Technologies of similarities and differences: on the interdependence of nature and technology in the Human Genome Diversity Project

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Chapter 2

Technologies of Population:
Making Differences and Similarities between Turkish and Dutch Males

Introducing the Argument

This chapter is about population. Its 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 examine how it is enacted in them. Towards this end, I analyse a forensic case. My analysis results in two arguments: first, that geneticists cannot know the individual without a population; second, that in genetics neither the individual nor population are inherently “biological.” Both are technologically assisted categories.

As has been discussed in the introduction, population is a subject of debate in the Diversity Project. In order to sample, study and compare populations, geneticists aim at achieving a consensus definition of what population is. This chapter, however, examines practices of population in laboratory routines and reveals the variety of what population “is” in such locales. In order to “know” a population geneticists study cell material from collections of individuals. In forensics, however, the vantage point is quite different. Forensic geneticists 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 also apply a category of population. 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.

Taking population as the main focus of analysis, little attention will be paid to the legal aspects of forensic DNA, a highly important matter in its own right. The site of study, rather than a courtroom, is a laboratory, the Forensic Laboratory for DNA research in Leiden, the Netherlands. But since my argument is organised around a forensic case, the narrative will enfold as a “trip” back and forth between laboratory and courtroom, viewing the
process of identification and examining the concepts of population embodied in that process of identification.

**In Court**

We are in a courtroom somewhere in the Netherlands. A murder case is in progress. Both the victim and the suspects 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 bloodspots, 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 individual in particular. The main suspect, however, 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. The 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: bloodspots, chewing 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 suggests that evidence and suspect DNA coincide. The DNA evidence supports the findings of the prosecutor that were based on circumstantial evidence. The defence objects to the results of the DNA tests and questions the testimony based on a figure of $10^{-7}$.

In order to trace the origin of the results presented in court, what they mean and how they play a role, we can 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 evidence DNA in the Netherlands, and then take a closer look at how DNA evidence is produced in that laboratory.

**DNA Evidence and its Laboratories**

In 1994 a new Dutch law on forensic DNA evidence was passed. The new law widened the use of this type of evidence in prosecutions and instituted an infrastructure of sites and regulations concerning the making of this evidence. According to this law, a suspect in a crime carrying a penalty of eight or more years cannot object to DNA testing. If there is other
evidence against that particular suspect, DNA testing is compulsory. Since a compulsory DNA test was considered a violation of the person’s bodily integrity, the 1994 law also regulates that the suspect has the right to apply for DNA contra-expertise. In cases of DNA evidence, two laboratories may be involved. The tests conducted on behalf of the prosecutor are primarily done in the Laboratory of Criminal Justice, Rijswijk (Het Gerechtelijk Laboratorium, Rijswijk), whereas the counter-expertise analyses are conducted in the Forensic Laboratory for DNA Research, Leiden. If the amount of evidence material does not support two studies, the suspect may decide which of the two laboratories should conduct the one and only test.

The Forensic Laboratory, hereafter Lab F, is part of a broad network of 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 cost of DNA testing (for prosecutors and suspects) and to make counter-expertise available to “every-body,” Lab F is entirely funded by the Dutch government.

In the next section, we encounter forensic laboratory work. We are introduced to Lab F’s rites and rituals, its protocols and procedures, and the particular alignment of technology and trace, to produce DNA evidence. Lab F will first be introduced from the perspective of a newcomer, which will reveal materialised institutional arrangements in that particular context and will familiarise us with the laboratory’s culture. Then we will learn more about the lab’s procedures and its organisation of work around DNA identification. Finally we will focus on DNA identification and how this was accomplished in the forensic case introduced above.

Off to the Forensic Laboratory

I was in Lab F. I was not merely an observer: I had asked for a short introduction to the basics of genetic research. For three and half months I participated in a project concerned with typing chimpanzee DNA and 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, to study a different culture, to take notes and hold interviews and to develop common ground for an understanding of what was going on.

In order to participate in this laboratory I was initiated in 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 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 accounts of forensics and experiences in the field, which enabled me to enter the discourse of the laboratory.

