



# **DNA-DATABASE MANAGEMENT REVIEW AND RECOMMENDATIONS**

**ENFSI DNA Working Group  
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## **Table of contents**

1	Introduction.....	3
2	Establishing a forensic DNA-database.....	3
3	Inclusion criteria.....	4
3.1	Source of the DNA-profiles.....	4
3.2	Choice of loci.....	6
3.3	Number of loci.....	8
3.4	Supplier of profiles.....	10
3.5	DNA-profiles produced from low levels of DNA.....	10
3.6	Rare alleles/chromosomal anomalies.....	11
3.7	Wild cards.....	12
3.8	Mixed profiles.....	12
3.9	Sequence variation between STR alleles of similar size.....	14
4	Deletion criteria.....	14
4.1	End of maximum storage time.....	14
4.2	Non-conviction of a person.....	15
4.3	Match of stain with person.....	15
4.4	Duplication.....	15
4.5	Match with elimination database.....	16
4.6	New information demonstrating that the DNA-profile should not have been included.....	17
5	Matching rules.....	17
5.1	Match/hit definition.....	17
5.2	Search modes.....	17
5.3	Number of matching loci/match probability.....	18
5.4	Near matches.....	18
5.5	Match validation.....	19
5.6	Dispositioning.....	19
5.7	Match counting.....	20
5.8	Output/efficiency measurement.....	21
6	Likelihood of finding adventitious matches.....	22
7	Reporting results.....	24
8	DNA-database software.....	25
9	Data integrity control measures.....	28
10	Inclusion of case information and personal data.....	29
11	Interaction with other databases.....	29
12	Automation of working processes.....	30
13	Storage of cell material.....	31
14	Legislative matters.....	32
15	Financing.....	33
16	Personnel requirements.....	33
17	Governance.....	33
18	External Communication.....	34
18.1	Annual report.....	34
18.2	Internet site.....	34
19	International overviews.....	35
20	International comparison of DNA-profiles.....	35
	Annex 1: Summary of ENFSI-recommendations.....	38
	Annex 2: Changes in the 2009 document relative to the 2008 document.....	41

## 1 Introduction

The DNA-database & Legislation subgroup of the ENFSI DNA Working Group has published and updated several documents during its existence:

- ENFSI Report on DNA Legislation in Europe
- ENFSI survey on DNA Databases in Europe
- ENFSI DNA Working Group - Terms and Abbreviations
- ENFSI Report on Criminal Cases in Europe solved by ILS (DNA Mass Testing)

These reports can be found at: <http://www.enfsi.eu/page.php?uid=98>

This document discusses the different aspects of forensic DNA-database management and makes recommendations where this is deemed useful. Questions, remarks and additions in relation to this document can be sent to the chair of the DNA-database & Legislation subgroup of the ENFSI DNA Working Group Dr. Ir. C.P.(Kees) van der Beek MBA (k.v.d.beek@nfi.minjus.nl) who has compiled this document with the help of the members of the ENFSI DNA Working Group and other experts. The first (2008) version of this document was approved at the 28<sup>th</sup> ENFSI DNA Working Group meeting which was held on 23rd - 24th April 2008 in Prague. This second version of the document was approved at the 29<sup>th</sup> ENFSI DNA Working Group meeting which was held on 23rd - 24th April 2009 in Lisbon. Every year the document will be updated and republished on the ENFSI website.

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The use of a (separate) DNA-database to find matches between (relatives of) missing persons and unidentified human remains is not discussed (yet) in this report.

## 2 Establishing a forensic DNA-database

The power of a forensic DNA-database is that it can assist in the investigation of crimes by linking DNA-profiles of crime-related biological trace material to possible donors (or their relatives) of that biological trace material. Over the past 10 years forensic DNA-databases has proven to be very powerful in this respect. In spite of this success not all ENFSI-member-countries have a DNA-database yet.

The Council of the European Union has already invited Member States in 1997 to consider establishing DNA Databases<sup>1</sup>. And in 2001 a European Standard Set (ESS) of loci was established to enable comparison of DNA-profiles from different countries<sup>2</sup>. In June 2008 the Council of the European Union has converted the Treaty of Prüm into EU-legislation (The EU-Prüm-Decision) . The new EU-

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<sup>1</sup> Council Decision of 9 June 1997 on the exchange of DNA analysis results

<sup>2</sup> EU-Council resolution 9192/01

legislation will require every EU-country to establish a forensic DNA-database and to make this database available for automated searches by other EU member states. As DNA-profiles are regarded as personal data, national privacy legislation derived from the European Data Protection Directive 95/46 also applies to forensic DNA-databases. This has certain disadvantages which will be explained in chapter 14. It is therefore better to have specific DNA-database legislation.

The DNA-working Group of the ENFSI strongly feels that every EU-country should have a forensic DNA-database to enhance:

- # the possibility to solve crimes
- # the number of crimes that are solved
- # the speed with which crimes are solved
- # the time the police can spend on other work
- # the possibility to link unsolved crimes
- # the possibility to identify false identities

The purpose of a National DNA database usually is defined in the legislation (e.g. intelligence tool, evidence provider, combat volume crime, combat serious crime, identify donors of stains, link crime scenes etc.). This defined scope determines which categories of individuals should be included in the National DNA database.

#### **ENFSI-recommendation 1**

Every EU/ENFSI-country should establish a forensic DNA-database and specific legislation for its implementation and management.

### **3 Inclusion criteria**

Several criteria determine whether a DNA-profile can/will be included in a DNA-database. In the paragraphs below, these criteria are discussed.

#### **3.1 Source of the DNA-profiles**

In most countries with a DNA-database specific DNA-legislation regulates which DNA-profiles can or should be included in that DNA-database. Some countries require an additional specific authorization of a magistrate. Because the purpose of a DNA-database is to find matches between crime-related stains and persons, these two types of DNA-profiles are usually always present in a DNA-database.

##### Crime-related stains

These are the DNA-profiles which are assumed to originate from presumed perpetrators of crimes. It is the responsibility of the police to collect crime-related samples. When the origin of a sample is unclear, reference samples (e.g. from the victim or from witnesses) should be collected and their DNA-profiles should be compared to those of the crime related samples to prevent DNA-profiles from innocent people to be included in the DNA-database. DNA-testing in high-volume-crime (burglaries etc.) often is very standardized and automated to increase the number of samples tested and to decrease the

throughput time from sampling at the crime scene to inclusion in the DNA-database. Samples taken at these type of crime scenes should be chosen in such a way that the likelihood of them originating from a perpetrator is as close as possible to 100%. Examples of such “safe” samples are: bloodstains (e.g. on broken windows), saliva stains (e.g. on tins, cups, bottles), cigarette butts and chewing gum, of which people who live in a burglarized house can testify that they did not produce those samples.

Usually the types of crime from which the stains originate correspond with the types of crime for which persons can be forced to take a DNA-test. However in some countries there are no limitations with regards to the types of crime from which stains can be included in the DNA-database. In practice stains related to minor crimes are not collected due to the priority given to more serious crimes but the absence of limitations on crime scene stains opens up the possibility of solving minor crimes (like littering or damaging public or private property) if the person corresponding to the stain has already been included in the DNA-database for a more serious crime. Moreover linking minor to more serious crimes may yield additional investigative information which may speed up the investigation into the more serious crime.

#### **ENFSI-recommendation 2**

The type of crime-related stain DNA-profiles which can be included in a DNA-database should not be restricted.

