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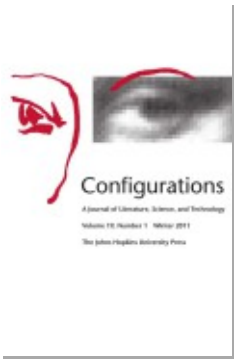

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Technologies of Population: Forensic DNA Testing Practices and the Making of Differences and Similarities

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This article is about population. My aim is to answer the question, what is *population*? Instead of defining it myself or asking geneticists what it is, I want to trace *population* in genetic practices and to observe how it is embodied in them. Toward this end, I analyze a forensic case. My analysis results in two arguments: first, that geneticists cannot know the individual without a population; second, that in genetic practices neither the individual nor the population is inherently "biological"—both are technologically assisted categories.

Population is a category of debate specifically in the Human Genome Diversity Project,[1] and in population genetics at large. Geneticists aim at achieving a consensus *definition* of what population is, in order to sample, study, and compare populations. In this article, however, I examine *practices* of population and attend to its variety in laboratories. In order to "know" a population, geneticists study the cell material of collections of individuals. In forensics, on the other hand, the vantage point is quite different. Forensic geneti-

1. This article is part of my Ph.D. research on the Human Genome Diversity Project, which was initiated in 1991 by the population geneticist Luiga Cavalli-Sforza and the biochemist Alan Wilson. In an attempt to understand human migration history, the diversity in populations, and population structures, the goal of the project is to map human genetic diversity by collecting samples from hundreds of populations and studying their DNA. The project had become very controversial, due to the emphasis placed on "isolated populations" and populations that allegedly did not undergo a great admixture; see Amâde M'charek, "Mediating Homogeneity and Diversity: On The Interdependence of Nature and Technology in the Human Genome Diversity Project," Ph.D. diss., University of Amsterdam, 2000.

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cists are interested in the individual: their aim is to identify individual A as similar to, or different from, individual B. Yet, I have chosen this very practice as a site for examining population. For, in order to know an individual, forensic geneticists apply a category of population as well. Hence, in order to produce *differences* (between individuals), geneticists need to presuppose *similarities* (within a population). I will examine practical decisions about individuality and population, and hence about similarities and differences. On the basis of one forensic case, various concepts of population will be interrogated.

Taking population as the main focus of my analysis, I will pay little attention to legal aspects of forensic DNA, a highly important matter in its own right. Rather, the site studied is a laboratory, the Forensic Laboratory for DNA research in Leiden. Since my argument is organized around a forensic case, the narrative unfolds as a "trip" back and forth between laboratory and courtroom, observing the process of identification and examining concepts of population embodied in the case.

In Court

We are in a courtroom somewhere in the Netherlands. A murder case is in progress. Both the victim and the suspect are Turkish. The victim was kidnapped and killed. Evidence was found in a house next to the victim's body, and also in a car belonging to one suspect; the evidence material consists of traces, such as blood spots, chewing gum, and cigarette butts. The evidence at the scene of the crime indicates that more people were present. Other circumstantial evidence made the prosecutor suspect one person in particular. The main suspect has denied any involvement. Since the victim no longer has a voice, the question remains: can the suspect be identified as the perpetrator?

In court, a relatively new type of expert witness is present to help in the process of identification.[2] This expert witness is a geneticist, called in to present and clarify the DNA evidence based on the suspect's cell material and on the evidence: the blood spots and chew-

2. On expert witnessing in American lawsuits, see Sheila Jasanoff, *Science at the Bar: Law, Science, and Technology in America* (Cambridge, Mass.: Harvard University Press, 1995). For a comparative study on expert witnessing in the Netherlands and the United States, see Petra T. C. van Kampen, *Expert Evidence Compared: Rules and Practices in the Dutch and American Justice System* (Antwerp/Groningen: Intersentia Rechtswetenschappen, 1998). See, for several other discussions, a special issue of *Social Studies of Science* (December 1998), edited by Sheila Jasanoff and Michael Lynch, prompted by the well-known O. J. Simpson trial.

ing gum, and especially the cigarette butts. The DNA evidence consists of a DNA fingerprint with a number, 10^{-7}, which represents the likelihood that the evidence comes from any other person in the population; according to the expert witness, this number indicates that evidence and suspect DNA coincide. The DNA evidence supports the findings of the prosecutor that were based on other circumstantial evidence. The defense objects to the results of the DNA tests and questions the testimony based on a power of 10^{-7}.

In order to trace where the results presented in court came from, what they mean, and how they play a role, we may best enter the Forensic Laboratory. This site is of great importance to the significance of the DNA evidence presented in court. We will first consider this laboratory in the context of DNA evidence in the Netherlands, and then take a closer look at how DNA evidence is handled in the laboratory.

DNA Evidence and Its Laboratories

In 1994, a new Dutch law on forensic DNA evidence was passed, which enlarges the use of such evidence in prosecutions, and has initiated an infrastructure of sites and regulations concerned with making this evidence.[3] According to this law, a suspect in a crime that carries a penalty of eight or more years cannot object to DNA testing. If there exists other evidence against that particular suspect, DNA testing is compulsory. A suspect cannot be convicted on the basis of DNA evidence only. Further, the rights of the suspect, embodied in the Dutch state, give him or her the opportunity to apply for DNA counterexpertise, which is also a product of laboratories. In cases of DNA evidence, therefore, two laboratories may be involved. The tests conducted on behalf of the prosecutor are primarily conducted in the *Laboratory of Criminal Justice, Rijswijk* (Het Gerechtelijk Laboratorium, Rijswijk), whereas the counterexpertise analyses are conducted in the *Forensic Laboratory for DNA Research, Leiden.* If the amount of evidence is too small for two studies, the suspect may decide which of the two laboratories should conduct the one and only test.[4]

3. The revision of 1994 is actually an addition to the Dutch Criminal Code (articles 151a, 195a, 195b, and 195d): see De Ministerie van Justitie, A. Kosto, *Staatsblad van het Koninkrijk der Nederlanden,* 522 (1994). A short description of forensic science in the Netherlands can be found in Livia Jacobs, ed., *Gerechtelijke Laboratoria in Beeld: Een Kennismaking met Beoefende Deskundigen* (Laboratories of criminal justice in the picture: A first acquaintance with experienced experts) (Groningen: Wolters-Noordhof, 1995), pp. 107–111.

4. According to the Dutch Criminal Code (Wetboek van Strafvordering, Artikel 151aj, 195a), only laboratories assigned via "de algemene maartregel van bestuur," the politi-

The *Forensic Laboratory,* hereafter Lab F, is embedded in a broad network comprising governmental regulations and laws, the Laboratory of Criminal Justice and the Board of Accreditation, the university's Department of Human Genetics and the Sylvius Laboratory in Leiden, pharmaceutical industries, and (inter)national networks of scientists in the fields of forensics and population genetics, including the Diversity Project. In order to reduce the high prices of DNA testing (for prosecutors and suspects) and to make counterexpertise available to "everybody," Lab F is entirely funded by the Dutch government.

In the next section, we shall encounter forensic laboratory work. We will be introduced to Lab F's rites and rituals, its protocols and procedures, and the particular alignment of technology and material trace, to produce DNA evidence. First Lab F will be introduced. From the perspective of a newcomer, we will make visible materialized institutional arrangements in that particular context and will familiarize ourselves with the laboratory culture. We shall then learn more about the Lab's procedures and its organization of work around DNA identification. Finally, I will focus on DNA identification and how it was accomplished in the forensic case introduced above.

Off to the Forensic Laboratory

I was in Lab F.[5] I was not merely an observer: I had asked for a short introduction to the basics of genetic research. During three and half months, I participated in a project concerned with typing

cal and judicial arrangement for forensic science, may produce DNA evidence. In the Netherlands there are two of these: the Laboratory for Criminal Justice (Rijswijk), and the Forensic Laboratory for DNA Research (Leiden).

5. I learned that laboratories do not necessarily have to be the immured sanctuaries, the domains of no entrance for outsiders, that Bruno Latour, for example, describes. When I started my studies I had several talks with Professor Gert-Jan van Ommen, head of the Department of Human Genetics to which the forensic laboratory is linked, and vice president of the Human Genome Organization (HUGO). He advised me to visit one of the Human Genome Diversity conferences organized by HUGO (in Barcelona, November 1995) to get to know that scientific community. Since I was especially interested in daily laboratory routine, he suggested that I talk to Dr. Peter de Knijff, head of the forensic laboratory, who, as he told me, was also working on human genetic diversity. Dr. de Knijff was enthusiastic about an outsider interested in genetic practices and was willing to arrange training for me in his laboratory. Having attended the conference in Barcelona and other international meetings, I learned, to my surprise, that many laboratories participating in the Diversity Project were actually very open to outsiders. In the two where I conducted my research, I combined a "hands-on" project (a training or a small genetic research project) with ethnographic work. Therefore I kept two journals: one lab journal on which I worked in the laboratory, and an

the DNA of chimpanzees, and I learned to perform some of the basic tasks of a technician. Since this training constituted my first observational study, I was also learning to observe scientists at work: learning to study a different culture, to take notes and interviews, and to develop common ground for an understanding of what was going on.

In order to participate in this laboratory I had to be initiated into institutional regulations. Like all laboratory members, I had to sign a medical declaration, I had to be insured against laboratory risks, and I had to swear to maintain secrecy about ongoing cases. I was also expected to participate in the weekly in-house meetings as well as the weekly joint meetings of Lab F and the Diagnostics Laboratory of Human Genetics. On a more informal level, my daily supervisor and the rest of the members shared with me their personal accounts of forensics and experiences in the field, which enabled me to enter the discourse of the laboratory.