On my first day, after having been introduced to the lab members, the head of Lab F appointed a supervisor for me, 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 where 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 managed to run the PCRs (DNA copying technology) necessary for identification.  

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 research projects of the Lab. Whereas most of the technology applied by the technicians is standardised, 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 and gain 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 legal details of the case, (all cases are assigned a registration number once they enter the lab) they have developed a laboratory-specific typology. The cases could be referred to in terms of the registration numbers. However in practice they are attributed 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. Our case had acquired the adjective “Turkish.” The ethnographic contents of the adjective Turkish 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 the case was important to this laboratory. The material for the case in this
chapter is the result of many talks during my training and is based on interviews I conducted towards the end of the training.

The Lab

Lab F is a predefined environment in terms of protocols, technology, knowledge, and space. Any step in the analysis is recorded on specified forms on which the case number, the name of the technician as well as information about the utilised chemicals (such as “lot numbers” and expiry date), kits, and technical devices appear. Also all analyses and technology 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 concerns in this respect is the confusion or contamination of samples. Prompted by concerns about contamination, the most pivotal spatial division is the division of the lab into pre-lab and post-lab.

Contamination is one of the major worries of all forensic laboratories. In 1996 the US Committee on DNA Forensic Science produced *The Evaluation of Forensic DNA Evidence* on behalf of the National Research Council in Washington D.C. This report, which aimed at redirecting forensic DNA research, addressed the risk of contamination at 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.” 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 on hearing a chorus of voices shouting: “Lab coat! Lab coat! Take it off!” I looked down and realised 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 effort. The movement from pre-lab to post-lab is easy but the other way around requires extra measures (sterilisation of instruments, putting on of gloves or a lab coat). My overt confusion made the lab members laugh and, after a moment of despair, I closed the door and ran back 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 real. The certificate of the Board of Accreditation hanging on the wall
became more meaningful and serious. I noticed the friendly but critical eye of the quality control manager much more often. Furthermore my lab coat, the rubber gloves, and the mask I occasionally wore became strict borders between foreign material and the DNA on which I was working. What is foreign does not have to be strange. My supervisor told me that all lab members have typed their DNA profiles. This information enables the staff to trace the source of potential contamination and to exclude the possibility that the occasional foreign material is theirs.

The lab is divided into pre-lab 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 sample remains in this lab and is used in small amounts for the different analyses. For each of the 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 visualisation. This copying procedure, also called DNA amplification, constitutes the very division between pre-lab and post-lab: the names in full are pre-amplification-lab and post-amplification-lab. Thus the PCR machine sets the boundary and is placed 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 (synthesised DNA fragments), the enzyme, and other PCR-chemicals. This mix of chemicals and the PCR amplification are 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. 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 distillate water, ddH₂O) 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 run their primary course. The subsequent experiments are conducted carefully 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 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 labs in the field of human genetics, but it is perhaps even stronger in the context of Lab F. This laboratory is a forensic laboratory: the results of experiments conducted here have decisive consequences for the
imprisonment or liberty of a suspect and for the kinship or identity of an individual. Mistakes or ambiguities in the DNA analysis are reviewed and should not appear in the final report. Lab F operates predominantly on behalf of the suspect or the accused (the alleged father, blackmailer, murderer, or rapist). In analysing DNA this lab 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. Our focus will be on 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.

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 cell material did not support two studies and the defence requested Lab F to produce the one and only DNA evidence.

According to protocol, the evidence 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. The latter is an extra measure to prevent the technicians 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 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 them. The profiles are compounds of genetic marker information. A genetic marker can be seen as a small fragment of DNA whose length may vary between individuals according to the number of nucleotides, i.e. the number of DNA building blocks, it contains. 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 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 on that basis.

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 STR (Short Tandem Repeat) marker. The Poly-markers are a standardised package of five markers located on five different chromosomes; they show polymorphisms (i.e. variations between individuals) based on one single base-pair substitution in each DNA fragment. 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 informative for the very reason that their appearance 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 probability and produces a more individual profile. By typing the whole set of markers - Poly-markers, HLA and STRs - the lab obtained individual profiles of suspects and evidence DNA.

