

# **Human Genomics as Identity Politics**

**Dr Christine Hauskeller**  
**ESRC Centre for Genomics in Society**

**Award Paper for  
Young Scholar Conference  
Cornell University  
7-9 April 2006**



## 1) Introduction

A basic assumption underlies current understandings of genes and genomes: The properties of cellular genomes mould and produce the properties of physiological bodies, not the other way round (Nelkin & Lindee 1995). There is debate amongst experts as to what genes or genomes are and how we conceptualize them properly (see, e.g., the Representing Genes Project). These differences are expressed in attitude, laboratory practices and theoretical concepts but also in the various metaphors used to speak about genomics. Metaphors such as code, map, blueprint, script, text, or programme (Kay 2000, Keller 2000, Nelkin 2001, Nerlich & Dingwall 2003, Turnbull 2004) obviously have different implications. Despite these differences in gene-images the experts (biologists, philosophers, historians, medical scientists and clinicians, social scientists, media studies people etc.) share a powerful basic understanding of what genomes are which also underlies public understandings of genomes. This minimal agreement encompasses the view that DNA and genomes exist as material entities. As such they connect the molecular body to the phenotypic appearance of a person and the phenotypic appearance to the person's life history, the bodies (and lives) of her ancestors, and to her current environment. This positioning of genomes and the science that investigates and familiarises them, genomics, means that genome knowledge implies identity knowledge. Life history, ancestry, and environmental influences can be translated into the humanities and social studies concepts of self, kin and origin, and society – they thus represent the key dimensions of personal identity as understood in current Western philosophy and social science. Given this close connectedness of genome, body, and identity, genomics seems ideally suited to help determine personal identity, to add an essential quality to these social categories.

What counts as a social marker, how this changes over time and the margins within which certain positions in society can be claimed are extremely flexible. In social structures in which lineage and social class of the birth family do not predetermine the margins within which an individual lives, but on the contrary personal freedom of development is deemed to be a basic right of each person, status has to be negotiated. This implies also that acquired positions need regular re-affirmation and societal recognition. The abandonment of an 'innate' social status goes hand in hand with the need to form oneself into a subject, to develop an identity – actually many different dimensions of personality that stand for uniqueness. In a democratic political structure in which every adult human is a full citizen of the state and may participate in politics, the chance is offered to take and use the power attributed to the state for certain personal or group interests. To represent one's own interests is to raise a voice, to become visible as a member of the state, to be someone specific. Individuals aim for different kinds of acceptance and recognition from others: the love and respect of friends and family are very different and bring to the fore different identity aspects from those brought by social recognition in a public role. Both, however, are reliant upon identity, upon self-knowledge as the confidence of a self and upon the possibility provided for others to recognize that person as her. In the Judeo-Christian tradition, uniqueness and identity were derived from God's administration of his creative activity, which assured that humans were made in his image and each was unique. In secular societies there is an empty space in the social logic of status and worth of the individual which Western model democracies fill with the individual herself. The individual is free and is forced to develop her identity. Her success in so doing is confirmed by the acceptance of her efforts by others. Becoming someone, having identities (or the acquisition and security of a subject position – to say it in the words of my PhD thesis, Hauskeller 2000), is the task, the pre-requisite for participation and social existence.

The resulting identity is unavoidably weak and fragile, because of its incalculable dependence upon others and upon societal recognition patterns. The stability of social recognition is dependent upon the success of an identity 'performance'. The occurrence of psychological problems such as depression and melancholia signify the insecurities regarding body, emotional engagement, sense of reality etc., caused by the ambiguous duty to self-direct the creation of a 'me', the social 'reality' of which depends on its recognition by others alone (Butler 2003; Hauskeller 2006). Far from suggesting that social power is distributed and executed as a zero-sum-game, I will suggest that, although firm identity presentations are obligatory, power can be subdivided in many ways and that such diversification is the main function of genomics in society.

This paper is about human genomics as a technology of identity fabrication. My hypothesis is that the major effect of human genomics in society is the proliferation of a multiplicity of identities that are all very meaningful and significant in present evaluation. Furthermore, science, social practice and ethics bolster each other in border construction work safeguarding ideas of humanity which refer back to novel genomic knowledge. I interpret genomics as a social tool used to create identities in a certain way. This interpretation is based on the observation that with genomics the three borders demarcating and signifying humanity have become heavily renegotiated. Two borders designate the space of the human in the order of things: one is the species border that distinguishes between humans and other life forms; the other confirms the individual human being as the prominent unit of reference (see e.g., Hauskeller 2004, Lindemann 2005). The third border is actually a plurality of different segregation lines along which intra-species classifications and groupings happen. This third border will be the centre of attention in this paper.

All three borders are fundamental for human self-understanding, and their cultural construction is heavily affected by the essentialism and kind of truth which the science of genomics contributes to their current social renegotiation. Genomics causes shifts and inconsistencies regarding all three borders, but in radically different ways, which I will briefly explain. Intense and important socio-political and moral debates have been and are currently circling around these borders. Basic values and ethical achievements are at stake, including the meaning, extension, and adequate application of human rights and human dignity. I will not argue here that society uses science and loads onto it these meaningful dimensions and ethical problems, therewith abusing science – clearly genetic knowledge is of great use in medical diagnosis. Rather, I will argue that science freely offers to engage with human self-understanding and its societal and ethical dimensions, claiming to be able to define humanity. Statements delivered by scientists on what genomics is about overlap significantly with the ways in which various social actors utilize genomic knowledge, namely as a practice of defining human identity.

The historical thread of the prevalent concepts of a genome leads from the acknowledgment of somatic inheritance of traits such as, for example, in Gregor Mendel's experiments with pigmentation lineage in seeds, to the identification of DNA and genes seen as producing qualities or limiting the range of properties an organism may develop in exchange with its environment. If genomic substance produces and determines basic properties of a body and some of these properties are socially evaluated as important features according to which status and treatment of that person are decided, then genomes determine social identity and status. Genomes are identified as the distinct substance that determines what and who a living being is. Consequently, knowledge about a person's genome is extremely powerful with regard to her social position and needs authorization. The special epistemic status and social importance of genomic knowledge have accompanied its creation and justified control and regulation of its use. Governments were challenged to acknowledge that the disclosure of genomic data is highly problematic and that public welfare demands careful guidance about the implementation of testing regimes and access to data. Access to

the data by health and life insurers may result in discrimination of individuals who seem over-proportionally at risk of illness.

Over the past 15 years the exceptional potential of biology as a hard science to deliver unquestionable proof of inherited bodily and social properties, data the use of which can undermine people's right to self-determination, created novel social institutions, advisory boards and commissions, and space and positions for new experts such as genetic counsellors, bio-ethicists and genomic-related interest groups. The scientific epistemological status of genomics has fed hopes that a 'truth' about identity traits of oneself, other people or social groups can be discovered. Genomics can provide confirmation of inheritance and physiological properties because it investigates directly the very essence that is the thread to the ancestors and triggers physiological processes. Genomics equips identities with both the special robustness of scientific truth and a pre-social reality. The umbrella of medical utility serves as legitimate cause to engage widely in such searches for 'truths' and the fast improvement of the present genomic data collection and banking is willingly taken on by a global network of sequencing laboratories and associated clinics.

Innumerable kinds of social identities have been constructed, and the political contexts and purposes for which those identities are mobilized are accordingly many and diverse. I will briefly mention a few in which genomics plays an important role. Women with confirmed increased breast cancer risk may claim and receive more frequent and different health check-ups by health care institutions. Ethnic groups all over the world demand genomic tests as proof of their being 'black Jews', a superior ('whiter') status in many environments even if the Jewish Patriate does not grant full recognition (Parfitt 2003, Parfitt & Egorova 2006). Native Americans and First Nation people are seriously threatened by multiple genomic tests on y-chromosomes (Lell et al. 2002) which show that the three most common male lineages in groups in North and South America originated in Siberia. Such non-American origin implicitly challenges the grounds on which legal treaties granting certain land rights are based (Kaestle 2003). On DNA-based evidence (or lack of confirmation) individuals have been reprieved from the death penalty and released from prison, or not charged with child murder in cases of doubted sudden infant deaths, while others have been identified and convicted for rape or murder. National legislation in Germany has used the fusion of the two parental genomes to the personal genome of the fertilized egg cell as the marker for the beginning of human life (German Embryo Protection Act, 1990). People who thought they would no longer have any paternal or maternal family find a relative, while others learn about a biogenetic relation or the lack thereof they did not expect. The accumulation of such cases and their reporting in the media sprouts increasing desires to know. Businesses that invite, respond to and serve these 'truth' desires have been developing rapidly over recent years. A fast-growing biotech sector sells genomic testing services (e.g. Ancestry by DNA 2006, Family Tree DNA 2006), often alongside allegedly related nutritional and life-style advice (e.g. SCIONA) or a tourist trip to a homeland in Scotland or Africa, for example, including a pre-organized visit to the ethnic group identified as genetically related. All this has triggered a basically unquestioned identity buzz that expands to special peer-reviewed journals, research priorities in national funding bodies, and an 'identity industry'. Individuals have to have multiple identities, the personal, social and political success of which depends on their firmness.

Genomic tests have troubled many social identities, but hardly yet satisfied the high expectations about definite and not doubttable clarification of status regarding individual health, origin, or belonging. Huge investments, both material and immaterial, are made into better future knowledge of the irregularities of genomic transmission and expression and large reference data banks. With those in place, the Personal Genome Project (Harvard 2005) may promise better 'truth' delivery. Population genomics in all its variants is, despite its low medical and social utility, not

widely regarded as dispensable or even as undeserving. Its inevitable racializing implications, when separating species, ethnic groups, places of origin and migration movements, resonate with the social need for hierarchies manufactured alongside distinction markers between some humans and others. Michel Foucault called this marking of intra-species borders 'racism' in his lecture on biopolitics on 17 March 1976 (Foucault 2003). Today, as in 1976, race is an infamous word and concept and genomic scientists in the Human Genome Diversity Project have always held that socio-political concepts of race do not translate into genomics, that there is no biological basis for race (Cavalli-Sforza 2000, VIII).

Concerning the species and the uniqueness borders as I understand them, Foucault is not very helpful. He does not address or problematize these demarcations on the level of their bodily presentation but rather presupposes their factuality. Yet his concept of inevitably racist biopower is of high explanatory value with regard to intra-species borders if updated to deal with specific aspects of the present case. Foucault restricted his analysis to the late eighteenth to twentieth centuries, ending with the war-based socialist regimes of eastern Europe and elsewhere, and National Socialism, which he described as the ultimate perversion of this power mode of the modern state. Much of what biopower can mean today needs to be reinterpreted given the changes in moral evaluation, international agreements and declarations concerning individual human rights and the decreasing acceptability of racism along the lines of phenotype or origin. I shall briefly introduce Foucault's chain of argument in this paper and my own interpretation of its explanatory value for the current situation because these conceptual thoughts carry my understanding of the function of genomics in society along the intra-species border.

According to Foucault, sovereignty is absolute power. In an aristocratic society the God-derived sovereignty found its ultimate expression of power in the right to take life, to kill those who offended the sovereign. In a society in which the state exercises this right as a representative of all its citizens, this right cannot be granted. The sovereign is only the life of its citizens and subsequently the right to kill has to turn into a power formation that expresses itself in its acts aimed at the protection of life – no one can have the power to take another person's life (Foucault 2003, 241). The state is only for the sake and duration of the life of its citizens. Their life is its precondition and basic legitimacy source and hence it nurtures, safeguards, insures, fosters and even, today, creates life instead of taking it. Prevention of death and disease are the state's logical task. Foucault calls this biopower. The disciplinary power to control and hedge life combined with the development since the late eighteenth century of biopower introduces the ideology of biological purity and quality and this is the groundwork for a new biological kind of racism that becomes a technique and technology of the execution of the power of the State for the first time in European history.

"The first function of racism is to fragment, to create caesuras within the biological continuum addressed by biopower" (Foucault 2003, 255). Its second function, he says, is of a positive type: "The very fact that you let more die will allow you to live more" (Foucault 2003, 255). Because death is in principle outside of the reach of biopower, executing power through the ultimate means of killing requires methods that allow the singling out of those who do not deserve life and support, the death of whom will provide better life for others. Racism in Foucault's sense corresponds with what I have been calling intra-species border construction. Racism is the technology that justifies the exception of the pro-life duty: it sets aside those who deserve a better life in terms of biological purity by inserting discriminatory lines throughout the body of the sovereign or between nation state populations. Racism is the segregation of the significant and 'deserving' from their 'inferior' other. Although this might seem an unconventionally loose

definition of racism, it is precise when we examine the role of genomics in society regarding identity reification, which is the negative aspect of creation of intra-species borders.

