of human populations,' *Nature genetics* 26 (2000); Wells, *The journey of man. A genetic odyssey* 52-3

[44] Wells, *The journey of man. A genetic odyssey* 67, 56

[45] Ibidem 125

[46] Spencer Wells, *Pandora's seed. The unforeseen costs of civilization* (2010) 15

[47] Wells, *Deep ancestry. Inside the Genographic project* 139

[48] Maltby, "The journey of man," [pt3]

Sforza's history included a similar hypothesis, albeit somewhat differently dated.[49] Like Cavalli, Wells associates modern behaviour with improved communication skills, that is, spoken language with a complex syntax. Indeed, he presents such skills as cause and precondition for human development. Wells illustrates the development of complex language by analogy with the way children learn to speak.[50]

This behavioural 'leap' was dubbed 'the Great Leap Forward' by Jared Diamond.[51] Man developed what Wells calls 'killer applications': more diverse, efficient and sophisticated technology associated with the Late Stone Age.[52] The Genographic website states that "these developments may have had their roots in a genetic mutation that boosted cognitive function".[53] This is when man becomes fully modern: "[o]ur birth as a species in the crucible of a marginal and changing environment" came down to the selection of inventiveness and plasticity – "we are biologically adapted to adapt"[54] – a literal echo of Huxley's famous remark that man "specialised in despecialisation". The biological preconditions, a modern brain, started to develop several millions of years ago, when man had left the trees for the grasslands. The necessity to hunt for a living and to escape predators drove this early, gradual development of the human brain.[55] But the bottleneck catalysed the fulfilling of this potential, the development of a "powerful, abstract mind, to take on the world."[56] In most of Wells' works, this is presented as a revolutionary event.

At the end of the last Ice Age, drought drove people to the coasts, to live off the sea. This provides Wells with an argument for the theory of a coastal route to Australia, the first migration from Africa (around 60,000 years ago): travelling alongside the coast would not require the changing of diet and food gathering strategies.[57] Around 50,000 years ago, the effects of climate change again "pushed"[58] modern man out of Africa, a second wave of migration, this time into its "nursery" in Central Asia. There, it 'matured' to face the challenges in Asia and Europe it wasn't ready to face yet when it had just emerged from its homeland and Asia. According to Wells, this 'maturation' may explain

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[49] Cavalli-Sforza et al., *The history and geography of human genes* 155
[50] Wells, *The journey of man. A genetic odyssey* 86-89
[51] Ibidem 85; with reference to Diamond's book 'The third chimpanzee' (1991)
[52] Ibidem 85
[53] Genographic Project, *Atlas of human journey* ([cited 15 April 2011]); available from https://genographic.nationalgeographic.com/genographic/lan/en/atlas.html: "genetic markers"/M168
[54] Wells, *The journey of man. A genetic odyssey* 89
[55] Ibidem 89
[56] Spencer Wells, 'Out of Africa,' *Vanity Fair* (2007)
[57] Wells, *The journey of man. A genetic odyssey* 68
[58] Wells, *Deep ancestry. Inside the Genographic project* 128

why modern man replaced the Neanderthals, who, he explains adapted biologically rather than culturally to difficult Eurasian environments, and were therefore no match for the moderns with their sophisticated hunting techniques.[59] Modern man's profile emerges from Wells comparison with these "distantly related cousins",[60] which is somewhat reminiscent of David and Goliath: "[w]hat modern humans accomplished with tools and brains, Neanderthals seem to have done with brute force;"[61] Neanderthals had "brutish ways".[62] The moderns won because of their "complex social structures" that facilitated elaborate hunting strategies and reserved a didactical role for old people, so that the continuity of knowledge was safeguarded. The replacement of Neanderthals did not necessarily take the form of a bloody battle; it may have been the modern's mere demographical dominance – "it was natural selection that did them in."[63]

Man left this "nursery" march into Europe and Asia, the latter of which is presented as the great test, the "school" where mankind toughened up and faced the depths of the Ice Age. The necessity to obtain food, that is, meat, "led them into the freezer": they shot across the "Steppe Highway" to the East.[64] The "Icy evolutionary laboratory" again selected those with an "intellectual capability of surviving".[65] Finally, man emerges as a cunning hunter of large animals, adapted to the cold, and carrying "technology such as "finely crafted tools", "portable dwellings" and "clothing against the cold." He entered the Americas via the Bering landmass (in *Journey of man* Wells states that this crossing took place no earlier than 20,000 years ago[66]). In the New World, these "pretty tough people"[67] were presented with something of a promised land after the endurances in the arctic, a "land of plenty" where they spread and multiplied.[68] Then, another revolution took place, comparable to the "Big Bang" of the development of the human mind: the shift to agriculture. This Neolithic revolution ended the great migrations and created the first elements that characterize modern civilization: the human ability to mould the environment, to control destiny – and increasing population densities, with the accompanying diseases.[69]

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[59] Wells, *The journey of man. A genetic odyssey* 133; Wells, *Deep ancestry. Inside the Genographic project* The Neanderthals were "trapped" in biological specialization, moderns "outcompeted" them with their "brain power." 110

[60] Wells, *Deep ancestry. Inside the Genographic project* 106-7

[61] Wells, *The journey of man. A genetic odyssey* 130

[62] Wells, *Deep ancestry. Inside the Genographic project* 106

[63] Wells, *The journey of man. A genetic odyssey* 130-1

[64] Ibidem 117

[65] Ibidem 135

[66] Ibidem 138-9

[67] Maltby, "The journey of man," pt11

[68] Ibidem pt 11

[69] Wells, *The journey of man. A genetic odyssey* 158-9

The stylistic device that cuts this narrative into thematic episodes analogous to the phases in an individual human life – birth, maturation – is also connected to the genetic data it is based on. Wells speaks of "genetic signposts,"[70] mutations that emerged at a particular location, in a particular phase of the journey. These often correspond to a particular split in the family tree. They are geographic entities; the markers occur in high frequencies in specific regions. And they are also genealogical; sometimes they were defined in terms of the first man in whose DNA the mutation occurred, which produces sub-Adams, so to speak – "Eurasian Adam", for instance. And they are narrative entities: each represent a chapter in the narrative. In Landau's approach, the building blocks would be: the birth of modern man; a climatic challenge; and the maturation into a fully modern human, all three both in Africa. Subsequently, departure(s) from the African cradle, and into the nursery; or training in central Asia. Then the test in frozen Asia, and finally, the arrival in the Americas with all its riches - the fulfilment of the journey, the "conquest" of the earth.[71]

The forces that drive the migrations are predominantly climatic. Some of the reasons for people to migrate "we will never grasp"; about other ones we can speculate. Man may have followed the animals he hunted, searched for water, plants, stones for tools, or moved because of conflicts with other groups. "[T]he journey must not be seen as a conscious effort to traverse the continent, but rather as a gradual expansion in range driven by seemingly insignificant local decisions", and "climate is the stick and carrot of scenario."[72] It is climatic change too that was the catalyst for the "Great Leap Forward". Wells explains that the severe selective pressure was due to climate changes that resulted from the last Ice Age. A crash in population numbers down to, possibly, as little as 2,000 individuals amounted to a bottleneck that may have let only the adaptive and most cunning through.[73] This Great Leap Forward also left a "genetic trace": subsequent population expansions of groups independent of each other, alleged reflections of the success of the new 'killer app', which can thus be "traced around the world".[74]

This modern mind evolved in Africa and is therefore shared by all humans. After that, the environment, drift, and possibly sexual selection physically shaped humanity.

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[70] Ibidem [pt13]

[71] "This is the story of your family and how they conquered the earth", Maltby, "The journey of man," [pt1]

[72] Wells, *The journey of man. A genetic odyssey* 94-5

[73] Ibidem ; Wells, *Deep ancestry. Inside the Genographic project* 139

[74] Wells, *The journey of man. A genetic odyssey* 93

Adaptive flexibility is thus at once a human universal and an explanation of differences. Apart from external ("superficial") changes, such as skin colour, adaptation takes place on a cultural level, again echoing the UNESCO consensus that man has "specialized in despecialization."[75] The idea that "every single person [...] on earth [...] is African"[76] therefore also settles the question of cultural and mental equality, as maturation of these traits took place in Africa. The swiftness and shortness of the colonisation of the earth is not only an argument for the unity of the human family. It also allows the GP to tell a heroic story, and add an adventurous veneer to it. It provides a moral message, but also has narrative benefits.

Narrativisation

Wells uses imaginative language, analogies and metaphors to present and explain his research. The most prominent metaphor, 'journey', has several epic synonyms: a "great coastal exodus" from Africa,[77] a "blitz" across Eurasia,[78] an "odyssey" into Polynesia[79], and a "leap into the unknown" when people left the coast.[80] Migrations of numerous people over numerous generations are often assembled in one single episode or narrative component. For instance, groups "broke away" in the Central Asian steppes to embark on "a journey that would not stop until reaching the Americas."[81] And obviously, the whole 'Journey of man' is often presented as a single episode, with a beginning and an end. As he introduces the documentary *Journey of man*: "this is the story of your family and how they conquered the earth."[82] The swiftness and heroic nature of this journey is emphasized: "[i]n just 40,000 years our species travelled from East Africa to Tierra del Fuego, "braving deserts, towering mountains and frozen wastelands."[83]

Wells consistent use of 'Adam' and 'Eve' for the shared common ancestor reinforces the personification of humanity. As mentioned before, the mtDNA evidence for 'Eve' triggered a search for her male counterpart, in which Cavalli participated. This

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[75] quoted in Delisle, 'Adaptationism versus cladism in human evolution studies,' 111
[76] Wells, 'Out of Africa,'
[77] Wells, *Deep ancestry. Inside the Genographic project* 129
[78] Wells, *The journey of man. A genetic odyssey* 99
[79] Ibidem 147
[80] Ibidem 96
[81] Wells, *Deep ancestry. Inside the Genographic project* 183
[82] Maltby, "The journey of man," [pt1]
[83] Wells, *The journey of man. A genetic odyssey* 150

search took many years, because geneticists initially could not find enough variation on the Y-chromosome to distinguish between samples. When in the late nineties new methods were developed in Cavalli-Sforza's lab to assess this variation, Wells "dropped everything" to "help find Adam". This was eventually done and published in the abovementioned 2000 article in *Nature genetics*.[84] Although Wells has called the name 'Eve' for the first coalescence point (a mere "statistical inevitability") "evocative",[85] he consistently uses it, as well as 'Adam', as the multiplication of 'Adams' illustrates. Wells' Y-chromosome based story often narrates of a single, male character. Unsurprisingly, the personification is most prevalent in the earliest African phase of his history of humankind, before humanity branched into subgroups.