#### Persons

Several categories of persons may be included in a DNA-database.

- Convicted persons, persons who have been found guilty of a crime by a court of law and may (or not) be (conditionally) convicted to imprisonment, a penalty, labor, hospitalization or combinations of those. A conviction can be overturned by a successful appeal to a higher court. In some countries it is possible to include persons in the National DNA-database who have been convicted in the past and who have already completed their imprisonment. This is called retrospective sampling.
- Suspects, persons who have not yet been found guilty but are officially the subject of investigation and/or prosecution.
- Arrestees, persons who have been taken into custody by the police but are not (yet) a suspect.
- Volunteers, persons outside the abovementioned categories who have agreed to give a DNA-sample for investigative purpose. In some countries volunteers can also be included in the national DNA-database. Two examples:
  1. In the UK persons who have voluntarily provided a DNA sample, for example for participation in a DNA-mass-screen, are asked if they object to the DNA profile being included in the national DNA-database. A once given approval for database loading cannot be withdrawn.
  2. In the Netherlands previously convicted persons who have already completed their imprisonment can be included in the national DNA-database on a voluntary basis. This is meant for persons who don't want to be repeatedly confronted with a request for a voluntary DNA-test to exclude them from being the culprit of a crime.

- (Deceased) victims of unsolved crimes. The purpose of including victims of unsolved crimes is the hope to find in the future a match with a stain on an object that has been in contact with the victim during the crime but which was taken by the culprit. The “risk” of including victims is getting matches with other unsolved crimes in which case the victim becomes a suspect. Therefore still living victims, like other volunteers, should be informed and asked to give their consent.

The legal criteria for the inclusion of convicts, suspects and arrestees in a national DNA-database are usually either specific types of crime or the maximum punishment the law allows for a crime.

Obtaining a DNA-sample from convicted persons, suspects and arrestees may involve several steps.

- A person may be asked first to give a sample on a voluntary basis,
- An official police or judicial order may be given to provide a sample, either directly or upon refusal to give the sample on a voluntarily basis
- Various actions are possible in different countries upon refusal to provide a sample: conviction for the refusal, physical force to obtain a sample or taking a sample from an object with cell material from the person. A conviction for the refusal does not result in the production of a DNA-profile (and the inclusion of the DNA-profile in the National DNA-database) and hence is not a logical measure in DNA(-database) legislation.

Since the match of a stain to a reference sample depends on the presence of the perpetrator in the DNA-database, more matches can be expected if more persons are included in the DNA-database. Moreover the persons included in the DNA-database should fit in the scope of the DNA-database. Including high volume crime scene stains but only persons convicted of sexual and capital crimes will not produce many matches.

### **ENFSI-recommendation 3**

To increase the chance of DNA-profiles of stains to match a person, the number of persons in a DNA-database who are likely to cause matches with those stains should be as high as legally (and financially) possible

Apart from nationally collected DNA-profiles also DNA-profiles originating from international legal comparison requests may be included to enable repeated comparisons against newly added DNA-profiles. See also § 20.

The inclusion of DNA-profiles in the DNA-database for contamination detection purposes is dealt with in § 4.5

## **3.2 Choice of loci**

Most countries use commercially available kits to produce DNA-profiles for inclusion in their DNA-databases. Table 1 shows the contents of the different commercially available kits as well as the composition of the different standard sets discussed below. Some kits are included which are no longer sold commercially (e.g. QUAD, SGM). Historically these kits were used in relation to the first DNA-databases but their discriminating power is insufficient to generate



Standard Set of Loci (ISSOL) is equal to the European Standard Set plus the Amelogenin locus.

The European Standard Set of Loci presently contains only 7 loci. This is enough for occasional exchanges of DNA-profiles between countries. However when massive exchanges of DNA-profiles are undertaken as has been made possible by the Interpol DNA-database and the EU-Prüm-Decision, 7 loci will not be enough because the chance of adventitious matches will no longer be negligible. In addition each DNA-database contains a significant portion of partial profiles with much higher probability to match randomly. That is why ENFSI has recommended that the European Standard Set of Loci should be extended by 5 additional loci. The Police Cooperation Working Party of the European Union has expressed its support for this work and has invited ENFSI to present a proposal for their approval when this evaluation has been completed (Room document PCWP 2007-04-12/01). Two companies have already produced kits which contain these new loci and have asked laboratories to evaluate them.

When DNA-profiles of crime related biological material and of reference samples in a DNA-database have been generated with different kits, the manager of the DNA-database should be aware of the possibility of missing matches due to the occurrence of so-called “null-alleles”. These are alleles which are not amplified in the PCR-reaction due to a mutation in the primer region. When 2 kits use different primers for the same heterozygous locus and the DNA of a person contains a mutation in the primer region used in one kit but does not contain a mutation in the primer region which is used in the other kit, the former kit will detect only one allele (apparent homozygote) and the latter will detect two alleles (heterozygote). The presence of a null-allele may be detected by the expected low peak height of the apparent homozygote but this requires an attentive DNA-analyst or intelligent allele-calling software. When the detection of null-alleles cannot be guaranteed, the search strategy in the DNA-database may be adapted to allow for one mismatch. Depending on the specific situation in a country this adapted “less stringent” search strategy may be used permanently or occasionally and for all profiles or only for a minority of profiles produced by a different kit than the majority of the DNA-profiles in the DNA-database (see also § 5.4).  
More information about the occurrence of null-alleles can be found at:  
<http://www.cstl.nist.gov/biotech/strbase/NullAlleles.htm>

### **3.3 Number of loci**

For the comparison of DNA-profiles between European countries the use of a DNA-kit which contains the European Standard Set or the Interpol Standard Set of Loci is necessary. For comparison of DNA-profiles in a single country however other criteria may apply. DNA-profiles of crime-scene stains may not contain all the loci present in the kit(s) used in a country to produce DNA-profiles. These partial DNA-profiles are included in the national DNA-databases however provided they have a high enough evidential value (random match probability) and the chance of producing adventitious matches is not too high (see § 6). Two criteria commonly used for the inclusion of partial profiles are 1) minimum number of loci and 2) maximum random match prob-

ability. The second criterion is better because a DNA-profile containing only 4 or 5 loci may have a lower random match probability than a DNA-profile containing 6 loci if (some of) the alleles in the former are rare.

If different but sufficiently overlapping partial profiles are obtained from a crime scene sample, these profiles may be combined into a composite profile containing more loci than the contributing profiles.

At the 28<sup>th</sup> ENFSI meeting in Prague in April 2008 Tacha Hicks Champod of the University of Lausanne presented the results of a simulation study in which she showed the influence of including DNA-profiles with lower numbers of loci on the number of genuine and adventitious matches generated in a simulated Swiss DNA-database.

**ENFSI-recommendation 4**

Managers of national DNA-databases should establish (together with other stakeholders) criteria for the inclusion of partial DNA-profiles to obtain an acceptable balance between the minimum allowable level of evidential value (maximum random match probability) of a DNA-profile and maximum number of adventitious matches a partial DNA-profile is expected to generate.

Sometimes an unsolved crime is so serious that a DNA-profile which does not meet the minimum criteria for inclusion in the National DNA-database still is searched against a National DNA-database accepting the fact that many of the matches which are found are adventitious matches. Tactical police work is then necessary to find out if one of the matches leads to a potential suspect. When no potential suspect is found by the police the search action may be repeated after some time or at regular intervals because new persons will have been added to the National DNA-database. The CODIS-autosearcher-mode produces only the new matches in these types of search actions which saves work in sorting out the old and the new matches.