After the Second World War an international stigmatisation of racism took place that expressed itself in the United Nations' Universal Declaration of Human Rights in 1949 and the UNESCO Declarations on Race from 1950 and its more recent versions. According to my interpretation of the development of biopower, this public and universal rejection of racism in its previous forms led to a constellation of powers in which identity and identity politics have taken on the role of racism. Racial pride and stigma are replaced by the positive relationships individuals have to develop toward themselves, their distinctiveness, and the groups they belong or wish to belong to and what makes these special. Particular identity and the markers that signify it stand in for the discarded concept of distinct human races with marked status. A society that is based ideologically on equality and the dignity of each person requires either drastic means of de-humanisation to reach beyond the limits of power it has committed to, or it needs strong ties of belonging (and a multitude of them) in order to practice in- and exclusions as the dominant practices of social life and death. A familiar ethical interpretation of such practices has been called 'bottom up' or 'individualized' eugenics in the context primarily of abortions of unborn human life subsequent to prenatal testing. Regarding the consumption of life from other species in order to facilitate the future better life of humans, racism as speciesism is practised in the billions on a daily basis in animal farming for food and research purposes, for example. Ethicists and animal rights activists have spoken of animal concentration camps in this regard (Pleasant 2004, 201; Costelloe 2003). The use of boundary case terminally ill humans or human tissues, organs and cells has also become both common to the degree of industrialisation and criticized therefore. Manifest racism has become much more widely contested morally, hence, modern racism has become more complex and subtle, implying that there are some qualities that make their possessors less deserving of life or certain rights.

In order to be a full human being, identity is required. Many laws and regulations are based on the assumption that no happy and mentally healthy life can be lived without self-confidence, self-knowledge and recognition of equality Foucault states that a new racism modelled on war evolved at the end of the nineteenth century and that it:

was required because a biopower that wished to wage war had to articulate the will to destroy the adversary with the risk that it might kill those whose lives it had, by definition, to protect, manage and multiply. The same could be said of criminality. Once the mechanism of biocriminal was called upon to make it possible to execute or banish criminals, criminality was conceptualized in racist terms. The same applies to madness and the same applies to various anomalies (Foucault 2003, 258).

Selection and the delineation of worthiness are the faces of current, biological racism. Individuals and state institutions find out about ties and properties of people with regard to sex and future health, biogenetic, ethnic, and bio-geographic origin. This is the creation of ties, of groups of some who belong together. From this togetherness and shared problems, socio-political claims might derive and be formulated. I interpret these practices as active racism that leads to a steadily increasing compartmentalisation of society. Everybody can identify positively in many different ways and hence build all sorts of alliances of belonging that are exclusions for those who do not share the relevant property. The consequence of not belonging and exclusion is not literal death in most of these cases; however, the paternity tests used in immigration offices, for example, might well exclude many who do die soon thereafter and who would not have had they been given the right to live in a comparatively safe and rich country. Death metaphorically speaking is executed

through institutions of care for disabled or elderly people, asylum seekers, criminal or pathological cases, and the effective silencing of the non-normal in socio-political life. Political correctness, however, is often seen as a Trojan horse. The biopower of genomic identities ties the stigmatic marker to the body or to the genome more precisely. This implies lifelong dependence upon the generosity and morality of social forces that grant these rights and special treatments for all those with confirmed need.

From this perspective the identity functions of genomics are neither arbitrary nor irrelevant, but genomics becomes the strongest weapon in racism that in most cases is now inverted and defused as identity politics. As I will show, genomics is happily and effectively engaging in this duty to separate, order and classify according to any trait one can possibly put an identity marker on. Genomics appears as the perfect instrument to start off social fireworks of identity worry, creation, and celebration. It diversifies and multiplies. Genomics, bioethics and political needs collaborate in an ongoing process of demarcating old and new borders through the body of the sovereign. The genomic contribution is special, for it subjects the bodies of humans to a supposedly culture-independent 'truth', provided by an ever more subtle and clever progressing science.

## 2) **Multiple identities, tests, actors, and ends**

This section introduces the relationship between genomic science and society. The more recent term 'genomics' is used throughout instead of 'genetics', understanding genomics as encompassing genetics as one of many techniques that search for DNA features such as repetitive sequences, transcription information or RNA or proteins as the products of a genome in action. I will then provide a systematic account of the current relations between genomics and human identities. Descriptive accounts of kinds of identities, genomic tests, actors who mandate tests and some of the ends they aim to reach by so doing, will, without claiming completeness, present a picture of the complexity and diversity of the interactions of genomic science and society.

A list of the types of identity will be followed by an account of the basics of DNA tests available at present; I will then list the actors using genomics and conclude with some examples of actual political struggles currently going on in which genomics is involved and used in order to achieve self-knowledge and/or socio-political change or recognition.

### Identities

If the following properties are traceable through analysis of genomes, then genomics helps to establish 'truths' regarding: sex and gender; biogenetic kinship (parent/sibling/twin/ancestor); status as a patient, future patient or carrier of a genetic disease; genomic health with respect to medical normality (prenatal testing); ethnicity and race; lines of descent and ancestry and bio-geographic origin; personal presence at a certain place at a specified time (forensics).

This range of identity qualities shows that genomics is, if not a panacea for all the weakness of previous socially constructed identity knowledge, then at least of extraordinarily wide utility in the social reaffirmation of aspects of a person's identity. Presuming we take for granted the trustworthiness of the information genomics delivers, it can make firm the links between an individual or group and its past and future - it confirms basic markers of identity humans have long desired to gain certainty about. This enormous potential has arisen quickly over the past 50 years. Different and ever more complex tests, matched to the variety of test purposes and genome properties, are being constantly developed and refined, with costs declining and application options and the sensitivity of the tests growing steadily. In recent years exponential growth has come

through advances in bioinformatics which provide novel levels of data management capacity and hence the ability to interpret comparatively quickly data from 1000 and more genomic markers for a specific test goal. With these technological advances at the genomics-informatics crossing, prices for a complete sequencing have decreased 500-fold in only six years. This technological improvement is particularly relevant both for disease susceptibility and ethnicity testing and conditional for technology applications such as those envisaged in the Personal Genome Project.

## Tests

Different tests reveal different features of a (human) genome.

Fluorescence in-situ hybridisation (FISH) is a technology used at a certain phase of the cycle of cell division – namely when the chromosomes are individually formed. The fluorescent substance makes visible the chromosomes and they can thus be counted. This method might still be most frequently used in human genomics, since it is employed for everyday prenatal genetic testing.

Specific alterations in the cellular DNA of a person or unborn can be sought by using polymerase chain reaction (PCR) in order to multiply the DNA and search for single nucleotide polymorphisms (SNPs) that might or might not be relevant for phenotypic traits. If a specific gene alteration is sought, laboratories use marked artificial DNA tools (micro satellite polymorphisms or micro array panels) that cling to specific versions of that particular string of DNA and give it visibility under the microscope. Such tools support the investigation of the degree of relatedness between individuals, provided that corresponding data is available for the relevant group members. With the fast-growing amount of genomic data from individuals from all over the globe, conclusions regarding both the biogenetic relatedness and the ethnic affiliation of a person can be drawn.

Other kinds of tests address not the order of amino acids but the actual organisation and functioning of genomes. This depends on the packaging state and locations at which a certain methyl group is attached to the amino acid sequences. The lack of or search for specific genome products such as ribonucleic acids (RNA) or the joint products of these, proteins, invites conclusions regarding the organisational state in which a cellular genome is or is not. So-called genetic disease is frequently a lack or overproduction of certain proteins, and medical genomics aims often to trace back the path from these missing RNA products to the genomic sequences that ought to control their production.

This paper is not about explaining in detail how genomic analyses are executed, but it is important to be aware that there are distinct methods of testing which provide different kinds of information, all of which need to be related to some genome product or trait of a body if they are to carry any significance for medicine, for science or for any other agent using genomics. Hence genomic knowledge becomes meaningful only when related to something else and there are, as mentioned above, a number of intermediary steps of translation from DNA sequence to something relevant. An important step to improving reliability of genomic findings is therefore to collect more genomic data at all levels of the genomes-property relationship in order to establish correspondence more solidly. Genomic data banks have become established and aligned to research aims in a growing number of national and international projects and institutions.

In most cases of disease and general genomics the current state of information concerning both genomic knowledge and relevant other data on the life conduct and physiology of the patient is insufficient. The relation between DNA and a physiological trait or identity feature such as bio-

geographic or ethnic origin, for example, seems increasingly complex and it requires an assembly of test types. The y-chromosome tests on some Native American groups, for example, relied on studies that had accounted for certain DNA repeat sequences (DYS1 system and alphoid) and the discovery of two y-chromosome SNPs (C => T at DYS 199 called Marker M3, and C=>T at RPS4Y) that were taken as signifiers of two different haplotypes; a third haplotype was discovered using micro satellite variation (Lell et al. 2002, 192). These three markers allowed the linking together of population groups and hence it was concluded that there had been three different males (or three large populations) in ancient history who travelled from Siberia to North or South America and settled in either place. The connection between complex diseases and susceptibility to them is similarly unreliable, although for different reasons. It is not the speculative nature of the narrative content of a story that leads back many thousands of years, but the unknown in the present interaction between genomics and environments that undermines our ability to be definite. Genomic reification of relevant properties of a human body – the relevance of which is socially determined - is still a promise for the future. Very recent (and future) high-tech applications such as the Personal Genome Project aim to deliver more conclusive data.

To present a rich picture of genomics and identity politics the list of the areas of identity tested for and the technologies used will be supplemented with a list of the agents using genomics in social practice and their purposes in order to stress the current degree of social implementation of genomic testing.

### Actors and Ends

Below is a list of actors who commission different genomic tests for different purposes. A selection of those aims and the subsequent social practices that evolve follows, in order to give some descriptive account of the interactions emerging from this web of identities, testing tools, actors, and aims in everyday social life.

#### Actors:

- Clinicians and medical scientists issuing tests for patients or the medicine of the future
- Individual persons for self or kin-related investigation of properties and relatedness
- State institutions (police, courts, immigration offices, child benefit agencies)
- Companies (to select employees, to sell insurance or other services)
- Scientists (population genomics, medicine)

#### Ends:

Medical applications have, together with the autonomous, self-determined uses of genomic tests by individuals, always presented the strongest positive reason for the pursuit and refinement of genomics. In the medical arena there are, for example, clinicians who order a test to find out about the health status of a patient or an unborn. Medical scientists engage in the development of interventions to trigger gene action or try to increase the medically relevant body of genomic data by expanding and improving the data banks that are indispensable reference resources. Depending on their specific projects these scientists use all kinds of genomic tests and methods, from the search for chromosomal anomalies and multiple gene loci PCR to the use of micro satellites and

SNPs, or the search for gene expression patterns for refined identification of a lack or weakness of molecular function of a certain tissue.

People who are or might be affected by heritable disease want to know whether they themselves or their offspring are at risk of suffering and may wish to plan their life accordingly. This potential to plan one's life from a well-informed basis is currently the strongest argument put forward to justify genomics ethically. But while a generous interpretation of this line of thought serves to legitimize almost all genetic tests which an individual chooses to take regarding her own genomic properties, other actors employing those same tests to find out about people face more ambiguity. In European bioethics it is widely held and put into regulation that autonomous decision making of the person concerned is needed for any such test to be legitimate. There is no limit to the desires of the free individual and consumer to find out about herself, though, as long as it appears to be a so-called autonomous decision. By contrast, although aim and test are the same, the conduct of paternity tests by child benefit agencies or immigration offices or the mother-in-law or a journalist is not at all ethically and socially unchallenged. A right to know or not to know is assigned only to the individual tested, so ethicists argue and many regulations judge. However, a genetic test of one individual regarding any particular property of her genome inevitably delivers knowledge regarding the probability of the specific genomic feature in her relatives, too (see Hauskeller 2004).

Other agents who use the tools genomic science has provided are the police and legal institutions such as courts, where genomic evidence can, in principle, play as many roles as there are different identities for which genomic verification is rendered appropriate or valid. There are obvious problems with identification in the case of monozygotic twins or multiples, and hence the number of genomic markers tested for when delinquency in cases of rape or presence at any crime scene is investigated has risen steadily from seven to beyond a hundred, and into the thousands if one wants to delineate all the various ethnically or bio-geographically significant specificities in a certain genome. In the courtroom genomic evidence regarding origin, ethnicity, or specific disease markers is becoming increasingly relevant, too. Genetic markers for increased risk of sudden infant death syndrome, for example, have recently sufficed to discharge parents accused of or convicted for child murder, attracting great media attention.