On my first day in, after I was introduced to the members, the head of Lab F appointed me a daily supervisor, explained the project I was going to work on, and told me that before the end of the day I would have done my first DNA extraction. In the afternoon we were indeed extracting DNA from blood. During this laborious work my supervisor, a technician, told me that he and his colleague were working on two forensic cases and that he was particularly happy that day because he had managed to do a rather difficult extraction. It was nothing like our task, he said, where the identity behind the blood spots is unambiguous and the blood is "clean": "his" DNA was extracted from some "dirty" blood spots on a lampshade. The DNA, so he told me, was still dirty, but he had managed to run the PCRs (DNA copying technology) necessary for identification.[6]

During my training I learned that the complexity of extractions and the social relevance of identification cause all technicians, without exception, to prefer working on forensic cases rather than on the

ethnographic journal, which I often had to write at home. At the end of my laboratory research I conducted interviews with laboratory members.

6. Polymerase Chain Reaction (PCR) is the revolutionary cloning technology of the late eighties. This technology, which mimics a "natural process" that takes place in the cell, namely DNA replication, allows geneticists to copy a target fragment of DNA in a short time. The enormous number of copies produced by PCR enables the visualization of a DNA fragment. For an exciting account of the different actors involved in the making of PCR, see Paul Rabinow, *Making PCR: A Story of Biotechnology* (Chicago: University of Chicago Press, 1996). On the adaptation of PCR to fit the various needs of scientific worlds, see Kathleen Jordan and Michael Lynch, "The Dissemination, Standardization, and Routinization of a Molecular Biological Technique," *Social Studies of Science* 28 (1998): 773–801.

research projects of the Lab. Whereas most of the technology applied by the technicians is standardized, the starting point of the cases, the extraction of DNA, demands insight, experience, and care. At the beginning of the procedure, the technicians have to assess the evidence material: they have to have an idea of how many extractions can be made from it, or whether it is possible at all to extract DNA.

It is also at this stage that the cases acquire colloquial names. Since the Lab members do not know the juridical details of the cases, all cases are assigned a registration number according to a laboratory-specific typology. The cases could be referred to in terms of these numbers. However, in practice they are given more communicable names, such as the case of the lampshade, the case of the stamps, the case of the bracelet, the rape case, the blackmail case, the paternity case; and even a case called number 9 gains another meaning in this context. These attributions may contain ethnographic information.[7] Our case had acquired the adjective "Turkish"; the ethnographic contents of the adjective will be addressed later.

The Turkish case was closed before I came to the Lab. Yet it continued to be mentioned on various occasions, and it became clear to me that it was important to the Lab. The material for the case in this paper is the result of many talks during my training and is based on interviews I conducted toward the end of this training. For aid in understanding the course and importance of the case, I owe a great deal to the members of Lab F.

The Lab

Lab F is a predefined environment in terms of its protocols, technology, knowledge, and space. Any step in the analysis is written down on specified forms in which the case number, the name of the technician, and complete information about chemicals (such as "lot numbers" and expiration date), kits, and machines used should appear. Also, all analyses and technologies applied are carefully defined in the various protocols. These measures are aimed at the transparency and repeatability of research, even after years have passed. One of the major concern in this respect is the confusion or contamination of samples. Prompted by concerns about contamination, the most pivotal spatial division is the separation of the Lab into pre- and post-labs.

7. For laboratory-specific typology and the ethnographic practice it may embody, see Annemarie Mol, "Pathology and the Clinic: An Ethnography of Two Atheroscleroses," in *Intersections: Living and Working with the New Medical Technologies,* ed. M. Lock, Alberto Cambrosio, and Allan Young (Cambridge: Cambridge University Press, forthcoming).

Contamination is one of the major worries of forensic laboratories in general. In 1996, the Committee on DNA Forensic Science produced *The Evaluation of Forensic DNA Evidence* on behalf of the National Research Council in Washington, D.C.[8] This report, which aims at redirecting forensic DNA research, addresses the risk of contamination in the different stages of the identification: "*Contamination* has been used as an umbrella term to cover any situation in which a foreign material is mixed with an evidence sample. Different kinds of contamination have different consequences for the analysis."[9] The committee recommended a number of measures to reduce the risk of contamination in forensic work.

In the Lab, I learned quite soon that measures against contamination were taken very seriously. On the Wednesday morning of my second week, I was "setting up a PCR" in the pre-lab. I had a question about the storage of reagents, and since my supervisor was working in the post-lab, I went over there to find him. In the doorway, however, I froze, due to a chorus of voices shouting "Lab coat! Lab coat! Take it off!" I looked down and realized I had forgotten to take off my pre-lab coat while planning to enter the post-lab. Of course I knew rule number one: Equipment for the pre-lab should remain there, and if it enters the post-lab it cannot be taken back without extra efforts. The movement from pre- to post-lab is easy, but the other way around requires special measures (sterilization of instruments, putting on of gloves or a lab coat). My overt confusion made

8. National Research Council, *The Evaluation of Forensic DNA Evidence* (Washington, D.C.: National Academy Press, 1996). This committee was installed in 1989, and issued an earlier report in 1992: National Research Council, *DNA Technology in Forensic Science* (Washington, D.C.: National Academy Press, 1992). The 1992 report regulated the use of DNA evidence in forensic cases, but was also seen as highly critical of this method, contributing to controversies around evidence DNA. William Sessions, a former director of the FBI, asked the National Research Council (NRC) to initiate a follow-up study in order to counter the controversial character of DNA evidence.

9. NRC, *Evaluation* (above, n. 8), p. 82. Since in the Netherlands only laboratories accredited by the Board of Accreditation are allowed to produce DNA evidence, elaborate protocols describing each step of the experiments and taking into account the risk of contamination were already operative in 1994. For almost all other laboratories in Europe (including Germany and Great Britain) as well as in the United States, such protocols did not exist yet, and the NRC report became a guideline for forensic practices. Nevertheless, in the Netherlands it also functions as a point of reference, and it became especially directive for the application of statistical analyses and for calculating matching likelihood estimates in cases of population admixture. For the relevance of the NRC report in the domain of statistics, see the article by the statistician and the head of the Laboratory of Criminal Justice (department of forensic DNA): Marjan Sjerps and Ate D. Kloosterman, "On the Consequences of DNA Profile Mismatches for Close Relatives of an Excluded Suspect," *International Journal of Legal Medicine* 112 (1999): 176–180.

the Lab members laugh, and after a moment of despair, I closed the door and ran back to the pre-lab to take off my coat in order to keep it free from (post-lab) contamination. From that moment on, the risk of contamination became very vivid. The certificate of the Board of Accreditation hanging on the wall became more real and serious, and I noticed the friendly but critical eye of the quality-control manager much more often.[10] Furthermore, my lab coat, rubber gloves, and the mask I occasionally wore became strict borders between *foreign material* and the DNA I was working on. What is *foreign* does not have to be strange: my supervisor told me that all Lab members have typed their DNA profiles;[11] this information enables the staff to trace the source of eventual contamination and to exclude the possibility that the occasional *foreign material* is theirs.

As stated above, the laboratory is divided into pre- and post-lab areas. The pre-lab is the more sensitive environment. This is the space where the cell material of all cases comes in, and where DNA is extracted from it. The extracted DNA samples remain in this lab and are used in small amounts for the different analyses. For each of those analyses the DNA will have to be copied using the PCR copying technology. With the help of a thermostable enzyme (polymerase), the PCR machine produces a millionfold copy of a particular DNA fragment, and so enables its visualization. This copying procedure, also called DNA amplification, constitutes the very division between pre- and post-lab: the full names would be pre-amplification- and post-amplification-lab. The PCR machine is located in the post-lab, where the amplification takes place. Before the DNA leaves the pre-lab for the purpose of copying, it is mixed with additives necessary for that step, such as nucleotide (DNA building blocks), primers (synthesized DNA fragments), the enzyme, and

10. The Board of Accreditation is the highest institution that monitors and assesses the technological preconditions for forensic work. There are several of these boards in the Netherlands, but both laboratories involved in evidence DNA are accredited by the strictest board, the so-called SterLab. Every year an audit takes place and all aspects—laboratory space, technologies, paperwork concerning how cases are reported and stored, and protocols of the laboratories—are inspected. Whereas this board is an evaluative institution, both laboratories also have a quality-control manager who supervises the daily work—that is, the laboratory space and protocols, and the conduct of laboratory members within this space (which tests should be done in flow cabinets, which under the "hut"/fume-hood)—and who makes sure that everyone takes notice of the clothing regulations (when to wear gloves and masks, lab coats, etc.).

11. Information about the DNA of the Lab members is source of many practical jokes. Specific behavior of individuals is then jokingly linked to their genetic outlook: a very strong Y-chromosome, and yet not so good a football player; or a strange peak that could indicate an extra X-chromosome, in the case of a male member.

other PCR-chemicals. This mix of chemicals and the PCR amplification is powerful, making the copying procedure sensitive to contamination by free-floating DNA fragments, which are more likely to be found in the post-lab. Therefore the mix is prepared in the pre-lab in a "flow-cabin," where such floating DNA fragments are least likely to be found. Before the mixture leaves the flow-cabin it is placed in lidded cups. Furthermore, as a routine check of possible contamination, with each PCR reaction a positive control (a DNA sample of which the information is already known) and a negative control (usually double-distilled water, ddH_2O) join in every step when typing the DNA of a case.

Once the technician enters the post-lab with a rack of cups containing the mixtures, the chemicals have taken their primary course. The succeeding experiments are carefully conducted in order to avoid mistakes when adding other chemicals to post-PCR DNA solution (the so-called PCR-product), or to avoid interchange between the prelabeled cups. The results are then dependent on the right tools being used and the results being read correctly.

The emphasis on reducing the possibility of contamination is essential to most laboratories in the field of human genetics, but it is perhaps even stronger in the context of Lab F. This is a *forensic* laboratory: the results of experiments conducted here have decisive consequences for the imprisonment or liberty of a suspect, and the kinship or identity of an individual. Mistakes or ambiguities in the DNA analysis are reviewed and should not appear in the final report.[12] Lab F operates predominantly on behalf of the suspect or the accused (the alleged father, blackmailer, murderer, or rapist). In analyzing DNA this laboratory studies the same tissue, hair, or blood studied on behalf of the prosecutor in the Laboratory of Criminal Justice. Reports on both studies are then submitted and presented in court. As stated before, if there is not enough evidence material to support two studies, the suspect may choose where the only possible DNA evidence should be produced.