For historic reasons the countries who started early with their DNA-databases (like England and The Netherlands) still have DNA-profiles in their DNA-databases which were produced by the older commercial kits like QUAD (4 loci) and SGM (6 loci + Amelogenin). For economic reasons these DNA-profiles often are only upgraded when they produce a match. This also implies however that these profiles often do not fulfill the criteria for international comparison which is a missed chance to solve the case from which the DNA-profile originates. An upgrade of a DNA-profile is of course only possible if the cell material or the DNA-extract still is available for further testing.

**ENFSI-recommendation 5**

DNA-profiles produced by older commercial kits should be upgraded (if possible) after a match in the National DNA-database to increase the evidential value of the match and also to fulfill the criteria for international comparison if a country wants to include DNA-profiles produced by older commercial kits in international search actions.

The number of loci in reference samples should be the maximum of the number of loci present in the kit(s) used for the production of the DNA-profiles of the reference samples to enhance the chance of finding relevant matches with partial DNA-profiles

**ENFSI-recommendation 6**

The number of loci in reference samples should be the maximum of the number of loci present in the kit(s) used for the production of the DNA-profiles of the reference samples to enhance the chance of finding relevant matches with partial DNA-profiles.

### **3.4 Supplier of profiles**

It goes without saying that the reliability of the matches produced in a DNA-database is dependent on the reliability of the DNA-profiles participating in the match. A wrongly called allele may prevent a match and a sample mix-up may produce a false match. That is why labs producing DNA-profiles for DNA-databases should objectively be able to show that they produce DNA-profiles with quality-driven processes meaning for example that there must be arrangements in place whereby the laboratory can demonstrate:

- The validation of its analytical processes
- Arrangements for continuous monitoring of data quality and consistency
- Arrangements for error identification, error handling and incorporation of corrective and preventative actions

**ENFSI-recommendation 7**

Labs producing DNA-profiles for a DNA-database should, as a minimum, be ISO-17025 (and/or nationally equivalent) accredited and should participate in challenging proficiency tests (for Europe: e.g. GEDNAP).

### **3.5 DNA-profiles produced from low levels of DNA**

DNA-profiles produced from low levels of DNA, either by the standard number or an enhanced number of PCR-cycles, can contain allele drop-ins and allele drop-outs even if a consensus profile is produced from repeated determinations. Hence they may never cause matches when included in a DNA-database if all alleles are required to match. So if DNA-profiles produced from low levels of DNA are included in a DNA-database they should be recognizable and a dedicated match strategy (allowing one or more mismatches) should be used for them as will be discussed in § 5.4.

**ENFSI-recommendation 8**

When DNA-profiles produced from low levels of DNA are included in a DNA-database they should be recognizable and a dedicated (near) match strategy should be used for them.

### 3.6 Rare alleles/chromosomal anomalies

For each commercial kit the known alleles of each locus and their frequency (in several different populations) is described in the manual of the kit. From time to time new alleles are observed in DNA-profiles and the question is whether these new alleles should be included in the DNA-database and which frequency they should get in order to calculate the random match probability of the DNA-profile. When a new allele is observed its appearance should of course be confirmed by repeated DNA-isolation, PCR, Capillary Electrophoresis and allele calling. Before including the new allele in the DNA-database a literature search may be conducted to see whether the new allele has been observed and/or sequenced before. A good source for this is the DNA-database of NIST (<http://www.cstl.nist.gov/biotech/strbase/index.htm>). If a new allele has not been sequenced yet it can be sent to NIST for sequencing. Only new alleles of which the size can be accurately determined using the internal DNA-size-standard, should be included in the DNA-database. An additional criterion for including a new allele in the DNA-database is the number of internal or/and external observations of the new allele.

The frequency attributed to a new allele may be one divided by the size of the reference database used to calculate the random match probability, a predetermined (low) frequency or a frequency calculated according to the Balding<sup>3</sup> size correction formula.

#### **ENFSI-recommendation 9**

When a new allele is observed in a DNA-profile, its presence should be confirmed by repeated DNA-isolation, PCR, Capillary Electrophoresis and allele calling of the DNA-profile. Only new alleles of which the size can be accurately determined using the internal DNA-size-standard, should be included in the DNA-database.

Sometimes chromosomal anomalies are observed in DNA-profiles. As a result a locus may show more than 2 peaks. As these chromosomal anomalies are rare and hence contribute to the evidential value of the DNA-profile it would be logical to recommend that they should be included in the DNA-database. However extra peaks can also be caused by somatic mutations which may only appear in certain tissues/body fluids. This means that DNA-profiles from different sample types (e.g. buccal scrape and blood) may not fully match. They can of course contribute to the evidential value after the match has been found in the DNA-database. An inventory of tri-allelic loci observations can be found at: [http://www.cstl.nist.gov/biotech/strbase/tri\\_tab.htm](http://www.cstl.nist.gov/biotech/strbase/tri_tab.htm)

#### **ENFSI-recommendation 10**

Alleles from loci with chromosomal anomalies should not be included in a DNA-database as they may be caused by somatic mutations which may only occur in certain tissues/body fluids.

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<sup>3</sup> Balding, DJ (1995) Estimating products in forensic identification. J. Am. Stat. Assoc. 90:839-844

### 3.7 *Wild cards*

If there is uncertainty about the presence or absence of an allele in a DNA-profile, a so-called wild-card may be included in a DNA-profile. This may be the case with low peaks of which the DNA-analyst is not sure whether it is a homozygote peak or a locus of which one allele has dropped out.

In some countries a wild card is used to replace a rare allele which is not in the ladder-range of the DNA-kit used. In this case the wild card represents a designated allele which can be used to verify a match with a DNA-profile containing such a wildcard. Searching with wildcards means that any allele is accepted as a match for the wildcard-allele. This increases the chance of finding adventitious matches. Therefore wild cards that do not represent a designated allele should not be part of the minimum number of loci/alleles required by the Prüm-matching rules.

#### **ENFSI-recommendation 11**

Wild cards that do not represent a designated allele should not be part of the minimum number of loci/alleles required by the Prüm-matching rules.

Different countries use different designations for their wildcards. For the international comparison these national designations have to be converted into mutual designations. Countries that exchange DNA-profiles under the terms of the EU-Prüm-decision use an “\*” for a wildcard which represents a designated allele and intend to use a “B” for wildcard which represents an unknown allele.