Based on the DNA analyses, the profile of one of the suspects matched the evidence DNA. But a match based on a similarity for the set of markers does not guarantee identification. It does not as such contribute to the suspect’s identification as the perpetrator. More work is required to achieve that. In order to be sure that the match between the profile of the suspect and that of the evidence DNA was the most likely, Lab F computed a matching probability based on profiles in the control population. This step is crucial. Forensic work is based on the presupposition that the suspect is innocent and that the evidence DNA was left by somebody else at the scene of the crime. 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 that are in its databank. On this basis, a probability was calculated expressing the chance that the marker profile of the evidence DNA could be found in the 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 databank in the following percentages: allele for marker I is represented in the data bank by 10%, allele for marker II is represented by 5%, and that of marker III can be found in 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, i.e., the population 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 to that of any other individual in the population from which the samples were drawn. This calculated probability, the matching likelihood number, 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 to those of the court.\(^{18}\) The figure was therefore presented in court as evidence of an exclusive match between suspect and evidence DNA, and thus as the identification of the evidence material. 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 recorded in a report drawn up 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 the court. A copy of the report printed on red paper, signalling 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.

From this discussion it became 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 defence had problems with the results presented in court. Let us now have a closer view at these objections and at how these relate to the T-case.

**Back in Court**

In court, the DNA tests of Lab F supported the findings of the prosecutor. These tests established a link between the evidence, found in the car and in the house next to the victim’s body, and the main suspect. But there appeared to be a problem. The defence did not accept the DNA
evidence and started to ask questions about how the matching likelihood number was produced, how the comparison was done, and about the control population upon which the figure 10^{-7} was based. Given that information, the defence argued that their client was not just a suspect, but a Turkish suspect. Their client is, after all, of Turkish descent. Did Lab F take that into account and can 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, the comparison was 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 in question. The defence 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 is 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 defence emphasised 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 it, no special attention was paid to the possibility of non-Dutch descent. Lab F used its Dutch control population as usual. Thereupon the defence raised the question of whether one could presuppose the absence of differences between Dutch and Turkish genetic makeup.

The scepticism of the defence raised a number of problems for the court. Would the matching likelihood be 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 can we be sure that the match between evidence and suspect DNA (inclusion) means that the suspect is indeed the perpetrator (identification)?

Although the traces of DNA based on evidence in the car and the house seemed to match with 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 assumptions, procedures and negotiations 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 Counter Expert**

Unlike the United States and Great Britain, in the Netherlands forensic DNA did not become an issue of public debate until the mid 1990’s. Before introducing the 1994 amendment to the Dutch Criminal Code permitting DNA evidence in lawsuits, a committee was appointed to investigate its impact and assess its future use. In that very context, discussing the reliability of technology, references were made to controversies in the United States and Great Britain. The committee considered technology to be no longer unreliable and spent most of its time regulating the rights of the suspect.

However despite the absence of controversies in the Netherlands, the defence may have been informed about controversies surrounding DNA evidence abroad and may have intended to use these as jurisprudence. One such controversial case 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. The case has been described by Richard Lewontin (1991) in *The Doctrine of DNA*. The judge in this case discarded the DNA evidence because it was obvious that not all inhabitants of Franklin County had an equal chance to access 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 databanks of other populations in the county, there was none for the Abenaki Indians. Therefore the suggestion to compare the DNA profile of the suspect, who was an Abenaki Indian, with various other ethnic groups living in the region was deemed inadequate and unreasonable. The DNA evidence was deemed inadmissible and the court dismissed the case.

Emphasising the need for an appropriate control population, the defence in our case seems to call forth a similar dilemma. Before returning to the case, however, we will 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 will try to understand the traffic of DNA evidence between laboratory and court by applying a theoretical notion, that of an “immutable mobile.”

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?”