There is obviously no easy telling of good or bad, legitimate or ethically unjustified use of genomics when looking at institutional actors and individual cases. Similarly ambiguous are the positions taken in regulation and advisory committee statements concerning, for example, the use of genomic tests by employers (EGE 2003). Tests can be used in order to select for staff not likely to show adverse reactions to certain chemicals, a goal that can be seen as benefiting both employee and employer, if the structural power imbalance between them is neglected in the assessment.

Until recently, there was some agreement in Europe that life and health insurers should not be permitted to request or use any genomic test results from their clients in order to assess genomic risk and individual monthly premiums. However, a growing number of ethicists and social scientists now argue that it is patronizing and against the personal rights of individuals to prevent them from exploiting the benefits they might have from insuring only their personal risk if it is negligible (e.g. Lemke 2005). This is structurally the debate about whether everybody should contribute toward the treatment of the poor health of smokers and alcoholics. The difference or similarity depends upon whether personal genome properties are considered luck or individual responsibility – which reflects an increasingly important controversy in genomics. The principle of insurance and how general versus individual risks are balanced in calculating contributions is a socially important issue, and obviously genomics opens a window to realign common and individual risk in a new way in the health sector. On the customer side of genomic tests being used for questioned purposes, are

companies using them to select staff or to determine work-related health risks? And then there are the businesses that rely on the genome-identity relation and offer specific genomic tests and other products chosen in accordance with the test results, companies such as SCIONA, GeneTree™, Family Tree DNA, and Ancestry by DNA.

Amongst the offers by GeneTree™ is forensic testing, advertised on the webpage as Crime Scene Profiling. Nowhere is there a note which says whether there has to be shown any proof that the samples are from the scene of a crime under active police investigation. The charges for service in this rubric are three times and more the usual price of a paternity test, a cost probably explained by the customer group envisaged:

“GeneTree brings state-of-the-art **DNA forensic testing services to crime labs, district attorneys, private investigators and other professionals**, looking to DNA for answers. On the right side there is a list of crime scene specimens that DNA evidence can possibly be obtained from:

GeneTree is focused on providing DNA analysis in the following **four different areas of forensic DNA testing**

- **DNAWitness 2.5\* Profiler:** Matches DNA profile from evidence found at a crime scene to a geopolitical database and photo database to get a clearer picture of who that DNA evidence may belong to.
- **EyeColor Profiler\*:** Matches DNA profile from evidence found at a crime scene to an eye color in order to get a clearer picture of who that DNA evidence may belong to.
- **DNA Profile Identification Match:** To match an identity between DNA evidence and DNA specimens on a swab.
- **Discreet DNA Relationship (Paternity) Testing:** To match DNA evidence from an alleged father or child to DNA specimens collected on a swab.

- **Sweaty t-shirts**
- **Undergarments**
- **Semen stains**
- **Vaginal Stains**
- **Paper or plastic cup**
- **Glass**
- **Ear wax**
- **Fingernail clippings**
- **Socks**
- **Urine**
- **Licked stamps**
- **Cheek swabs**
- **Hair with roots**
- **Hair without roots**
- **Dried blood**
- **Whole blood**
- **Chewed gum**
- **Dental floss**
- **Cigarette butts**
- **Used tissue**
- **Dried skin**
- **Used razor**
- **Other biological specimens**

**For more details, call our crime scene evidence experts ...”**  
Tree Detective 2006)

(Gene

Then follows a free phone number, and details about the simplicity of the procedure and the waiting time for the results (about three weeks).

The internet provides open access to genetic identification tests for ancestral and bio-geographic markers, phenotypic appearance markers, identification of the chewer of the particular piece of gum or dental floss, biogenetic relatedness, origin and ethnic belonging, and ancestral markers. All these tests can be found for less than \$1,000, while a private home paternity test kit - and the webpage states: for father and child, mother optional - can be had for about \$200 - results within a week of ordering. Genomics has, in some places more than in others, obviously, become a

surveillance tool, one which everybody who can afford it can use to control and check on anybody from who they can get the required body fluid samples. In principle, it seems, anyone can become an actor in this and there is no requirement to provide any reasons legitimating their interest in some other person's identity. I find this very disconcerting, but will not go into more ethical discussion of this aspect in this paper. My impression is that this needs more attention than has been given to it so far (but see e.g. Human Genetics Commission 2002). All the various factors for which genomic testing is being used are in principle marketable via the web. Genomic identity tracing can become a hobby of everyday entertainment, but it is also a freely available surveillance tool which can be used to practise public and private control of people's activities and whereabouts, just as are CCTV cameras and other recent inventions.

The following table illustrates the heterogeneous assembly of technologies, actors, and status markers, which engage in various relations with each other for specific socio-political or private ends, all of which are identity-related.

<b>Technologies</b>	<b>Actors</b>	<b>Status marker/Identity</b>
FISH	Individuals	Uniqueness
PCR	Relatives	Patient /carrier
Micro Arrays	Medical staff	Other health (prenatal)
Micro Satellites	Police and legal institutions	Sex and gender
SNPs	Immigration offices	Relatedness
RNA	Child benefit agencies	Bio-geographic origin
Proteins	Employers	Ethnicity and race
Mitochondrial DNA	Insurers - Companies	Time and place (forensics)
y-chromosome	Scientists	Species belonging

The following section presents one more actor in genomics, namely the science of genomics, which has a medical and a biological dimension that are increasingly merged. I will expand on it a little more here in order to make sense of the multiplicity of genomic usages presented in society. Ordering the field according to either technologies or identities or actors or purposes does not lead to a meaningful explanatory frame. Yet, there is another route via which a systematic and meaningful interpretation of the function of genomics in society can be given.

### 3) **Genomics and the three borders of humanity**

“Over the decades and centuries to come this sequence will inform all of medicine, all of biology,

and will lead us to a total understanding of not only human beings but all of life. Life is a unity, and by understanding one part you understand another. When you look at all the possible combinations of all the variations in the human genome, of which there are possibly ten million, then the number of combinations vastly exceeds the number of particles in the known universe. We can be pretty sure, very sure, that we will never get two identical human beings unless they come from the same split egg, that is identical twins.” Dr Sulston said the wider message of the human genome pointed to two profound truths about humankind - the remarkable similarities between people, and with other life forms, and the wonderful differences between individuals. “In every 1,000 of the genetic letters, there are two differences between people. Most of the letters of the code are the same between us - but that still leaves an awful lot of differences. My way of looking at it is that we should take both morals from it. We should certainly regard ourselves as similar and take responsibility for one another in that way, but we also have to respect our differences.” The scientific proof that humans are 99.9% similar was highlighted by Dr Dexter as a far-reaching cultural icon of the work. “We have powerful new ways to see what it is that makes each individual unique - but perhaps more importantly we have new tools to see what it is that makes us all the same. Our common humanity is set out in the wonderful spiral staircase that is our DNA, and at last we can read its letters”. (Human Genome Project (HGP) 2000)

This long quotation is from the official press release announcing the completion of the draft sequence (97%) through the International Human Genome Sequencing Consortium. It quotes in particular John Sulston, Director of the Sanger Institute, a research institution which was set up by the Wellcome Trust in order to conduct the British part of the HGP, and Michael Dexter, who at the time was Director of the Wellcome Trust. According to both Sulston and Dexter the product of the HGP, the sequence of the order of amino acids, and the counting of genes (30,000) are useful for the establishment of the biogenetic uniqueness of each individual human and the identity of the human species.

It might seem surprising that in the context of my analysis of the function of genomics in society, statements by scientists on what the work is about count as a relevant source. Can we have such an uncontested belief in science that we take for granted the explanations genomicists give for what genomics is all about? My reasons to take these explanations seriously are the following. If the concept of a ‘knowledge society’ describes the present dominance of science, then science is epistemologically granted enormous authority in defining its own purposes. If science itself is asked to set the social agenda of what it is about and can be used for, it is simultaneously assigned the performative power of self-determination and self-definition. But science is not independent of society – it needs to legitimize its aims adequately in order to survive economically and in this authoritative position. To some degree the scientist’s account has to be convincing regarding the genuine potential of fulfilment and meaningful to the public in order to maintain this general epistemological positioning of science in society. This means quotes such as the one above are effective because a certain degree of self-fulfilling prophecy merges with clever academic salesmanship and spin. Scientific accounts can, therefore, be a good starting point for critical exploration.

Genomics, not only in the HGP but also as an idea of essential identity, interferes with all social border constructions. Below I will introduce the Human Genome Diversity Project and population genomics in general and the role they play in the reawakening and reaffirmation of the third boundary type and the remainder of the paper will focus on this area. However, I would like to mention briefly the confusions and alterations that occur along the other borders as a result of the existence and conduct of genomics. The notion of uniqueness and the epistemological definition of an individual human, particularly the beginning of its existence, have been re-debated. Research on

human embryos and the ethical debate about it has made genomics the science of reference for those who insist on embryo protection. This definition of the unique genome as the marker of the individual, however, resonates with other cultural concepts and increasingly contributes to a conflation of the species and the uniqueness border. The species and uniqueness distinction was shaken by the novel understandings of chimerism that developed slowly and almost unnoticed within transplantation medicine and oncology. The ‘chimerism factor’ is the measure of success of bone marrow transplantation. But this idea of the unique genome in each individual human’s body is increasingly unsustainable. Irregularities, such as that a person may have developed from two fused heterozygous twin embryos and is therefore living with a patchwork pattern of genomes in her body, cannot commonly be perceived. Incoherent findings from genetic tests, for example for inherited diseases or relatedness of parents and offspring, may apparently show that a biological mother and her child are genomically unrelated, when there is no doubt about their kinship and more precise tests can establish its existence. Without genomic uniqueness ideas and the frequency of genomic tests to establish relatedness, descent and health, the idea of the unique individual genome as a marker of identity and worth of the person could not have occurred as a concept and would not make any sense. The species border is, however, contested more severely by the fact that genes are shared between humans and other species – that humans share all their genes with chimpanzees and (more problematic especially for the conduct of science) mice, the ultimate ‘model’ organism. Genome sequencing unintentionally troubled naïve ideas of a direct link between the number of distinct genes or length of DNA sequence and the self-assigned status of the human species in the hierarchy of living beings. Humans have about twice as many genes as nematode worms and about the same numbers of genes as mice (and chimpanzees) – presumably there is a mouse gene equivalent to every human gene. Whole parts of the genome sequence of both species are indistinguishable. This makes the mouse an ideal ‘model’ organism for biomedical experimentation. In order for such utilisation to be ethically permitted, the moral significance of the gene sequence carrier as relevant other has to be assigned only to human but not to murine carriers – regardless of their genomic similarities. Of course, mice do not have moral status at all – in the USA not even as an animal (Animal Welfare Act, 2<sup>nd</sup> Amendment 2002). With genomics, species borders become construed in a fragile and interesting way. I will, however, focus on the borders of intra-species racism and explain the way in which its social prevalence was already effective in the conduct of the sequencing project, and then move on to argue for the discursive explosion genomics caused in this arena of identity politics and power negotiation.

Neither competing sequencing project, HGP and Celera Genomics, sequenced a complete human genome, which has all chromosomes twice in different versions (except the x or y that indicates sex), but each sequenced each chromosome only once, including the y-chromosome. Additionally, in order to take account of political sensitivities, they did not sequence chromosomes of one person but a composition of chromosomes carefully selected from individuals from different human ‘races’ and both sexes. Although their sequenced genomes therefore clearly do not represent a genome that could be active in a human body at all, this ‘human genome’ has gained paramount symbolic value as an emblematic reference for genomic uniqueness and species identity and the ideology of both.

Sulston and Dexter (HGP 2000, Dexter 2002) point out two traditional and highly charged axes of classification: the one that separates humans from other animals and the one that defines the unit of moral and conceptual significance, the individual person. The reason to select participants from the five continents, each of which had to be represented in the reference human genome, was strongly emphasized by pictorial means in the respective announcements by the HGP Consortium and Celera (Venter et al. 2001; Nature 2001). Adam Bostanci has examined the complex technical,

political, commercial, and ethical considerations that went into the production of DNA sequences publicly celebrated as drafts of the human genome. He used the cover pages of the human genome issues of *Nature* and *Science* to show that different scientists and artists were actually working with different conceptions of the human genome which reflected the diverging scientific strategies of the HGP and Celera (Bostanci 2004 and 2006). This selection of different individuals, which at first sight seems a mere attempt at political correctness, actually points towards a third border. This border is drawn in multiple ways through humankind and the epistemological and social status of it has been more debated than that of species and person: the division of the human species into subtypes, kinds of humans.