### 3.8 *Mixed profiles*

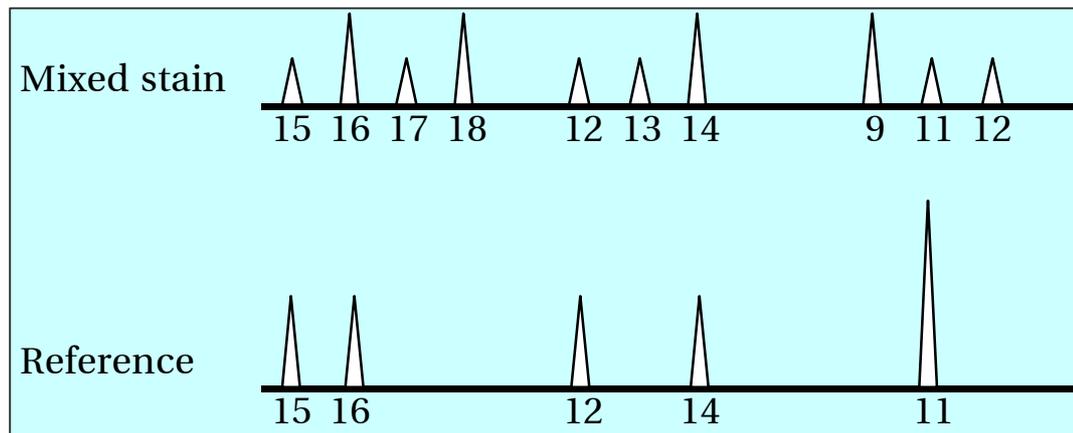
Mixed profiles can occur when two or more suspects have left cell-material on the same object (e.g. smoking from the same cigarette or drinking from the same bottle) or when cells of a suspect are mixed with cells of a victim (which often occurs in rape-cases). If possible mixed DNA-profiles should be interpreted and designated into their contributing DNA-profiles. Mixed profiles from (known) victims and (unknown) suspects sometimes can be resolved because the alleles of the DNA-profile of the victim can be subtracted from the mixed profile. The remaining alleles must belong to the suspect. Mixed DNA-profiles from two suspects however can often only be completely designated into separate contributors if there is a significant difference in contribution between the two participants (Major-Minor-situation). A working group of the ISFG has produced a document with guidelines for the analysis of mixed profiles.

#### **ENFSI-recommendation 12**

The guidelines in the document of the ISFG-working group on the analysis of mixed profiles should be used for the analysis of mixed profiles.

In some DNA-databases (like CODIS) mixed DNA-profiles can be included and searched against. This is very useful when a mixed DNA-profile cannot be reliably resolved in its contributing components. In CODIS it is even possible to designate remaining alleles as “required” if one of the participants of a mixed DNA-profile has been identified. Matches with reference samples will only be

shown if these required alleles are present in the reference sample DNA-profile. A numerical match between a reference sample and a mixed profile must always be checked against the plots of the DNA-profile because a numerical match may not be a real match as shown in figure 1. For this reason mixed profiles cannot be used at this moment for automated international comparison of DNA-profiles like the comparisons which are performed under the terms of the EU Prüm Decision and comparisons in the Interpol DNA-database.



*Figure 1: Three loci of a mixed stain and a reference sample which match on a numerical basis but are clearly not a match when the mixed profile is designated into its contributors*

**ENFSI-recommendation 13**

A numerical match between a reference sample and a mixed profile must always be checked against the plot of the mixed profile.

Mixed profiles of more than 2 persons should not systematically be included in a DNA-database because they generally will produce too many adventitious matches. Manual searches with this type of profiles may however be useful.

**ENFSI-recommendation 14**

Mixed profiles of more than 2 persons should not systematically be included in a DNA-database because they generally will produce too many adventitious matches.

Special software exists to designate mixed DNA-profiles into possible contributors. These possible contributors can then be searched against a national DNA-database of a country. Some people have expressed their concern that this will lead to an increase of false positive matches. Compared to the situation where mixed profiles themselves are included in a DNA-database (which can be done by countries using CODIS) searching with possible contributors of a mixed DNA-profile will not lead to more false positive matches.

### **3.9 Sequence variation between STR alleles of similar size**

The present designation of STR-alleles is based on their number of repeats as determined by their size in capillary electrophoresis. More sensitive analyses using ion-pair reversed-phase high-performance liquid chromatography electrospray-ionization quadrupole time-of-flight mass spectrometry (ICEMS) have shown however, that STR-alleles in general display considerable sequence variability that may result in additional discrimination for alleles with identical sizes<sup>4</sup>.

These findings have significant consequences for forensic DNA-typing:

- Match probabilities may be lower than presently calculated
- Identical alleles as determined by capillary electrophoresis may be differentiated with ICEMS due to sequence variability
- Capillary Electrophoresis may have to be replaced by ICEMS in the future
- The discrimination power of DNA typing can be enhanced which is important for mixtures and partial DNA profiles.
- The established DNA databases can still be used.

## **4 Deletion criteria**

In this chapter the reasons for deleting DNA-profiles from DNA-databases are discussed. Regardless of the reason for deletion, the deletion of a DNA-profile should always be recorded in a verifiable way including the reason for deletion. Deleting a DNA-profile from the DNA-database may also require the destruction of the cell material and hardcopies of the cell material. Deletion of DNA-profiles from back-ups or analytical data files usually is more difficult to do.

### **4.1 End of maximum storage time**

In most countries there is a maximum time during which DNA-profiles are stored. Below is a list of criteria which are used by different countries for reference samples:

- Fixed time after inclusion
- Variable time after inclusion depending on the type of crime
- Variable time after inclusion depending on repeated convictions
- Until the death of a person
- Fixed time after the death of a person
- Variable time after the death of a person depending on the type of crime
- Until no longer relevant (criterion from data-protection legislation)

In all but the first two situations the custodian of the DNA-database is dependent on external information for the determination of the deletion date of

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4 Oberacher et al. Human Mutation 29(2008) 3: 427-32. Increased forensic efficiency of DNA fingerprints through simultaneous resolution of length and nucleotide variability by high-performance mass spectrometry

Oberacher et al. Electrophoresis 29(2008) 23: 4739-50. The next generation of DNA profiling - STR typing by multiplexed PCR - ion-pair RP LC-ESI time-of-flight MS"

a DNA-profile. In these cases the custodian should have access to this information preferably by means of automated messages after an event which influences the deletion date of a DNA-profile.

**ENFSI-recommendation 15**

If the removal of a DNA-profile from the DNA-database is dependent on external information, a process should be in place to give the custodian of the DNA-database access to this information preferably by means of an automated message after an event which influences the deletion date of a DNA-profile.

For DNA-profiles of stains which do not match, the storage time is usually fixed or variable depending on the type of crime or the statute of limitation of the crime. For DNA-profiles of stains which do match see § 4.3.

## **4.2 Non-conviction of a person**

Suspects, arrestees and convicted persons who have successfully appealed against their conviction may have to be removed from the DNA-database if they are not convicted. If the law prescribes this, the manager of the DNA-database is dependent on information about the conviction or acquittal of these persons. Experiences in several countries have learned that this kind of information is not always provided in time by the courts or the public prosecution service. This has resulted in matches with persons who should have been removed from the DNA-database and courts have ruled that these matches are inadmissible as evidence. The ENFSI-recommendation in the previous paragraph is equally applicable to this removal condition.

## **4.3 Match of stain with person**

When a reference DNA-profile has matched a DNA-profile from a crime-scene-stain in the DNA-database and the match has been dealt with by the judicial authorities, the latter may be removed from the DNA-database because it has fulfilled its purpose. If the match occurs within the same case this is called a benchwork-match. In some countries (like The Netherlands) a crime-scene-DNA-profile can not be removed from the DNA-database until the custodian of the DNA-database has received a message that either the suspect has been convicted or that the prosecution has decided not to use the DNA-evidence. The ENFSI-recommendation in paragraph 4.1 is equally applicable to this removal condition. For various reasons countries may retain crime-scene stain profiles in their DNA-database even after they have shown a match with a person. The Nuffield Council for Bioethics even recommends this in their 2007 Bioethics report to verify possible future doubts about a match.<sup>5</sup>

## **4.4 Duplication**

Sometimes persons are sampled repeatedly for inclusion in the DNA-database. As this is a waste of resources there should be a system which can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA-database.