In a National Geographic Channel documentary called "The search for Adam" (2005), to which Wells contributed, the personification takes on explicit forms. The documentary attempted to "discover [Adam's] lost Eden," and, at an "unexpected crossroads of Bible and biology";[86] "confirms [..] the Biblical story."[87] It presents "scientific Adam," to whom every man on earth is linked by "microscopic clues". A forensic facial reconstruction expert literally personifies this common ancestor: he models Adam's face, based on a 100,000 year old excavated skull and that of a modern chief of the Ha'adzabe, the people allegedly genetically linked most closely to 'Adam'.[88]

In the documentary, this Adam is not only presented as a common ancestor; he is also individually associated with the "Great Leap Forward", which is estimated to have taken place around the time the coalescence point is dated, around 60,000 years ago. The voice over: "Wells has a theory - cutting edge, highly controversial: Adam may have been the first human able to think as we do. The first truly modern man."[89] His mental superiority would explain the spread of his genes and the dying out of the lineages of his contemporaries. Thus, this Adam represents humanity as a whole as a common ancestor, literally embodies the evolution of mankind, and represents the origin of what we now are, the "birth of our species". In a more recent book, Wells nuances his "cutting edge theory", and the revolutionary view of the modernization of the human mind. He discusses the debate about micro- vs macroevolution, and recounts how Lenski et al. proved in 2003 that microevolution can lead to complex traits, such as the capacity for

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[84] Underhill et al., 'Y chromosome sequence variation and the history of human populations,'

[85] Wells, *Deep ancestry. Inside the Genographic project* 156-7

[86] "DNA mysteries: The search for Adam," (National Geographic Channel, 2005) [pt1]

[87] Ibidem, [pt5]

[88] Ibidem,

[89] Ibidem, [pt4-5]

abstract thought. If this is how the "Great Leap Forward" has taken place, there was no revolutionary change in behaviour in a single individual, he explains.[90] Also, on the website, it is emphasized that "Adam does not literally represent the first human."[91]

Towards the end of the documentary, Wells explains that our common descent means that "effectively, we're all members of an extended family, we're all distant cousins." The voice over summarises: "the message of genesis."[92] These "family members" are often depicted as tribes, and consistently called "clans" in Genographic language. They are defined by markers, which "like a clan", define unique lines of descent.[93] Regional Adams and Eves gave rise to Eurasian, central Asian, Coastal, European and Siberian clans[94]. Wells explains that that is what haplogroups essentially are: "ancestral clans." Europe, for instance, has "seven clans", "Founding Fathers" of the continent.[95] Haplogroups are organized into "macrohaplogroups," or "superhaplogroups" which share markers that define "deeper" relationships.[96] In 'The search for Adam" these are computer animated as branches on trees with a human figure, the common ancestor of that part of the tree, in every split. The perspective sinks lower and lower until the lowest split, with "Adam" in it, comes into sight.

The vocabulary used to describe these groups, c.q. lineages, derives from genealogy. Thus, the Q lineage is a "cousin" of the R haplogroups, because the lineages share an M45 "grandfather."[97] (In "haplogroup nomenclature" letters define a "broad haplogroup affiliation," and numbers and other letters define subgroups within them).[98] Wells travels to Australia to search for "the ancestral grandfather of the aboriginals."[99]

Nash's observation of the way "discourses of family relatedness provide a grammar for translating the complexities of new genetics into public culture" and the way models of "family and historical genealogies provides tangible physical and temporal scales that mediate between the micro-scale of molecular genetics and the long time span of human evolution." seem especially appropriate for these popularisations. She continues:

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[90] Wells, *Pandora's seed. The unforeseen costs of civilization* 111

[91] Project, *Atlas of human journey* ([cited) Journey highlights/Adam

[92] "DNA mysteries: The search for Adam," pt5

[93] Wells, *Deep ancestry. Inside the Genographic project* 40, 60

[94] Wells, *The journey of man. A genetic odyssey* 111, 114, 120, 132, 139, respectively; also, see Project, *Atlas of human journey* ([cited)

[95] Wells, *Deep ancestry. Inside the Genographic project* 53

[96] Ibidem 100-101

[97] Ibidem 101

[98] Ibidem 49

[99] Maltby, "The journey of man," pt5

> *“ geneticized genealogy joins naturalized notions of biological kinship to the truth of science.* [It] *brings us back to genealogical time: linear, progressive, one directional, modelled on descent and the transfer of property from father to male offspring. At the same time, it produces new versions of genetic kinship, in the form of Y-chromosome genetic brotherhood, mtDNA clan membership and global genetic kinship.*[100]

Indeed, a family metaphor is used to illustrate the ideological message, which is already delivered by the very use of this vocabulary: that “we’re all brothers and sisters, separated by a mere 2000 generations.”[101]

Identifying groups

Indigenous populations hold the key to – literally embody - these relationships: they “retain some of their ancestors’ way of life”, are “isolated from immigration”, and are presumed to “have been living in the same place for a long period of time.” In other words, their lifestyle, their geographic location (both allegedly relatively unchanged), and their genetic composition (allegedly relatively unadmixed) are all essential pieces of evidence needed for the reconstruction of the past. “Has anyone, including indigenous populations, really been that removed from the effects of global migration?” Wells asks rhetorically. “In some cases, yes.” [102]

Therefore, these historical groups and the currently existing populations that are presumed to be their descendants are often strongly associated, and almost identified with each other – as was the case in Cavalli-Sforza’s research, and despite protests against this view. Wells warns against the danger of implicitly ascribing backwardness to the sampled populations. Africans, for instance, inhabit the region of human origins, but are not frozen in “some sort of ancestral evolutionary limbo”. Each of the branches of the family tree evolves continuously; and all change at the same rate, which is why greater African diversity indicates greater age of the African branch.[103] Elsewhere, he is less careful: the Andamanese are thought to represent a “relic” of the pre-Mongoloid

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[100] Nash, 'Genetic kinship,' 25

[101] Maltby, "The journey of man," pt13

[102] Wells, *Deep ancestry. Inside the Genographic project* 4, 45

[103] Wells, *The journey of man. A genetic odyssey* 39

population of Southeast Asia; "'living fossils', if you will."[104]

In the films, the equation is more explicit and dramatized than in his books - perhaps unsurprisingly, as the language of the screen requires moving images and allows for fewer nuances. In the documentaries, the San Bushmen are presented as almost interchangeable with their ancestors. But both in popular and in scientific publications, they are depicted as 'remnants': "Khoi and San (Khoisan) people of South Africa [...] are considered to be a unique *relic* of hunter-gatherer lifestyle and to carry paternal and maternal lineages belonging to the deepest clades known among modern humans."[105] The Hadzabe "offer the next best thing to time travel: a window into Adam's world".[106] Visiting them in Tanzania is "like visiting the preagricultural era".[107] Other examples that indicate a 'relic' view of the indigenous include a discussion of the language of the Tajik Yagnob as a "linguistic artefact", descendant from the "Silk Road lingua franca".[108] Also, carriers of M91, the marker associated with 'Adam', "often practice cultural traditions that are representative of the ways of life of their distant ancestors. For example, some live in traditional hunter-gatherer societies once common to all humans. They also may still speak ancient click languages".[109] Language, next to geographic location, genes and lifestyles, provides another important link to the past, in a way analogous to genetics: currently spoken languages are considered to be indicative of 'ancestral' languages.

Language correlates with genes, Wells explains, referring to Cavalli-Sforza's work on this subject.[110] The loss of languages is an indication of the loss of genetic group identities[111] - Wells remarks that increasing occurrence of "language death" indicates that human mixing is now "accelerating."[112] He agrees with Cavalli that the historical development of languages is analogous to that of gene pools, and that therefore, linguistics and genetics can inform and complement each other. When it comes to the question how many waves of migration there were into the Americas, linguistics

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[104] Ibidem 75

[105] Doron M. Behar et al., 'The dawn of human matrilineal diversity,' *The American Journal of Human Genetics* 82 (2008) emphasis mine

[106] "DNA mysteries: The search for Adam," pt5

[107] Wells, *Deep ancestry. Inside the Genographic project* 134. This rather blunt designation contrasts with a somewhat indignant remark about how the government treated the Hadzabe until recently as an "embarrassing anachronism". Wells explains that the hunter/gatherer-way-of-life is an extremely successful adaptation; "its stability over thousands of years is sign of strength, not of backwardness."

[108] Wells, *The journey of man. A genetic odyssey* 186

[109] Wells, *Deep ancestry. Inside the Genographic project* 204

[110] Wells, *The journey of man. A genetic odyssey* 162-3

[111] Wells, *Deep ancestry. Inside the Genographic project* 4

[112] Wells, *The journey of man. A genetic odyssey* 191-2

provides insights,[113] while genetics can help "search for an Indo-European ancestral form".[114] Wells discusses the linguistic hypothesis of an equivalent for the root of the genetic world tree: a single ancestral language, or common linguistic origin, of all languages today – an idea Cavalli also discussed in *History and geography*. Wells is very careful in his discussion of these speculations: there is "no clear genetic data to support this model"; he argues that the alternative view that language spread via cultural dissemination rather than with speakers themselves may also hold. Furthermore, maybe "superlanguages" have never existed; perhaps they were "simply collections of unrelated languages that show random similarities", or perhaps subgroups do exist while many other languages are unrelated. He concludes that it's all speculation and that no one knows how long it takes for an original language to disappear. Nevertheless, the "contentious and exciting new field," dedicated to the "search for the language of Adam and Eve," is an exciting one, to which Wells thinks genetics can contribute.[115]

Next to language, he also seems to consider the physical characteristics of present-day populations informative of genealogical relationships between groups. We already saw how the present physical appearance of the Khoisan was used as a basis for the reconstruction of "Adam's" looks. Wells' attention to physical features is perhaps unexpected in the light of the conceptual separation of the physical and the genetic level, with the argument that the latter are useless for the construction of taxonomies or family trees. Wells too argues that "beneath the skin we're more similar than our surface would make us believe."[116] Nevertheless, he often refers to physical appearance when discussing possible relationships or lines of descent between populations; more explicitly than Cavalli-Sforza. It is illustrative for the broad perspective Wells takes on human history, as well as his popularising style, that he includes questions about such topics– "do the San give us a glimpse" of the looks of our ancestors? "It is difficult to imagine what [they] looked like". He states that informed speculation is the only possible approach, "like in any historical science"[117] – but, as the very posing of these questions implies, not a senseless one. Elsewhere, he even presents the physical similarity between Africans and Australians as "a piece of evidence" for a "direct link

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[113] Ibidem 142
[114] Ibidem 163
[115] Ibidem 163
[116] Wells, *Deep ancestry. Inside the Genographic project* 153
[117] Wells, *The journey of man. A genetic odyssey* 58

between Africa and Australasia".[118] Interestingly, this resemblance had often been used in genetics as an illustration of the fallacies of morphological taxonomies, which lumped these genetically distant populations together.

Next to lifestyle and language, the correlation of other cultural features with genetic patterns was also the subject of GP research. In 2010, Genographic researchers, Wells among them, published an article reporting on research into genetic make-ups of religious communities in Lebanon. They found that "the great religions in Lebanon were adopted within already distinguishable communities. Once religious affiliations were established, subsequent genetic signatures of the older differentiations were reinforced. Post-establishment differentiations are most plausibly explained by migrations of peoples seeking refuge to avoid the turmoil of major historical events."[119] However, there were "no noticeable or significant genetic differentiation between the Maronites as a group and the major non-Maronite communities (Greek Orthodox Christians, Greek Catholic Christians, Sunni Muslims, Shiite Muslims, and Druze) that occupy modern day Lebanon." This was taken as a strong indication that "the various communities have a shared genetic history that might result from a common origin, gene flow between them or additional populations, or a combination of these factors."[120] Previous GP research considered Y chromosome diversity in Lebanon, and found that the Lebanese Muslim population carried a genetic imprint that could be traced to its origins on the Arabian Peninsula, carried into Lebanon with the Islamic expansion in the seventh century.[121] Genetics was used to gain insight into recent historical events as well.