This boundary type was brought up in ethical discussion on the HGP, but not resolved or even very clearly addressed. It did, however, become the basis of a simultaneous genomic enterprise: the Human Genome Diversity Project (HGDP), and also its successor, the Haplotype Mapping Project (HapMap 2002).

The genetic diversity of people harbors the clues to the evolution of our species (Cavalli-Sforza et al 1991).

Luigi Luca Cavalli-Sforza, who in practice started to merge molecular biology and anthropology to create what has become known as ‘genetic anthropology’, was the driving force behind the HGDP. This project collected DNA from different ethnic groups, preferably indigenous populations with as little admixture with other ethnic groups as possible, in order to reconstruct migration movements in the evolutionary past of humankind. Cavalli-Sforza pointed out repeatedly in this context and with reference to the genomic findings that the phenotypic common-sense notion of race is a social construct and has no biological or genetic foundation, and that the genetic differences between any two individual humans are more significant than those between populations (Cavalli-Sforza 2000, VIII).

Jenny Reardon has analysed in detail the processes of methodological and ethical debates and alterations made during the course and development of the HGDP (Reardon 2005). Her presentation stresses in particular the paradoxical fact that any alternative molecular or genetic race concepts Cavalli-Sforza and others had promised to deliver with this research, namely a “genetic definition of race” (Cavalli-Sforza & Bodmer 1999) would de facto reinscribe racism as the structural means of social segregation. In the call for the HGDP (Cavalli-Sforza et al. 1991), it was argued that the epistemic aim to map the evolutionary development of the various human subspecies was urgent, because admixture and cultural invasions into native tribal life forms are about to destroy quickly and irrecoverably the last traces of the ancient history of human racial variation still detectable in genomes of isolated native groups.

Migration history on an evolutionary time scale – including identifying the part of Africa from which the ancestors of a certain percentage of a European or Asian population moved many tens of thousands of years in the past - does not mirror in any way the basis of concepts of race that have structured social classification over the past two centuries. But many social identities of ethnic groups, ancestry, or people’s traditional land of origin or belonging, rely heavily on myths that can easily conflict with the basic science around which genetic anthropology is framed. Native American groups and many people who claim to be of Jewish descent make different uses of the testing methods and markers the HGDP developed in order to discover human evolution and population history. Although legally rejected and opposed by majorities in public debate, racial and ethnic distinctions still structure social politics today, often with the help of the intended remedy ‘affirmative action’. The HGDP and its successor projects, despite all efforts to increase their

credibility with the explicit rejection of any racist goals and many attempts to convince the public of the medical utility of the data collected, inevitably operate with concepts of intra-species differences, and therefore rely on ideas of biogenetic differences between populations.

Despite their fundamentally similar claims to reveal aspects of human identity, the HGP and the HGDP did not claim to explain the same kind of human identity. The HGP created a human genome 'ideal' from genomes of different people from different parts of the world. This artificial human genome assembly was then divided into a great number of pieces that were spread to the different participating laboratories on the globe to become sequenced bit by bit. So it did not 'read the letters' of the genome of a viable human being but of a human genome construct. Complicated ethical negotiations and political sensitivity justified this approach. The construed identity of the species herewith analysed could hardly be more transparent. Of course, the question arises what these data are good for, and it has to be said that the location, closeness or distance between gene sequences known to be involved in particular diseases, for example, is helpful in medical genetics in particular.

Genomics became ever more important after the HGP was finished because its findings were that only the whole genome as a structural and functional unit in exchange with its environment makes the difference between a mouse and a human, not the sequence nor the genes alone. Genomics now encompasses the subdisciplines transcriptomics (the science of the messenger RNA transcripts from active genes); proteomics (the study of expression and function); structural genomics; comparative genomics (the science that delivers the above numbers and insights regarding genome size, gene number and functional difference between species); and others depending on what people like to subsume or exclude from genomics in the first place. Implicit in saying that the meaning of genomics has expanded, however, is that genomics proper is understood to have started only after the sequencing projects had reported such low gene numbers in humans. Some tend to speak of the above '-omics' as post-genomic science.

The above introductions to the HGP and the HGDP aim at assessing their achievements and stated goals in the context of human identities. Two kinds of identity seem most prominent: the species identity and its history and intra-species identities. In other words, the projects operate along the boundary between humans and other living beings and the boundaries between kinds of people. The third boundary, demarcating individual uniqueness, is socially highly relevant, since much of current morality is conceptually reliant upon the significance of the concrete and implicitly irreplaceable other (in terms of responsibility, harm, hurt, life protection etc.). Although this boundary is not really within the scope of either of the large genomic projects, its validation is claimed by the HGP, probably for publicity reasons. Affirmative reference to individual uniqueness calms and comforts ethical critics aiming to assert a clear relation between genomics and human dignity.

Genomics seemingly safeguards the three crucial boundaries that establish the basic identity of humans – in a complex interplay between its own interests and values and the programmatic functions it is invited to take on in disharmonious concert with the legal, regulatory and political spheres. Genomes are the essential proof of the adequacy of most fundamental social beliefs in individuality, the particularity of humankind and, of course, that there are different kinds of humans – with respect to sex, race, disease propensity, etc. Genomics is all about identity, or, to put it the other way round, identity has been identified as the major task when it comes to the social functions of human genomics. Concerning the intra-species difference, the HGP was released from the charge to deliver. The HGDP and the HapMap Project took on this dimension. The unique individual and the species category both seem precise: the individual being any token human the uniqueness of

whom is recognized as the basis of morality and human civilisation; the species boundary being like one big circle and all elements imaginable can be placed either within or outside. Intra-species borders or groups of humans that share some property, on the contrary, can be created in multiple ways and social organisation is all about how this is being done.

All three borders have a long cultural tradition and carry heavy moral baggage, since every inclusion is an exclusion of other species, people, or possible entities of conceptual and moral significance and hence needs to be negotiated. Genomics inserts new elements of definiteness in ongoing border negotiations and shakes up some formerly solid criteria of classification. The uniqueness of each person assigns her moral importance as not being exchangeable for another person, child, or unborn. The classifications along which people sharing certain defined characteristics have been considered significantly different from other humans with regard to place in society, influence and esteem, medical treatment, etc. have been negotiated in debates on race, disability, patient status, class and so on. The species boundary has become heavily debated recently in the course of scientific developments that require reductionist definitions of what it is in humans that makes them worthy of ethical and legal protection against exploitation, murder, etc. It has become blurred in ways that hardly allow the drawing of the conventional line between humans and great apes, for example, or the argument that research on humans should be governed in radically different ways from research using other animals which are also able to feel pain and react in self-determined ways.

While what genomics is and can be could be negotiated and in balance with social needs to safeguard basic distinctions of ordering the world and having important boundaries confirmed, genomics can also be seen as a tool for creating identity trouble in a society that demands firm identities. In the following section I will show how the kind of evidence genomics delivers in society and the variety of actors using it in different settings produces an enormous fluidity and sprouting or shifting novel identities. These identities carry the dignity of supposed scientific truth and yet do not form a new system of social markers and classifications that would replace the previous social categories of status. Genomics is related to shifts in traditional attitudes, it moves related concepts of identity, but in effect it also establishes a parallel universe of socially significant identities and differences. I see genomics as engaged in the interactive creation of additional identities of increased or ambiguous value to those who carry them.

#### **4) Genomics facilitates identity trouble**

##### A) New patient identities: Huntington's Chorea

It was long known that certain diseases run in families and affect some but not all of their members. The paradigmatic cases where genomics is changing the meaning of this knowledge are those very few in which it can provide fairly definite information on whether or not a particular person is likely to suffer from a certain disease in the future. The most certain genomic prognoses are for Huntington's Chorea and very rare and specific forms of breast cancer.

Huntington's Chorea is a severe 'monogenetic' disorder which always leads to an early death after about 15 years of suffering from a disabling neurological disease. The 'faulty gene' was identified on chromosome 4. It is called IT 15 and it took about 15 years from the start of the systematic search for it to the finding of it in 1983. Leonore Wexler was diagnosed with Huntington's Chorea in 1968. Her family set up a foundation, the Hereditary Disease Foundation, to find the gene, and one of her two daughters, Dr Nancy Wexler, played a major role not only in the identification of the gene through her research activity but also by arranging for that research to

happen in the first place. When the test became available, Nancy Wexler, who was then 38 years old and who had for 15 years invested her ambition and built up her scientific career on and in the search for the gene and the development of the test, publicly expressed her personal ambivalence about taking it. She said that knowing her fate would not change the decisions she had made early on – to not have children and risk passing on the gene, and to continue the search for a cure (Time Magazine 2002). However, there is still no cure. In 2000 a report on trials in transgenic mice of treatments for Huntington's raised hopes that the disease process might be reversible by using regular tetracyclines to suppress gene-expression. But the number of patients, between 30,000-50,000 in the USA, is not high enough to motivate the pharmaceutical industry to invest in research into treatment. What has been developed is a screening test usable in pre-implantation genetic diagnosis to identify embryos that carry the gene before implantation in the uterus (Drury et al. 2001). Less than 3 percent of people at risk for HD who are over age 18 and eligible for testing have been tested. "It's a big issue," says Dr Karen Marder, from Columbia's Huntington's Disease Society of America Center for Excellence at the New York State Psychiatric Institute. "We have a genetic testing program here, and we spend a huge amount of time — instead of just sending out a lab test — discussing what they might do or not do if they had that knowledge," Dr Wexler and Dr Marder agree. "Once an individual knows this information, you can't take it away" (Kolb 2003).

In terms of its politics this example contains interesting notions of identity. There is the policy made by relatives of patients: the Wexler family engages strongly in the search for the gene and then a possible cure. Its activities are directed toward public visibility of the disease and problems concerning the lack of treatment and funding for research. Both are involved in fundraising activities through an especially set-up foundation and criticise the pharmaceutical industry for its lack of interest in developing drugs. This type of patient activity has become a regular occurrence in biopower relations, and this area of so-called 'genetic citizenship' is well studied – examples are: PXE International, Little People of America and the Breast Cancer Societies (Little People of America 1995; Terry & Terry 2001; Rapp 2001; Stockdale & Terry 2002; Taussig et al. 2003; Rose & Novas 2004).

There is a strong identification with the group of patients and possible patients in a person like Nancy Wexler, who has devoted her life to pursuing the aim of finding the gene and effective treatments, not knowing if she would suffer from the illness herself. A test providing certain knowledge does enable patients to make particular kinds of decisions. Before the test was available, the, in principle, threat of Huntington's motivated family members not to have children of their own and often to seek to adopt. Yet the public knowledge about the uncertainty of their life expectancy has become a severe obstacle for being accepted as suitable for adopting a child by the responsible public institutions. The risk of getting to know one will suffer from the disease in the future equals the likelihood of escaping the problems: 50:50. After the test one will know whether there is no obstacle to having children of one's own or whether the decision to not father or mother biologically will be accompanied by social stigma and institutional regulations that impose to live without the alternatives to become a fully responsible parent. A confirmed positive result can mean subsequent trouble with employers, health insurances and so on if it becomes known, and hence mean a massive limitation to individual plans for the future, especially as there is no cure available or in prospect.

Huntington's is a prime example of the shifts and novelties that occur in long-known cases of hereditary disease in families when the individual's and her family's identities, previously tied together inextricably, become subject to various separate knowledge practices. The genomic knowledge forms a new definite identity for each family member. Genomics unties the shared family bond regarding the disease. Because of this it forecloses some possibilities and modes of

self-identity formation while opening up chances to plan better a life which will or will not be doomed by this particular illness. The status of a patient or likely patient, ambiguous and ambivalent as it is, creates space for new political claims and changes a vast array of situations both in the affected people's lives and in the societal handling of the particular problems and needs related to such diseases. The availability of genomic tests confronts, not only but most clearly, members of families affected by Huntington's or the rare but highly predictive breast cancer genes called BRCA 1 or 2 with a reshaping of the relationship between family belonging and individuality. The tests distinguish clearly between individuals positive or negative for the particular genomic feature. A family bond which in the past had over many generations often been affirmed with reference to the threat posed by the disease which struck, but unpredictably, is dissolved by the individual marking of people of one or the other kind in the family. Ambivalent experiences in respect to belonging and self-identity have been reported both by people who received negative and by those who received positive test results.

The certainty that genomics brings to medical diagnosis in these few cases of life-threatening diseases has ambiguous consequences for the individuals. The breast cancer gene hysteria at one point extended to almost routine offers to BRCA 1 or BRCA 2-positive young women to have their breasts removed as a means of prevention. This drastic measure has turned out to be not sufficiently effective. But when, for example, a patient group negotiates more frequent or intense cancer screening than is usual with an institution such as the UK National Health Service, genetic results can serve as a strong argument in favour. At the same time, the individualisation of inherited disease risk provides a useful entry point to single out institutionally or socially in various ways those who are problematic in these families and leave alone those who are 'normal'.