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 that we think 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 either easier to transport or to 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. 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 how to understand the DNA evidence. The understanding implied is that DNA fingerprints are easy products. And the suggestion is that even in daily life anybody 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.”25 Thus, understanding a DNA fingerprint in terms of a conventional fingerprint mobilises a previous and successful individuality-determining practice in forensics. While facilitating this reading, the analogy seems to prohibit another, namely a complex view of DNA fingerprinting. What knits the two practices together also seems to set them apart: 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.”26 This feature of DNA fingerprints is emphasised by the matching likelihood number.

The second immutable mobile, the matching likelihood number (especially an impressive number like $10^7$) mobilises a scientific practice. It mobilises a complexity, hidden from the view of those “who haven’t been there.” This scientific practice is a number-producing 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, “unravelled” and made into a DNA fingerprint. The matching likelihood number therefore mobilises and establishes the complexity of these procedures as well as the scientific prestige attached to the production of DNA evidence. The information that comes out of the laboratory is a DNA fingerprint with a number.

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, mobilises a scientific practice where numbers as facts are produced out of human cell material. Whereas the former suggests familiarity, the latter evokes strangeness.27 If we put this in the context of our case, it is exactly this strangeness the defence sought to challenge. The objection of the defence can be seen as an objection to the immutability of both the matching likelihood number and the DNA fingerprint presented. Thus the defence 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 chapter 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 Turks contribute to different concepts of population.

**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 Lab F, 50 males were selected from Dutch hereditary-diseased families at Department of Human Genetics in Leiden. The samples come from healthy men related by marriage to the diseased families. These samples were selected by family name only. A second set of 50 female samples was randomly 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 Organisation for Applied Scientific Research). The 68 male samples were also 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. This study was conducted in three regions of the Netherlands, represented by the towns of Doetinchem, Leiden, and Amsterdam.

Hence the control population of the Lab as a whole was based on both genealogical ties (as expressed in family names) and on specific ties to the Dutch medical system. 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 lab. In compiling the control population, the Lab was not so much interested in those individuals as such but rather as representatives of a population as a whole. Yet the choice for 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 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 belong to the same family; the way to reduce this chance was by excluding samples that come from siblings sharing family names.
What, in view of the above, are the practices embodied in the sampled population, the source of the control population in the Lab? On the one hand the choice of names as an overall criterion for samples guarantees the representativity of the samples. On the other, it also suggests that family names make populations. In this practice a population consists of individuals linked by names. It 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 traced in the objection of the defence, and the emphasis placed on the Turkishness of the case. At stake is the matching likelihood number and the basic statistical presupposition it expresses. 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 defence opposed this by questioning whether this presupposition would hold if suspect and 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 the Lab was ignoring the statistical proposition of forensics: the possibility that any other person could have committed the crime?

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 failed to 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 databank (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, the laboratory practice provides some clues. For Lab F, the control population is the databank as usual, and the suspect is a suspect as usual. A T-suspect is not a common occurrence in this laboratory. Having compiled its databank with care, the Lab has grown to view it as the
control population full stop. The databank has thus become “a black box.” The stake in this black-boxing is not the content or the composition of the databank but the daily routine of forensic work in which it is used. Normally the databank does the task of a control population quite well and is therefore “reflexive” of that routine practice. One could say that due to daily routine, the Lab seemed to have developed a blind spot for T-cases. Thus the second concept of population is a product of laboratory routine and daily practice in which the population becomes the control population as usual.

**Proposing Differences**

For the benefit of its client, the defence questioned the matching likelihood probability based on the control population of the laboratory. This indicates a third concept of population. Whereas the Lab presupposed similarities between Dutch and non-Dutch, the defence considered the possibility of differences. By pleading that the case should be viewed as a Turkish case, the defence questioned the “representativity” of the control population applied. 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 issue of genetic distance. Are Turks and 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 which is exclusive within the context of a Dutch control population might be less convincing if comparison were based on a different population. Emphasising the fact that the suspect is of Turkish descent, the defence pleaded that these differences should be taken into account.

This objection suggests 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.

From these analyses it became clear that in forensic practice there is no such thing as the population, that different practices of population may be
in play at the same, and the specific concept produced has consequences for individuality. To know 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 to a Turkish population.