In the footsteps of Cavalli-Sforza, the GP has also investigated the spread of 'farmer communities' in the Neolithic.[122] They argued that the "Neolithic transition (8,000–4,000 B.C.) from hunting and gathering to agricultural communities was one of the most important demographic events since the initial peopling of Europe by anatomically modern humans in the Upper Paleolithic (40,000 B.C.)." But the population studied "also showed unique genetic features including a clearly distinct distribution of mitochondrial haplogroup frequencies, confirming that major demographic events continued to take place in Europe after the early Neolithic." Sometimes, the research

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[118] Ibidem 74-75

[119] Marc Haber et al., 'Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon,' *European Journal of Human Genetics* 19 (2011) (Epublication date December 2010). 1

[120] Ibidem 6

[121] Pierre A. Zalloua et al., 'Y-Chromosomal diversity in Lebanon is structured by recent historical events
' *The American Journal of Human Genetics* 82 (2008) 873

[122] Wolfgang Haak et al., 'Ancient DNA from European early Neolithic farmers reveals their near eastern affinities,' *PLOS Biology* 8 (2010)

focused on historical populations of that are only known from the historical record. This was the case in the GP study of "Phoenician" genes. "Phoenician-influenced sites" were chosen as sample sites; people currently living in these regions were sampled in search for genetic traces of the historical population. By "comparing historically documented Phoenician sites with neighboring non-Phoenician sites" they identified "weak but systematic signatures shared by the Phoenician sites that could not readily be explained by chance or by other expansions" [123]

One of the earlier scientific GP publications reported about research into "The dawn of human matrilineal diversity". It paid "particular attention to the Khoi and San (Khoisan) people of South Africa because they are considered to be a unique relic of hunter-gatherer lifestyle and to carry paternal and maternal lineages belonging to the deepest clades known among modern humans. Both the tree phylogeny and coalescence calculations suggest that Khoisan matrilineal ancestry diverged from the rest of the human mtDNA pool 90,000–150,000 years before present."[124] They inferred that African populations lived fairly isolated before humans left Africa, and that "of the more than 40 mtDNA lineages in Africa at the time modern humans left Africa, only two of the variants, (L3) and (L3), gave rise to the entire wealth of mtDNA diversity outside of Africa."[125]

From the links – geographical, linguistic, behavioural, physiological and genetic - thus forged between current communities and their 'ancestral groups', identities emerge that are stable over vast amounts of time. These historical group identities also facilitate, are translated into, individual, *personal* identities of the GP participants. The GP website presents the details of each lineage's story, characteristics and route across the globe. Participants, who sent a cheek swab to the GP, can log in to receive their results online, and can subsequently check an "Atlas of human history" for the section discussing their own lineage. Bennett Greenspan of Family Tree DNA, the company that provides technical support for this GP branch, explains: one can "find out about [one's] *personal* migration pattern over the last tens of thousands of years."[126]

Historical group identities, which are complexes of genetic markers, regional and indigenous identities, and historical narratives, also serve as the stuff of individuals'

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[123] Pierre A. Zalloua et al., 'Identifying genetic traces of historical expansions: Phoenician footprints in the Mediterranean,' *The American Journal of Human Genetics* 83 (2008) 633

[124] Behar et al., 'The dawn of human matrilineal diversity,' 1130

[125] Ibidem 1138

[126] "Family tree project helps trace deep history," emphasis mine

genetic selfhood.

Sometimes GP media imply the literal localisation of such identities in a single currently living individual. This is the case in *Journey of man*, when Wells visits Niazov, an "extraordinary" man living in central Asia. "Niazov is directly descendent" from a mutation that arose in a central Asian individual 40,000 years ago, 'the central Asian marker'. "After nearly 2,000 generations, Niazov *still lives* in Central Asia".[127] Wells tells him: "I can tell you with absolute certainty that your Y chromosome has been here for 40,000 years.' Niazov responds to this news, which is received in a celebratory atmosphere, that "this means [his] blood is pure".[128] This sits rather awkward with the rejection of language of 'purity' by the GP, and by anthropological genetics in general. Therefore (one gets the impression), the remark is skipped over by Wells - on the other hand, the scene is included. The episode is telling of the fragile equilibrium between the discourse of brotherhood and the emphasis on group identities.

The confrontation of GP history with personal or group histories, as mentioned above, was not always as welcome as this. In the documentary Journey of man, Wells meets an aboriginal artist from Queensland in Australia, who asks him: "if our stories are myth, as you might believe they are, and we know they're not - why wouldn't the tree branch out from us, from Australia?" To which Wells responds: "DNA stories are DNA stories: our version as Europeans of how the world was populated, our songline. We use science to tell us that because we don't have a sense of direct continuity, our ancestors didn't pass down our stories, we've lost them. So we use science, which is a European way of looking at the world. You guys don't need that." The artists confirms: "that's right, we know where we come from, and we know about creation, we don't come from nowhere else". In voice over, Wells says: 'this really isn't going very well. Tradition rarely sits well with cutting edge science."[129]

In America, a similar confrontation takes place. Wells meets Phil Bluehouse, a Navajo Indian, who tells him about Navajo origin stories. Wells responds: "I have my own story: people are closely related, we're part of one big family, all related to people living in Africa 50,000 years ago. We all are essentially African." Characteristically, Bluehouse speaks of 'us', while Wells story is also about 'you', about the Navajos. Wells story is also about Bluehouse, while Bluehouse's story says nothing about Wells'

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[127] Maltby, "The journey of man," pt8
[128] Ibidem [pt9]
[129] Ibidem [pt5]

ancestry. After Wells has told him his story, Bluehouse asks: “why do you call that what people tell you a myth? It sounds like a substandard event.” Wells responds: “my bias as a scientist is that I want to see evidence for things.” In voice over he adds: “I’m getting pretty good at this.” The documentary continues with the revelation that Bluehouse carries a Central Asian marker, to which Bluehouse responds enlightened. Wells narrates: “my story came of no surprise to the Navajo; migration was central to their creation stories.” And Bluehouse adds: “science and tradition complement each other.”[130] Apparently, some cosmologies – or rather, some individual interpretations of them – are more suitable for accommodating scientific views than others.

Models and methods

Because Wells focuses predominantly (although by no means exclusively) on popular media, and the Genographic output takes the form of public presentation in films and documentaries, it is more difficult to gain insight into the methods and assumptions that underlie the research. Wells has not published an overview of the field as Cavalli-Sforza has done, nor elaborated on dilemmas and alternative views. His, and the GP’s scientific output is therefore restricted to a collection of articles on divergent subjects, referred to above.[131] The translations of this research into popular works, however, are plenty, compared to Cavalli’s output.

Wells explains that the Genographic project aims to “elucidate the relationship among genetic, linguistic, cultural, and historical data.”[132] Haplogroups are lines of descent, as represented by the markers accumulated over time, and are also geographical entities.[133] Furthermore, they have cultural (e.g. linguistic), social and narrative dimensions. These multidimensional entities are clearly delineated – partially due to popularizing shorthand, and partially due to the methods themselves. As is the case in Cavalli-Sforza’s work, the emphasis lies on separate lineages and not on

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[130] Ibidem [pt12]

[131] Behar et al., 'The Genographic Project public participation mitochondrial DNA database,' ; Behar et al., 'The dawn of human matrilineal diversity,' ; Haak et al., 'Ancient DNA from European early Neolithic farmers reveals their near eastern affinities,' ; Haber et al., 'Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon,' ; Zalloua et al., 'Identifying genetic traces of historical expansions: Phoenician footprints in the Mediterranean,' ; Zalloua et al., 'Y-Chromosomal diversity in Lebanon is structured by recent historical events
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[132] S. Wells and T. Schurr, 'Response to decoding implications of the Genographic Project,' *International Journal of Cultural Property* 16 (2009)

[133] Wells, *Deep ancestry. Inside the Genographic project* from 175 onwards provides an overview of haplogroups, their “ancestor”, their lines of descent, accumulated markers, their geographic journeys, and current knowledge of their ages and distribution.

admixture; populations and historical group identities are presented as branches on trees. Wells emphasizes that these are statistical entities, and is clear about uncertainties, the limits of metaphor and analogy. Nevertheless, there remains a tension between these reservations and the less nuanced GP vocabulary, concepts and visuals – a tension Cavalli's critics views found in the HGDP and Cavalli's writings.

Wells combination of cultural and genetic definitions and his use of trees puts him in the research tradition of tree building to which Cavalli-Sforza contributed with Edwards and Feldman and many others. Indeed, Wells places himself in this tradition.[134] He explains that "the goal, when drawing a tree, is to minimize the number of genetic changes required to explain relationships,"[135] which indicates that 'simplification' is not just a matter of popularization, but is inherent in the methods used. This minimization requires a "leap of faith": the theory of parsimony. This is explained by Wells as follows: "[i]f mutations occur very rarely, [...] then we should assume that sequences differing at ten positions had only ten mutational changes since they last shared a common ancestor. [...] In genetics, as in physics, the simplest explanation is almost always correct." Parsimony could be translated as the idea that the 'molecular clock', counting mutations, never runs backwards nor hesitates: that mutations are almost never undone. To increase the strength of this hypothesis of parsimony, those positions on the genome that are relatively stable are selected for study, while the hypervariable ones are ignored.[136] The mutation rates differ depending on part of the chromosome – as we saw, mutations on the Y-chromosome are so infrequent that it took some years before variation was detected.[137] The 'molecular clock' ticks at different paces on different parts of the genome; the principle of parsimony assumes that it does so stably and continuously.

Geneticists search for and focus on the variable regions of the genome, looking for markers, to discover patterns of relatedness among groups. What the GP is looking for, Wells explains in an online GP video, is a "measure of relationship, similar to a totem or family crest."[138] The voice over adds: "markers allow us to connect people through history. [...] They also serve as a kind of clock, to estimate when people lived. And by looking at how markers cluster, they can even act as roadmaps, to show us where our

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[134] Ibidem 23
[135] Ibidem 23
[136] Ibidem 89-90
[137] Ibidem 75
[138] Ibidem 40; 44

ancestors came from, and where they moved."[139] Wells states: "A marker is a glimpse of a person who lived at some point in the distant past.[...] They [i.e., markers] don't change the way you look, or give you a disease, or make you better than anyone else, they're just baggage that gets passed on through the generations".[140] In other words, 'historical' markers are also selected to have no clear relationship with the phenotypic level – also because selection would distort the molecular clock.[141] This can be contrasted with the HGDP reference to possible medical insights from diversity research. Therefore, this selection could be regarded as the final separation of what Marianne Sommer has dubbed the "anthropological gene" from other notions of the gene:

> *[T]he anthropological gene and genome gained their status as the most fundamental, clean, and direct records of historical information. [...T]he kind of information the anthropological gene and genome are supposed to carry is special in that it can be of a narrative nature. The anthropological gene is then understood as a record of past events. It is therefore performed in the semantic field of historical reconstruction.*[142]

The emphasis on the historical and otherwise neutral nature of the markers studied in the GP distinguishes them from 'medical genes' and studies of genotype-phenotype relationships – from the level of commonsense, everyday identities. The GP ethical framework explicitly rejects medical research questions, and requires scientists who collaborate on the project to do likewise.[143] Contrastingly, in GP popularising publications, references to the phenotype level of physical characteristics abound.

Although at first sight the Genographic visuals are very similar to those encountered in Cavalli-Sforza's work, there are significant differences. They reveal more of the complexity of the migration patterns they depict. This may be a result of the use of a different medium – Cavalli's visual material is printed, whereas the Genographic's predominantly has the form of interactive online maps and animations. The website's

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[139] "Genetic roadmaps", *The human family tree* http://channel.nationalgeographic.com/episode/the-human-family-tree-3706/Overview#tab-Videos/07082_00 (accessed 18 April 2011)

[140] "Genetic roadmaps", *The human family tree* http://channel.nationalgeographic.com/episode/the-human-family-tree-3706/Overview#tab-Videos/07082_00 (accessed 18 April 2011)

[141] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 517

[142] Ibidem 473, 476

[143] Genographic Project, *Ethical framework* ([cited 18 April 2011 2011]); available from https://genographic.nationalgeographic.com/staticfiles/genographic/StaticFiles/AboutGenographic/Introduction/Genographic-Project-Ethics-Overview.pdf

atlas shows an entangled web of migration routes and lineages, evoking a complex image of migratory history. The vocabulary derived from these models is also more imaginative, again probably because of differences in media - and public. Trees dominate not just the metaphoric but also the visual vocabulary. For instance, Wells uses Aspen trees as a metaphor for the historical relationships that his population trees depict. Apparently unrelated Aspen trunks are connected under the soil, and "spring from a common source." Haplogroups are connected in a similar way: "if we dig down far enough in the genetic soil", we find that "all humans share a common ancestor."[144]

Figure 11 "Atlas of the human journey" depicting "mtDNA and Y chromosome migration routes." The orange dots indicate "journey highlights" such as the possible emergence of proto-Indo-European and "migration to Great Britain". The 'M9' label, which emerges with the movement of the mouse pointer over a route, indicates the marker associated with the route, or lineage: in this case, one that started with "A man born around 40,000 years ago in Iran [sic] or southern Central Asia [who] gave rise to a genetic marker known as *M9*, which marked a new lineage diverging from the Middle Eastern clan."[145]

Wells refers to Lewontin's landmark study of variation between and within human groups to explain that variation unites humanity, rather than separates it. He explains that his former tutor's results indicated that the bulk of human variation is "shared".[146] As Wells sees it, these new approaches not only transformed biology from "an anecdotal science to one that strove with ever increasing rigor to apply statistical

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[144] Wells, *Deep ancestry. Inside the Genographic project* 88

[145] Genographic website accessed June 26 2011 https://genographic.nationalgeographic.com/genographic/lan/en/atlas.html

[146] Wells, *Deep ancestry. Inside the Genographic project* 21

tests to better understand the underlying cause of the observations."[147] The statistical definition of groups, populations and races also separated them from commonsense concepts, much like the divorce from 'medical' and other known coding genes. He does not refer to the criticism raised against the Lewontin study.