#### B) The biogenetic kinship bond

The consequences for relationships of the use of paternity testing kits bought via the internet have received plenty of media attention. A presumed paternity could be checked for via blood tests regarding immunological markers in the blood in the past. However, this only made it possible to rule out as likely fathers men with certain properties of their blood and to establish a likelihood that another recognized candidate was the biological father. It did not make it possible to determine paternity, or, for it is the same test, to determine who out of thousands of suspects committed a rape crime. SNPs testing makes it possible definitely to establish the identity of a person or the relatedness of two or more people – except for doubts remaining in the case of monozygotic twins. This chance to find out who committed a rape, or who is the biological father or mother, or whether there is a biological tie to the presumed grandparents etc. through what has become called 'genomic fingerprinting' allows for a previously unknown degree of certainty regarding biological kinship. A notoriously unstable foundation of the social organisation and in particular the family in all patrilinear kinship systems, sexual fidelity, has become testable.

With this new knowledge the social contracts and legal regulations that order the field around family stability in marriage and inheritance law need to be renegotiated. What is the role of social and deliberate parenthood with regard to biological ties? Many regulatory changes have happened around this testing possibility in family and criminal law and, as the rape example shows, since the same test has many possible usages there is no clear boundary to be drawn between family and the police, crime and kinship. I will, however, concentrate on the kinship rather than the criminal situation in this section.

The anthropologist David Schneider described three ties of kinship which together create the European or Western model of relatedness: the emotional or social, the legal and the biological tie.

In his 1968 study on American kinship he started reinterpreting the biological as a biogenetic tie (Schneider 1968). Following on from there other anthropologists such as Kaya Finkler introduced the concept of a geneticisation of relatedness, or studied the meaning of essence and substance (Finkler 2000; Carsten 2003). In the past, the biological bond was uncertain with respect to the paternal side and the legal bond secured social status of relatedness regardless of actual sexual couplings. The tests for biogenetic ties have been utilised in many ways and are of huge importance in relation to traditional family concepts and the everyday social practices of governance and status identification that derive from them. What is a child of one's own, which care obligations and responsibilities derive from various types of social and biological parenthood and what areas in this kin organisation around the raising of children need regulation, are some of the questions currently being raised and renegotiated. I will give a few examples to point out the diversity of usages, settings and environments on and in which this novel certainty of information about biogenetic kin relations has an impact on people's lives and social interactions.

People find or lose presumed fathers or (given egg cell donation) mothers, and the histories of origin and belonging that came with this kin knowledge. Couples fight about infidelity and the obligations to care and share in divorce settlements when the number of fathers and/or mothers increases. Individuals adopted or grown up without a father and paternal family line enter into a search for their fathers and mothers and do or do not find long-lost or never-known-about relatives. Child benefit agencies, when ascertaining for example who is in charge of refunding their support payments to a single parent, usually a mother, try to pin down the parent with a genomic test. Not very much attention is paid in public to the single mother who argues with social workers, nurses, and institutions about whether or not information about the possible father ought to be delivered or acquired, or to the societal impact of systematic testing in cases of rape and teen pregnancies, especially involving child abduction and incest. The disturbance to certain beliefs and norms structuring modern Western societies is not limited to those societies internally. The use of genomics in order to establish relatedness in cases of subsequent immigration of family members, for example, enforces the image of the biologically related nuclear or extended family onto cultures with different traditions in ascribing parental responsibility. Where paternal rights and responsibility are assigned to the brother of the birth mother and not the sexual partner by whom she became pregnant, the logic of kin designation requires less rigid contractual social support and surveillance than the norms that structure Western marriage and inheritance systems. Beyond the imposition of a certain family concept, genomic testing in cases of the immigration of related family members also neglects the pressures under which immigrants act and how hardship can rebound wider family circles. People may feel close enough to removed cousins and their children or the children of unrelated neighbours to have the desire and take the responsibility to help others in extremely disadvantageous or traumatizing circumstances such as poverty or political or religious prosecution. During and after periods of war in Europe kin extended to a much wider group of relatives than that which is included as relevant responsibility today and genomically testable.

In public representation, paternity testing is mainly about individuals trying to find relatives, with a rather less outspoken subtext concerning infidelity in relationships and the control of women's sexual and reproductive choices. The control of reproduction here is very specifically oriented towards safeguarding the legitimacy of offspring. Reliable contraceptives and reproductive medicine allow stronger enforcement of the male claim to be protected from 'bastards' in his nest. Previous pragmatic choices by women to try another man's sperm for the creation of the desired offspring rather than or before undergoing invasive infertility treatment (still an option outside the geneticisation discourse) thus becomes a forbidden option and genomic testing is the technology of its successful prevention.

An enlightening case regarding the reconstructions of belonging, relatedness and shared history has been described after it was confirmed with DNA fingerprinting tests that Thomas Jefferson did indeed have children with his slave Sally Hemings. The offspring of Hemings' children and of Jefferson's legitimate children were tested and the findings confirmed that all but the eldest son of Sally Hemings were biologically related to Jefferson. The Jeffersons and the Hemings started having joint parties once a year and everybody who belongs is invited - except the family of Hemings' eldest son, of course (Davis 2001; Jefferson and Hemings 2003).

Speaking in Foucauldian terms, genomic testing as a means to clarify kin relations is at the same time a practice of governing sexual reproduction. It is the iconic present example for the crossing of the two power strategies of discipline and biopower in genomic utilisation. Personal identity and the ideal of an autonomous, self-governed lifestyle encourage the individual to look after her health in order to protect and save her life, which every citizen as a member of the sovereign is entitled to do. Not coincidentally, it is in the sovereign's general best interest to secure public health in the general population for financial and functional reasons. A health-protective lifestyle hence services both powers, discipline and regulation, and can thus be seen as the ultimate normative principle in present democratic societies.

Of course, this ideological reason for the endorsement of these imperatives in society is based on the assumption that knowledge of biological ancestry is the safest way to identify a person's disease susceptibilities. To rate family history as a better risk indicator than genomic testing for multiple gene loci when it comes to predicting disease likelihood and weaknesses of the physiological apparatus, does not reflect the general belief in the certainty of genomic knowledge and is surprising for that very reason. The firm belief that genomic knowledge is highly reliable is at the bottom of all discourses about the protection of individuals against the (mis-)use of genetic data. If this data would not be seen as more reliable predictors of disease, for example, than health behaviour, why invest so much into the safeguarding of genetic data in order to prevent exploitation and disadvantage of individuals or groups through its use by insurers or employers. This exceptional status of genomic information serves a double function regarding the social implementation of this kind of knowledge: it delivers reasons as to why ancestry is so very relevant for individual identity and simultaneously provides grounds to assume that information about individual disease risks cannot be gained by direct and simple routine testing. Subsequently kin knowledge becomes necessary to establish health status. If genomic knowledge was indeed as precise in predictive power and less dangerous than is assumed in exceptionalist bioethics, then health information could be gained without reaffirmation of the blood tie by testing the individual directly.

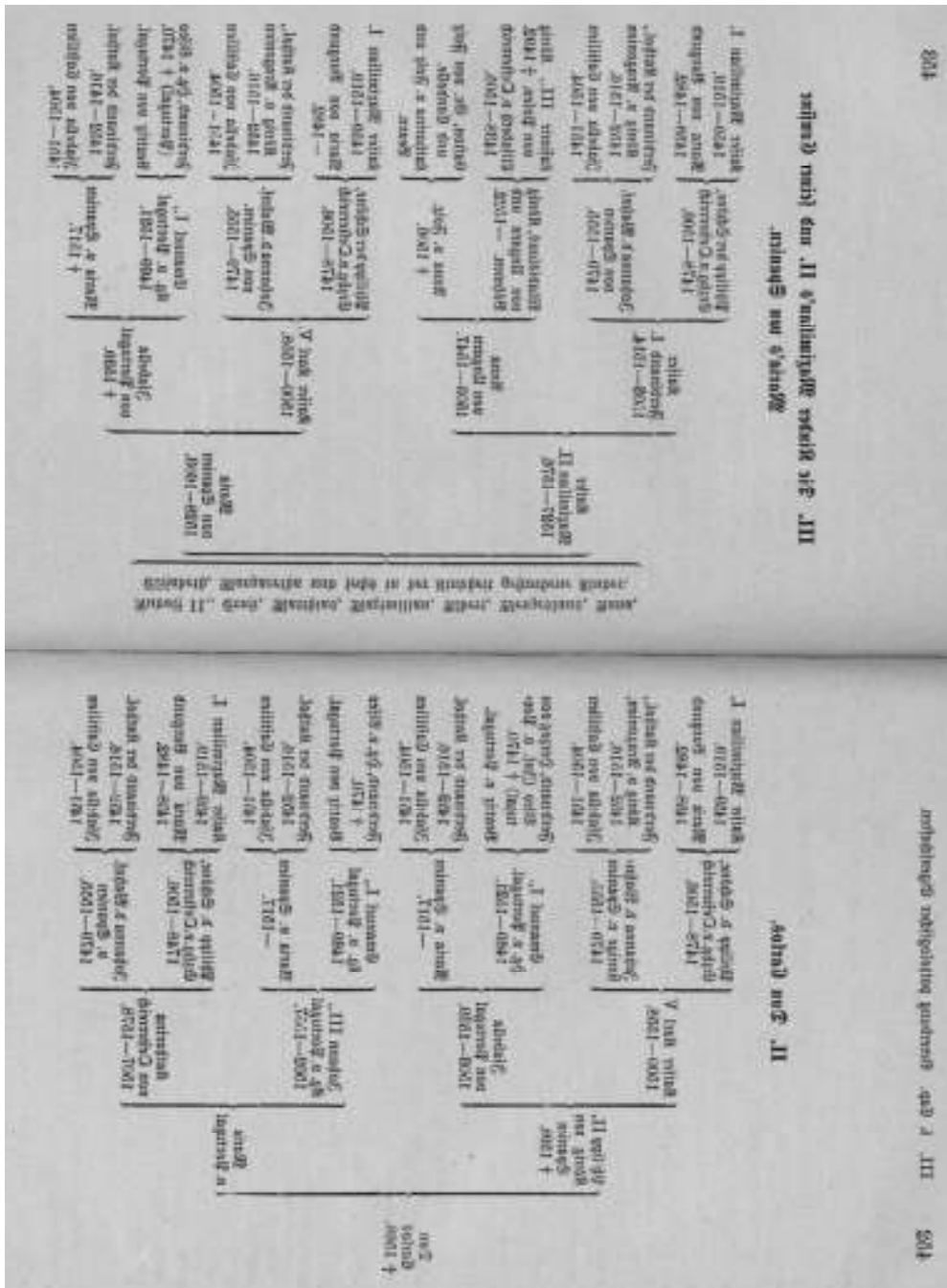
UK legislation introduced in April 2005 rules that in the case of gamete donation being used in infertility treatment the Human Fertilisation and Embryology Authority has to register all donors and to ensure that any resulting child will have access to information about the identity of the gamete donor when of age. The main argument publicly brought forward in favour of the conversion from strict donor anonymity to full disclosure to the child was the need for the child to be able to find out about health issues and biogenetic inheritance but also to develop a strong self-identity (Klotz 2006). Donor children were associated with adoptees and the legislation aims to prevent donor children experiencing stigmatisation similar to that which adoptees endured in the past. With increasing demand in medical practice for risk assessment with regard to diseases and the causes of death running in a family, this scenario of discrimination seems to have persuaded the UK legislators.

The special truth assigned to genomic knowledge opens up a wide space for interpretations and usages. It invites inconclusive and contradictory but obviously in any case multi-fold societal responses. The positive identity dimension on the individual level has remained underdeveloped in this description so far. What is it individuals seek when they search for a father or mother? The aim as frequently reported is to find some form of root that carries the promise to equip a person with something considered important; origin and a history and a lineage in the form of a chain of ancestors. A combination of the SNPs tests used to establish close relatedness, and PCR to search for specific genetic alterations shared amongst a type of people is used to establish ethnic belonging and local origin. The emotional reasons to undergo tests which establish belonging to a group correspond to the positive associations mentioned by individuals who actively seek to find a father, birth mother or a sibling. Identity confirmation as the motive to undergo testing will be discussed in the chapter below.

### C) Tracing Ancestry: Origin, Race, and Rights

Testing for ancestry is about establishing a physical connection to a group or place. Genomes as the material substance passed on through the generations indicate relatedness and belonging of an individual to a people or group. I will present some details of biological assumptions underlying this utilisation of genomics before discussing a few prominent examples.