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 is not possible to identify the Turkish suspect on the basis of routine and standardised 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.” The Lab tried to meet the request 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 defence:

The question of “representativeness” raised by the defence 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 (south-eastern Turkey). The suspect is also from the South-East of Turkey. They are all Caucasians 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.

As a response to the defence, Lab F compared the DNA profiles of the suspect to 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. Hereupon, the matching likelihood was recalculated as $10^{-6}$ instead of $10^{-7}$. This means that the chance that the profile of the suspect would match with any other Turkish person has 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 allowed it to calculate a new matching likelihood probability. The papers that provided the lab with the data were included as scientific evidence. Again, the defence was not convinced and stated that even the matching likelihood number based on the data of the German study may not have accurately represented the case at issue.

The objection of the defence 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 defence aimed at just the opposite. It had mobilised more data about the Turkish population living in Brussels and argued that Turkish populations may be similar for some markers, but can differ for others. Since the markers used in the Lab and those in the German studies differed considerably, the defence 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 also makes them sensitive for population sub-structures. The defence 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. In forensics genetic markers are also subjects of great debate and discord, as they are often matters of life and death in forensic cases. 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.

In studies of genetic diversity as well as forensics, genetic markers are selected on the basis of three criteria. First, markers in the non-coding region of the DNA are preferred over those found in the coding region. Contrary to non-coding DNA, coding DNA has crucial functions in the cell because it helps produce proteins. Hence its pattern of change and of inheritance may be restricted to the functions it has in a living cell. In forensics the underlying and most important supposition concerning markers is that their
change is not restricted and that they are randomly inherited. As a consequence the supposition is that the variety of its alleles is randomly distributed within a population. This is based on the assumption of “random mating,” according to which people choose their partners at random and also pass on their genetic material at random. 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.”

Therefore the preference is for markers in non-coding 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 that bear this proposition. This does not mean, however, 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 are inherited independently. Preferably, they look for markers on different chromosomes, as in the case of the five poly-markers.

Second, 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 the 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 databank (a few hundred or more).

Finally a marker should not be too polymorphic. This has to do with other types of cases that one can find 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 two individuals. However forensic DNA is not only concerned 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 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 marker for both DNA evidence and paternity testing, not having to train laboratory members to work with too many markers and for reasons of economy), markers are chosen that are polymorphic but not “hyper”-variable. This choice is also involved in statistical models. For example the models of
Lab F do not take into account the occurrence of mutations. But if the Lab were to choose for hyper-variable markers for the purpose of identification, it would have to change its statistical models to be able to use those markers for paternity testing as well. Thus the practicability of markers in a specific laboratory context puts constraints on which of these will be considered good in forensic DNA practice.

Now that we have outlined 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 in the previous section.

**Arguing for Similarities**

A fourth concept of population can be traced in the interview excerpt quoted above. When talking about the problems of representativeness, the head of the laboratory mentioned in passing that Turks, like the Dutch, are Caucasian.46 This notion of population seems to warrant the first and 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 have indicated, the lab was not informed about the descent of the individuals involved. Taking their names for granted suggests 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.47 Race is an ambiguous but nevertheless relevant category for geneticists. The Caucasian, Negroid, and Mongoloid races are seen as the three main races of the world.48 According to this taxonomy, “races” within the three main races are called “population substructures” or “sub-populations.”49 In a way this suggests that “population” is nothing but another term for race. Even though genetic technologies blur clear-cut categorisation 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.50 In this concept of population, Turkish and Dutch are included in one race, namely Caucasian. In this practice of population, racial boundaries coincide with population boundaries and suggest a classical biological basis for similarities and differences.51

A fifth concept of population draws upon the German study, as it is referred to in this case. On the basis of the German study, Lab F could draw the conclusion that Turks are not Dutch when it comes to their genetic
material. The German study showed that allelic frequencies differ more between Germans and Turks than they do among Turkish people. Two Turkish groups were studied, one of which lives outside Turkey. This group had migrated to Brussels in the 1960s and had been living there ever since. No indication is given of the group’s place of origin in Turkey. That did not seem to be an issue. The conclusion in one of 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.” 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 contribute to what may be seen as Turkish. This concept of population thus suggests that it is a matter of national boundaries.