The GP shares the HGDP viewpoint that modern times have brought radical change. The tree that the GP constructs may be a complicated one with numerous branches and missing links; it only becomes properly entangled at the top.[148] Globalization and admixture are turning its crown into a jumble. Thus, another narrative building block is added to Wells' historical narrative, structured by milestones in the development and migration of the human species. The mobility revolution, the "final Big Bang"[149] (the others being the "Great Leap Forward" and the ascent of agriculture) caused geographic homogenization, bringing together lineages that had been separated for thousands of years.[150] As a 'Balkanized' world comes to an end,[151] hunter-gatherer groups are the last links to this world, and will soon be immersed in the global melting pot too.

In Wells' book *Pandora's seed. The unforeseen costs of civilization* (2010), the indigenous groups take on another role. In the book, the focus lies on more recent phases in human history. Wells dates the onset of modern times with the shift to agriculture. What is more, he also traces the problems humanity currently deals with back to this change of lifestyle. These problems are urgent: (nutritional) diseases, overpopulation, mental illness, stress, unsustainable economies, and ruthless exploitation of resources. They all relate to a mismatch between human nature, which is the result of thousands of years of hunter-gatherer existence, and our sedentary lifestyles. The effects of the "transgenerational powers" that we unleashed when we took destiny in our own hands, by exploiting the environment, are too large for our minds to imagine.[152] "[W]e are at a critical juncture, a time unlike any other, when our culture threatens to destroy the essence of what it means to be human".[153]

Wells blames our 'logos', our instrumental world view, of which the agricultural

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[147] Ibidem 20

[148] Illustrated by an animated tree in "DNA mysteries: The search for Adam," pt2

[149] Wells, *The journey of man. A genetic odyssey* 184

[150] This convergence of lineages is illustrated in an online video about several participants in the GP public participation section. In Jorge Gonzales, "lineages that had been separated for long long times reunited in Jorge. His son is even more admixed." *The human family tree* http://channel.nationalgeographic.com/episode/the-human-family-tree-3706/Overview#tab-Videos/07082_00 (accessed 18 April 2011)

[151] Wells, *Pandora's seed. The unforeseen costs of civilization* 203

[152] Ibidem 58

[153] Ibidem 209

managing and moulding of the environment was the first largescale expression. He advocates a “new mythos”, and argues that hunter-gatherer societies are the sole carriers left of such an alternative world view. Wells argues that they deal with their resources in a sustainable way, out of necessity; they are relatively egalitarian[154] and peaceful[155]; they limit the number of children they have[156] and never acquire more than they can carry.[157] These groups represent the way man has lived during most of human history. Because this history has shaped us biologically, they present us with a mirror of ourselves – our better, or more natural selves, that is. Subtly, Wells elevates them to a morally superior position, to propose at the end of the book to take their world view “as a moral guide.” “Maybe we can learn to want less.”[158] He emphasizes that he does not “advocate a return to a hunter-gatherer lifestyle, [...] “but we can learn something about the state of modern society from these ancestors.”[159] The unifying message that we’re “all Africans” thus acquires an additional meaning: a diagnosis of present ills and a moral guideline for the future. Interestingly, this view was also used in the 1950s discourse about the equality of races. The argument was that humanity was threatened by modernity, to which no race was adapted: mankind was united by its shared afflictions.[160]

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[154] Ibidem 53
[155] Ibidem 195
[156] Ibidem 38
[157] Ibidem 192
[158] Ibidem 184, 208
[159] Ibidem 195
[160] Haraway, *Primate Visions. Gender, race, and nature in the world of modern science* 217, 223

Chapter five - Criticism continued – or not?

Like the HGDP, the GP was opposed by indigenous organizations, but the opposition didn’t hit the project as hard as the HGDP. Organizations that had criticized and battled the HGDP, such as the *Indigenous Peoples Council on Biocolonialism (IPCB) and Cultural Survival, pointed to similarities between the projects. They thought the aims and methods of the Genographic Project sounded “all too familiar”: they accused its initiators of not having learned from its precursor’s mistakes*[1]*. In 2005, the IPCB launched an attack on the GP. In the press release, Debra Harry, the executive director of the Indigenous People’s Council on Biocolonialism, called the GP “a recurrent nightmare”.* “It’s essentially the same project we defeated years ago. Some of the actors are different, but also some are the same. With the founder of the HGDP serving on this new project’s advisory committee, I can’t help but think this is simply a new reiteration of the HGDP.” The IPCB’s legal analyst Le`a Kanehe stated that “It’s interesting how in the past racist scientists, such as those in the eugenics movement, did studies asserting that we are biologically inferior to them; and now, they are saying their research will show that we’re all related to each other and share common origins. Both ventures are based on racist science and produce invalid, yet damaging conclusions about Indigenous cultures.”[2]

The Genographic relied on approvals by the Institutional Review Boards of the institutions it worked with. This went wrong for the project in Alaska. The IRB of the University of Pennsylvania had approved the collection of samples, but the Alaskan IRB was still considering the request, when the GP had already started sampling in Alaska. In 2006 the Alaskan IRB criticized the GP consent procedure.[3] The Genographic responded by temporarily stopping all sampling efforts to review the regional protocols.[4] By then, the GP had collected about 18,000 samples. Of these, only 100 were collected by Theodore Schurr, the coordinator of the North American branch, and he was forced to send back 50 of these that were collected in Alaska, and to start sampling all over again. The Genographic continued to negotiate the retaining of the samples, with reference to

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[1] http://www.culturalsurvival.org/publications/cultural-survival-quarterly/none/genetic-research-collecting-blood-preserve-culture; “There has been criticism that the Project has repeated the failings of past endeavours, such as the HGDP and the Arizona State University genetic research.” Rimmer, 'The Genographic Project: Traditional Knowledge and Population Genetics,' 43

[2] "IPCB press release: indigenous peoples oppose National Geographic & IBM genetic research Project that seeks indigenous peoples’ DNA," (2005)

[3] International Journal of Cultural Property (2009) 16

[4] https://genographic.nationalgeographic.com/genographic/lan/en/update_safeguards.html

the Pennsylvanian approval, and shifted its focus to other communities.[5] Many North American tribes refused cooperation. This was perhaps the result of a controversy that emerged when samples used for a diabetes study by Arizona State University were used without consent from the sampled Havasupai tribe members to reconstruct their migration history. The study linked them to Asian populations, which contradicted the Havasupai belief that they originated in the Grand Canyon.[6]

The whole episode evoked the remark from a professor of law that "IRB approval is [disconnected] from subjects and their protection, especially subjects outside the United States."[7] Marks voiced the more general objection, that the GP evaded ethical issues by seeking private funding, which allowed it to circumvent approval procedures and made it independent from public funds – factors which had prevented the HGDP to proceed.[8] The "ethical opacity that accompanies private sponsorship" allowed for the HGDP to reappear, he argued, in the form of the GP.[9] He also asserted that the GP was formulated without the input of bioethicists.[10]

Scientists and their critics met on 20 May 2006, when Cultural Survival hosted a meeting of GP scientists and representatives of the indigenous in New York.[11] A GP press release emphasized afterwards that communications were "open and respectful" and that "all parties remained committed to a future dialogue." It also emphasized that sampling was always preceded by a consent procedure. However, it couldn't prevent a recommendation by the UN Permanent Forum on Indigenous Issues to suspend the project, and call for an investigation of its objectives by the WHO and the Human Rights Council.[12] In July, *Cultural Survival called for a moratorium on the whole project;*[13] *and in* December, the project was reported to be 'on hold'.[14] Victoria Tauli-Corpuz, chairperson of the UNPFII, explained in *Geographical Magazine* that the main objection was that the project didn't align its priorities with those of the indigenous people it claimed to

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[5] Marks, "Human genome diversity studies: Impact on indigenous communities,"

[6] Amy Harmon, 'DNA gatherers hit snag: tribes don't trust them,' *The New York Times*, December 10 2006

[7] George J. Annas, 'Anthropology, IRBs, and human rights,' *American Ethnologist* 33 (2006) 542

[8] Jonathan Marks, 'Science, samples, and people,' *Anthropology Today* 28 (2010) 3

[9] Marks, 'Lessons from history,' 202

[10] Marks, "Human genome diversity studies: Impact on indigenous communities," 3

[11] https://genographic.nationalgeographic.com/staticfiles/genographic/StaticFiles/ProjectUpdates/Genographic-Project-Cultural-Survival.pdf (accessed June 30, 2011)

[12] "The Permanent Forum recommends that WHO and the Human Rights Council conduct an investigation of the objectives of the Genographic Project which proposes to collect 100,000 DNA samples from the indigenous peoples of the world in order to formulate theories on historic human migrations, that the Genographic Project should be immediately suspended and that they report to indigenous peoples on the free, prior and informed consent of indigenous peoples in all communities where activities are conducted and planned." UNPFII, "Report on the fifth session," (New York: 2006) 15; Amy Harmon, DNA gatherers… NYT 2006; http://www.ipcb.org/issues/human_genetics/htmls/unpfii_rec.html; zoek UNPFII doc

[13] Harmon, 'DNA gatherers hit snag: tribes don't trust them,' ; http://www.culturalsurvival.org/publications/cultural-survival-quarterly/none/cultural-survival-calls-genographics-moratorium

[1414] Ibidem

collaborate with: "[o]ur history is not the main thing that indigenous peoples are concerned about at the moment. […] All over the world we are being killed, we are being displaced. And while this is going on, the Genographic Project is spending millions of dollars on a study that hopes to show the patterns of population migrations. It's hard to see how this is a cooperation. Why don't they bring that money to us and ask us what we really need?" A secondary objection seems to have been that the Genographic didn't talk to the appropriate indigenous institutions.[15]

One line of indigenous criticism addressed issues of profit, related to patenting, as was the case with the HGDP. This critique has been studied extensively.[16] But as the Havasupai case illustrates, next to these issues of power and profit, the genetic historical narratives, and occasionally the accompanying ideological message, also raised objections, and sometimes plainly clashed with indigenous histories and origin stories. As described in the previous chapter, GP publications occasionally documented these clashes, albeit concisely.