Generally there are two conceptual and methodological problems with genomic ancestry tracing. The first problem is the arbitrariness of ancestral DNA transmission: due to the peculiar property of genomes they usually reassemble by keeping together large allele units. Subsequently the 'leftovers' from ancestors in a particular genome may indicate - depending on the selected parts and which test kits are used - one specific ancestor out of many. In theory the number of ancestors of a person grows exponentially – two parents, four grandparents, eight great-grandparents, and on to 256 ancestors after eight generations, which is estimated to be between 160 and 240 years of ancestral history. This theoretical number is actually reduced by overlaps that occur when one draws the family tree as a descent line, because of grandcousin marriages etc. Hence, the mathematical model based on full panmixia is never adequate, yet is frequently used in genomic ancestor chart debates. There is most likely considerable reduction of the number of ancestors over generations, the more so the smaller the communities with greater intermarriage rates.



(Lorenz 1898)

But for ancestry genomics and its scientific status as representing something adequate, more important than the empirically reduced number of ancestors in the family chart is that many ancestors may not have left any trace at all in a descendant's specific genome, because she inherits only one set of chromosomes from both her parents. Meiosis may assemble the inherited set of chromosomes in a particular egg or sperm so that over generations in the case of an individual only some of her ancestors are represented therein. But while meiosis might use a cocktail from both biological parents of the father and mother who contribute to a particular embryo, it might as well not. Specific chromosomes and other DNA are considered to be passed on almost unchanged from father to son and mother to her children: namely the y-chromosome and mitochondrial DNA (mtDNA). Hence whole lineages which are nominally equal parts of a person's ancestry might not be presented in her genome.

The chances are that over as few as eight generations genomic influences from many ethnic groups and bio-geographic regions accumulate to form one individual person's particular genome. A small number of dominant lines of ethnic origin may be present in the genome of an individual if she is from of a small, intermarrying community such as the Amish, for example (Lindee 2003). A person's genome is a patchwork of ancestral DNA, but many ancestors might not be part of it.

Every person carries chromosomes transmitted from both her parents, but intermarriage on the one hand and the arbitrary assembly processes in the creation of germ cells on the other do leave space for many ancestors of the person to be unrepresented in her genome. A rather underrepresented ethnic group, only feeding into the germ line of that family once, many generations back, might have left a mark, while the majority of ancestors all of similar Italian or Nigerian background, say, might fail to appear in her DNA yet might dominate the social and cultural environment of her life.

Especially useful parts of genomes for ancestry testing are the y-chromosome, because it is passed on virtually unchanged from father to son, and mitochondrial DNA (mtDNA). Details concerning these two testing techniques and their implications will be described below, but I will mention here that present knowledge is that each informs only about either the paternal or the maternal route of descent. Regarding the incompleteness of ancestor representation these two elements are highly specialised and rather precise when certain markers are sought. According to the current theory of inheritance the mtDNA or the y-chromosome a testee carries equals that of only one out of four grandgrandmothers or grandgrandfathers respectively.

This selectivity and almost detachment of genomic traces and social environment has led social and biological scientists to be very critical of ancestry testing. At the centre of this discussion are those groups who are most likely to seek confirmation. The most prominent examples are Black Americans, Native Americans in the US and the many groups that claim Jewish descent worldwide. These groups all have a long history of discrimination, rejection of their claims for equality and for recognition of their particularity. A confirmed, essentialist and proven identity as Black from x in Africa or definitely Native American etc., so they hope, would improve the odds for power struggles to lean toward their interests.

### C.1) Finding ethnic roots in Africa

The discrimination felt by adoptees and children not knowing father or mother, referred to above, structurally reappears in the practices of disempowerment endured by the victims of racism, slavery and ethnic discrimination. Many people of colour in the USA desire to find out about where their ancestors came from, which country they originated from, which place or name they can affiliate themselves with that is not the land or name of the former slave owner, rapist, and exploiter present in their family history. The socio-political history reflected in the official identity of a discriminated-against person, family, or group is often seen as a legitimate reason to refuse that identity or to enrich it with dimensions beyond the dark history of slavery and subjugation. A connection to any ethnic group living independently somewhere in Africa (or elsewhere) seems supportive, given the social demand for self-determination and self-confidence in order to succeed and claim equal rights in a racially divided social environment. Given the uncertainties and selectiveness of genomic leftovers from ancestors in one's genome anyway and that rape and abuse left genomic engravings of slavery and colonialism most clearly detectable in the male-determined parts of genomes, mtDNA testing has become established as the preferred ancestry test for Black people.

It seems from documents, self-stories and the online adverts of the servicing gene-companies, mostly in the USA, that the argument regularly brought forward by social scientists and critics of genetic testing as presented above, is missing the crucial point of the reasoning behind the searches. The weakness of the linkage, the likely arbitrariness of any identified close connection with a particular ethnic group revealed by the test is recognised in the published self-understandings of the testees and the adverts of those selling the tests. The tests are usually not testing for sophisticated genetic profiles anyway. The companies refer to databanks with 1,600 or 20,000 samples identifying ethnic relatedness with respect to the particular features of the mitochondrial DNA in the cells.

As of **3/21/2006** Family Tree DNA hits new milestones solidifying its leadership with the largest DNA database in the field of Genetic Genealogy:

- **2922 SURNAME PROJECTS!**
- **45355** unique surnames
- **57318** Y-DNA records in the database
- **16403** distinct 12-marker haplotypes
- **19672** distinct 25-marker haplotypes
- **20106** mtDNA records in the database. (from FamilyTreeDNA.com)

The DNA in the mitochondria, often called the cell's power stations, is most likely left over from a process of ongoing symbiosis between former bacteria and the nuclear DNA – so increasingly the DNA from the former bacteria that entered to live in conjunction with the nuclear DNA moves into the nucleus and the mtDNA gets shorter and less complex. In humans, mitochondria only produce a very small number of proteins from their own genome, but those are crucial for all developmental processes in the cell and many proteins are probably produced in some exchange of the mtDNA and nuclear DNA or the products of both. This symbiotic process and generally alteration in mtDNA is estimated to be very slow, that is at a rate of one alteration in 10,000 years.

The current state of knowledge has it that there are a certain number of types of mtDNA that are found in all humans. The maximum number currently seems to be 18 daughters of Eve, only seven of which seem to be present in Europeans, but not restricted to them, of course (Johnston et al. 1983, Sykes 2004, Jennings 2006). The seven primordial mothers of humankind stand for seven different stems of bacteria that entered the human germ line at some point and engaged in the mutual beneficial process of co-production with some bit of what is now human nuclear DNA. These ancestral mums or bacteria can all be traced back to Africa, where the marriage between nuclear DNA and mtDNA seems to have occurred millions of years ago. This view of 18 'Eves' has been challenged, but there is no need for too much detail on scientific controversy in population developments and evolution. However many Eves and when, general scientific belief at present holds that mtDNA is transmitted from mother to offspring as an integral part of the egg cell, while there is presumably no mtDNA passed on with or in the sperm.

Against a background of slavery in which 'white' intrusion into the lineage was most likely to happen through rape and sexual abuse of black women by white men, the female line of ancestry

represented in the mtDNA of Black people is more likely to select positively for an African, Jamaican or other origin. Hence the analysis of mtDNA is the preferred instrument to find roots in Africa and to locate more or less roughly a group in Africa, or elsewhere – given frequent migration movements - that shows the most similar mtDNA pattern.

That is what both the identity search and desire of individuals from discriminated social groups and also the tourism companies concentrate on, identifying some relatedness to some pre-slavery group and origin. Looking at the function of genomic testing in identity politics this seems, in my view, to be a case where, quite knowingly, an identity is sought and found that helps the personal confidence of the individual in her everyday life. The test has a therapeutic function that is not dependent upon its scientific appropriateness in terms of the proof of derivation of lineage or anything like that. The information provided to the customers indicates - and so do some reports online by such customers - that it is not pressing to find out dominant percentages of ancestral lineage, but rather to find any connection in the past that enhances self-esteem. Those who are troubled by the results of such genomic tests are those identity seekers who find themselves related to a slave-holding or trading tribe in Africa that collaborated with the USA in the slave trade, for instance, people who find not a positive but a discouraging descent line.

The strategy employed here is symbolically very fascinating in so far as it simultaneously re-inscribes and twists the logic of the one-drop rule. The test only shows a connection to one out of 16 or 32 or, given intermarriage, maybe 29 ancestors. But this is all that is needed to become someone who belongs to a group that has a cultural tradition, a language, customs and rites not reflected in the life chances of abductees during and after slavery. Of course, there is market logic at work here that adds to the fragility of this identity construction. To select for an ethnic group that may not be closest in mtDNA-pattern in post-colonial Africa but does promise a memorable, self-assuring visit doesn't seem far-fetched. Similarly, Africans might be paid to perform ethnicity rites on occasions, just as European tourists in Tunisia can book trips to places in the desert to watch natives in traditional costumes and body paintings grind corn with a huge stone mortar (while the cars with which those natives commute to their workplace are well hidden in a garage close to the displayed traditional sandstone cave). Despite the commercial setting, this identity technique may still help individuals to rebuild personal strengths on the establishment of an ethnic bond to their past. The technique used here, namely to lay open, embrace and hold dear the trait of stigma was developed by Black activists in the US and has become useful to many groups or individuals who are, or who feel they are, discriminated against for some special feature of their body or personality.

Affirmative action policies accepting those claims, however, usually require proof of the stigma and proof of membership, and this is where the negative side of this type of ancestry tracing hits not the Black American but the Native American and First Nation peoples.

## C.2) Native Americans and their Rights to the Places of Origin

Native Americans have certain rights to claim the land in which their ancestors are buried and which is therefore holy according to their beliefs. The regulations that seem to recognise the rights and value-systems of Native Americans were created by, for example, the Allotment Act of 1887. The major problem with those regulations is that they, seemingly legitimately because land-rights cannot be guaranteed to anybody who just claims to be Native, may be enforced only to the advantage of those who fulfil certain requirements. As Troy Duster states, US legislation makes certain rights dependent upon proof of belonging. Each individual that intends to claim this right has to prove "Nativeness" – formerly measured using particular markers in the blood, now increasingly tested genetically. The requirement may be "half-blood" (Allotment Act 1887) or

“one-quarter blood” (as for being allowed to call oneself a “Native Artist”) (Duster 2003, 267). Frederika Kaestle analysed the use and discourses around the testing of DNA from archaeological samples in this context (ancient DNA) and argues that the cultural affiliation of a particular group of people often does not match with data derived from genetic or other biological studies about their ancestry or region of origin. Kaestle stresses that laws such as the Native American Graves Protection and Repatriation Act were written as human rights legislation and that scientific results now trouble the balance of negotiation between the Government and the Native Americans. “In addition to having legal and political implications, DNA evidence could be interpreted as contradicting the creation myths of the tribes living in the region, many of whom believe they were created *de novo* in the area where they currently live” (Kaestle 2003, 287). Tribal history and origin as an autonomous group-identity were in line with the particular system of religious and cultural beliefs of that group. Now they are confronted with scientific evidence, gathered heteronomously, that demands reorientation.

### C.3) Jewish identities all over the globe – the Lemba and the Bene Israel

Many ethnic communities in all parts of the world from India and Yemen to various parts of Africa and the Caribbean to China have claimed, often for hundreds of years, to be Jews. This is documented in historic records by missionaries, for instance, as Tudor Parfitt, Professor of Modern Jewish Thought at the School of Oriental and African Studies, London, has admirably researched and communicated. This story has fascinated many and it is particularly special regarding the role of genomics in the verification of those claims, because Judaism is traditionally inherited by the maternal line: a Jew is a person who was born to a Jewish mother. The most important theological-political role in Judaism, however, is assigned to the male priests, who are sons of Moses. Jewish priesthood is passed on from father to son. Hence both maternally transmitted mtDNA and y-chromosome testing have become significant in establishing these population groups as Jewish.