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<sup>5</sup> [http://www.nuffieldbioethics.org/fileLibrary/pdf/The\\_forensic\\_use\\_of\\_bioinformation\\_-\\_ethical\\_issues.pdf](http://www.nuffieldbioethics.org/fileLibrary/pdf/The_forensic_use_of_bioinformation_-_ethical_issues.pdf)

**ENFSI-recommendation 16**

There should be a system that can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA-database.

Sometimes people use a false identity and for that reason duplication of sampling is not always avoidable. Therefore a rapid biometric identification system like fingerprints should be linked to the system indicating whether a person is already present in the DNA-database.

**ENFSI-recommendation 17**

The system which can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA-database should be combined with a rapid biometric identification system like fingerprints to verify whether a person is already present in the DNA-database

The analysis of unintentional and (low level) intentional duplicates however is a useful quality control instrument. When removing a duplicate, the sample with the least chance of being removed in the future should be selected (if legally possible)

#### **4.5 Match with elimination database**

Any DNA-database should have a so-called elimination DNA-database (or databases) associated with it, that contains the DNA-profiles of persons which may have caused cross-contamination of the investigated samples. Such elimination databases should include of course anybody working on the DNA-samples in the DNA-lab but also people cleaning the labs or performing any other kind of maintenance. Also people earlier in the chain of custody such as the police and other persons present at the scene of crime should be included. In addition unidentified DNA-profiles found in negative control samples which may come from people involved in manufacturing disposables and/or chemicals should be included and shared with other ENFSI countries. When a DNA-profile in the DNA-database matches a DNA-profile from the elimination DNA-database, it should of course be deleted because it is not meant to be included. However this should not be done before the contamination incident has been analyzed to confirm the presumed cause of the match (contamination) and actions have been formulated to prevent this (and similar) accidents happening again. Laboratories supplying DNA-profiles to the DNA-database may have their own elimination databases to exclude their own employees as a possible source of contamination.

**ENFSI-recommendation 18**

Any DNA-database should have an associated elimination DNA-database (or databases). This should include laboratory staff of all categories as well as visiting maintenance personnel. Profiles from those with access to samples (e.g. police) should also be included in addition to unidentified DNA-profiles found in negative control samples which may originate in manufacturing disposables and/or chemicals. The latter category of DNA-profiles should be shared with other ENFSI-countries

#### **4.6 New information demonstrating that the DNA-profile should not have been included**

Sometimes during a police investigation new information becomes available showing that a sample, which was thought to be relevant to the crime, has another origin. If the DNA-profile of such a sample has already been included in the DNA-database, it has to be removed to prevent unauthorized DNA-profiles to be present in the DNA-database.

### **5 Matching rules**

This chapter describes the criteria which are used to label the resemblance between DNA-profiles as a match.

#### **5.1 Match/hit definition**

The words match and hit are sometimes used in different ways. The Dutch police use the word match if DNA-profiles of crime related stains are identical and the word hit if a DNA-profile of a crime related stain is identical to a DNA-profile of a reference sample. In the USA the word match is used if two DNA-profiles in the CODIS DNA-database correspond to each other and the word hit is used if a match is confirmed by a DNA-expert. In this document we use the definition of the ENFSI <sup>6</sup> which does not differentiate between a hit and a match:

*Hit/Match: A confirmed match between DNA profiles discovered by a database search at a single instant in time. It can be stain to stain or stain to person*

In this document the word match will be used.

#### **5.2 Search modes**

DNA-profiles can be compared in different ways. In CODIS these are called search-stringencies:

- High-stringency means that all alleles of the loci which are present in both DNA-profiles must be equal
- Moderate-stringency means that of two DNA-profiles the alleles of a locus with the least number of alleles must be present in the corresponding locus of the other DNA-profile. This stringency is used when comparing mixed DNA-profiles with single DNA-profiles. Because in CODIS homozygotes are designated by only one allele value, searching at moderate stringency with single DNA-profiles also detects an allele drop-out in one of both DNA-profiles (e.g. 12/13 will match 12/ or 13/)
- Low-stringency means that in each locus which is compared between two DNA-profiles at least one allele of that locus must be present in the other DNA-profile. This stringency is used to find parent-child-relationships.

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<sup>6</sup> <http://www.enfsi.org/ewg/dnawg/db/exfile.2004-09-20.3012308078/attach/ENFSI%20DNA%20WG%20Terms%20and%20Abbreviations.pdf>

In some countries a search strategy called “familial searching” is allowed. This means that apart from searching for full matches it is also allowed to search for matches with possible relatives of a crime scene associated DNA-profile. This search strategy includes the above mentioned “low stringency” search mode to find possible parent-child relationships and also searches for profiles which:

- share higher than the average number of alleles in random unrelated DNA-profiles (which may indicate a possible sibling)
- contain rare alleles (which may indicate a possible family member)

The outcome of the search is a starting point to find the real owner of the crime-scene-stain by tactical police-work. This police-work may be preceded or accompanied by likelihood ratio calculations and/or Y-chromosomal and/or mitochondrial DNA testing to decrease the number of candidates and/or their priority order.

### **5.3 Number of matching loci/match probability**

The number of matching loci depends on the number of loci of the DNA-profiles which can be compared. The lower the number of loci, the higher the match probability of the DNA-profile, the higher the chance of an adventitious match especially with large DNA-databases. For this reason DNA-profiles which are included in the DNA-database on a permanent basis should have a minimum number of loci or even better a maximum random match probability as indicated in § 3.3. For reference samples the number of loci is usually 10 or higher to increase the chance of finding a match with a (partial) DNA-profile of crime related biological material. At a national level a lower number is also possible but then the DNA-profile should have a low match probability. This is the case in Germany which uses the 7 ESS loci plus the highly discriminating locus SE33. The matching rules of the EU-Prüm implementation decision require a minimum number of 6 fully matching loci.

### **5.4 Near matches**

When an allele is incorrectly called, a typing error is made when a DNA-profile is entered manually into the DNA-database or an allele drop-in or drop out has occurred (as can happen in low level DNA-profiling), that DNA-profile will never result in a correct match when all alleles are required to match. This may also happen when one of two corresponding DNA-profiles contains a null-allele (see § 3.2). That is the reason why some countries allow one or more mismatches when comparing DNA-profiles<sup>7</sup>. Other countries such as Switzerland and the UK regularly perform quality control checks by searching for near matches, which are then checked for possible mistakes. Searching for matches with one mismatch may lead to matches with close relatives, hence the pros and cons of this strategy should be evaluated in advance. (See also chapter 9) When setting up a new DNA-database the allele calling and the DNA-database import process should be automated as much as possible to avoid this problem. Manually entering DNA-profiles into a DNA-database has been shown to be the greatest source of errors, hence this should be done by a process which detects typing errors such as the double blind method (entering

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<sup>7</sup> Also the countries who are member of the EU-Prüm-Decision allow for one mismatch when comparing their DNA-profiles with other member states

a DNA-profile twice without seeing the first one and the database software checking if both entries are equal).

#### **ENFSI-recommendation 19**

The occurrence of errors in DNA-databases as a result of human mistakes associated with data entry should be avoided as much as possible by automating the allele calling and the DNA-database import process. When DNA-profiles are entered manually into the DNA-database this should be done by a process which detects typing errors, for example by double (blind) entry of data.