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. The scepticism of the defence could be rephrased as addressing exactly the presumption of an “easy” spread of alleles within national boundaries.

**Arguing for Differences**

The defence’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 defence presented data that showed just the contrary. Therefore the idea that the country as a whole may have a general allelic 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 defence asked for more comparisons. As a check, it suggested a comparison with the markers and data used in the Laboratory for Criminal Justice, Rijswijk.

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, population may be produced differently. 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 a 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 defence demanded a clearer answer about the clustering of alleles, and how genetic makeup is affected when different markers and different data about the control population are being applied.\textsuperscript{54} From this it can be stated that population is a product of genetic markers. Depending on what type of markers are 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 us take a second look at the matching likelihood number and the DNA fingerprint as \textit{immutable mobiles}. We will focus on the stakes in 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 mobilise worlds, practices, and conventions, and to function as a convincing argument for those who have not been in the laboratory. I have also argued that DNA fingerprint and matching likelihood number 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 material can be used for identification (the whole print of all fingers, of one finger, half a finger, or even a vague print may do). For DNA evidence one cannot “examine” all of the material.\textsuperscript{55} Therefore a selection is made based on variable regions on the DNA, the genetic markers. Categorising DNA testing as a kind of fingerprinting suggests that one can read genetic information of each and every individual separately. This can be done in conventional fingerprinting. 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 ruling out of a match between the suspect’s fingerprint and any other member in the control population and especially in the population at large.\textsuperscript{56} 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.\textsuperscript{57} Whereas the conventional fingerprint gives a yes or no, i.e. identity or no identity, the DNA fingerprint is based on frequencies and comes with a probability number.

In his “Galton’s Regret and DNA Typing” Paul Rabinow also addresses this analogy.\textsuperscript{58} Rabinow 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 the hope of developing a tool of classification between populations. In this he did not succeed.\textsuperscript{59} The fingerprint showed no population structure. 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 has become 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 travelling back and forth between laboratory and court room. Both DNA fingerprint and matching likelihood number 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, whereas a Turkish suspect, a Dutch control population, and various Turkish populations found their way to the laboratory. Latour argues that the power of immutable mobiles is dependent on their ability to “recombine” different practices.\textsuperscript{60} 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 the courtroom?

In the following we will view how Lab F enabled the DNA fingerprint to be brought back to the courtroom. We will see that in order to achieve this the Turkish suspect is required to become a T-suspect once again.

Back to the Lab: Making Similarities

Given the objections and questions of the defence, 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,\(^1\) 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 \(10^6\). 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 round the problem of a suitable control population until another scientific paper appeared to show a way out of this stalemate situation and to help take the DNA evidence back to court. The paper suggested a method for blurring the specificity of population.\(^2\) Its authors had compared individual profiles with different reference populations, leading 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 suggested. But also, so the paper suggested, the ties between an individual and a population are loosened if more genetic markers are typed.\(^3\)

In the beginning of our case it was stated that the DNA fingerprint produced in Lab F was based on seven genetic markers. With these markers it was possible to produce a DNA profile and to compare it with that of another individual (as in the case of evidence and suspect DNA). But this information did not lead to 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 having 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 be on the side of population: the absence of an appropriate control population. As we will see below, the solution was, however, sought on the side of
individuality. Since the problem raised by the defence 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 fifty percent. But when using 25 markers, the chance is $3 \times 10^{-8}$. 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 individuals 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 markers 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 this made the Turkish suspect into a T-suspect, who had thus become a member of a much larger population; for the very reason that all members of that population look less alike and had become more individualised. 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” to 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 into 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 should be set apart in order to be sure that the specific combination of alleles (which make up the DNA profile) is unique and does not occur in the population. But to achieve this the suspect should also be
sufficiently similar to the control population that helps estimate this probability. Without the presupposition of “similarity,” i.e., that the genetic profile of the suspect is represented in the population, identifying him proved to be impossible. The very presupposition of similarities and objections to it have already revealed six different concepts of population. As we saw above, population might be a product of family names, of laboratory practice and routines, or of genetic proximity and distance. But it could also be a product of race, national boundaries or of genetic markers and their specific clustering in different population. This makes clear the “problems” or the variety in the practice of population. Lab F, however, sought a solution on the side of individuality. It used more genetic markers. By introducing more markers, both the profiles of the Lab’s control population as well as those of evidence and suspect became more individualised. 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 either with a set of seven markers. Using ten markers, however, blurred 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 quoted it became clear that all the individuals in the world become part of one population when 25 markers are used.