Now we will follow the procedure of DNA identification. We will learn more about what counts as evidence and what does not, and about the possibility of identifying a unique individual. The focus will be on our case, the case of the Turkish suspect, and for reasons that will become clear later, at this stage it will be referred to as the "T-case."

12. This is different from, e.g., the United States, where reports should include an error rate for the results.

The T-Case, DNA Profile Typing

In the T-case there were two suspects. Although one was more suspect than the other, the cell material of both was supplied for DNA analysis. In this case, the amount of evidence material found at the scene of the crime was too small to support analyses in both laboratories. The defense requested Lab F to produce the one and only DNA evidence.

According to protocol, the cell material did not travel alone: it was accompanied by a short description of the case and of the material. In order to guarantee the privacy of the suspect, only the head of the lab receives this information. The technicians are not supposed to know the names of suspects, nor where the crime in question took place; this is an extra measure to prevent them from forming a biased view in cases where a crime becomes a public issue.

The T-case was treated routinely. Two technicians conducted two parallel and independent analyses, from the extraction of DNA from the cell material, to the typing of the DNA profiles. DNA profiles of the evidence material and of the suspects were typed in order to check for a match between the evidence profile and the profile of one of the suspects. The profiles are compounds of *genetic marker* information. A genetic marker can be seen as a small fragment of DNA, the length of which may vary among individuals according to the number of nucleotides, DNA building blocks, it contains.[13] The various lengths that can be found in different individuals are referred to as *alleles* (allelomorphs). For example, an individual, A, who carries a sequence fragment of 290 base pairs,[14] may be said to carry a different allele from that of an individual, B, whose sequence fragment is 294. It is this variation in sequence length, or alleles, in individuals that makes genetic markers useful for profile typing and for comparing individuals with one another.

In order to produce the DNA profiles, Lab F typed three groups of markers: five Poly-markers, one HLA (Human Leucocyte Antigen) marker, and one Short Tandem Repeat (STR) marker. The Poly-markers are a standardized package of five markers located on five different chromosomes; they show polymorphisms (i.e., variations

13. This is one of the possible understandings of genetic markers. Markers can best be seen as hybrids, being simultaneously objects of study, the technology to do that, and signs.

14. A *base pair* consists of a bond between two nucleotides, one located on each of the two strands of the DNA molecule. Since the nucleotides comprise chemical groups, the ways they can bond with each other are limited; the commonest possibilities are A-T (adenine-thymine) and C-G (cytosine-guanine).

between individuals) based on one single base-pair substitution in each DNA fragment.[15] HLA markers are located in several hundred genetic sites on chromosome 6 and are responsible for the antibody system. The STRs consist of short sequences of two to five nucleotides that repeat in tandem, such as the tandem CTAT, which may repeat eight to twelve times, or ATT, repeating ten to sixteen times in different individuals. This set of markers—Poly-markers, HLA, and STRs—is called informative for the very reason that what they look like may differ between individuals, either in length or in sequence composition. However, there is a fair chance that two individuals might "look alike" for one of the markers; using more markers reduces this chance and produces a more individual profile. By typing the whole set of markers the Lab obtained individual profiles of suspects and evidence DNA.

Based on the DNA experiments, the profile of one of the suspects matched the evidence DNA. But a match based on a similarity between these two genetic profiles does not guarantee identification. It does not make the suspect into the perpetrator. The Lab computed a matching probability using profiles in the control population, in order to confirm that the match between the profile of the suspect and that of the evidence DNA was the most likely. This step is crucial. Forensic work is based on the presupposition that the suspect is innocent and that the evidence DNA was left by someone else at the scene of the crime.[16] Therefore, the Lab has to estimate the chance of a match between evidence DNA and any other individual in the population. Since it is not feasible to type the profiles of all the individuals in a population, Lab F works with a control population based on a "random" collection of Dutch people. In calculating the matching likelihood, the Lab compared the profile of the evidence DNA with those of 168 males and females in its data bank. On this basis,

15. The Poly-markers are: LDR, GYPA. HBGG, D7S8, and GC. Some of these are in coding DNA; others are in introns (the flanking regions of a gene) and are thus far not known to be involved in vital functions of the cell. Note that these markers are not based on variation in fragment length, but on "molecular weight," a substitution of a base pair by another. Since the different nucleotides consist of different chemical groups, they differ in weight.

16. NRC, *Evaluation* (above, n. 8), p. 29. Although, in the case as whole, other evidence may reduce the chance of this probability, the Lab is tied to this working hypothesis, according to the 1994 lawsuit in the Netherlands. One could say that the conduct of law and science leads to another type of evidence, sought in laboratory practice rather than courtroom practice. See also Sheila Jasanoff, who addresses this difference and analyzes what counts as fact in court and in science: Jasanoff, *Science at the Bar* (above, n. 2), pp. 49–68.

a probability was calculated expressing the chance that the marker profile of the evidence DNA could be found in the population at large. The procedure for this is as follows:

Suppose that for three markers, the specific fragments found in the evidence DNA, the *alleles,* can be found in the data bank in the following percentages: the allele for marker I is represented in the data bank by 10%, the allele for marker II by 5%, and that for marker III by 2%. To calculate the chance that the three marker fragments (alleles) *combined* may occur in the population, the frequencies are multiplied. In this specific example, the chance would be $10/100 \times 5/100 \times 2/100 = 100/10^6$. Hence the chance is one in ten thousand. This number is also called the *matching likelihood number.* The matching likelihood number is therefore the result of a simulated comparison between the suspect's DNA profile and those of the population at large—that is, the society of which this individual is considered a member.

In the T-case, based on seven markers and the Lab's control population, a matching likelihood of 10^{-7} was calculated. In other words, the chance was one in ten million that the profile of the suspect would match the profile of any other individual in the population from which the samples were drawn. This calculated probability of a match with another individual makes the DNA profile of the suspect into a *DNA fingerprint.* The figure 10^{-7} was considered acceptable according to the standards of the Lab and those of the court.[17] The figure was therefore presented in court as evidence of an exclusive match between suspect and evidence DNA, and thus as an identification of the suspect. One could say that 10^{-7} was the basis for the DNA evidence in this case; a higher matching likelihood would counter the testimony of the DNA comparison and challenge the authority of the DNA fingerprint.

For Lab F, this chain of procedures usually ends when the information is sent to court. The DNA profiles, the matching likelihood number, and the methods of analysis are written down in a report by the secretary, and after a simultaneous check of the report by a technician and the head of the Lab, it is signed, sealed, and sent to court. A copy of the report printed on red paper, signaling that the case is closed, remains in the Lab. In our case, the head of Lab F was invited to the hearing as an expert witness to present the results and to answer any questions.

17. This figure may differ depending on the judge who is conducting the trial: some accept a higher matching likelihood number, while others demand a much lower matching figure.

From this discussion it becomes clear that DNA fingerprints are technical products, intertwining a specific nature of individuality and of population. We will go back to our case and follow the technicality of both categories. As indicated before, the defense had problems with the results presented in court. Let us now take a closer look at those objections and at how they relate to the T-case.

Back in Court

In court, the DNA tests of Lab F supported the findings of the prosecutor by showing that the evidence DNA found in the car and in the house next to the victim's body matched the DNA of the main suspect. But there appeared to be a problem: the defense did not accept the DNA evidence and started to ask questions about how the matching likelihood number was produced, about how the comparison was done, and about the control population upon which the figure 10^{-7} was based. Given that information, the defense argued that their client was not just a suspect, but a Turkish suspect, being of Turkish origin. Did Lab F take that into account, and could the Lab guarantee that the control population is representative of their client's DNA profile?

What do these objections mean?

In order to calculate the matching likelihood number and to produce the DNA fingerprint, Lab F had compared the profile of the Turkish suspect with those of a Dutch control population. As stated before, this procedure is based on the presupposition that the suspect is not guilty and that the perpetrator is "out there," in the population; thus, theoretically, any other person in this population has an equal chance of having committed the crime. The defense questioned whether this presupposition was still maintained, given the Turkishness of the case. It argued that since the victim, the suspect, and other individuals at the scene of the crime were all apparently of Turkish descent, it was not plausible to presume an equal probability that any individual in Dutch society could have been the perpetrator. Questioning the control population used means doubting the matching likelihood number of 10^{-7} and, consequently, questioning the validity of the DNA evidence. Whereas the defense emphasized the "Turkishness" of this case, Lab F had not been informed beforehand about the descent of the individuals involved. While their names might have suggested they were Turkish, this possibility was not taken into account and Lab F used its Dutch control population as usual. Thereupon the defense raised the question of whether one could presuppose the absence of differences between Dutch and Turkish genetic makeup.

The skepticism of the defense raised the following problems for the court: Would the matching likelihood have been equally low if the evidence DNA had been compared with a Turkish control population? Did the Lab use the appropriate control population to determine the DNA fingerprint of the suspect? And consequently, could the court be sure that the match between evidence and suspect DNA (*inclusion*) meant that the suspect was indeed the perpetrator (*identification*)?[18]

Although the traces of DNA evidence in car and house seemed to match the profile of the suspect, the court decided that the matching likelihood probability contained no evidential power without further information about a more "appropriate" control population. Lab F was asked to take the Turkishness of the case into account, to investigate the possibility of using genetic data of a Turkish population, and to recalculate the matching likelihood number for establishing the *identification* of the suspect.

We shall see below how Lab F responded to this request. Furthermore, it will become clear that answering these questions opens up a broad field of presuppositions, procedures, and negotiations that are crucial to forensic work, to population genetics as well as to forensic DNA evidence. To understand what is at stake in our case, let us make a brief detour to another forensic case where the DNA evidence was challenged.