### **5.5 Match validation**

There are several reasons why a DNA-database match may need to be validated:

- Confirmation of the original DNA-test
  - Some countries require a new sample to be taken from the suspect and have that new sample re-analyzed.
  - Some countries perform a second analysis on a duplicate sample previously taken from the involved person but not yet analyzed.
  - Some countries require a new sample and re-analysis because a database match may influence a jury in court (because this is an indication of earlier convictions).
  - Some countries do an independent duplicate analysis for all their reference samples, avoiding any match validation needs.
  - The requirement for a duplicate analysis may be linked to a suspect making a plea of not-guilty, and contesting the DNA evidence.
- Possibility of an adventitious match  
In this case more loci should be determined if possible to increase the evidential value of the match
- Near match (one allele does not match)  
In this case the original data of both DNA-profiles should be checked to eliminate the possibility of a typing- or an allele calling error.
- Match with a mixed DNA-profile  
A DNA-database match based on numbers of a single DNA-profile with a mixed DNA-profile is not necessarily a real match (see § 3.8). A DNA-expert should indicate whether this type of match can be a real match or not.

### **5.6 Dispositioning**

After finding a candidate match in the DNA-database this match has to be confirmed. When a match is found between two full DNA-profiles, this confirmation can be done by the DNA-database personnel or in an automated way. However, matches with partial and/or mixed profiles have to be examined and given a final disposition by a DNA-expert. The final disposition of a match can also usually be registered in the DNA-database to prevent the same match from being reported again after a new search action.

## 5.7 Match counting

One of the parameters to determine the efficiency of a DNA-database is the number of matches it generates. The counting of matches between two DNA-profiles is easy. In serial crimes committed over a period of time however different approaches are possible. Table 2 shows the number of matches that will be found when a single (unknown) individual commits a series of 7 crimes over time and leaves his DNA at all these crime scenes.

DNA-profile	Nr of matches	Description of the matches
A	-	
B	1	B -> A
C	2	C -> A&B
D	3	D -> A&B&C
E	4	E -> A&B&C&D
F	5	F -> A&B&C&D&E
G	6	G -> A&B&C&D&E&F
H	7	H -> A&B&C&D&E&F&G
Total	28	

*Table 2. Number of matches that will be found when a single (unknown) individual commits a series of 7 crimes over time and leaves his DNA at all 7 crime scenes.*

For a series of X crimes the number of matches is  $(X-1)X/2$ . For high volume crime cases this way of counting leads to match counts which are not representative as compared to the number of cases involved. That is why the ENFSI counts matches in serial crimes in a different way. The following definition is taken from the document: "ENFSI DNA Working Group Terms and Abbreviations"<sup>8</sup>

*For statistical purposes hits/matches with multiple identical profiles from the same case will be counted as one hit/match, but as separate hits/matches if they originate from different cases. In serial crimes, the total number of hits/matches is N-1 to the number of matching profiles (e.g.: a series of 8 identical stain profiles from different crimes yields 7 stain to stain hits/matches. If subsequently the DNA profile of a person matches the series, it yields 8 stain to person hits/matches. The number of stain to stain matches should then be removed from statistics.*

An expression that is also used in match counting is "the number of investigations aided". This equals the number of DNA-profiles involved in matches. In the example above dealing with a series of 8 identical DNA-profiles there are 7 matches and 8 investigations aided.

A series of matching DNA-profiles may be given a unique identification code to indicate that they are identical. In the Netherlands this is called the DNA-cluster-number and has proved to be very useful for the investigators in order to designate the series.

<sup>8</sup> [http://www.enfsi.eu/get\\_doc.php?uid=242](http://www.enfsi.eu/get_doc.php?uid=242)

## 5.8 Output/efficiency measurement

The output of a DNA-database is the number of matches it generates. During the 5<sup>th</sup> Interpol DNA users' Conference (2007, Lyon) Simon Walsh presented a formula developed in conjunction with John Buckleton which describes the output of a DNA-database:

$$H = \frac{\alpha N}{M} \times \omega C$$

Where...

*H* = number of hits/matches

*N* = number of persons on 'offender' database

*M* = active criminal population

*C* = number of crimes on 'forensic' database

*α* = quality factor (person sampling)

*ω* = quality factor (crime/exhibit sampling)

The two quality parameters in the formula determine the efficiency of a DNA-database. If *H*, *N*, *M* and *C* are known, the product of the two quality factors can be determined by transforming their formula into:  $\alpha\omega = HM/NC$ . Van der Beek has compared the efficiencies of the DNA-databases of the ENFSI member states in the Annual Report 2006 of the DNA-database of the Netherlands by dividing the number of stain-to-person-matches by the number of persons in the DNA-database (*H/N* in the formula of Walsh and Buckleton). Table 3 shows this parameter for the December 2008 version of the semi annual ENFSI DNA-database overview.

Country	Population size	Persons			Stains	Matches					Date	Stain-person matches per person
		S	CO	T		Person/Stain			Stain/Stain	Total		
						S	CO	T				
Austria (1)	8,100,000			116,258	32,032			9,973	4,485	14,458	Dec-08	0.09
Belgium	10,400,000	n/a	15,619	15,619	18,364	202	663	865	1,521	2,386	Dec-08	0.06
Bulgaria	7,900,000			17,012	1,073			369	112	481	Dec-08	0.02
Croatia	4,600,000			13,041	2,301			1,114	311	1,425	Dec-06	0.09
Cyprus	772,000											
Czech Republic (5)	10,300,000			12,639	4,740			4,537	5,587	10,124	Dec-06	0.36
Denmark	5,500,000			47,317	26,135			8,274	2,777	11,051	Jan-09	0.17
Estonia	1,500,000			20,558	7,159			2,396	767	3,163	Dec-07	0.12
Finland (1)	5,300,000			76,233	10,098			10,049	1,439	11,488	Dec-08	0.13
France (6)	59,300,000	618,618	238,293	856,911	41,920	12,309	4,318	16,627	2,993	19,620	Dec-08	0.02
Georgia	4,700,000											
Germany	82,400,000			611,867	145,122			60,118	18,015	78,133	Dec-08	0.10
Greece	10,600,000											
Hungary	10,200,000			66,111	1,158			65	88	153	Dec-08	0.00
Ireland	4,200,000											
Italy	58,000,000											
Latvia	2,400,000											
Lithuania	3,369,000			25,843	3,135					543	Jul-08	0.00
Luxembourg	500,000	205	13	218	226	3	3	6	18	24	May-08	0.03
Malta	400,000											
Netherlands	16,100,000	12,606	60,275	72,881	38,391			17,461	4,554	22,015	Dec-08	0.24
Northern Ireland	1,685,000											
Norway	4,500,000	1,275	11,745	13,020	4,602			2,066	705	2,771	Dec-08	0.16
Poland	38,200,000			20,037	781			27	27	54	Dec-08	0.00
Portugal (3)	10,300,000											
Romania	22,000,000		2,452	2,452	41		1	1		2	Feb-08	0.00
Russia (3)	143,800,000											
Scotland	5,062,000	130,809	94,725	236,202	9,987			18,410	2,046	20,456	Jul-08	0.08
Slovakia	5,500,000			12,736	3,767			834	517	1,351	Dec-08	0.07
Slovenia	2,000,000											
Spain (4)	44,800,000			30,723	32,213			5,838	26,158	31,996	Dec-08	0.19
Sweden	9,000,000	24,206	34,230	58,436	18,433	15,934	3,520	19,454	13,394	32,848	Dec-08	0.33
Switzerland (2)	7,360,000			104,625	21,278			19,365	4,787	24,152	Dec-09	0.19
Turkey	66,800,000											
UK (England & Wales)	53,700,000			4,458,340	329,482			873,613	48,052	921,664	Dec-08	0.20
Ukraine	47,600,000			1,723	176					22	Jan-07	0.00
<b>Total</b>	<b>768,848,000</b>			<b>6,890,802</b>	<b>750,614</b>			<b>1,071,462</b>	<b>138,353</b>	<b>1,210,380</b>		

Table 3. Semi annual ENFSI DNA-database overview.