**Reporting on Immutable Mobiles**

*This case has produced many confusions. It started out with making individuality and became an issue of making population. Identification started as a matter of DNA, to become that of technology. Meanwhile a T-suspect became Turkish and 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*
make a link between these practices. Yet when mobilising one practice to
another, their immutability was at stake.

Whereas the focus of the court is primarily on individuals and on their
identification, that of the laboratory is on variability in the DNA. However in
the interfering practice of law and science, the lab’s concern is to produce
individualised DNA. To do so, DNA is not treated in isolation but is both
part and product of the socio-material network of DNA evidence. The very
existence of this evidence could be seen as the work of laboratories and the
handling of DNA. However without the juridical regulation of laboratory
practice, or without taking into account the specificity of the case at issue, a
DNA profile may fail in a law practice. In the traffic between lab and
courtroom the DNA fingerprint and the matching likelihood number are the
centrepieces of DNA evidence. They embody the interfering practices of law
and science and usually express a “smooth” translation of scientific facts
into court evidence. This was different in the Turkish case. It began as a
routine case, the suspect’s profile being compared to the population as
usual. Since the victim and the initial two suspects were all of Turkish
descent, the defence started to question the lab’s routine. And thus the
practice of producing DNA evidence as also the practice of producing
individuals and populations was opened up for investigation. Whereas the
DNA fingerprint had to testify to the individuality of the suspect, the
matching likelihood number had to do so to the exclusion of other members
of the population. Various versions of population have been produced to
establish the individuality of the suspect and evidence on the basis of DNA.

Population may be a matter of family names, a matter of lab routine, or that
of genetic proximity and distance. Then again, it may be a product of racial
differences and similarities, of national boundaries, of genetic markers, or of
the number of markers applied. These different versions do not add up to
produce an integral picture of population. They are not pieces aiming at
completing a puzzle. One reason for this is that any version of population
embodies a specific set of techniques and materials and treatment of these
two. Population embodies specific kinds of practice. The transportability of
such practices (for example between laboratories) may be feasible, but it
may also be inhibited. For example, a version of population as national
boundaries, such as was used in the German Study referred to in this case,
required specific markers that were not part of Lab F’s practice. On the
other hand a population based on family names may not be feasible in other
contexts, because the social order implied in names may vary in different
parts of the world or because the routine of sampling may be a product of
divergent practices. Also in a context of genetic markers population could no
longer be practised as race since genetic markers structure groups of
individuals in ways that conflict with racial categorisations. The latter hints
at the second reason why the different versions of population identified here do not add up to one another. These versions may conflict, for they require different technologies for producing them. Population based on national boundaries may conflict with one based on language or on genetic proximity and distance, or again with a version based on a large number of markers.

Should this lead to the conclusion that since population can be made into different things, this variety is a random collection consisting of autonomous elements? The examination of the Turkish case points in a different direction. It shows that differences between versions of population are not natural or essential but matters of practice. It may be possible to make two conflicting versions fit. This, however, would require a change in laboratory practice: it would require additional technical interventions. Identifying the Turkish suspect also involved changes in practice, some of which were feasible, others not. For example, Lab F neither had access to the samples of the German Study, which embodies a practice of national boundaries, nor could it link the data of that study to its own practice of seven genetic markers. However a link between a population based on family names (the Lab’s control population) and an individual of Turkish descent was enabled by using more than seven genetic markers. This intervention accommodated a population in which Dutch and Turks could fit. Hence population does not exist by itself but is enabled in specific practices and inhibited in others.