Expert and Counterexpert

Unlike the situation in the United States and Great Britain, in the Netherlands forensic DNA did not become an issue of public debate. Before the introduction of the 1994 amendment of the Dutch Criminal Code that enabled DNA evidence to be used in lawsuits, a committee was appointed to investigate its impact and assess its future use. In that very context, discussing the reliability of the technology,

18. For a clear elaboration of the difference between *inclusion* and *identification,* see Paul Rabinow, "Galton's Regret: Of Types and Individuals," *Culture, Medicine and Psychiatry* 17 (1993): 59–65, at p. 60 (also published in Paul Rabinow, *Essays on the Anthropology of Reason* [Princeton, N.J.: Princeton University Press, 1996], pp. 112–129). See also Eric Lander, "DNA Fingerprinting: Science, Law, and the Ultimate Identifier," in *The Code of Codes: Scientific and Social Issues in the Human Genome Project,* ed. Daniel J. Kevles and Leroy Hood (Cambridge, Mass.: Harvard University Press, 1992), pp. 191–210, at pp. 191–193. Lander's contribution gives a clear overview of how DNA typing is done in forensics, and addresses some controversial cases in the United States and their implications for future forensic work.

references were made to controversies in the United States and Great Britain. The committee considered the technology to be no longer unreliable and spent most of its time on regulating the rights of the suspect.

However, despite this absence of controversy in the Netherlands, the defense may have been informed about controversies surrounding DNA evidence abroad and may have intended to use these as precedents.[19] One of these controversial cases took place in 1990 in Franklin County in Vermont, near the Canadian border. This was a rape case in a caravan-camp of Abenaki Indians; it has been described by Richard Lewontin in *The Doctrine of DNA* (1993). The judge in this case discarded the DNA evidence because it was obvious that not all inhabitants of Franklin County had equal access to the caravan-camp—or, in other words, there was a higher probability that the perpetrator was a member of the Abenaki Indian community. Franklin county is ethnically very mixed and the Abenaki Indians make up the largest population. Although there were genetic data banks of other populations in this county, there was none for the Abenaki Indians. Therefore, the suggestion to compare the DNA profile of the Abenaki suspect, with various other ethnic groups that live in this region was deemed inadequate and unreasonable. The DNA evidence was deemed inadmissible, and the court dismissed the case.[20]

Emphasizing the need for an appropriate control population, the defense in our case seems to call forth a similar dilemma. Before returning to the T-case, however, we shall take a closer look, first at matching likelihood estimation and DNA fingerprinting, and then at the different concepts of population that have been presupposed in the case thus far. With reference to matching likelihood and DNA fingerprinting, we shall try to understand the traffic of DNA evidence between laboratory and court by applying a theoretical notion, that of an "immutable mobile."

19. Since I have not talked to the defense myself, I introduce this example to show that this case did not stand alone, but links up with many debates and controversies surrounding evidence DNA outside the Netherlands.

20. Richard Lewontin, *Biology as Ideology: The Doctrine of DNA* (New York: Harper-Perennial, 1993). I used the Dutch edition, *DNA Doctrine: Biologie als Ideologie* (Amsterdam: Uitgeverij Bert Bakker, 1995), pp. 99, 100. Another well-known forensic case, the "Castro Case," became a controversy in the United States because of sloppy conduct in the laboratory. See Lander, "DNA Figerprinting" (above, n. 18), pp. 196–201; and also Jasanoff, *Science at the Bar* (above, n. 2), pp. 55–57.

Matching Likelihood Numbers and DNA Fingerprints: Immutable Mobile?

"[H]ow can distant or foreign places and times be gathered in one place in a *form* that allows all the places and times to be presented at once, and which allows orders to move *back* to where they came from?"[21] Bruno Latour raises this question in his "Drawing Things Together," where he addresses inscriptions of scientific practices and "worlds" onto objects. The objects he considers can be seen as representation conglomerates in which many worlds and practices are reassembled and "made presentable" in a different setting. Hence, these objects are transportable, and unchangeable during their transportation. What "form," then, should these objects take to do this job? Latour suggests thinking of graphs, models, figures, written texts, specimens, or samples, which combine various practices in a specific "form" or materiality; in this fixed condition they are immutable, and they are mobile because they are easy to either transport or reproduce—they are thus "immutable mobiles." Immutable mobiles, as representational devices, allow scientific practices to be transported from one laboratory to another, and from one field to another. Latour argues that immutable mobiles are "things" gathered, displaced, made "presentable" and convincing to those who have not been there. These "things" may combine and recombine different fields, because they are made flat and reproducible.[22] Here, I will consider matching likelihood numbers and DNA fingerprints as immutable mobiles.

In forensics, a DNA fingerprint cannot exist without a convincing matching likelihood number. Without this number the fingerprint would be just another DNA profile. Although the two accompany each other on a journey from laboratory to court, matching likelihood and DNA fingerprint reveal a different reality about where they come from.

Classifying a DNA profile as a fingerprint suggests an analogy with conventional fingerprints. This analogy does not always hold: the fingerprint of a *Drosophila* or a dog does not exist, yet both may have a DNA fingerprint. But the fingerprint analogy is instructive of

21. Bruno Latour, "Drawing Things Together," in *Representation in Scientific Practice,* ed. Michael Lynch and Steve Woolgar (Cambridge, Mass.: Harvard University Press, 1990), pp. 19–69, at p. 56 (second emphasis added). See also Bruno Latour, *Science in Action: How to Follow Scientists and Engineers Through Society* (Cambridge, Mass.: Harvard University Press, 1987), chap. 6.

22. Latour, "Drawing Things Together" (above, n. 21), pp. 26, 44–47.

how to understand the genetic profile.[23] The understanding implied is that DNA fingerprints are easy products, and the suggestion is that even in daily life, anyone can produce his or her own fingerprint, whether based on DNA or the print of a finger. Paul Rabinow describes the convenience of conventional fingerprinting as follows: "Little skill was necessary to obtain fingerprints and not much more was demanded to classify them. No confession was required, a physical impression would do."[24] Thus, understanding a DNA fingerprint in terms of a conventional fingerprint mobilizes a previous and successful individuality-determining practice in forensics. By facilitating this reading, the analogy seems to prohibit another one, namely, a complex view of DNA fingerprinting—because what knits the two practices together seems to set them apart as well. This is the belief that ever better technology and knowledge are produced to do the same job. It is the belief that DNA typing has superseded conventional fingerprinting and become "the ultimate identification scheme."[25] This feature of DNA fingerprints is emphasized by the matching likelihood number.

The second immutable mobile, the matching likelihood number (especially an impressive number like 10^{-7}) mobilizes a scientific practice. It mobilizes a complexity, hidden from the view of those "who haven't been there." This scientific practice is a number-generating machinery that produces facts out of human tissue. A stranger does not (need to) know what is going on in this machinery: how DNA is acquired, "unraveled," and made into a DNA fingerprint. The matching likelihood number therefore mobilizes and establishes the complexity of these procedures as well as the scientific prestige attached to the production of DNA evidence. The in-

23. An analogy can therefore be seen as an apparatus of signification; see Marilyn Strathern, *After Nature: English Kinship in the Late Twentieth Century,* 3d ed. (Cambridge: Cambridge University Press, 1995), p. 13. For a straightforward and motivated use of this analogy, see NRC, *Evaluation* (above, n. 8), p. 14. For an example of this analogy in practice, see Alec J. Jeffreys, Michelle Turner, and Paul Debenham, "The Efficiency of Multilocus DNA Fingerprint Probes for Individualization and Establishment of Family Relationships, Determined from Extensive Casework," *American Journal for Human Genetics* 48 (1991): 824–880. For a study of the use of (conventional) fingerprinting at the beginning of the twentieth century, see Simon A. Cole, "Witnessing Identification: Latent Fingerprinting Evidence and Expert Knowledge," *Social Studies of Science* 28 (1998): 687–712.

24. Rabinow, "Galton's Regret" (above, n. 18), p. 60.

25. Eric Lander, "Population Genetic Considerations in the Forensic Use of DNA Typing," in *Branbury Report* 32 (1989), quoted in Rabinow "Galton's Regret," p. 63.

formation that comes out of the laboratory is a DNA fingerprint with a number.[26]

The DNA fingerprint, as an immutable mobile, transports into the courtroom a (scientific) world, where fingerprinting is accepted as an individuality-determining practice. The matching likelihood number, on the other hand, mobilizes a scientific practice where numbers as facts are produced out of human cell material. Whereas the former suggests familiarity, the latter evokes strangeness. If we put this in the context of our case, it is exactly this strangeness that the defense sought to challenge. The defense's objection can be seen as an objection to the immutability of both the matching likelihood number and the DNA fingerprint. The defense herewith questioned the immutability of these mobiles and opened up the practices inscribed onto them and transported through them.

How to read the individual profile or the DNA fingerprint is now the central issue, and has become a matter of comparison between an individual and a population. Both sides of the comparison are of great importance. As already indicated, the main focus of this paper is population. So let us try to trace the different concepts implied in this part of the case. Special attention will be paid to where differences and similarities are located in the category population, and how similarities and differences between Dutch and Turkish contribute to different concepts.

Similarities Presupposed

The first concept of population is indicated by the control population of the laboratory. The control population of Lab F is based on three population samples; combined, they are deemed to be representative of the Dutch population in general. The sampling procedure of the control population contains specific views of what counts as population.

Of the 168 samples in use in the Forensic Laboratory, 50 males were selected from Dutch hereditary-diseased families at the Department of Human Genetics in Leiden. The samples come from healthy

26. For the convenience of scientific prestige and its importance for the credibility of expert witnesses in court suits, see Cole, "Witnessing Identification" (above, n. 23). In his elegant paper Cole argues that the "ordinariness" or the familiarity of the fingerprint almost jeopardized its testimonial power in lawsuits. Its role in court was thus based on a delicate balance between strangeness, attending to a scientific practice, and familiarity, of which the validity could be observed in the courtroom. One could say that this double role in the case of DNA evidence is nicely delegated to the two components: the DNA profile, and the matching likelihood number.

men who are related by marriage to the diseased families and they were selected by family name only.[27] A second set of 50 female samples was drawn from a large study on contraceptives in Dutch women; while the samples were drawn at random, the collection as a whole is known from elaborate medical records. These samples, as well as the third set of 68 male samples, were made available by the TNO (Dutch Organization for Applied Scientific Research). The 68 male samples were drawn randomly from a larger number of samples: 2,018 thirty-five-year-old males taking part in a large-scale TNO study of (susceptibility for) heart disease in the Dutch population;[28] this study was conducted in three regions of the Netherlands, represented by the cities of Doetinchem, Leiden, and Amsterdam.