The last column shows the ratio between the number of stain-to-person-matches and the number of persons in the DNA-database. This ratio can be followed over time to monitor the efficiency of the DNA-database. It can also be applied to subgroups of persons in the DNA-database. In the Netherlands, for example, this ratio was 0.52 for suspects (in 2005) and 0.06 for convicted persons (in 2006).

The number of stain-to-stain-matches can either be expressed as the number (or percentage) of stains involved in matches (investigations aided) or as the number (or percentage) of profiles giving a match at inclusion, which is lower because the first profile of a cluster does not result in a match (see table 2 in § 5.7)

As a national DNA-database regularly is subject to attention from the public, politicians and the media, a DNA-database manager should consider establishing performance parameters and making these publicly available.

**ENFSI-recommendation 22**

As a national DNA-database regularly is subject to attention from the public, politicians and the media, a DNA-database manager should consider establishing performance parameters and making these publicly available.

## 6 Likelihood of finding adventitious matches

As DNA-databases become larger the chance of finding adventitious matches also increases, especially with partial and mixed profiles and DNA-profiles of relatives which have higher random match probabilities. If a crime stain DNA-profile has a random match probability of 1 in 1 million and a DNA-database contains 3 million DNA-profiles, a mean of three matches can be expected and none of them may be the actual originator of the crime stain DNA-profile. Therefore every DNA-database manager should be able to determine the chance of finding adventitious matches in his/her DNA-database. Table 4 may help in this respect. In this table the expected number of adventitious matches is given when a DNA-database of a given size is searched with a DNA-profile with a given match probability.

		Size of the DNA-database			
		10,000	100,000	1,000,000	10,000,000
Random Match Probability (1:X)	10,000	1	10	100	1,000
	100,000	0.1	1	10	100
	1,000,000	0.01	0.1	1	10
	10,000,000	0.001	0.01	0.1	1
	100,000,000	0.0001	0.001	0.01	0.1
	1,000,000,000	0.00001	0.0001	0.001	0.01
	10,000,000,000	0.000001	0.00001	0.0001	0.001

Table 4: Expected number of adventitious matches when searching a DNA-database of a given size with a DNA-profile with a given random match probability

The expected numbers of adventitious matches in table 4 are the expected numbers for one search with a DNA-profile with a given random match probability in a DNA-database with a given size. On an annual basis the number of searches usually is much higher than one. Hence on an annual basis the expected number of adventitious matches is the expected number of adventitious matches of one search times the annual number of those searches. So a DNA-database to which many crime scene DNA-profiles are compared can expect more adventitious matches on an annual basis than a DNA-database of similar size to which much less crime scene DNA-profiles are compared per year. An estimation of the annual expected number of adventitious matches can be made by splitting up the crime related DNA-profiles in match probability classes and estimating how many of each class are compared to the reference samples in the DNA-database

Table 5 gives a theoretical example of a DNA-database which contains 4 million reference DNA-profiles to which 70.000 crime related DNA-profiles of different random match probabilities (RMP) are compared on an annual basis and calculates the expected number of adventitious matches from those figures.

DNA-database size	RMP crime related stain	Number of searches	Exp. Nr Adv. Matches
4.000.000	1 : 10.000.000.000	50.000	20
	1 : 1.000.000.000	10.000	40
	1 : 100.000.000	5000	200
	1 : 10.000.000	3000	1200
	1 : 1.000.000	2000	8000

*Table 5: Theoretical example of a DNA-database which contains 4 million reference DNA-profiles to which 70.000 crime related DNA-profiles of different match probabilities are compared*

Another factor which influences the expected number of adventitious matches is the presence of relatives in the DNA-database. This results from the fact that the match probabilities between relatives are higher than the random match probability. Table 6 lists the approximate match probabilities between different kinds of relatives as compared to a random match probability of 1 in 1 billion.

<b>Relationship</b>	<b>Match Probability</b>
No relationship	1 in 1 billion (random match probability)
First cousin	1 in 100 million
Half-sib or uncle/nephew	1 in 10 million
Parent or child	1 in 1 million
Full-sib	1 in 10.000

*Table 6: Approximate match probabilities between different kinds of relatives as compared to a random match probability of 1 in 1 billion<sup>9</sup>*

<sup>9</sup> L.A. Foreman, I.W. Evett, Statistical Analysis to Support Forensic Interpretation of a New Ten-Locus STR Profiling System. International Journal of Legal Medicine 114 (2001) 147-155

Identical twins of course have the same DNA-profile.

The exact expected number of adventitious matches due to the presence of relatives in a DNA-database is impossible to calculate without knowing the numbers and types of relatives present.

The impact of the presence of relatives in a DNA-database on the expected number of adventitious matches seems limited however as shown in the next example: If 50.000 full SGM+ DNA-profiles from crime related stains are searched against a DNA-database of 4.000.000 reference profiles and 10% of the crime related stain donors has a brother in the DNA-database, 5000 DNA-profiles will have a match probability of 1:10.000 instead of 1:1.000.000.000. The extra expected number of adventitious matches caused by the DNA-profiles of these 5000 persons who have a brother in the DNA-database is  $5000 \times 1/10.000 = 0,5$ . This is only a small extra number as compared to the 20 adventitious matches which are expected anyway by searching a DNA-database of 4.000.000 reference profiles with 50.000 DNA-profiles from crime related stains of persons which are unrelated. The effect of relatives on the expected number of adventitious matches will increase over time as more persons related to each other in some way will be included in the DNA-database. At this moment we are only dealing with one generation of relatives but in 10 years also a next generation of relatives may be present

Because the risk of adventitious DNA-database matches can not be neglected, a warning should be included indicating the factors that increase the possibility of finding an adventitious match (size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members) when reporting a DNA-database match

#### **ENFSI-recommendation 21**

DNA-database managers should be aware of the possibility of adventitious matches and be able to calculate their expected numbers for the matches they report. When reporting a DNA-database match, a warning should be included indicating the factors that increase the possibility of finding an adventitious match (size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members)

To compare theory based numbers of adventitious matches with actually occurring ones, a DNA-database manager should record adventitious matches and the conditions under which they were found (size of the database, number of searches, etc) for future analysis.

## **7 Reporting results**

Matches in DNA-databases often are so-called “cold hits” meaning that there was no prior evidence suggesting that the match would occur. And also in cases where there is prior evidence, this usually is not known to the DNA-database-manager. This means that reporting should be done in such a way that it does not create misconception in the mind of the person receiving the match report.

Apart from reporting a match between two DNA-profiles (which may contain different loci) as a fact, the match probability of the corresponding loci/alleles should be reported to give the person receiving the report an idea about the evidential value of the match. It should be stated however that the match should only be used as evidence if other information supports the involvement of the named individual in the crime. The evidential value of matches with mixed profiles may be reported as the likelihood ratio of two alternative propositions e.g. 1) the mixture is composed of the suspect profile and a random profile and 2) the mixture is composed of two random profiles.