This treatment of population and of the practices in which it emerges suggests that (im)mutability and mobility are not issues restricted to the traffic of “things” between different domains, such as the domain of science and that of the law. The (im)mutability and mobility of scientific facts may also be at stake in the exchange between laboratories. Thus their fate also expresses the tension between similarities and differences between scientific practices.

To conclude

Whereas geneticists claim to know an individual by his or her DNA, the aim of this chapter was to show that more is involved to achieve this. 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.

Geneticists working in the Diversity Project aim at defining population according to linguistic criteria. By way of 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 as many as
seven different versions of population may be found in forensics and in population genetics at large. Depending on the particular practice, population may come to embody 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 population are treated as matters of definition. The conduct of scientific practice is heterogeneous, and the handling of scientific objects requires various different technologies, contributing to a diversity in what these objects "are." The question prompted by this concerning population, is of course, how do we want to be made into population?
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Notes to Chapter 2


3. The revision of 1994 is actually an addition to the Dutch Criminal Code (articles 151a, 195a, 195b, and 195d): see het 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
4. According to the Dutch Criminal Code (Wetboek van Strafvordering, Artikel 151aj, 195a), only laboratories assigned via “de algemene maatregel van bestuur,” the political 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, as described by Bruno Latour, for example. 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 Organisation (HUGO). He advised me to visit one of the Human Genome Diversity conferences organised by HUGO (in Barcelona, November 1995) to get to know that particular 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 (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 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 1980s. 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 visualisation 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

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).


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 at the time, 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.

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 obeys 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 behaviour 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.

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

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; see Chapter 3 for an analysis of markers.

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).

15. The Poly-markers are: LDR, GYP A, 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. A significant part of this work is done with juridical means and argumentation; see M'charek, Hagendijk and de Vries (forthcoming).

17. 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 law 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 analyses what counts as fact in court and in science: Jasanoff, Science at the Bar (above, n. 2), pp. 49-68.

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

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


27. For the convenience of scientific prestige and its importance for the credibility of expert witnesses in court cases, see Cole, “Witnessing Identification” (above, n. 24). In his elegant paper Cole argues that the “ordinariness” or the familiarity of the fingerprint almost jeopardised 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.
28. 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.
29. 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.
30. 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.
31. In an article written in collaboration with the Forensic Laboratory for DNA Research, the following is stated: “The two groups of unrelated males analysed 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. 30], p. 1032).
32. Whereas before 1960 most immigrants in the Netherlands came from former Dutch colonies (such as Indonesia and 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 labour 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).

33. 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).

34. 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.


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

38. Dr. Peter de Knijff, personal communication.

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


41. My focus in this analysis is on criteria and the more “technical” features of genetic markers as applied tools in forensics; see Chapter 3 for an elaboration.


44. 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.

45. 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 - since 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.

46. Also in the German study, the Turkish population in Turkey is referred to as Caucasian: Alper et al., "HumFES/FPS" (above, n. 36), p. 93.

47. 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. 24): "The only preselection of data for this study was that of ethnicity [Caucasian], which was determined on the basis of photographic evidence" (p. 825).

48. 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, 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. 44), pp. 119-130.


51. 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).

52. Alper et al., “Frequency Profiles” (above, n. 36), p. 112 (emphasis added).

53. 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. 47), 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. 40), 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 of and an 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).


55. 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 early 1990s). Their argument is that DNA fingerprints do not contain as much information as conventional fingerprints: Lewontin and Hartl, “Population Genetics” (above, n. 40), p. 1746. Recently, in a personal communication, Richard Lewontin made clear that DNA profile typing has become more powerful thanks to more and convincing genetic markers (5th Annual Meeting of the Society for Molecular Biology and Evolution, Garmisch-Partenkirchen, Germany, June 1-4, 1997).

56. Nowadays, in the late 1990s, the amount of information stored in large databanks 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. 48); and esp. idem, “Genetics, Race, and Crime” (above, n. 50).

57. 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.

58. Rabinow, “Galton’s Regret” (above, n. 19).


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


63. 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).