Wells juxtaposed the numerous attacks and petitions with the willingness of large numbers of indigenous peoples to participate, and pointed to the informed consent procedure that precedes the taking of each sample. At a forum dedicated to the GP, "Decoding Implications of the Genographic Project" at the 39th Annual Chacmool Conference on "Decolonizing archaeology" in 2006 at the University of Calgary in Canada, Wells stated that the GP representatives were "not given the opportunity to speak substantively" at the UNPFII meeting.[17] "We have encountered little resistance to the project in the field, where we are able to explain the project directly to prospective participants. The vast majority of those we have approached – more than 95 per cent – have agreed to participate. In parts of North America and Russia, we've even had communities approaching us. Those who have refused have done so because of a fear of needles or something, not because they object to the project."[18] He stated that "it is paternalistic to imply that indigenous groups need to be kept from the knowledge that genetics might offer." "I don't think humans at their core are ostriches. Everyone has an

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[15] Quoted in *Geographical dossier: The Genographic Project*, (Geographical Magazine, 2006 [cited 7 April 2011]); available from http://www.geographical.co.uk/Magazine/Dossiers/The_Genographic_Project_-_September_2006.html

[16] 'Chacmool conference forum "Decoding implications of the Genographic project",' *International Journal of Cultural Property* 16 (2009); M'Charek, 'De onzichtbare (f)actor. Standaardisatie, ras en genetische diversiteit,' ; M'Charek, 'Een kwestie van technieken. Over de buitensporigheid van de genetica en de onbestendigheid van ras,' ; A. M'charek, *Technologies of similarities and differences. On the interdependence of nature and technology in the Human Genome Diversity Project* (Amsterdam 2000); Reardon, 'Decoding race,' ; Reardon, 'The human genome diversity project: A case study in coproduction,' ; Reardon, *Race to the finish. Identity and governance in an age of genomics* ; Rimmer, 'The Genographic Project: Traditional Knowledge and Population Genetics,'

[17] Wells and Schurr, 'Response to decoding implications of the Genographic Project,' 186

[18] *Geographical dossier: The Genographic Project*, ([cited)

interest in where they came from, and indigenous people have more of an interest in their ancestry because it is so important to them."[19] Wells reported that the GP sent written answers to questions raised during the session to Cultural Survival, and that "[s]ince this time, neither the UN nor its related offices, nor the World Health Organization [...] with whom we sought to explain our work, have raised any questions about our goals and methods."[20]

Indeed, many indigenous people were interested in the research. They felt that the results could "bolster their cultural pride" and even "force an acknowledgment that they were here first, undermining those who see the government as having 'given' them their land."[21] For instance, the Seaconke Wampanoag requested to participate in GP 2005. Tallbear, who, remarkably, judged from photos that they were "a virtual rainbow of 'admixture'", stated that they were not federally recognized as a tribe; that there was a lack of historical evidence to base their land claims on, and that they therefore turned to the GP. She argues this was a "mismatch": "The mtDNA and Y chromosome analyses that the project performs to look for 'Native American markers' do not point to specific relations, tribal affiliations, and recent tribal histories. Genographic's DNA analyses cannot tell the Seaconke Wampanoag who they are as Wampanoag."[22] However, the very participation with the Project and the press attention it generated confirmed their status as indigenous. Whatever the outcome (which could remain confidential), "the two parties offer each other a great deal in terms of their respective cultural and public relations needs [...]. [The Wampanoag] accrue indigenous cultural capital, and Genographic is portrayed in the American press as "collaborating" with a U.S. tribe."[23]

The GP researchers published an article tracing the descent of the Wampanoag in 2010 stating that to West Eurasian and African lineages ("reflecting the extent of their contacts and interactions with people of European and African descent"); "a range of Native American, West Eurasian, and African haplogroups" and via a paternal lineage to New Guinea and Melanesia. Furthermore, they stated that "Comparison of the genetic data with genealogical and historical information allows us to reconstruct the tribal history of the Seaconke Wampanoag back to at least the early 18th century."[24] Although

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[19] Harmon, 'DNA gatherers hit snag: tribes don't trust them,'

[20] Wells and Schurr, 'Response to decoding implications of the Genographic Project,' 187

[21] Harmon, 'DNA gatherers hit snag: tribes don't trust them,'

[22] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 420

[23] Ibidem 420

[24] Sergey I. Zhadanov et al., 'Genetic heritage and native identity of the Seaconke Wampanoag tribe of Massachusetts,' *American Journal of Physical Anthropology* 142 (2010) 579

the study pointed to nonindigenous origins of both Y chromosome and mtDNA haplotypes, they argued that admixture was not unusual for Native tribes. “the genetic data clearly support the extensive genealogical information and tribal records gathered by the Seaconke Wampanoag Tribe. Some of these genealogical records indicate Native American ancestry in past generations that would not appear through the analysis of mtDNA and Y-chromosome variation because direct maternal and paternal links to indigenous ancestors had been lost due to population loss or admixture.”[25]

Many objections were raised to the use of genetic knowledge to define indigenousness. Debra Harry, of the IPCB, stated that “If we have genetic scientists saying their research suggests that certain Indigenous peoples really are recent immigrants from somewhere else, this denies those peoples’ claim to their own indigeneity.”[26] A participant of the Chacmool conference claimed that there had been cases where American indigenous peoples excluded groups from land they claimed for themselves with reference to genetic data.[27] The problem for Tallbear lay with the precedence that genetics took over other sources of knowledge. She protested against Wells’ “proselytizing and totalizing” message. “It leaves no room for alternative meanings by which human beings want to and should be able to live.”[28] She quotes Phil Bluehouse, the Navajo participant who appeared in Journey of Man, to say that the “Genographic is not a research project that is in opposition to indigenous beliefs and desires. Rather, it is in sync both scientifically and spiritually with the beliefs and desires of the Dinè,” (Navajo).[29] Tallbear remarks that “a Navajo creation story is far older than the computer code metaphors that predominate in descriptions of that molecular form. Yet are we supposed to believe that mid- to late-20th-century metaphors are inherent to ancient Navajo knowledge?”[30] She argues that the GP webcasts indigenous accounts that do not provide insight in indigenous stories, but warps them into GP versions laden with DNA metaphors and genetics concepts:[31]

> *“the video is also a culturally authoritative performance on Genographic’s part.*

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[25] Ibidem 586

[26] Hollowell and Nicholas, 'Decoding implications of the Genographic Project for archaeology and cultural Heritage: Transcript of a panel discussion held at the Chacmool conference “Decolonizing archaeology” University of Calgary, Alberta, Canada, November 2006,'

[27] Ibidem

[28] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 422

[29] Quoted from video on GP website (no longer available online) by Ibidem 418

[30] Ibidem 419

[31] Ibidem 419

> *It adds a scientific gloss to what are already meaningful cultural, historic, and spiritual narratives in their own right. Even as it proposes to support indigenous meanings and original accounts, Genographic can be seen to hollow out the meanings of those accounts by attributing other meanings to them, the real meanings – the scientific meanings. It confirms indigenous accounts with the real evidence – scientific evidence. By colorfully reinforcing the truth of science, such indigenous origin stories are then worthy of being broadcast to the world".*[32]

Along similar lines, Ilkilic argued that "enriched notions of culture and ethnicity" should be developed, which are "not only based on genealogical information—such as most likely provided by projects like the Genographic Project—but understand the very nature of the construction of cultural identities as a historical, social and cultural process not caused by but rooted in our biological heritage."[33] He too argued that ethical aspects were not adequately addressed. Designing research such as the GP in a culturally, socially, and legally acceptable" way should contribute to "an epistemologically sound understanding of the different ontologies and cosmologies affected by and involved in research and thus contribute to both, freedom and responsibility of research and research subjects."[34] Consent procedures, to which Wells repeatedly referred, did not suffice because of this very difference between the scientific and indigenous cosmologies: "in the languages of many indigenous populations, elementary words used to describe the study such as gene, DNA, etc. do not even exist or [...] are invested with other meanings such as 'life spirit of mortals' or 'genealogy.'"[35]

Schurr and Wells characterized the clashes as conflicts "between certainty and probability, tradition and investigation, belief and knowledge." They proceeded to say that "While science can't define who you are, it can help you to understand more about yourself, including your ancestry. We understand why some people may not want this information, but we also hope that they understand why many people do." [36] However, some argued, the implications of research stretch beyond the individual who agreed to have his blood sampled; furthermore, in some indigenous communities the 'self' was

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[32] Ibidem 422

[33] Ilkilic and Paul, 'Ethical aspects of genome diversity research: genome research into cultural diversity or cultural diversity in genome research?,'

[34] Ibidem 33

[35] Ibidem 32

[36] Wells and Schurr, 'Response to decoding implications of the Genographic Project,' 187

conceptualised as a 'collective self', as opposed to the Western. "liberal", individualist notion.[37] This was why consent procedures were considered inadequate: it was not always clear who could speak for the whole community, and reconstructions of history based on a small number of individuals' DNA dealt with the history of the whole tribes to which they belong, and therefore had implications for non-participating individuals.

The priority for genetic over other accounts also evoked fears that "Scientific evidence that American Indians or other aboriginal groups came from elsewhere could undermine their moral basis for sovereignty and chip away at their collective legal claims."[38] An ethicist and an anthropologist argued in 2009 that "A very real possibility exists that courts or other legal forums will place more weight on DNA results over and above other forms of evidence when it comes to claims of cultural continuity such as oral histories, ethnographic accounts, or even archaeology."[39] Wells responded that if this was true, "this would, indeed, be a concern":

> *"We are well aware of this issue and understand its sensitivity to Native American communities across North America. Indigenous and traditional peoples [...] have a long history of poor and shameful treatment at the hands of government entities, and land that belonged to their ancestors has been taken in the past. However, DNA was not responsible for these injustices; social policies based on racist ideology were. The fault lies not in our genes, but in our society."*[40]

He argued that the meaning of DNA research results did extend this far:

> *"DNA alone cannot aid or undermine advances that have been made by indigenous groups over the past century. No Native American tribes, for example, define membership solely on the basis of an individual's mitochondrial DNA or Y-chromosome haplogroup status. To do so would be to ignore the other 99% of the genome, which also provides information about individual and human history, as well as written records and oral traditions, which contain the*

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[37] Jenny Reardon, '"Anti-colonial genomic practice?" Learning from the Genographic Project and the Chacmool Conference,' *International Journal of Cultural Property* 16 (2009) 206

[38] Harmon, 'DNA gatherers hit snag: tribes don't trust them,'

[39] Julie Hollowell and Gearge Nicholas, 'Introduction,' *International Journal of Cultural Property* 16 (2009) 136

[40] Wells and Schurr, 'Response to decoding implications of the Genographic Project,' 185-86 emphasis mine

> *same kinds of details. Such DNA markers tell you about some of your history, but they don't completely define who you are. Moreover, to the extent that DNA says anything about land rights, all genetic evidence supports the view that the ancestors of Native Americans were the first people to enter the New World."*[41]

In other words, the information DNA can provide on these issues is limited, and if it does provide arguments that are useful in legal contexts, these are in favour of the indigenous case. Moreover, genetic information is neutral; society is responsible for the way it is dealt with. Dorothy Lippert, coordinator of the repatriation of indigenous human remains and artefacts for the Smithsonian National Museum of Natural History, held a different view. She argued that power relations were inherent to the term 'indigenous' itself: "The truth is that one really only gets to be indigenous if one's ancestors were colonized. By identifying the subjects of the research to be indigenous peoples, the Genographic Project automatically sets itself up within the historical framework of colonization." Wells had hit a familiar sore spot with his explicit endorsement of the much-criticised view of indigenous as "isolates," "vanishing" in the genetic melting pot: "This description of indigenous people as *vanishing* is all too familiar to Native Americans. We were once defined as vanishing; in reaction, anthropologists struggled to scientifically acquire information about our communities. In this process, human remains and sacred objects were removed often with little regard for whether or not this was the ethical thing to do."[42]

Rimmer concluded that "The [Genographic] Project, the HGDP, and the Arizona State University diabetes project were each undermined by mutual distrust between scientific researchers and Indigenous communities regarding the legal and ethical issues of intellectual property, informed consent and benefit-sharing." He argued that ethical protocols had been insufficient and that indigenous needed greater legal protection, for which the United Nations Declaration on the Rights of Indigenous Peoples provided a blueprint.[43] This declaration, issued in 2006, stated that 'Indigenous peoples have the right to maintain, control, protect and develop their cultural heritage, traditional knowledge and traditional cultural expressions, as well as the manifestations of their sciences, technologies and cultures, including human and genetic resources, seeds,

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[41] Ibidem 185-86

[42] Dorothy Lippert, 'Science and humanity,' *International Journal of Cultural Property* 16 (2009) 197

[43] Rimmer, 'The Genographic Project: Traditional Knowledge and Population Genetics,' 49

medicines, knowledge of the properties of fauna and flora, oral traditions, literatures, designs, sports and traditional games and visual and performing arts. They also have the right to maintain, control, protect and develop their intellectual property over such cultural heritage, traditional knowledge, and traditional cultural expressions."[44]