The Lemba in Zimbabwe and South Africa are a community of about 70,000 people who live mainly as Christians but claim Jewish ancestry and have been ridiculed and belittled for believing in their Jewish origins in the past, prior to the proof offered by genomics. Parfitt notes of the Lemba that they are “often referring to themselves as ‘the white men who came from Sena’, they have a number of Semitic customs and have tentatively been identified as Jews by missionaries and other observers for about a hundred years” (Parfitt 2003, 114). A marker called the Cohen Modal Haplotype (CMH), which has been linked to a mutation in the genome of one of Abraham’s sons – Cohen - is considered to indicate direct descent and kin with the Jewish Priesthood. This genomic variation has been found on Lemba y-chromosomes with a significant frequency. Hence, it appears genetically proven that they have some Middle-Eastern male inheritance contribution and that their Jewishness is ‘genuine’. Parfitt’s observations during the last few years show that this newly confirmed identity has motivated some Lemba (almost all of whom are Christian and often puritan and rigorous) to abandon their previous habits and to practise Jewish customs instead. With regard to their social status this is only logical, as colonialists who had classified them as Jewish had always assigned a higher social status to them (and had more interest in Christianising them, too) than to other ethnic groups living in the area. Questions of who is black and not black and of who is Jewish and not Jewish structure the public reception and the self-perception of the Lemba in changing patterns. Laurie Zoloth considers the meaning of that ‘proof’ of a lost-tribal identity for the Lemba and stresses that “the research on the Cohen Modal Haplotype raises immediate questions about citizenship and the obligation of the Israeli state to support any Jew anywhere” (Zoloth 2003, 131). The Lemba’s Jewishness gave new emphasis to the question of the social status of Jews in various populations and nations and has been linked to the discourses about the creation of Whiteness in the USA (Allen 1997, Brodtkin 1999, Parfitt & Egerova 2006, Chapter 4).

Parfitt and Egorova compare the situation of the Lemba with that of the Bene Israel, a Jewish group in and around Mumbai in India. The Bene Israel, who have also long claimed Jewishness, were recently shown to carry a high frequency of the CMH without specific insertions in the y-chromosomes. Those factors together mean, according to Parfitt and Egorova, that they are most probably an ancient Jewish group that originated from the Middle East. The genomic confirmation of the Bene Israel's Jewishness attracted a surprising amount of media attention. The *Times of India* carried a report on the front page and a longer article. "But now, after the test, the article argues, the Bene Israel 'could well claim to be the purest of the pure'" (Parfitt & Egorova 2006, 111). Regarding the effect this particular form of test had in India, Parfitt and Egorova conclude:

"In Indian terms the test appeared to the Bene Israel to confer upon them caste dignity, priestly status and purity. In the light of their social situation in India it was not so surprising that the Bene Israel tended to construct the genetic results as proving the 'purity' of their Jewishness combined with the traditions, according to which the Brahmans of India were actually Cohanim, the 'purest' of the Jews, made the Bene Israel even purer than the Brahmans" (Parfitt and Egorova 2006, 119).

## 5) Conclusions

Michel Foucault, in his reflections on the functions and limits of biopower, uses the term 'race' to denote a whole set of social practices that insert intra-species distinctions. Race in this meaning becomes inscribed into the mechanisms of state power, as "a way of fragmenting the field of the biological that power controls. It is a way of separating out the groups that exist within a population" (Foucault 2003, 255). As described in the section on the Human Genome Diversity Project, intra-species borders in terms of race or ethnicity were greatly debated in the context of population genomics and its aims. The forms taken by this desire for belonging and the ways in which genomics delivers the confirmations that individuals seek privately or publicly are framed differently in the examples above. Descent and belonging are regarded as important dimensions of identity, as the paternity, inheritance, and origin debates described above show.

Considering these are but a few examples out of many that could have been presented, and in much more detail than was possible here, it seems that genomics is a much appreciated tool in identity politics, at least. My argument goes much further, though. I aim to show that genomics is actively engaging and participating in the inversion of racism as a strategic tool of difference and in doing so is safekeeping its place in society as the major institution of the delivery of truth.

That identity politics is racist in its structure and that the way in which groups and individuals use genomic tests as evidence actually supports this ideological framing of genomics as an instrument of racism becomes most obvious in the examples of the HGDP, in the tests used by Black people not living in Africa to establish a distinctive African root, and conversely in the example of the Lemba, many of whom began to enact their Jewishness more strongly after it had been genomically affirmed – which only expresses the mutual interaction of public recognition and everyday practices and self-understandings.

The idea of purity, which is a major concept in all racism, runs through these examples in very specific and heterogeneous ways, but is always recognizable. The one-drop rule reappears, inverted, when – despite the almost complete arbitrariness with which an mtDNA test relates an individual to one out of so many female ancestors – it is consciously rendered valuable for personal identity development. The effect that identity-positive genomic findings had on the social status of the Bene Israel in India is interesting: similar images to the one-drop rule are invoked to establish superiority of race in a racial society through notions of purity. In the case of hereditary disease the

identity trouble is of a similar type: the clarification of carrier status replaces the shared family history by one in which definite in- and outsiders of groups of carriers and one of non-carriers are identified, bringing with it new tensions, empowerment and disempowerment. The 'belonging' in kinship and biogenetic kin testing is more complicated, because the various levels at which legal and social constructions refer to presumed or real biogenetic ties to parents, ancestors or a place cannot be described along a dual line but are more complex. This does not mean, however, that the idea of the quarter-blood or half-blood rules that are legally in place to define whether a person's art can be called Native or whether she can claim land rights, cannot be tested or proven genomically in principle – an idea which so far has been opposed forcefully by the Native American communities.

The relationship between identity practices and testing technologies and science is one of mutual affirmation, referencing and justification. The specificity of genomics, supposedly providing certain knowledge about inherited traits of a person, on the one hand and the immediate medical and wider societal utility of the knowledge genomics is seeking on the other, has created an interplay of social actors that aims for a specific social formation of true knowledge on significant differences. In Foucauldian terms, the genomics and identity politics relationship can be described as a basic strategy and technique of power, as a 'dispositif' of genomically essentialised identity formations. The problem with the often used co-production language in this context, it seems to me, is that co-production implies some product that is consciously aimed at. Although I am aware that the concept can well be invoked without the intention to convey this, it is difficult to avoid the association with this rhetoric. Foucault's concept of dispositif allows emphasizing the enormous social power that is accumulating around and in the genomics-identity hubs without denying the multi-fold forms in which it appears and is used. The concept of dispositif contains the idea that there is no plan or super-agent behind all this, but a huge number of conflicting mini-agents, each of which is strongly encouraged to go her way by the firm identities built upon genomic test results. This leads to an explosion of certainties and identities that express themselves, cross out and override each other both in individual and in group contexts, causing conflicts and tensions that lead to mini-wars of stigmatisation and social death.

Biopower fosters life and its strengths, hence it benefits from strong identities in people. In order to remain powerful, however, it also needs to act and its act is one of purification, of improving the chances for the strongest. Competition for strong and not unalienable identities can be a valid instrument in a struggle for social status and place and genomics can make itself useful in various ways in such competitions.

To conclude with a self-critical comment about the involvement of social scientists and ethicists in this activity: both the declaration of an exceptionalist status that requires governance of genomic testing as much as the appreciation of certain identity struggles and movements that arose from or were 'won' with genomics, stress that we are a very active part of the formation and transformation of this dispositif. Not that one could remain outside – certainly not in writing on it.

Genomes fly through the air (as cells and skin particles etc.). Each organism carries, to say it metaphorically, a cloud of her DNA around her. Much tested DNA will hence be mixed with minute traces of DNA from the tester. This fundamental and practical weakness in genomics is only relevant when there are only very small amounts of testable (amplifiable) DNA from the testee available, which is the case with ancient DNA, forensic and some prenatal testing. Contamination of probes is a serious threat to adequate test findings. This is not a problem when the amount of DNA of the organism that is intended to be tested is a multiple of the DNA that might have dropped in from imperfect cleaning procedures in the lab or unqualified handling so that an accidental drop

of some DNA from a police-officer, lab technician etc. enters the sample. The impurity becomes visible in an SNPs test, for there are visible some grey traces where there should be either clear dark marks or no mark at all or when specific markers are found in different probes (e.g. Gilbert et al, 2004.1). This is, of course, a recurring problem for all analysis for which signal to noise issues are confounded by possibilities of external contamination. While there are various established control procedures for optimizing discrimination under such circumstances, the analyst as well as the legal official and the customers of the technology should be aware of the statistical confidence limits of the work that seemingly relate to the number of loci examined.

I make this observation here for two reasons. First, to show that the assumed precision of genomics is not as easily maintained or achieved as assumed because DNA is not safely locked up into cells that for their part stick to their organism firmly. Second, to show that the image and language of racism runs through and appears in genomics at all levels from aims to everyday lab practices. The problems of purity and contamination of genomic test samples, which has remained almost unproblematised so far in public discussion, has been a serious problem of molecular biology since the 1950s and has been phrased in racist language from early on, as in the example of HeLa cells “taking over” whole laboratories (Landecker 2000). Indeed, the term ‘contamination’ in particular, but also sometimes ‘purity’, is used in scientific accounts of the problem in ancient DNA analysis in particular. Since this is not as clearly separated from origin and medical history testing as might be supposed (see Gilbert et al 2004.2), the identity truth factory may be even less reliable than already assumed in ethics and social science debates. The conceptual relatedness between purity and definiteness of knowledge mirrors the crossing over between a technological, societal and policy discourse in identity and points out why and how DNA as seemingly exceptionally reliable means to know became such a useful instrument in identity politics. The complementary power structures of discipline and biopower both foster racism in attitudes toward knowledge about oneself, and consequently in relation to others.

### Acknowledgements:

This paper was first presented at Cornell University in April 2006 as part of the Ethics in Public Life Young Scholars Award. I would like to extend my sincere appreciation to the Ethics and Public Life program for honouring me with this award and to those who generously participated in the two days of discussion of my work. I wish to give special thanks to Michele Moody-Adams, Director and Hutchinson Professor of Ethics and Public Life at Cornell. The success of the Young Scholars Award weekend was due in great measure to Professor Moody-Adams' capaciousness as director, host, and, above all, intellectual interlocutor. In all that she does, she realizes the ideal of women in philosophy. I am also thankful to the many esteemed colleagues who gave me their time and honest yet encouraging critique. In particular, I thank Kimberly Leighton and Chloe Silverman for their challenging and careful commentaries.

The Young Scholars Award weekend was one of the intellectual highlights in my experience so far, and I hope to be able to do justice to the rich and thoughtful advice I received. I have continued to develop the projects I presented there at various venues and am presently working on expanding the present paper into a monograph. I have also pursued this work through the creation of the ESRC Genomics Network Workstream "Genomics and Identity Politics" which is taking place from spring 2008 to summer 2009.

For their help with the production of the paper itself, I wish to thank Michael Hauskeller, Harriet Barry and Claire Packman for reading carefully through this manuscript; Gesa Lindemann for the inspiring and clarifying discussions on border regimes and Foucault; and Barry Barnes for his constant support and advice on many theoretical and conceptual issues. I further thank Bernd Gausemeier, who provided me with knowledge about ancestry charts and the page from Lorenz. I also wish to acknowledge the many scholars, colleagues and experts whom I have met and exchanged ideas with over the past several years and whose writings and/or contributions were not directly noted in my references. In particular I wish to express my indebtedness to Barbara Katz-Rothman for many long and intense discussions; other important exchanges happened with Nadia Abu-el Haj, Martin Dannecker, and John Dupré.

This paper was part of my work at Egenis, the ESRC Centre for Genomics in Society at the University of Exeter, which is funded by the UK Economic and Social Research Council.

## Bibliography:

Allen, T.W. (1997) *The Invention of the White Race: Volume Two: The Origins of racial oppression in Anglo-America*, New York: Verso.

Allotment or Dawes Act, 1887:

[http://www.rootsweb.ancestry.com/~okmurray/images/daws\\_act\\_of\\_1887.htm](http://www.rootsweb.ancestry.com/~okmurray/images/daws_act_of_1887.htm)

AncestryByDNA (2006) [Online], Available, [13 June 2008]:

<http://www.ancestrybydna.com/welcome/home/index.php>

Bostanci, A. (2004) 'Sequencing Human Genomes' in Rheinberger, H.-J. and Gaudilliere, J.-P. (eds.) *The Mapping Cultures of 20th Century Genetics*, Abingdon: Routledge, pp 158-179.

Bostanci, A. (2006) 'Two Drafts, One Genome? Accommodating Human Diversity in Human Genome Research', *Science as Culture*, Vol. 15, No 3, pp. 183-198.

Brodkin, K. (1999) *How Jews Became White Folks and What That Says about Race in America*, London: Rutgers University Press.

Butler, J. (2003) *Giving an Account of Oneself: A Critique of Ethical Violence*, Amsterdam: Van Gorcum Ltd.

Carsten, J. (2003) *After Kinship (New Departures in Anthropology)*, Cambridge: Cambridge University Press.

Cavalli-Sforza, L.L., Wilson, A.C., Cantor, C.R., Cook-Deegan, R.M & King, M.C. (1991) 'Call for a Worldwide Survey of Human Genetic Diversity: A Vanishing Opportunity for the Human Genome Project', *Genomics*, Vol. 11, (No.2), pp. 490-491.

Cavalli-Sforza, L.L. & Bodmer, W. F. (1999) [1971] *The Genetics of Human Populations*, New York: Dober Publications.