Hence, the control population of the Lab as a whole was based both on genealogical ties (as expressed in family names) and on specific ties to the Dutch medical system.[29] Although the medical records contain a large amount of information about the individual samples and about the sampling procedures, the medical ties are not of particular importance to this laboratory. In compiling the control population, the Lab was not interested in those individuals as such, but as representatives of a population as a whole. Yet the choice of healthy men, in the first collection mentioned above, is indicative of a practical consideration: the Lab aimed at compiling a *normal* control population. Not a population of individuals living in the Netherlands, but a *normal* Dutch control population was the goal. Names, just like health, were treated as devices to produce a homogeneity in that population. Furthermore, since the control population consists of 168 samples only, it was of statistical significance to know that a genetic profile was not doubly represented because two individuals belonged to the same family; the way to reduce this

27. Note that the Department of Human Genetics is part of the laboratory network. Moreover, it is the so-called pen wielder of the Forensic Laboratory, through which the Lab can be treated as part of Leiden University.

28. TNO (Nederlandse Organisatie voor Toegepast-Natuurwetenschappelijk Onderzoek) has a close tie to the TNO-Leiden, where the head of the laboratory used to hold a position conducting and guiding research on heart disease.

29. This type of sampling is called convenience sampling, as opposed to simple sampling. The latter is based on a random sampling procedure, whereas the former is based on a random selection of already-existing samples (from blood banks, paternity testing, or laboratory personnel): NRC, *Evaluation* (above, n. 8), pp. 30, 186. For further information about the male samples, see Peter de Knijff, "Genetic Heterogeneity of Apolipoprotein E and Its Influence on Lipoprotein Metabolism" (Leiden University, 1992), p. 57; L. Roewer et al., "Analysis of Molecular Variance (AMOVA) of Y-Chromosome-Specific Microsatellites in Two Closely Related Human Populations," *Human Molecular Genetics* 5 (1996): 1029–1033, at p. 1032.

chance was to exclude samples that came from siblings sharing family names.[30]

What are, on that account, the presuppositions behind the sampled population, the source of the control population in the Lab? Choosing names as an overall criterion for samples guarantees, on the one hand, the representativity of those samples. On the other hand, it also suggests that family names make populations. In this concept a population consists of individuals who are linked by names. This concept of population thus indicates that Dutchness is in the name: names function here as an attempt to capture an unambiguous genealogy of what Dutchness is, and consequently of what a population is.

A second concept of population can be deduced from the objection of the defense, and the emphasis placed on the Turkishness of the case. At stake is the matching likelihood number and the basic statistical presupposition expressed by it. The number presented was the result of a comparison with a Dutch control population, and presupposed that any citizen of Dutch society had an equal chance of having been at the scene of the crime. The defense opposed this by questioning whether this presupposition would hold if the suspect and the victim were Turkish. Lab F had not been informed about the descent of these individuals: the information contained their names only. Their names would of course suggest a different descent, but this was not taken into account. Did the laboratory have a reason not to do so? Lab F works with the general presupposition of forensic DNA research, namely, that the suspect is innocent. Comparing the evidence DNA profile with that of the control population means looking for a possible match, other than the match between the suspect and the evidence DNA. Despite the fact that more non-Dutch individuals were at the scene of the crime—which reduces the chance that any citizen might theoretically have been there—the laboratory considered its control population to be representative. Does this mean that they were ignoring the statistical proposition of forensics: the possibility that any other person could have committed the crime?

30. In an article written in collaboration with the Forensic Laboratory for DNA Research, the following is stated: "The two groups of unrelated males analyzed in this study (70 Germans and 89 Dutch) comprised controls routinely used for the validation of forensic genetic markers. Care was taken that none of the males share last names, and that all were white Caucasians" (Roewer et al., "Analysis of Molecular Variance" [above, n. 29], p. 1032).

Seen from a different perspective, taking the conduct of Lab F seriously could lead to a different conclusion: The Lab did take this proposition into account, but did not make a distinction between what might count as Dutch and what might count as non-Dutch. From this perspective, the "material" basis of the laboratory's data bank (the samples drawn from individuals) moves to the background and the data come to represent a much larger population. The data seem to represent not only a Dutch population, but a more general population. What concept of population would include Dutch and non-Dutch as belonging to one category? Here, it appears that laboratory practice plays an important role. For Lab F, the control population is the data bank *as usual,* and the suspect is a suspect *as usual.* A T-suspect is not a common occurrence in this laboratory.[31] Having compiled its data bank with care, the Lab has grown to view it as the control population *tout court.* The data bank has thus become a "black box." The stake in this black-boxing is not the content or composition of the data bank, but the daily routine of forensic work in which it is used.[32] Normally it does the task of a control population quite well and is therefore "reflexive" of that routine practice.[33] One could say that due to daily routine, the Lab

31. Whereas before 1960 most immigrants in the Netherlands came from former Dutch colonies (such as Indonesia and the Surinam), or from southern European countries, since the 1960s a large group of (male) immigrants have been recruited in Turkey and Morocco by government officials to counter the tension on the Dutch labor market. The recruitment initiated a much bigger migration wave from these countries, especially due to family unification. Of the two million immigrants living in the Netherlands nowadays, around 240,000 are of Turkish descent and live in high concentrations in large cities; see Marcel Metze, *De Staat van Nederland: Op Weg naar 2000* (The "state" of the Netherlands: Toward the second millennium) (Nijmegen: SUN, 1996). Despite the fact that this group of immigrants has been part of Dutch society for almost four decades, they often appear to be "a special group" or "an outgroup" (ibid., p. 32).

32. Compare Harold Garfinkel where he addresses routine practices embodied in the records of an outpatient psychiatric clinic. He argues that these records may cause "normal, natural troubles" for a sociologist who uses them for research, because the practices they embody are not made explicit and tend to escape the eye: "'Normal, natural' troubles are troubles that occur because clinic persons have established ways of reporting their activities; because clinic persons as self-reporters comply with these established ways; and because the reporting system and reporter's self-reporting activities are integral features of the clinic's *usual* ways of getting each day's work done—ways that for clinic persons are right ways" (Harold Garfinkel, *Studies in Ethnomethodology* [Cambridge: Polity Press, 1967], pp. 186–207, at p. 191; emphasis added).

33. For this notion of reflexivity, see ibid.; Michael Lynch, *Scientific Practice and Ordinary Action: Ethnomethodology and Social Studies of Science* (Cambridge: Cambridge University Press, 1993). For a comprehensive elaboration of the difference between *reflexivity* in the approach of ethnomethodology and *self-reflexivity* in other sociological approaches, see Lynch, *Scientific Practice,* pp. 34–39.

seemed to have developed a blind spot for T-cases. Thus, the second concept of population suggests a category based on laboratory routine and daily practice in which the population becomes the control population *as usual*.

Proposing Differences

For the benefit of its client, the defense questioned the matching likelihood probability based on the control population of the laboratory. This indicates a *third concept of population*. Whereas Lab F presupposed similarities between Dutch and non-Dutch, the defense considered the possibility of differences. By pleading that the case should be viewed as a Turkish case, the defense questioned the "representativity" of the control population used. Could the identification of the Turkish suspect be established on the basis of the proposed matching likelihood number, or would the profile be more common if compared with a Turkish population? Challenging the claim of *identification* embodied in the matching likelihood number calls upon the presupposition of genetic distance. Are the Turks and the Dutch genetically close enough to be situated in one population, or does a difference in descent indicate a genetic distance between groups of people?

These objections can be viewed within the realm of population genetics, where it is argued that groups of people from different parts of the world may differ in genetic makeup. Such differences often concern the frequency with which alleles occur within specific populations. In this respect a matching likelihood number that is *exclusive* within the context of a Dutch control population might be less convincing if comparison were based on a different population. Emphasizing the fact that the suspect is of Turkish descent, the defense pleaded that these differences should be taken into account.

From this objection we can deduce a concept of population based on genetic proximity and distance. Individuals are members of a population when their genetic makeup/profile is represented in this population. Thus, people from different parts of the world are included in or excluded from a population on the basis of genetic nearness or distance.[34]

From these analyses it becomes clear that in forensic practice there is no such thing as *the* population—that different concepts of popula-

34. On the clustering of alleles according to population, see HUGO, "The Human Genome Diversity (HGD) Project: Summary Document" (Sardinia: Human Genome Organisation, 1993), p. 24.

tion may be at issue at the same time, and that the specific concept applied has consequences for individuality. Determination of the individuality of the Turkish suspect is thus dependent on population. We shall now go back to Lab F and view how it responded to the court's request, to solve the problem of the control population and to seek comparisons with a Turkish one.

Back to the Lab

The Lab's control population had become a Dutch control population, while the T-suspect had become a Turkish suspect. And it had become clear that it was not possible to identify the Turkish suspect on the basis of routine and standardized laboratory practice. Matching likelihood, control population, and DNA fingerprint had all become matters of more decisions than usual. Studies of Turkish populations were therefore gathered and considered. Two published papers were found to be of specific importance; I will refer to them as the "German study."[35] The Lab tried to answer the questions of the court by calculating a new matching likelihood number based on the Turkish data referred to in the German study. In an interview I held with him retrospectively, the head of the Forensic Laboratory stated the following about the questions of the defense:

> The question of "representativity" raised by the defense is a relevant question. In Germany a study was conducted measuring the allelic frequencies of two different Turkish groups: Turkish migrants living in Brussels, and Turkish groups living in the Adana region. The suspect is also from the southeast of Turkey. They are all Caucasian, by the way, just like the Dutch. For most genetic features there is little difference in the allelic frequencies among Turkish people, but if compared with Dutch males, differences do occur.[36]

As a response to the defense, Lab F compared the DNA profiles of the suspect with the data of the German study. With the information about the allelic frequencies of the Turkish population contained in that study, a new statistical analysis was carried out for the suspect DNA and the matching likelihood was recalculated as 10^{-6} instead of 10^{-7}. This means that the chance that the profile of the

35. These two publications are based on collaborations between scientists in Turkey and Germany: B. Alper et al., "HumFES/FPS and HumF13B: Turkish and German Population Data," *International Journal for Legal Medicine* 108 (July 1995): 93–95: B. Alper et al., "Frequency Profiles of 3 STRs in a Turkish Population," ibid., pp. 110–112. The third study is S. Meneva and Ü Ülküer, "The Distribution of the HLA-DQa Alleles and Genotypes in the Turkish Population as Determined by the Use of DNA Amplification and Allele-Specific Oligonucleotides," *Science and Legal Justice* 35: 3 (1995): 259–262.