There were objections about the scientific claims of the GP as well. Marks objected to statements, made on the basis a GP test, about an Alaskan woman not descending from the Aleuts "but from their one-time enemies, the Yup'ik Eskimos."[45] "I know enough genetics to know that there is no test that can distinguish between the members of any particular group and their neighboring enemies. DNA can no more distinguish an Aleut from a Yup'ik than it can tell an Israeli from a Palestinian, a Shia from a Sunni, or a North Korean from a South Korean. Those kinds of differences are constituted independently of the structure of the gene pool."[46] And Tallbear criticized GP speculations that are "not the stuff of science", such as those about Ghengis Khan descent, which she argued are based on speculation and oral history.[47] Greely objected against the participation branch, which claimed participants would take part in a research project, but (he argued) doesn't require personal information beyond that "necessary for the credit card transaction" He wondered how the GP would do research on human history without background information about the person's ancestry.[48]

With private funding, and due to the National geographic context, the GP's scientific visibility is limited: its research strategies were less topic of debate, as no formal proposal had to be published and evaluated by academic funding institutions. There were scientific articles published by its researchers, and it provides a database for research to the scientific community, but the bulk of the output is popular which does not go into detail about the way research is done. It is therefore less the focus of discussions and debates about the methods. Criticism generally concerned the way results were presented, identities constructed, and the use of concepts and metaphors. The debate between multiregionalists and those who favoured the Out of Africa theory, for instance, received new input with Neanderthal research, but was hardly reflected in Genographic publications. As mentioned in chapter four, Wells dedicated attention to the sequencing of sampling Neanderthal DNA for the first time, and considered this the

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[44] United Nations, *United Nations Declaration on the rights of indigenous peoples* (2006 [cited June 26 2011]); available from http://www.un.org/esa/socdev/unpfii/documents/DRIPS_en.pdf

[45] Harmon, 'DNA gatherers hit snag: tribes don't trust them,'

[46] Marks, 'Lessons from history,' 202

[47] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 421

[48] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 222

end of multiregionalism. One of the first publications of the Genographic Project confirmed the findings in 2007.[49]

However, debate has continued to the present day, with research into ancient human DNA producing mixed results. There was debate about the possibilities and methodological problems of using of ancient DNA.[50] In 2007, Templeton argued strongly against Out of Africa, referring to multilocus studies.[51] The correlation of geographic distance and genetic variation, one of the arguments of the multiregionalists, however, was dealt a blow with research that showed that within-population diversity decreased with the distance of the populations from Africa. This was interpreted as strong evidence for Out of Africa, as it could only be interpreted as difference in “founding times” of the populations.[52] A year before, in 2006, the ‘Neanderthal genome project’ was launched. It is led by Svante Paäbo, who was responsible for the study Wells referred to, in which he reported that Neanderthals and modern humans did not admix.[53] Over the years, the project has revised these results. recently, it produced tentative evidence of admixture between humans and Neanderthals, which was nuts to the multiregionalists and challenged the version of the Out of Africa theory that included the replacement of Neanderthals by modern humans. These discussions are seldom addressed by the Genographic; although Wells mentions debates between palaeoanthropologists about the question whether archaeological finds are representative.[54] In his books, Wells considers Out of Africa as proven.

Criticism of the Genographic focused not on scientific viewpoints, nor on methods. It came mainly from anthropology, ethics and science studies, and addressed, next to problematic relations with the indigenous, issues of power relations and racism. Tallbear remarks about Wells’ statement that ‘racism is scientifically incorrect’: “I read that statement as a non-sequitur. What does racism have to do with scientific correctness? She proceeds to point out that scientists, in the history of anthropological genetics, have found difference when they looked for it, and now find “connectedness”[55]

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[49] “it is clear that our results do not support the existence of mtDNA samples of Neanderthal (or other archaic Homo) origin in our database.” Behar et al., 'The Genographic Project public participation mitochondrial DNA database,' e104

[50] For instance, in Svante Paabo et al., 'Genetic analyses from ancient DNA ' *Annual review of genetics* 38 (2004)

[51] A. R. Templeton, 'Genetics and recent human evolution,' *Evolution* 61 (2007) 1507

[52] Weaver and Roseman, 'New developments in the genetic evidence for modern human origins,' 72-4

[53] “the Neandertal sequence falls outside the variation of modern humans. Furthermore, the age of the common ancestor of the Neandertal and modern human mtDNAs is estimated to be four times greater than that of the common ancestor of human mtDNAs. This suggests thatNeandertals went extinct without contributing mtDNA to modern humans.”Matthias Krings et al., 'Neandertal DNA sequences and the origin of modern humans,' *Cell* 90 (1997)

[54] Wells, *Deep ancestry. Inside the Genographic project* 107-8

[55] Tallbear, 'Narratives of race and indigeneity in the Genographic Project,' 415

- science delivers whatever society or political correctness requires. Some have pointed out that this does not necessarily has adverse effects. For instance, the launching on the web of the "Book of Icelanders", a genetic database of most of the Icelandic population, made data accessible to Icelanders. This created a sense of community among them, based on genetic kinship ties.[56] Others pointed to the dangers inherent in the new genetic identities that anthropological genetics carried with it: "a new racism, based on the result of the new genetics, may emerge from a one-sided identification of contemporary human beings with archaeological remains and the soil in which they are found."[57] And a distinct and strong line of criticism addresses the commercialisation of genetic ancestry testing, as described in chapter three.

All in all, the Genographic is fairly different from the HGDP, despite the many similarities. Both used phylogenetic trees, often pasted onto geographic maps. Both focused on indigenous groups. Both provided narratives of unity based on common descent, an African homeland, and a recent and short period history of human migration, dated between approximately 60,000 and 10,000 years ago. Both focused on this short history, and used it to explain current human diversity - and the other way around: both focused on those patterns in the human gene pool that could be used to infer the details of this historical period. Both interpreted markers as lineages connecting present and past ancestral populations. The views of history of the projects are similar. These emphasized sharp caesuras: the 'Great Leap Forward' sometime before 60,000 years ago, the shift to sedentary lifestyles between approximately 10,000 and 5,000 years ago, and the mobility revolution in modern times. Both used metaphors and language that, intentionally or not, reinforced an 'insular' view of genetic diversity, while both emphasized the clinal nature of variation. Both presented their research as fundamental in the battle against racism.

And both projects encountered criticism. Indigenous peoples opposed the projects with similar arguments. They placed them in a tradition of exploitation, objected to the precedence genetic information took over other historical sources, and opposed the scientific cosmologies that redefined their own histories and identities. Anthropologists objected to what they considered to be a flawed view of history, to the emphasis on population splits, the downplaying of genetic exchange and the historical

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[56] Pálsson, *Anthropology and the new genetics* 79

[57] Lucassen et al., 'Migration history: multidisciplinary approaches,' 35

complexity and muddiness of population histories. They also objected to the view of indigenous populations as 'living fossils', to the reification of genetic populations, and the presentation (and in the case of the GP, the selling) of the identities that emerged from the research. Moreover, they objected against the ideological message with which research was presented, to what they thought was a mergence of science with ideology, and the dependency of the latter on the truths of the former. They objected to the authority that anthropological genetics acquired, to its dominance over other disciplinary and lay bodies of knowledge. Because of the way both projects were presented, the way HGDP and GP research results were interpreted and appropriated, and also in the criticism the projects encountered, boundaries between science and culture are difficult to discern.

However, the projects operated in different historical contexts, and differed in some fundamental ways. One of the most striking differences is that between institutional contexts. The HGDP was a conglomerate of prominent, established anthropological geneticists working in an academic environment. Therefore, it was dependent on public funds and endorsement by the scientific community. The work of these geneticists predominantly took the shape of scientific publications, and popularisations were secondary, informative, and educational. These provided one-way communication from informed scientist to uninformed publics. Because the Genographic is a National Geographic project, and it is sponsored by IBM, it depended less on public money, on academic criteria and endorsement from the scientific community. Because of this, and because of the NG focus on education and popularisation, the GP addresses, and conforms more to, the uninformed public it tries to reach - and persuade to donate and participate. The nature of criticism levelled against the projects is therefore different. The HGDP's scientific home and visibility (due to controversies), as well as Cavalli's many publications and his important role in the field, inspired debates about methods and models. The GP's low scientific visibility and Wells extensive popular work resulted in a different emphasis, which lay predominantly on issues connected to the role his research played in a wider cultural context and lay discourse.

When the HGDP started, anthropological genetics had just burst onto the public scene. In the context of the end of the Cold War, the 'Eve' study and the Human Genome Project appealed to the public imagination and to a sense of a shared humanity. There were high hopes of genetics' potential, from the elimination of racial prejudice to the prevention of disease, albeit accompanied with emerging fears of genetic essentialism. Fifteen years later, the GP was launched in a different world. Ethnic conflicts that followed the collapse of former communist countries and the disappearance of the Cold War ideological umbrellas seemed to indicate a return of nationalism, of the importance of ethnic identities. Perhaps the fading of the hype that had surrounded genetics in the 1990s played a part too. Debates in and about anthropological genetics, of which the HGDP became a focal point, had tempered enthusiasm about research into genetic variation. Such research had also been tainted by the publication of several scientific and popular works about the reality of racial categories. Long-held viewpoints about the insignificance of genetic differences were questioned as more data became available, and was studied by an increasing number of scientists. Criticism from other disciplines and from indigenous groups had discredited anthropological genetic attempts to reconstruct human history. Meanwhile, taboos on biological differences were broken. Promising possibilities for preventive screening, genetic medical research had moved to the study of population differences, providing them with genetic identities. Lay demand for such genetically defined group identities emerged, and companies started to sell genetic ancestry tests. Genealogy incorporated the new genetic methods of reconstructing descent, and extended its historical scope, as it included, next to the reconstruction of family history, that of "deep" population history. These group histories and identities occasionally entered the political arena of tribal membership and indigenous status. In short, while the GP can be considered a descendant of the HGDP, the history of the two projects also illustrates the way anthropological genetics has changed in the past two decades.

Conclusion

The HGDP and GP narratives of human history and the population concepts that lay at their basis had implications for the way in which human unity and difference were defined. Notwithstanding the ambitions of the scientists involved to put an end to racism, or at least, to scientific and pseudoscientific legitimizations of racial views, their research possessed an ambiguity that had since long characterised diversity research - one could argue unavoidably. This ambiguity resulted from the tension between, on the one hand, arguments for the unity of mankind, and on the other, the categorisation and subdivision of that same humanity into clusters. The former referred to a shared and recent history, and the insignificance of genetic differences, while the latter resulted from the use of just such genetic differences as means to organise the human gene pool, and as historical sources. The tension pervades the methods, the tree models, the vocabulary and metaphors they used.

Although Cavalli problematised the use of trees as models, and admitted that their representativeness and use was limited, he stuck to them. While he developed methods to incorporate admixture into his models, he continued to emphasize fissions. Indeed, he selected data that were useful to construct tree models. Moreover, if the data did not fit a tree model, that is, if admixture had taken place, or populations had converged, he referred to this, rather than to the tree model itself, as a "source of error"[1]. He did argue that "the validity of a tree depends on exchanges being small"[2] and on "populations splitting cleanly",[3] emphasizing that this had not always been the case. But the language he used often suggested that it was the other way around – that the data were less 'valid' when they did not fit the model. For instance, he remarked that the "effect of admixture on trees" could be predicted by statistical methods and was visible in matrices of genetic distance as deviations from "standard patterns."[4]. It has been argued that his use of linguistic information was equally selective; that Cavalli chose controversial theories of linguistic 'splitters' and those who inferred ancestral, primal languages, because these fitted his tree models. As Nei remarked: "the authors do not really compare the genetic

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[1] Cavalli-Sforza et al., *The history and geography of human genes* 39
[2] Cavalli-Sforza and Cavalli-Sforza, *The great human diasporas* 190
[3] Cavalli-Sforza, *Genes, peoples and languages* 36
[4] Cavalli-Sforza et al., *The history and geography of human genes*

tree with the language tree. In fact, they compare the genetic tree with Ruhlen's taxonomy of languages."[5]

Perhaps this tree view of human descent, on a scientific, epistemological level, remained suspended between the status of a real representation of evolutionary or genetic history on the one hand, and that of nothing more than a convenient model on the other. And possibly this undefinedness was understood and accepted by many anthropological geneticists. Whether or not this was the case, it remains clear that his tree models carried with them the ambiguity of unity and difference: they provided a single root, yet conceptualised human populations as discrete branches, as stable throughout "deep history". And in the simplifying discourse of popularisation, the lay media and public appropriation, his nuances were often lost.