Cavalli-Sforza, L.L. (2000) *Genes, Peoples and Languages*, New York: North Point Press.

Costelloe, T. (2003) 'The Invisibility of Evil: Moral Progress and the 'Animal Holocaust'', *Philosophical Papers*, Vol. 32 (2).

Davis, D. S. (2000) 'Groups, Communities, and Contested Identities in Genetic Research', *The Hastings Center Report*, Vol. 30.

Davis, D. S. (2001) *Genetic Dilemmas: Reproductive Technology, Parental Choices and Children's Futures*, New York: Routledge.

Dexter, M. (2002) The Wellcome Trust and The Sanger Institute, Press Conference to Announce the Finished Draft of the Human Genome Sequencing Project, 26. June 2002.

Drury, K.C., Liu, M.C., Lilleberg, S., et al. (2001) 'Results on single cell PCR for Huntington's gene and WAVE™ product analysis for preimplantation genetic diagnosis', *Molecular and Cellular Endocrinology*, Oct. 22, Vol. 183/1, pp. 1-4.

Duster, T. (2003) 'Buried Alive: The Concept of Race in Science', in: Goodman, A.H., Heath, D., Lindee, M.S., in *Genetic Nature/Culture: Anthropology and Science Beyond the Two-Culture Divide*, Los Angeles: University of California Press.

EGE (2003) European Group on Ethics in Science and New Technologies to the European Commission: "Ethical Aspects of Genetic Testing in the Workplace". .

Family Tree DNA [Online] Available, [13 June 2008]: <http://www.familytreedna.com/>

Finkler, K. (2000) *Experiencing the new genetics. Family and kinship on the Medical Frontier*. Philadelphia: University of Pennsylvania Press.

Foucault, M. (2003) *Society must be Defended: Lectures at the Collège de France 1975-1976*, New York: Picador.

Gene Tree 2008 [Online], Available, [13 June 2008]: <http://www.genetree.com/>

Gene Tree Detective 2008 [Online]: <http://www.genetree.com/product/dnadetective.asp>

German Embryo Protection Act, [Online]: <http://www.bmj.de/files/-/1148/ESchG.pdf><http://www.jura.uni-sb.de/BGBl/TEIL1/1990/19902746.1.HTML>

Gilbert, M.T.P., Wilson, A.S., Bunce, M., Hansen, A.J., Willerslev, E., Shapiro, B., Higham, T.F.G., Richards, M.P., O'Connell, T.C., Tobin, D.J., Janaway, R.C., Cooper, A. (2004) 'Ancient mitochondrial DNA from hair'. *Current Biology*, Vol.\_14, R 463-R 464.

Gilbert, M.T.P., Cuccui J., White, W., Lynnerup, N., Titball, R.W., Cooper, A., Prentice, M.B. (2004) 'Absence of *Yersinia pestis*-specific DNA in human teeth from five European excavations of putative plague victims'. *Microbiology*, Vol.\_150, Part 2, pp. 341-354.

HapMap 2008: International Haplotype Mapping Project, [Online], Available, [13 June 2008]: [www.hapmap.org/](http://www.hapmap.org/)

Harvard 2005: Personal Genome Project Webpage, [Online] Available, [13 June 2008]: <http://arep.med.harvard.edu/PGP/>

Hauskeller, C. (2000) *Das paradoxe Subjekt. Unterwerfung und Widerstand bei Butler and Foucault*, Tübingen: Discord.

Hauskeller, C. (2004) 'Genes, Genomes and Identity', *New Genetics and Society*, Special Issue the Meanings of Genomics.

Hauskeller, C. (2006), 'Verteidigung des abhängigen Subjekts: Warum es gewaltlose Ethik nicht gibt', in: Haker, H. & Konnertz, U. (eds.) *Ethik, Geschlecht, Wissenschaft*. Paderborn: Mentis Verlag, in press.

HGP 2000: Sanger Centre Main Press Release "The first draft of the Book of Humankind has been read", 26.6.2000: [Online], Available, [13 June 2008]: <http://www.sanger.ac.uk/Info/Press/000626.shtml>

Human Genetics Commission 2002: Consultation Document: 'The supply of genetic tests direct to the public', July 2002, accessed June 2008:

<http://www.hgc.gov.uk/Client/document.asp?DocId=35&CategoryId=3>

The literature on Jefferson and Hemings is wide – a controversy about the use of genetic data is particularly salient for our context, see the links below or the whole evaluation as pdf at:

<http://www.monticello.org/plantation/hemingscontro/dnareport6.html>

[http://www.monticello.org/plantation/hemingscontro/minority\\_report.html](http://www.monticello.org/plantation/hemingscontro/minority_report.html)

Jennings, K. (2006) 'Eve's Secret', [Online], Available [13 June 2008]: Genetics and the Origin of Women webpages: <http://gtalumni.org/Publications/magazine/win91/wallace.html>

Johnson, M. J., Wallace, D.C., Ferris, S.D., Rattazzi, M.C. & Cavalli-Sforza, L.L., (1983) 'Radiation of human mitochondrial DNA types analyzed by restriction endonuclease cleavage patterns', in *Journal of Molecular Evolution*, Vol. 19, No. 3-4, pp. 255-271.

Kaestle, F.A. (2003) 'The Good, the Bad and the Ugly: Promise and Problems of Ancient DNA for Anthropology', in: Goodman, A.H., Heath, D., Lindee, M.S. (eds.) *Genetic Nature/Culture: Anthropology and Science Beyond the Two-Culture Divide*, Los Angeles: University of California Press.

Kay, L. (2000) *Who Wrote the Book of Life: A History of the Genetic Code*, Stanford: Stanford University Press.

Keller, E. F. (2000) *The Century of the Gene*. Cambridge, MA, USA: Cambridge University Press.

Klotz, M. (2006) "'HELLO DADDY!": The construction of gamete donors and their kin-relations in UK regulatory discourse on donor anonymity.' Manuscript under review at *New Genetics and Society*.

Kolb, E. (2003) 'Huntington's disease: Historical and Contemporary Connections', in: *P&S* Vol. 23, No. 1, [Online], Available, [13 June 2008]: <http://cpmcnet.columbia.edu/news/journal/journal-o/winter-2003/hd.html>

Landecker, H. (2000) 'Immortality, in vitro: A History of the HeLa Cell Line', in Brodwin, P. (ed): *Biotechnology and Culture: Bodies, Anxieties, Ethics*, Bloomington: Indiana University Press.

Lell J.T., Sukernik, R.I., Starikovskaya, Y.B., Su, B., Jin, L., Schurr, T.G., Underhill, P.A., Wallace, D.C. (2002) 'The Dual Origin and Siberian Affinities of Native American Y Chromosomes'. *American Journal of Human Genetics*, Vol. 70, pp. 192 -206.

Lemke, Th. (2005) 'Beyond genetic discrimination. Problems and perspectives of a contested notion', *Genomics, Society and Policy*, Vol.1/3, [Online], Available, [13 June 2006]: <http://www.lancs.ac.uk/fss/journals/gsp/index.htm>

Lindee, S.M. (2003) 'Provenance and the Pedigree: Victor McKusick's fieldwork with the Old Order Amish', in Goodman, A.H., Heath, D., Lindee, M.S. (eds.) *Genetic Nature/Culture: Anthropology and Science Beyond the Two-Culture Divide*, Los Angeles: University of California Press.

Lindemann, G. (2002) *Die Grenzen des Sozialen: Zur sozio-technischen Konstruktion von Leben und Tod in der Intensivmedizin*, Munchen: Wilhelm Fink Verlag.

Lindemann, G. (2005) 'The Analysis of the Borders of the Social World: A Challenge for Sociological Theory', in: *Journal for the Theory of Social Behavior*, Vol. 35: pp 69-98.

Lorenz, O.-K. (1898) *Lehrbuch der gesamten wissenschaftlichen Genealogie. Stammbaum und Ahnentafel in ihrer geschichtlichen, sociologischen und naturwissenschaftlichen Bedeutung*, Berlin

Marks, J. (2003) '98 % Chimpanzee and 35 % Daffodil: the Human Genome in Evolutionary and Cultural Context', in Goodman, A.H., Heath, D., Lindee, M. S. (eds.) *Genetic Nature/Culture: Anthropology and Science Beyond the Two-Culture Divide*, Los Angeles: University of California Press.

Nature (2001) International Human Genome Sequencing Consortium: 'Initial sequencing and analysis of the human genome'. *Nature*, Vol. 409, No. 6822, pp. 860-921.

Nelkin, D. & Lindee, S.M. (1995) *The DNA Mystique: the gene as a cultural icon*, New York: Freeman and Company.

Nelkin, D. (2001) 'Molecular metaphors: the gene in popular discourse.' *Nature Reviews/Genetics*, Vol. 2, pp. 555-559.

Nerlich, B. & Dingwall, R. (2003) 'Deciphering the Human Genome: The semantic and ideological foundations of genetic and genomic discourse.' in Dirven, R., Frank, M.R., & Pütz, M. (eds) *Cognitive Models in Language and Thought: Ideologies, Metaphors and Meaning*, Berlin: Mouton de Gruyter.

Parfitt, T. (2003) 'Constructing Black Jews: Genetic Testing and the Lemba – the 'Black Jews' of South Africa', in: *Developing World Bioethics*, Vol. 3/2, pp. 112-118.

Parfitt, T. & Egorova, Y. (2006) *Genetics, Mass-Media and Identity: A case study of the genetic research on the Lemba and Bene Israel*, London: Routledge.

Park, A. (2002) 'Pioneers of Molecular Biology, Nancy Wexler' *Time Magazine*, 9 February: [Online], Available [13 June 2008]: <http://www.hdfoundation.org/news/20030209-Time.htm>

Pleasant, N. (2004) 'The concept of learning from the study of the Holocaust', *History of the Human Sciences*, Vol. 17, No 2-3, pp. 187-210.

Rapp, R. & Ginsburg, F. (2001) *Enabling Disability: Rewriting Kinship, Re-imagining Citizenship*, in: *Public Culture*, Vol. 13, No. 3, pp. 533-556.

Reardon, J. (2005) *Race to the Finish: Identity and Governance in an Age of Genomics*, New Jersey: Princeton University Press.

Rose, N. & Novas, C. (2004) 'Biological Citizenship', in Ong, A. and Collier, S. (eds) *Global Assemblages: Technology, Politics, and Ethics as Anthropological Problems*, Malden, MA: Blackwell Publishing.

Schneider, D. (1984) [1968] *American Kinship*. Englewood Cliffs: Prentice Hall.

SCIONA (2008), [Online], available [13 June 2008]: <http://www.sciona.com/>

Stockdale, A. & Terry, S. F. (2002) 'Advocacy groups and the new genetics', in Alper J. S., et al. (eds) *The Double-Edged Helix: Social Implications of Genetics in a Diverse Society*, Baltimore: John Hopkins University Press.

Sykes, B. (2004) *The Seven Daughters of Eve*, Corgi Press.

Taussig, K.S., Rapp, R., Heath, D. (2003) 'Flexible Eugenics: Discourses of Perfectability and Free Choice at the End of the 20th Century', in Goodman, A. H., Heath, D., Lindee, M. S. (eds.): *Genetic Nature/Culture: Anthropology and Science Beyond the Two-Culture Divide*, Los Angeles: University of California Press.

Terry, S. F. and Terry, P.F. (2001) 'A consumer perspective on informed consent and third-party issues', in *Journal of Continuing Education in the Health Professions*, Vol. 21, No. 4 pp. 256-264.

Turnbull, D. (2004) 'Genetic Mapping: Approaches to the Spatial Topography of Genetics or Performing Genes through Mapping, Metamapping and Unmapping', in Rheinberger, H.-J. and Gaudillière, J.-P. (eds.) *Classical Genetic Research and Its Legacy: The Mapping Cultures of 20<sup>th</sup> Century Genetics*. Abingdon: Routledge.

UNESCO Statement on Race (1950) [Online], Available, [13 June 2008]  
<http://unesdoc.unesco.org/images/0012/001282/128291eo.pdf>

United Nations (1948) 'Universal Declaration of Human Rights', [Online], Available, [13 June 2008]: <http://www.un.org/Overview/rights.html>

Venter, J.C. et al. (2001) 'The Sequence of the Human Genome', *Science* Vol. 291, No. 5507, pp 1304-1351.

Wexler, A. (1995) *Mapping fate: A Memoir of Family, Risk and Genetic Research*, New York: Times Books, Random House.

Zoloth, L. (2003) 'Yearning for the long lost home: The Lemba and the Jewish narrative of genetic return', in *Developing World Bioethics* Vol. 3/2, pp. 127-132.