36. Interview with Dr. Peter de Knijff, at Forensic Laboratory, Leiden, January 17, 1997.

suspect would match with any other Turkish person had grown to one in a million instead of one in ten million.

Back in Court

In court, Lab F presented the new results, which showed that comparing the allelic frequencies of a Turkish population with the alleles of evidence and suspect DNA had allowed it to calculate a new matching likelihood probability of 10^{-6}. The papers that provided the laboratory with the data were included as scientific evidence. Again, the defense was not convinced and stated that even the matching likelihood number based on the data of the German study might not accurately represent the case at issue.

The objection of the defense at this point was not so much based on the representativity of populations, as on that of genetic markers. Whereas the markers used in the German study contributed to the conclusion that there is no difference among Turks, the defense aimed at just the opposite. It had mobilized more data about the Turkish population living in Brussels and argued that Turkish populations may be similar for some markers, but can differ for other markers.[37] Since the markers used in the Lab and those in the German studies differed considerably, the defense still had doubts about the matching likelihood presented. The German study, for example, was conducted solely on the basis of STRs, whereas the set of seven markers used in the Lab included only one STR marker. Furthermore, the six other markers used are found in so-called coding regions of the DNA, which makes them sensitive for population substructures as well. The defense suggested comparisons with the markers and data used in the Laboratory for Criminal Justice, Rijswijk.

At this stage, genetic markers became an issue of debate in DNA evidence. In the next section, we will have a closer look at this category in order to understand how they came to play a key role in this case.

Tools of Similarities, Tools of Differences: Genetic Markers in DNA Fingerprinting

Genetic markers are key categories in population genetics.[38] In forensics, they are also subjects of great debate and discord, as they

37. Dr. Peter de Knijff, personal communication.

38. For example, in November 1995 in Barcelona at the international conference *Human Genome Variation in Europe: DNA Markers,* a special plenary session was held on genetic markers for typing genetic variation. The main goal of the discussion was to develop a set of "priority markers" that could be used within the realm of the Human Genome Diversity Project. As a result, a preliminary document was produced in which

are often matters of life and death.[39] Likewise, in our case, markers are important actors that keep popping up. So, let us examine them more closely and focus on the roles attributed to them in forensic cases.[40]

In population genetics as well as forensics, genetic markers are selected on the basis of three criteria. First of all, markers in the noncoding region of the DNA are preferred over those found in the coding region. Contrary to noncoding DNA, coding DNA has crucial functions in the cell because it helps produce proteins; hence its pattern of inheritance may be restricted to the functions it has in a living cell.[41] In forensics, however, the underlying and most important presupposition concerning markers is that their patterns of inheritance are not restricted and that they are randomly inherited, so that the alleles are randomly distributed within a population. This is based on the assumption of "random mating," according to which people choose their partners at random and pass on their genetic material at random as well. In *The Evaluation of Forensic DNA Evidence,* it is argued that "for some traits the population is not in random-mating proportions. Mates are often chosen for physical and behavioural characteristics. . . . For example, people often choose mates with similar height, but unless a forensic marker is closely linked to a possible major gene for heights, the forensic genotypes will still be in random-mating proportions."[42] Therefore the preference is for markers in noncoding regions and not linked to genes. The so-called discrete alleles of such markers are supposed to meet the condition of random mating and therefore fit into the statistical models based on this proposition. This does not mean, however,

these markers were described: Jaume Bertranpetit, "Recommendations on the Use of Genetic Markers in Human Genome Variation Studies" (Barcelona, February 1996).

39. This discord is best visible in the publications of Lewontin and Hartl on the one hand, and Chakraborty and Kidd on the other: Richard C. Lewontin and Daniel L. Hartl, "Population Genetics in Forensic DNA Typing," *Science* 254 (1991): 1745–1750; Rannajit Chakraborty and Kenneth Kidd, "The Utility of DNA Typing in Forensic Work," ibid., pp. 1735–1739. For an account of the controversy around these papers in *Science,* see Lewontin, *Biology as Ideology* (above, n. 20), chap. 4. Furthermore, *The Evaluation of Forensic DNA Evidence* (above, n. 8), a coproduction of the National Research Council and the Commission on DNA Forensic Science, can be seen as a capstone in this debate. For paternity DNA studies and DNA fingerprinting on the basis of minisatellites, see Jeffreys, Turner, and Debenham, "Efficiency" (above, n. 23).

40. My focus in this analysis is on criteria and the more "technical" features of genetic markers as applied tools in forensics.

41. NRC, *Evaluation* (above, n. 8), p. 14.

42. Ibid., p. 26.

that markers linked to coding DNA are necessarily excluded—the HLA and some of the Poly-markers used in our case, for instance, are linked to functional DNA. Taking random mating into account and choosing markers in coding regions, geneticists strive for markers that are not linked to each other and that inherit independently. Preferably, they look for markers on different chromosomes, as in the case of the five Poly-markers.[43]

Secondly, a marker should be polymorphic within a given "population." This means that it should show different alleles within the sampled population. The discriminating power of a marker depends on the number of its alleles. If this number is too low, this will enlarge the chance of a match between two genetic profiles. Therefore, using markers with a low number of alleles requires the use of a larger data bank (a few hundred or more).[44]

Finally, a marker should not be *too* polymorphic. This has to do with the types of cases found in forensic laboratories, as well as with the statistical models used. If a marker has a high number of alleles, it would be an interesting marker for identification: the more variation, the smaller the chance of a match between suspect DNA and any other individual. However, forensic DNA is concerned not only with identifying possible criminals, but also with paternity testing. For the latter type of profiling, markers with many alleles are especially problematic. Many alleles or a high variability indicate that a particular DNA fragment changes or mutates relatively fast. Mutations may even occur in between two generations, distorting the results of paternity tests, which are based on similarities and differences between parents and offspring. For practical reasons—such as being able to use the same set of markers for both DNA evidence and

43. Personal talks with members of the Forensic Laboratory. In cases where markers on the same chromosome are chosen, the loci should be far apart to allow for independent inheritance; these loci are said to be nonhomologous. For an analysis of the concept of homology in the realm of the Human Genome Project, see Joan H. Fujimura and Michael Fortun, "Constructing Knowledge across Social Worlds: The Case of DNA Sequence Databases in Molecular Biology," in *Naked Science: Anthropological Inquiry into Boundaries, Power, and Knowledge,* ed. Laura Nader (New York/London: Routledge, 1996), pp. 160–173.

44. See NRC, *Evaluation* (above, n. 8), p. 34; furthermore, it is suggested here that markers with a number of alleles lower than five should be rebinned (grouped in bins containing at least five alleles). Note that for paternity testing the number of alleles should preferably be lower than for evidence DNA profile typing—for a higher variability indicates a higher mutation rate (in a locus); in these cases even mutations from one generation to the other may occur. See, for example, a review article by Mark A. Jobling and Chris Tyler-Smith, "Fathers and Sons: The Y Chromosome and Human Evolution," *Trends in Genetics* 11 (1995): 449–456.

paternity testing, not having to train laboratory members to work with too many markers, and for economic considerations—markers are chosen that are polymorphic but not "hyper"variable. This choice is also implicated in the statistical models applied. For example, the models used by Lab F do not take into account the occurrence of mutations. If the Lab were to choose hypervariable markers for the purpose of identification, it would have to change its statistical models in order to use those markers for paternity testing as well.

Now that we have framed the roles that genetic markers play in forensic research, let us go back to our case and have a second look at the different concepts of population that have been touched upon.

Arguing for Similarities

A fourth concept of population can be deduced from the interview-excerpt quoted above. When talking about problems of representativity, the head of the laboratory mentioned in passing that the Turks, like the Dutch, are Caucasian.[45] This notion of population seems to warrant the prior approach of the Lab not to distinguish between the two, where population was their "local" population as usual (*the second concept of population*). However, as I indicated, the Lab was not informed about the descent of the individuals involved. Taking their names for granted indicates that the control population, which was based on Dutch names, became part of a routine practice. Thus, using "Caucasian" in this context should not be understood in terms of *the second concept of population*. "Caucasian" is here a racial category, suggesting a taxonomy of population based on race.[46] Race is an ambiguous but nevertheless relevant category for geneticists: Caucasian, Negroid, and Mongoloid are seen as the three main races of the world.[47] According to this taxonomy, "races"

45. Also in the German study, the Turkish population in Turkey is referred to as Caucasian: Alper et al., "HumFES/FPS" (above, n. 35), p. 93.

46. On Mendelian population see, for example, Helen Macbeth, "Ethnicity and Human Biology," in *Social and Biological Aspects of Ethnicity,* ed. Malcolm Chapman (Oxford/New York: Oxford University Press, 1993), pp. 47–91, at pp. 51, 54ff. One striking example of how race "is done" in genetics can be found in Jeffreys, Turner, and Debenham, "Efficiency" (above, n. 23): "The only preselection of data for this study was that of ethnicity [Caucasian], which was determined on the basis of photographic evidence" (p. 825).