The tree remained the dominant visual and conceptual model for human migration, population and genetic history. Proposals of alternatives, which accommodated views of history that emphasize admixture, never seem to have provided a match for it. The reasons for the popularity of the tree model are difficult to establish. The power and ubiquity of trees as metaphors for descent in Western, or indeed, human culture,[6] and their long history of use in the biological sciences as well as in biblical study, may provide an explanation.[7] A comparison with their alternatives also gives the impression that the conciseness and catchiness of tree models may account for their success. 'Rhizotic' and 'trellis' models did not have the power of organisation and the insightfulness that trees possess. While this muddiness of such models is exactly what makes them superior in the view of those arguing that genetic history is complex, it may have been the reason why they never took root. The organisation of data, the scientific usefulness of a visually and conceptually powerful model, and the logic of lay discourse demanded simpler visions.

The resemblance of phylogenetic trees to genealogical family trees was paralleled by the use of family metaphors. Phylogeny, the history of groups of organisms, was described not only in the visual but also in the metaphorical language of genealogy, the history of families. Journey metaphors were the linguistic equivalent of the branches of the trees that were pasted onto geographic maps and interpreted as migration routes. Again, the use of such concepts may result from the cultural and, indeed, cognitive

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[5] Nei, 'The history and geography of human genes: Book review,'
[6] As explored in Laura Rival, ed., *The social life of trees. Anthropological perspectives on tree symbolism* (Oxford and New York, 1998)
[7] Bouquet, 'Family trees and their affinities: the visual imperative of the genealogical diagram,'

power of the journey metaphor. As Lakoff has argued, this metaphor is generally, perhaps universally used to conceptualise phenomena as various and fundamental as love relationships, careers, and individual's lives.[8] Of course, its use by the HGDP and GP is not surprising and not always metaphorical; after all, in these texts it refers to actual journeys – or does it? Lucassen et al argue that we should carefully consider what the inferred migrations meant on an individual level:

> *If we write that man migrated from Northeast Africa via the shores of Arabia, Persia, India and Indonesia as far as Australia, what does it mean for the individuals involved? Of course none of them has seen both Africa and Australia [...] Suppose that the whole coastal "trip" – 10,000 kilometres as the crow flies – actually meant a migration of on average not 200 metres but, say, 1 kilometer per annum, what was its impact on the short-lived life of most of our ancestors?*[9]

Another example of the influence of the choice of words is the naming of populations. This is part of the unavoidable categorisation of genetic data and, again, analogous to the branches on phylogenetic trees. It would be absurd to equate the naming of a population with reification, but the use of current tribe names to designate lineages does lend ancientness to the group identities in question. The view of the indigenous gene pools as pockets of ancient genetic makeups, harbouring "anthropological genes" (i.e. genes informative of migration history)[10] reified population categories and promoted an "insular view"[11] of genetic differences, however much admixture and similarities were emphasized. These population boundaries were made ahistorical - 'eternalised', so to say - with the historical narrative of the lineages with which they were connected to ancestral populations. The use of the words 'tribe' and 'clan' illustrate the focus of research on current tribal communities and discourses of descent and group membership. The (sometimes unintended and often implicit) identification of groups with the markers, which were "selected to be maximally informative"[12] of differences and history, reinforced the reification of the groups in question and evoked fears of

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[8] Lakoff, 'The contemporary theory of metaphor,'
[9] Lucassen et al., 'Migration history: multidisciplinary approaches,' 34
[10] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 477
[11] Pálsson, *Anthropology and the new genetics* 220
[12] Marks, 'Race. Past, present and future,'

genetic essentialism. “[N]aming groups in the past and in the present that are related through common maternal connection ‘clans’ [...] shore[s] up ideas of purity and biological distinction.”[13] Criticism of these views, rooted in ethnographic and anthropological field work, emphasized more fluid population definitions.

Wells and Cavalli did not address this tension extensively in their publications, and do not seem to have considered it damaging for the overall unifying message of their research. Often, their writings give the impression that they are hardly aware of the ambiguity in their research. Perhaps this results from their familiarity with models as merely models. They did critically discuss the concepts they used - but their trust that their various publics would appreciate such nuances, and their underestimation of the force of words and images, are striking. This trust sometimes turned out to be naive, as the opposition and their subsequent indignation illustrate. Cavalli shrugged off the attacks of the HGDP with the remark that “It is easy to recognize a pioneer: his back is full of arrows.”[14]

The question whether the scientists involved have failed in the explanation of the epistemological status of their concepts, because this was self-evident for them, or the whether the issue is rather the loss of nuance inherent in popularisation, remains an open one. It depends on which view one has of scientists’ responsibility for the way their research results impact non-scientific discourses. Cavalli’s and Wells’ engagement in such public discourses, and their claims that their results had social relevance, propagated the view that genetics had acquired cultural authority to speak about such issues. In this way, in a sense, they answered the question of responsibility: they encouraged non-scientific appropriations of their results, and attributed social and cultural meaning to them. Therewith, they made themselves vulnerable to accusations of irresponsibility.

Whether or not one agrees with such accusations, it is clear that their explanation of the tentativeness and complexity of the information that their research produced – which Cavalli did more extensively than Wells – was often contradicted by their language. That the use of words can be confusing even for informed readers is illustrated by a controversy between Cavalli and Bryan Sykes, a human geneticist, over Cavalli’s model for the spread of agriculture. Sykes took Cavalli’s term “wave of advance”

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[13] Nash, 'Genetic kinship,' : 21; Marks, '”We’re going to tell these people who they really are”: science and relatedness,'

[14] Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza*

to mean that the expansion was an "overwhelming" phenomenon, which was not what Cavalli believed. He merely considered 'wave of advance', derived from R.A. Fisher's mathematical model with the same name, a "classier" term for 'demic diffusion'. Cavalli had not investigated "how *major* [...] the expansion was, only "*how* it [...] spread". Cavalli stated that the term might have been "beguil[ing]".[15] This example illustrates the power of words to mislead – as Cavalli's biographers have it – even a specialist. Choice of vocabulary also seems to have obscured the nuances and reservations Cavalli presented with regard to his tree models and population concepts. The GP especially offers an example of how the use of enchanting or catchy language can contradict the nuanced and preliminary nature of genetic population concepts, as well as the overall message of unity. This resulted from the popularising nature of the GP, as well as the fact that it was more subjected to what Greely called the 'dynamics of the marketplace'.[16] The differences between the HGDP and the GP reflect the general movement during the past two decades of anthropological genetics knowledge from academia into the popular realm.

Apart from the way results were presented, the tension was inherent in the research itself, as scientific debates illustrate. It is striking that Wells' and other GP publications handle these issues more loosely: here, population categories are named more bluntly and less effort is taken to problematise them. This may be explained by the fact that, at the time the GP was launched, more elbow room had been created for ideas about differences between groups. The taboo on racial categories had been questioned by mainstream, respectable scientists who received far less tar and feather than the more marginalised authors of books arguing for 'the reality of race' in the 1990s. In addition, the emergence of a commercial market for genetic ancestry testing had created popular demand for genetic group identities. This marketability also took the sting out of such concepts.

It has been argued that genetics in anthropology has a history of scientism.[17] Cavalli's statements about the educational value of genetics research, and especially his quantitative modelling of culture,[18] place him in this tradition. Both Wells and Cavalli

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[15] Ibidem 94 emphasis original

[16] Greely, 'Genetic genealogy. Genetics meets the marketplace,' 230-1

[17] "human genetics began in America as a scientistic alternative to the non-racist anthropology Franz Boas was struggling to develop" Marks, 'Lessons from history,' 199; Nash refers to Steinberg who argued that "genetics [...] figured as the truthful antidote to inaccuracies and distortions of social science and historical research" Nash, 'Genetic kinship,' 22

[18] For instance, in a discussion of culture as the object of evolution in work by Feldman and Cavalli, the latter's biographers report that "Cavalli notes that we do not know what the physical bases for ideas really are', but that this in his view should not dissuade us

argue that their research produces insights that can inform a betterment of the human condition and their moral message extends the interpretations of their results beyond the boundaries of scientific research; it explicitly targets social problems. From better understanding ourselves, to curing the “disease” of racism, to providing direction for the ways the problems humanity faces at present (as Wells did in *Pandora’s seed*) - all of these possible benefits have been claimed for their research. While emphasizing the educational value of their work may not be characterised unambiguously as scientism, it is certainly an indication that ideological message and science were profoundly mixed. It was this kind of mixing that evoked scientists’ objections to the First UNESCO Statement in the 1950s. Ironically, it is also at the core of Cavalli’s biographers’ (and therefore most likely his own) objections to Lewontin, whom they accused of explicitly attaching a social message to his findings. Throughout the history of diversity research, scientists protested when the mantra of equality and unity was made dependent on ideology, while time and again, research results were nevertheless presented as evidence against racism; sometimes even by the very scientists protesting the conflation of social action and scientific research by others.

Cavalli’s scientistic inclinations can explain the opposition he encountered – this is certainly the case with his excursions into the study of culture and the cross-pollination of cultural and genetic concepts in his work. His explicit ideological message remained dominant and, so to speak, ‘politically correct’ during the period covered here, and is therefore less of an explanation for the ferocious criticism. Most of his critics attempted to acquire the same goal as he did: to discredit views of difference. It was not his antiracist message they attacked, and, remarkably, only occasionally the idea that science could be used to spread this message. They objected to what they perceived as latent racist elements in his research.

This also applies to Wells and the Genographic. The attempt to genetically identify not only ethnic but also religious communities illustrates a similar conflation of cultural and genetic population categories, which in Cavalli’s work received much criticism. Overall, GP research was based on the same theories and models, and therefore, scientific criticism (to the extent that there was any) of the GP was hardly different from the HGDP. Most of the criticism of the GP was a reaction against the

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from studying them; after all, when the basis of genetics was similarly unknown, we could already work with it.” In other words, the possibility of a physical basis for ideas is considered real. Stone and Lurquin, *A genetic and cultural odyssey. The life and work of L. Luca Cavalli-Sforza* 99 simplification inherent in popularisation and commercialisation, which rendered such conceptualisations of difference more explicit. This is clearly reinforced by the kinds of media Wells uses: television and film demands that the issues addressed are sensational, catchy and simple. Because Wells targets a lay public, not only the concepts but also the questions he asks are different from those guiding Cavalli's popular works. The latter are side-products of research. Wells' investigations seem more informed by and tailored to public interests.

Thus, perhaps it is the expansion of the interpretation of their research, from the mere reconstruction of *genetic* evolution to include population history, group descent and identity, ideology and ethics that evoked much of the criticism. Anthropological genetics has generally defied boundaries between 'science' and the public', and Wells and Cavalli positioned their research results squarely in the cultural domain of meaning and collective self-understanding. Even when they did not, their findings were often appropriated by non-scientists to be used for individual and group identity formation, as well as for political ends. As this trend took root in the 1990s and blossomed in the 2000s, anthropological genetics narratives and concepts were properly appropriated by the public.

The anthropological nature of the questions asked positioned this research in debates about fundamental issues of humanness and differences. Addressing age-old questions of origins, this research could hardly have remained restricted to purely scientific debates. With regard to the cosmologies propagated by the projects, it seems not much has changed. The world views and moral messages proposed by the two projects were fairly similar. In both HGDP and GP narratives, human unity was emphasized; a common ancestor and the trivialising of differences as 'superficial' served as counterbalances for the divisive potential of population categories. Wells nor Cavalli seem to have changed their basic ideas in response to criticism. The Genographic learnt from the history of the HGDP: it learnt not to 'immortalise' the samples they took; not to claim medical relevance; and to enrol the indigenous, whether by funding cultural preservation initiatives or providing them with the cultural capital of a genetic identity. But it didn't diverge fundamentally from the research strategy the HGDP had set out. The GP social message at most provided more room for explicitly formulated group identities.

A clear historical scheme emerges from the narratives these projects produced.

The emphasis on fissions and journeys, and the use of populations as protagonists, is clearly closely connected to the methods of choice, most notably the tree. They are structured by several caesuras, albeit sometimes dated somewhat differently: the maturation of modern humans during a cultural 'leap', the shift to sedentary lifestyles as a result of the invention of agriculture, and the modern mobility revolution. All three caesuras resulted from technological inventions (in response to climatological difficulties, at least in the case of the first and second caesura), in a broad sense: the first form the development of language; the second from a revolution in subsistence methods; and the third from the transport and industrial revolutions. In other words, the sense of radical and abrupt change that characterised their view of genetic and migration history is based on a similar view of cultural change. The emphasis on technology echoes the emphasis on culture as defining as well as uniting the human species, which has characterised biological thinking since the UNESCO Statements on race.

A recent argument against this view of historical discontinuity has been made. It can be regarded as an extension of multiregionalist 'uniformitarianism', which holds that continuity is the rule in human history. It is proposed by linguists and genetics in Lucassen et al's interdisciplinary overview of migration histories, who argue that migration patterns for hunter-gatherers and farming populations are not fundamentally different.[19] This challenges the idea that with the invention of agriculture, the population-genetic processes that created current genetic frequency patterns came to a halt. The view therefore undermines the rationale behind Wells and Cavalli's focus on the period before agriculture. It remains to be seen if such arguments will successfully challenge anthropological genetics views of history.

The general interest in the migration history of the whole human species, which informed the HGDP and GP, may not be surprising in a time when 'globalisation' was a buzzword. As the genre of world history developed, migration history followed in its wake.[20] In several recently published works, the 'traditional' historical sciences were merged with disciplines that focus on "deep history". Jared Diamond's *Guns, germs and steel* (1997) is an example of this, combining natural history with the historical sciences as practiced in humanities contexts. Patrick Manning's *Migration in world history* was

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[19] Lucassen et al., 'Migration history: multidisciplinary approaches,' 31

[20] In the slipstream of global history, history of migration is studied more and more on a worldwide scale. Ibidem 10-11

hailed as another, focusing on human migration, and covering the past 80 millennia. It was referred to as the first overview that engages with sciences that focus on "deep history" and are remote from historical studies.[21] "The book argues that although all species migrate, only humans migrate to other communities, because different groups of humans, distinguished by their unique language capacity, developed cultures of their own. This cultural proliferation (from technology to value systems) explains the advance of civilizations and clarifies why it was profitable for people, unlike animals, to migrate to other groups." [22]

Thus the timescale of the historical sciences expanded, and they started to incorporate insights from other disciplines, anthropological genetics among them. This has also resulted in a diversification of historical sources:[23] "The notion of migration needs to be broadened to include not just movement of individuals but also families, societies, genetic material, chemical constituents, words, languages, material culture, ideas."[24] Indeed, this trend is becoming visible in the genre of global history. This creates the danger of confusion of 'migrating objects'. The histories of languages, material cultures as identified by archaeology, or surnames, are easily conflated, exchanged, or interpreted as indicative of each other. As we have seen, some critics accused Cavalli and Wells of just such confusing of the history of genetic markers with the history of populations. In addition, the use of different timescales by historians and scientists investigating "deep history" may add to the confusion,[25] as it encourages the description and conceptualisation of long-term and gradual evolutionary change with the vocabulary of short-term history, which deals with groups and individuals. This is what critics of the use of family metaphors to explain genetic history warned against. Therefore, "Analysis of migration needs to be specific about what, precisely, is in movement."[26]

Among these different historical sources, the "anthropological gene," endowed with the authority and objective-scientific aura of genetics, acquired a special status. It became not only a new historical source, but also a new 'resource' of identity and claims about differences. Initially, this was considered dangerous, much in line with a long tradition of cautionary tales about scientific racism. The fear was that genetic evidence

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[21] Ibidem 16
[22] Ibidem 14
[23] Ibidem 30
[24] Ibidem
[25] Ibidem 14
[26] Ibidem 29

would shore up claims about the superiority of certain groups: what if, for instance, a gene for intelligence was found? Since the 1960ies,[27] population genetics moved from ‘classical’ to DNA polymorphisms, and away from the phenotypic level, by looking at non-coding regions of the genome. In the context of a more general trend from ‘genetics’ to ‘genomics’, the complexity of the relation between genotype and phenotype was emphasized, as well as the fact that very little of these interactions was known.[28] The inclusion of non-coding DNA reinforced the argument that genetic data could be separated from the everyday realities of mental and bodily differences. Nevertheless, population genetic research has continued to focus on both markers that have a known relationship to phenotypic differences and those that do not code, or ‘junk DNA’. The latter are even considered to be useful for the construction of ‘molecular clocks’: “despite assertions to the contrary, ancestry inferences are robust using a modest number of polymorphisms in either coding or non-coding regions.”[29] With the use of markers on such coding regions of the genome, as well as their references to phenotypic differences, Cavalli and Wells provided their critics with ammunition.

However, what is especially remarkable about the recent history of anthropological genetics is that genetic identities started to evoke enthusiasm as well as criticism. They were increasingly used ‘positively’, whether to claim land, group membership, and to define individuals’ and groups’ ethnic identities. Such uses paralleled more traditional uses of genetic narratives as resources of world views, whether to postulate a universal humanity to battle racism or to exclude groups and to emphasize the reality of differences. This positive use challenged a view of the indigenous and other communities that anthropological genetics dealt with as passive victims of racist ideas disguised as narratives of descent. Indigenous communities were enrolled in genetic ancestry testing, and made use of it as a resource that could empower them.

Yet such positive use of genetic knowledge evoked objections against its dominance and authority as well. Critics opposed the imperial nature of anthropological genetics, the discrediting and ‘hollowing out’ of alternative sources of knowledge and identitiy. Opposition from anthropologists targeted these issues. While such arguments were undoubtedly informed by authentic concerns about the possible disappearance of

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[27] Sommer, 'History in the gene: negotiations between molecular and organismal anthropology,' 475, 506

[28] Ibidem 517

[29] Michael Bamshad et al., 'Deconstructing the relationship between genetics and race,' *Nature* 5 (2004) 602

such alternatives, it can also be considered as boundary work between disciplines. After all, the historical and mythological narratives and cultural identities that were perceived to be threatened by genetic ones were among the traditional objects of anthropology. General fears about genetic essentialism were mirrored by disciplinary clashes. Marks provided the most outspoken example of this clash when he complained about the fact that anthropological genetics did not incorporate anthropological expertise. [30]

The imperial view of genetics can be contrasted with the multi-interpretable nature of genetic data. The genome is complex and harbours an incredibly large amount of information. As M'Charek has pointed out, the human gene pool can be organised in a large number of different ways, depending on which markers are used for this organisation. Genetics therefore has the potential to upset traditional taxonomies and boundaries between human groups. "The exciting thing about present-day genetics is its *licentiousness* [buitensporigheid]. And its denaturalising potential is a result of the excessive amount of objects it can produce".[31] However, she pointed out, within the scientific community, a selection of 'priority markers' has legitimised itself, as it allows and moderates scientific communication, and ensures the comparability of research results and databases.[32] In this process of defining 'normal science', in her opinion, the potentially upsetting power of genetics that she considers beneficial, threatens to be lost. She argued for the embracing of the ambiguity of genetic information, for accepting the existence of several ways of organising it, and for allowing the resulting, sometimes conflicting interpretations to exist next to each other. This would not only properly illustrate the fluidity of group categories, but also discredit the view that genetics has privileged access to knowledge about human similarity and difference. She argued that this would also benefit scientific research, and she illustrated this with the fact that

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[30] He places the HGDP in "a tradition of biogenetic studies that cast themselves in opposition to anthropology." And: "genetics portrays itself as modern alternative to anthropology." "The HGDP has claimed it has proved that races don't exist – but anthropologists already knew that." (Marks, '"We're going to tell these people who they really are": science and relatedness,' 355, 375). Precisely because of its history of scientific racism, as well as opposition against that, anthropology knows about the pitfalls of diversity research. Marks objected in 1996 to the addition of anthropologists to the HGDP "only as an afterthought." Interestingly, Kidd replied to Marks' accusations that "by any objective criteria [...] most people would agree that Luca Cavalli-Sforza, Mary Clair King and I are anthropologists." (Kenneth Kidd, 'letter: Anthropology's role in the HGDP,' *Anthropology Newsletter* (1996) 2.) "Actually, they probably wouldn't", Marks responded. (Marks, '"We're going to tell these people who they really are": science and relatedness,' 377). He explained in 2001 that this was more than just "turf patrolling"; if the difference between the two bodies of knowledge was not acknowledged, anthropological expertise would be neglected and a repetition of the history of scientistic alternatives for anthropology, such as eugenics, would be possible, he argued. Anthropological insights into the "cultural dimensions of all human activities, including science" were dismissed. Marks argued that the Project could have benefited intensely from biological anthropological input. Anthropologists could have taught the geneticists, for instance, about the relationship between named populations and natural categories. But the anthropologists enrolled in the HGDP were 'sycophantic', and geneticists saw no need for anthropological input. (Marks, '"We're going to tell these people who they really are": science and relatedness,' 377, 375)

[31] "Het spannende aan de hedendaagse genetica is haar *buitensporigheid*. En haar denaturaliserend vermogen zit 'm in de excessen aan objecten die zij voortbrengt." translation mine; emphasis original. M'Charek, 'Een kwestie van technieken. Over de buitensporigheid van de genetica en de onbestendigheid van ras,' 33

[32] Ibidem 32-33

medical science defines populations differently depending on the specialism.[33] Her plea is reminiscent of Allan Wilson's argument to "abandon previous concepts of what populations are" [34] in the HGDP sampling debate.

It remains to be seen whether such an approach would be viable. The recent public appropriation and the commercialisation of anthropological genetic concepts certainly have pushed developments in the opposite direction. And one wonders what the application of her ideas to genetic histories would look like. Their narrative nature requires protagonists and plots. Moreover, Wells' and Cavalli's ambitions are the reconstruction, not the deconstruction of history. Simplicity and insightfulness are important criteria for their models, which might be incompatible with the desire to do justice to the ambiguity and multi-interpretability of the genome. It can also be doubted whether the performance of these narratives as scientific equivalents of origin myths, and as effective carriers of ideological messages, benefits from an emphasis on undeterminedness and complexity.

The research strategies were based on decisions what differences matter; which are most informative of human history. The anthropological geneticists discussed here were not primarily interested in problematising their conceptual tools and inferences; their goal was to provide meaningful statements about genetic structures and interpret them as historical sources. They did, each to a different extent, acknowledge the ambiguity and uncertainty of their data, and this increased the validity of their inferences. The complexity of genetic data was also used as an argument for their ideological message of human unity. Nevertheless, even this message, like the research itself, required a reduction of this complexity to a manageable level, and with this simplification, a distortion of muddy realities. Therefore, the tension between unity and difference was not only the result of their vocabularies, ideological agendas, and visuals, and the way their publics interpreted these, but was inherent in their research itself.

What is striking is that in the GP narrative, group identities are less cautiously presented. Comparison of HGDP and GP origin stories leaves the impression that such concepts became more accepted in the past decade. Looking at diversity research from a bird's eye perspective, comparing discourses as they were established in the 1950s with those of the 2000s, the message of unity seems to have evolved slowly from one that

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[33] Ibidem 32-33

[34] Roberts, 'A genetic survey of vanishing peoples,' 1615

depended more on an explicit view of the equality of humans to one that subtly provided more room for difference. The view of variation in and diversity of the human species became a more explicit aspect of human unity, and seemed to be less dominated by fear of potential racist interpretations. Diversity became something to be celebrated rather than downplayed. However, the basic message remained the same: shared human origins and DNA patterns provide evidence for the unity of the human species and genetic differences, however informative, are insignificant.

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