47. An interesting feature of the use of racial taxonomies in population genetics can be found when comparing genetic discourse in the United States with that in Europe: in Europe the main races are Caucasian, Negroid, and Mongoloid, whereas taxonomies in the United States produce more races, such as Caucasian, blacks, Hispanic, East Asian,

within the three main races are called "population substructures" or "subpopulations."[48] In a way, this suggests that "population" is nothing but another term for race. Even though genetic tools blur clear-cut categorization along racial boundaries (whatever these may be), races are entry-points for genetic studies (sampling procedures and comparisons) as they are embedded in a long history of research in this field.[49] In this concept of population, the Turkish and the Dutch are included in one race, namely Caucasian. Hence, in this concept racial boundaries seem to coincide with population boundaries and seem to suggest a biological basis for similarities and differences.[50]

A fifth concept of population draws upon the German study referred to in this case. On the basis of that study, Lab F could draw the conclusion that Turks are not Dutch when it comes to their genetic material. The German study shows that allelic frequencies differ more between Germans and Turks than they do among Turkish people. Two Turkish groups were studied, one of which was living outside Turkey. This group had migrated to Brussels in the sixties and had been living there ever since; it is not indicated from where in Turkey they migrated, but that was not an issue. The conclusion in one of

and American Indian. For an example, see NRC, *Evaluation* (above, n. 8), p. 35. On the different taxonomies of race in genetics, see Troy Duster, "The Prism of Heredity and the Sociology of Knowledge," in Nader, *Naked Science* (above, n. 43), pp. 119–130.

48. See NRC, *Evaluation,* pp. 34ff.

49. For a history of race, crime, and the law, which takes the social construction of both crime and race into account, see Troy Duster, "Genetics, Race, and Crime: Recurring Seduction to a False Precision," in *DNA On Trial: Genetic Identification and Criminal Justice,* ed. Paul L. Billings (New York: Cold Spring Harbor Laboratory Press, 1992), pp. 129–141. On the intertwined history of race and genetics, see Daniel J. Kevles, *In the Name of Eugenics: Genetics and the Use of Human Heredity* (New York: Knopf, 1985); idem, "Out of Eugenics: The Historical Politics of the Human Genome," in Kevles and Hood, *Code of Codes* (above, n. 18), pp. 3–36; Chapman, *Social and Biological Aspects* (above, n. 46). For a historical debate on biology and the human races after World War II, see United Nations Educational, Scientific and Cultural Organisation (UNESCO), *The Race Concept: Results of an Inquiry* (Paris: UNESCO, 1952). For an analysis of this document, see Donna J. Haraway, *Primate Visions: Gender, Race, and Nature in the World of Modern Science* (London/New York: Routledge 1989), pp. 197–203. A broad collection of papers on race and the sciences is Sandra Harding, ed., *The Racial Economy of Science: Towards a Democratic Future* (Bloomington: Indiana University Press, 1993).

50. See, for example, L. C. Dunn, *Race and Biology* (Paris: UNESCO, 1951); the collision of population and race becomes clear in the following quotation: "Since biologically *races* are *populations* differing in the relative frequencies of some of their genes, the four factors noted above [mutation, selection, genetic drift, and migration/mixing] as those which upset the equilibrium and change the frequencies of genes are the chief biological process responsible for race formation" (p. 24; emphasis added).

the papers is that "neither Turkish *subpopulation* showed any significant differences for any of the three STRs, indicating that the time of geographical separation was too short to have had an influence on the allele frequencies."[51] Since the study answers the question of whether migration has had an impact on genetic "homogeneity," it becomes clear that "homogeneity" is located within a national context. Calling the two groups *subpopulations* indicates that they are derived from one *population,* an overall Turkish population. Hence, what is Turkish is correlated with being a subject of the nation-state Turkey. The national boundaries of Turkey therefore define what may be seen as Turkish.

More generally, within the realm of population genetics, national boundaries are seen as prohibiting conditions for "random mating" between members of different populations, and as enhancing random mating within the population. The spread of alleles is expected to be higher within national boundaries.[52] The skepticism of the defense could be rephrased as addressing exactly the presumption of an "easy" spread of alleles within national boundaries.

Arguing for Differences

The defense's objection to the presumed distribution of alleles within Turkey introduces *the sixth concept of population.* Contrary to the presumption of similar allelic frequencies within state boundaries, the defense presented data that showed just the contrary. Therefore, the idea that the country as a whole may have a general allele frequency representative of Turkish individuals at large is open to question. And since the markers used in Lab F differed considerably from those studied in the German paper, the defense asked for more comparisons. As a check, it suggested a comparison with the markers and data used in the Laboratory for Criminal Justice, Rijswijk.

51. Alper et al., "Frequency Profiles" (above, n. 35), p. 112 (emphasis added).

52. See Helen Macbeth about national and population boundaries (the former being referred to as a "conceptual boundary"). She suggests national boundaries as one possible approach to compare populations, since these boundaries often coincide with other "natural" boundaries: Macbeth, "Ethnicity" (above, n. 46), pp. 49, 78ff. The problems of this perspective are of course clear if one looks at, for example, the map of Africa. For a conception of differences within and between populations, see, e.g., Chakraborty and Kidd, "Utility" (above, n. 39), p. 1737. Moreover, the statement about differences within and between population is also used when other than national boundaries are seen as criteria of difference between populations. For a critique and elaboration on this argument see, e.g., Leon J. Kamin, Richard C. Lewontin, and Steven Rose, *Not in Our Genes: Biology, Ideology and Human Nature* (Harmondsworth: Penguin, 1984).

To doubt the content of 10^{-6} from this perspective suggests that populations may be tied to specific markers. Depending on which markers are used, a different classification of a population may be produced. Depending on markers, alleles may be equally spread over the whole world, they may be clustered in specific patterns, or they may be found in one population and not in another. The matching likelihood number correlates to the frequency of alleles in a given population. This means that to be able to say anything about matching probabilities, one needs to be sure that the specific profile is represented, in terms of alleles, in the population. For if the suspect is carrier of an allele B, and allele B happens to be common in the appropriate control population, but absent in the one used, then the matching likelihood number will be biased and will tend to show a lower figure. Therefore, the defense demanded a clearer answer about the clustering of genetic makeup, in case different markers and different data about the control population would be used.[53] From this, it can be stated that the concept of population here is based on genetic markers. Depending on the type of markers used, populations can be clustered anew.

Before going back to the Lab to see how it answered the question of genetic clustering in populations, let's have a look at how the matching likelihood number and DNA fingerprinting performed the role of *immutable mobiles*. We will focus on the stakes of their immutability and the effect of their mobility in this particular case.

Matching Likelihood Numbers and DNA Fingerprints: Immutable Mobiles

Earlier I suggested that DNA fingerprints and matching likelihood numbers can be viewed as immutable mobiles. Numbers are immutable mobiles par excellence, and as I suggested, analogies bear this power as well: both have the capacity to mobilize worlds, practices, and conventions, and to function as a convincing argument for those who haven't been in the laboratory. I have also argued that DNA fingerprints and matching likelihood numbers make an inseparable alliance in forensic cases, but that they transport different practices into court. The practice transported by the DNA fingerprint—familiarity with fingerprints as tools of identification—has proved to be questionable. With conventional fingerprints, all mate-

53. On population admixture, the clustering of markers within populations and subpopulations, and the calculation of matching likelihood probabilities, see Lander, "DNA Fingerprinting" (above, n. 18), p. 205; Lewontin and Hartl, "Population Genetics" (above, n. 39), p. 1746.

rial can be used for identification (the whole print of all fingers, of one finger, half a finger, or even a vague print of a finger). For DNA evidence, one cannot "examine" all of the material; therefore a selection is made based on variable regions on the DNA, the genetic markers.[54] Categorizing DNA testing as a kind of fingerprinting suggests that one can read the genetic information of each and every individual separately. With conventional fingerprinting, this can be done: there, a suspect can be identified if his or her fingerprint is included in "the population" of available fingerprints; the quest is then for the one and only match. In DNA fingerprinting, establishing identification requires the work of ruling out a match between the suspect's fingerprint and any other member in the control population, and especially in the population at large.[55] Thus, whereas conventional fingerprinting includes the suspect in the population, DNA fingerprinting seeks to exclude the suspect from the population. The difference between looking for other matches in the population and excluding or reducing the chance of a match in the population is paramount and may be difficult to overcome in DNA fingerprinting, as the example of the Turkish case shows.[56] Whereas the conventional fingerprint gives a yes or no—that is, identity or no identity—the DNA fingerprint is based on frequencies and comes with a probability number.

In "Galton's Regret," Paul Rabinow addresses this analogy as well.[57] He shows the irony in the promises made by both conventional and DNA fingerprinting. The British eugenicist and founding father of the fingerprint, Francis Galton, studied the fingerprint in

54. Lewontin and Hartl argue that the analogy does not hold water if one takes into account the material that can be studied in evidence DNA (only a fraction of the retrieved DNA is used), and the technology (the small number of markers that were available in the beginning of the nineties). Their argument is that DNA fingerprints do not contain as much information as conventional fingerprints: Lewontin and Hartl, "Population Genetics" (above, n. 39), p. 1746. Recently, in a personal communication, Richard Lewontin made clear that DNA profile typing has become more powerful, due to more and convincing genetic markers (5th Annual Meeting of the Society for Molecular Biology and Evolution, Garmisch-Partenkirchen, Germany, June 1–4, 1997).

55. Nowadays, in the late nineties, the amount of information stored in large data banks has grown dramatically, making it possible to look for matches between DNA profiles, especially if suspects have a criminal record. On the history of race and the incrimination of (groups of) individuals, see Duster, "Prism of Heredity" (above, n. 47); and esp. n. 49, above.

56. I thank Dr. Hans Zichler of the Laboratory for Evolution and Human Genetics, Munich, for having brought this point to my attention and clarified my thoughts about the analogy.

57. Rabinow, "Galton's Regret" (above, n. 18).

the hope of developing a tool of classification between populations. In this he did not succeed: the fingerprint did not show any population structure.[58] Instead, it established its prestige in forensics as a tool of individual identification. The DNA fingerprint has been developed and introduced into forensics as an ultimate tool of individual identification, but as becomes clear, individuality cannot be determined without situating the individual in a population. Galton's regret is indeed the weak spot in DNA evidence.

In this case, the fingerprint analogy seems to have lost ground. Therefore, the question is, has DNA fingerprinting ceased to be an immutable mobile? The matching likelihood number was instructive of the differences between both sides of the analogy. Matching likelihood computations blurred the fingerprint analogy and put the burden of proof on the markers typed, the reference population used, and the allele frequencies presupposed. Yet the matching likelihood number determined the fate of the DNA fingerprint. As we have seen, DNA fingerprints, and especially matching likelihood numbers, have been traveling back and forth between laboratory and courtroom. Both DNA fingerprints and matching likelihood numbers proved to be mutable: their inscriptions and the significance of the practices and information carried through them changed several times. Also, neither the courtroom nor the laboratory remained unchanged. Laboratory practice had been transported into court, and courtroom practices into the laboratory. Among other things, laboratory reports, control populations, different DNA profiles, and methods of computation entered the door of the courtroom, while a Turkish suspect, a Dutch control population, and various Turkish populations found their way into the laboratory. Latour argues that the power of immutable mobiles is correlated to their ability to "recombine" different practices.[59] Can the matching likelihood number, the number one immutable mobile, combine all these different worlds/practices and present them at once? In other words, is it capable of bringing the second immutable mobile, the DNA fingerprint, back to court?

In the following we will view how Lab F enabled the DNA fingerprint to be brought back to court. We will see that to do that requires the Turkish suspect to become a T-suspect once again.

58. Francis Galton, *Finger Prints* (London: Macmillan, 1892).

59. Latour, "Drawing Things Together" (above, n. 21), p. 45.

Back to the Lab: Making Similarities

Given the objections and questions of the defense, the DNA evidence seemed to be at risk. In the laboratory, different matching likelihood numbers were produced based on a set of markers of Lab F,[60] on the set of markers of the Laboratory for Criminal Justice, and on the data of the German study, all of which produced figures around 10^{-6}. All the sets used consisted of four to five markers. This figure did not seem to convince Lab F: not only was the matching likelihood number larger than 10^{-7}, but also the set of markers in each comparison declined as a result of trying to use comparable markers.

There seemed to be no way around the problem of a suitable control population, until another scientific paper seemed to show a way out of this stalemate situation and helped to take the DNA evidence back to court. This paper suggested a method for blurring the specificity of population.[61] Its authors had compared individual profiles with different reference populations, which led to the conclusion that allele frequencies may vary between populations depending on which marker is used. It was argued that errors that occur when determining the DNA profile of an individual from a population other than the reference population can be reduced when using the statistical model proposed. But also, so the paper suggested, the ties between an individual and a population are loosened if more genetic markers are typed.[62]

In the beginning of our case it was stated that the DNA fingerprinting of the Lab was based on the use of seven genetic markers. With these markers it was possible to produce an individual profile and to compare it with that of another individual (as in the case of evidence and suspect DNA). But this information did not make an identification; it could not tell who these individuals were. The DNA evidence was inhibited and the profile did not become a fingerprint. For that, a population was needed. Excluding a match with the rest of the population was not possible without access to the right control population; consequently, the individuality of the profile remained obscure. One could say that the problem of Lab F seemed to

60. The set of markers used at this stage is smaller and consists of STRs and HLA markers only.

61. R. Chakraborty, M. R. Srinivasan, and S. P. Daiger, "Evaluation of Standard Error and Confidence Interval of Estimated Multilocus Genotype Probabilities, and Their Implications in DNA Forensics," *American Journal for Human Genetics* 52 (1993): 60–70.

62. This argument is put forward in the following words: "[I]n general, the profile frequency is a decreasing function of the number of loci scored" (ibid., p. 68).

be on the side of population: the absence of an appropriate control population. As we will see below, however, the solution was sought on the side of individuality. Since the problem raised by the defense was deemed plausible, and since the Lab itself did not have access to Turkish samples, the way out of the impasse headed in another direction and the solution was laid in the hands of technology.

When I asked the head of the Lab to explain the meaning of the paper addressed, he stated the following:

> If one compares two brothers on the basis of a single marker, the chance of a match is 50 percent. But when using 25 markers, the chance is $3 \cdot 10^{-8}$. An arbitrary comparison between any two individuals based on 25 markers gives a matching probability equal to zero. So, generally, the more markers one uses, the smaller the chance that two people will look alike.

In terms of our case, the solution was to make the profile more individual by using more genetic markers: instead of seven markers, ten were used. In a way, this is a matter of statistics: the more variables one introduces, the more specific the units become. This refinement, using more genetic markers, made the profile of the Turkish suspect less population-specific. In a sense the Turkish suspect herewith was made into a T-suspect, who thus became a member of a much larger population. Also, the Dutch control population had become representative of a much larger population than the Dutch. The problem of "representativity" was resolved, because the control population of Lab F had become more sensitive, since all profiles had become more individual. The Lab was now in a position to calculate the matching probability of "the Turkish suspect" by comparing the profile of the "Turkish suspect" with those of the "Dutch control population." Based on this comparison, the Lab found a matching likelihood number of 10^{-10}. The DNA fingerprint produced was no longer the fingerprint of *the Turkish suspect* but that of *a suspect*. And, due to the number of markers, the DNA profile of this individual could become evidence, since it could be expressed in a population. The suspect had thus become similar enough to be identified as different from the rest of the population.

Similarities Established

The seventh concept of population is now introduced to the case. Earlier, it was argued that forensics works under the presupposition that the suspect is innocent and that the perpetrator is in the population. The task is to determine the individuality of the suspect's profile by simulating a comparison between the individual and all other members of the population. Thus, the suspect's profile should be set

apart in order to be sure that the specific combination of alleles (which make up the DNA fingerprint) is unique and does not occur in the population. But to do so, the suspect should also be sufficiently similar to the control population that helps estimate this probability. Without the presupposition of "similarity"—that is, that the genetic profile of the suspect is represented in the population—identifying individuals proved to be impossible. The very presupposition of similarities and the objections to it have already made visible six different concepts of population. As we saw above, population might be defined by family names, by laboratory practice and routines, or by genetic proximity and distance. But it could also be defined by race, by national boundaries, or by genetic markers and their specific clustering in different populations. This makes clear the "problems" or practicalities of *population*. Lab F, however, sought a solution on the side of individuality: it used more genetic markers, so that both the profile of the Lab's control population and those of evidence and suspect became more individualized. This introduces a new feature of genetic markers—namely, their number. First of all, more markers can distinguish better between individuals. The discriminating power of a marker (between individuals) is dependent on how many more markers can be used in a specific job at the same time. Secondly, the number of markers is crucial in producing differences or similarities between populations. Under *the sixth concept of population* it was shown that the set of markers used did produce differences between what should be viewed as Turkish and what as Dutch. That distinction was based on fewer than five markers, and as we saw earlier, it was not countered with a set of seven markers. Using ten markers, however, served to blur that distinction and incorporated a new concept of population assisted by technology. Hence ten markers produced a population in which both Turkish and Dutch could fit.

The concept of population we have here is based on genetic markers, and more specifically, on their number. The more markers, the larger the population becomes, and from the interview above it became clear that all the individuals in the world become part of one population when twenty-five markers are used.

Reporting on Immutable Mobiles

This case has produced many con-fusions. It started out with making individuality and became an issue of making population. Identification started as the work of DNA, to become that of technology. Meanwhile, a T-suspect became Turkish and then a T-suspect once again, while a control population became Dutch and then a

control population once more. There was a laboratory practice and a law practice and two mobiles in between: the matching likelihood number, and the DNA fingerprint. These were the very devices that could make laboratory facts into court evidence, and could forge a link between these practices. Yet in mobilizing one practice to another, their immutability was at stake; and as became clear in the course of the case, (im)mutability was dependent on the concept of population they embodied.

The first evidence produced by Lab F suggested a likelihood of one in ten million that the DNA profile of the suspect could be found (in another individual) in the population. At that stage, the case was treated routinely and the suspect's profile was compared with the population as usual. As we saw, that comparison was based on population samples that were deemed representative of the Dutch population. Since the victim and the initial two suspects were all of Turkish descent, the defense argued that the case should be treated as Turkish instead. This point was hammered home, and the question raised was whether genetic proximity and distance between populations—that is, between Turkish and Dutch—should be considered in the identification. Thereupon the Lab produced a second identification based on German studies of two Turkish "subpopulations," one living in Turkey and another living outside the country. Through a comparison with those studies, the likelihood increased ten times to become one in a million. But again the immutability of this likelihood number was challenged by the defense. Following the German studies, Turkishness was at that stage deemed to be connected to national boundaries. The defense, however, mobilized other evidence that indicated that the populations considered in the German studies might well be similar for the markers studied there, but that they differed for other markers. Taking population admixture into account, the question remained which population would be the appropriate one for this case, and would thus be representative of the suspect's profile? Hereupon the laboratory conducted more comparisons based on markers and data from the Laboratory of Criminal Justice. However, not having access to Turkish samples, Lab F decided to turn to its "mapping" technology. The technologies that had produced differences, the genetic markers, appeared to be capable of producing similarities as well—that is, if one considered their number. The power of markers to discriminate between populations had a breakpoint at seven: using more than seven markers—namely ten in this identification—created a population representative of Turkish and Dutch equally. Therewith the Turkish suspect

became once again a T-suspect and the Dutch control population, a control population as usual.

A population in which both Dutch and Turkish could fit allowed for the immutability of both the matching likelihood number and the DNA fingerprint. Since Turkish and Dutch had become similar by using ten markers, the control population of Lab F became an appropriate population for this case.

Whereas geneticists claim to know an individual by his or her DNA, it became evident that in the practice of genetics neither the individual nor the population is a *natural* category. Both categories are technology-assisted and established in the diverse practices of laboratory routines. I have examined how that is done.

In "global" endeavors of genetics, as in the case of the Human Genome Diversity Project, populations are *defined*—by language, for example. By contrast, my main concern here was to examine how populations are *produced* in the context of laboratory routines. Based on one particular case, I have shown that at least seven different concepts of population may circulate in forensics, and in population genetics at large. Depending on the circumstances, population may be embodied in laboratory routines, it may be a matter of practical reasoning, or a product of feasibility and access to data, technology, and samples. Thus in a laboratory setting neither the individual nor the population is treated as a matter of definition. The very conduct of scientific practice enhances and requires a variety in approach, contributing to a diversity in category. The question prompted by this is, of course, how do we want to be made into population?

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