Meester and Sjerps<sup>10</sup> have suggested including a table in the match report which describes the relation between the prior probability and the posterior probability given the match probability of the match to help jurors to determine the evidential value of the match.

The report should also contain a warning about the possibility of adventitious matches as mentioned in recommendation 21.

**ENFSI-recommendation 22**

A DNA-database match report of a crime scene related DNA-profile with a person should be informative and apart from the usual indication of the evidential value of the match (RMP) it should also contain a warning indicating the possibility of finding adventitious matches (as mentioned in recommendation 21) and its implication that the match should be considered together with other information.

## 8 DNA-database software<sup>11</sup>

Software programs which have been designed for at least the storage and the comparison of DNA-profiles are referred to as DNA-database software. Some programs also can do other things. DNA-database software can either be internally developed by a country to meet its own specific needs or it can be obtained from a producer which provides it without costs or offers it on a commercial basis. Examples of DNA-database programs which can be obtained without costs are:

- CODIS which has been developed by the FBI for the USA but which is also available for non-USA-governmental organizations. A private company SAIC which has developed the program, provides training courses and runs a well-organized and skillful helpdesk. CODIS has three levels of storing and comparing DNA-profiles: local, state and national which can be used to combine data if there is more than one DNA-database in a country e.g. Spain.
- STR-lab, a program developed in South-Africa which can be downloaded from: <http://strlab.co.za/>

Programs which are or have been commercially available are:

<sup>10</sup> Meester, R. and Sjerps, M. (2004) Law, Probability and Risk, 3, 51-62.

<sup>11</sup> The mentioning of trade names does not mean that ENFSI recommends these programs. ENFSI's aim is just to give an overview of what is available on the market.

- FSS-iD™ of the Forensic Science Service in the UK
- Dimensions of the Austrian company Ysselbach Security Systems
- eQMS::DNA of the Hungarian company Pardus (www.Pardus.hr)
- fDMS-STRdb distributed by the Czech Republic company Forensic DNA Service (<http://dna.com.cz/files/file/fdms-strdb.pdf>)

DNA-database programs should comply with national personal data-protection guidelines especially those dealing with data-quality, -integrity and -security.

Table 7 shows which DNA-database programs are used by the different ENFSI member countries

<b>Country</b>	<b>DNA-database program</b>
Austria	Self-developed program + Interpol
Belgium	CODIS
Bulgaria	Self-developed program
Croatia	CODIS + Interpol
Cyprus	Self-developed program
Czech Republic	CODIS
Denmark	CODIS + Self-developed program
Estonia	CODIS
Finland	CODIS
France	CODIS + Self-developed program
Germany	Self-developed program
Georgia	No DNA-database yet
Greece	CODIS
Hungary	CODIS
Ireland	No DNA-database yet
Italy	CODIS
Latvia	CODIS
Lithuania	Self-developed program
Luxembourg	Self-developed program
Malta	No DNA-database yet
Netherlands	CODIS
Northern Ireland	Self-developed program
Norway	CODIS
Poland	CODIS
Portugal	CODIS
Romania	Dimensions
Russia	No DNA-database yet
Scotland	Self-developed program
Slovakia	CODIS
Slovenia	Self-developed program
Spain	CODIS
Sweden	CODIS
Switzerland	CODIS
Turkey	No DNA-database yet
Ukraine	?
UK (England, Wales, Scotland, North Ireland) <sup>12</sup>	Self-developed program
Interpol	Self-developed program
Prüm-Treaty-countries (exchange-database)	Self-developed program

*Table 7: DNA-database programs used by the different ENFSI member countries and two international bodies.*

<sup>12</sup> Northern Ireland and Scotland have their own DNA-databases, even though their profiles are also loaded to the UK National DNA Database

## 9 Data integrity control measures

For forensic reasons but also required by personal data protection legislation, DNA-profiles and their associated information should be entered and stored correctly. That is why manual entry of DNA-profiles should be avoided. If this is not possible DNA-profiles should be entered using the double blind method.<sup>13</sup> A reliable professional database program should be used with proper logging of all actions and secure ways of importing the DNA-profiles as indicated in § 4.3. Access to the DNA-database should be limited by physical and organizational methods to those persons who need to have access. Regular back-ups should be made, stored in a safe place and put back at regular intervals to simulate recovery from a disaster. If the DNA-profiles and/or DNA-profile associated information are also registered in another system like a LIMS or a judicial or police system, the contents of these systems should regularly be compared to check whether the systems are still properly synchronized. Official recognition of compliance with personal data protection legislation may be sought by submitting the organization and its working processes to an independent external audit.

### ENFSI-recommendation 23

- DNA-profiles should be entered into a database in a way that guarantees their correct import.
- Access to the DNA-database should be limited to those persons who need to have access, by physical and organizational measures.
- Regular back-ups should be made, stored in a safe place, and put back at regular intervals to simulate recovery from a disaster.
- When DNA-profiles and their associated information are present in different systems, these systems should be regularly compared to check whether they are still properly synchronized.

The abovementioned recommendations are to prevent errors as much as possible. It has been shown however that despite of all these measures DNA-profiles may occasionally contain errors as a result of:

- Allele drop-ins or drop-outs
- Allele calling errors of long DNA-fragments
- Primer mutation differences between commercial kits
- Mixture interpretation errors by DNA-analysts

When searching at moderate stringency (see §5.2) DNA-profiles containing allele drop-outs and primer mutation differences will be found as a match between a heterozygote and an apparent homozygote but DNA-profiles containing other types of errors will not match their correct counterparts. To detect these false negative matches (e.g. matches which should be found but are not found because one of the DNA-profiles contains an error) regular full DNA-database searches allowing one or more mismatches should be performed, as indicated and recommended in §5.2. The software which is used by countries exchanging DNA-profiles under the terms of the EU Prüm Decision also allows for one

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<sup>13</sup> The double blind method is also used for changing passwords. A new password is entered twice while only asterisks are shown. The computer compares the two blind entries and only accepts it if both entries are equal.

mismatch. When a match between two DNA-profiles contains a mismatch in one of the loci, the original data of both DNA-profiles should be checked to see if one of the DNA-profiles contains an error.

**ENFSI-recommendation 24**

- To detect false negative matches (e.g. matches which should be found but are not found because one of the DNA-profiles contains an error) regular full DNA-database searches allowing one or more mismatches should be performed.
- When a match between two DNA-profiles contains a mismatch in one of the loci, the original data of both DNA-profiles should be checked to see if one of the DNA-profiles contains an error.

## **10 Inclusion of case information and personal data**

In some countries the DNA-database program also contains case and personal information but in other countries this is strictly separated for legislative or other reasons. The DNA-database program CODIS has only been developed to store and compare DNA-profiles so CODIS-using countries always need a second system to store other DNA-profile associated information. As indicated in the previous paragraph regular comparisons of the systems are then required to check whether they are still properly synchronized and if the DNA-profiles are correctly linked to their associated personal and/or case information.

Whether or not the DNA-profiles are kept separated from personal data, the identity of persons should be properly verified when they are sampled to avoid matches with wrong or non-existing persons.

## **11 Interaction with other databases**

It can be very useful for investigative reasons to combine DNA-information with other technical or tactical forensic information. If for example a series of crimes has been linked by the presence of a DNA-profile of an unknown person and on one of the crime scenes a fingerprint matching a known person has also been found, the combined information may solve the whole series of cases. Countries like the United Kingdom and the Netherlands are working on systems to combine the contents of different forensic databases and to visualize the links between different cases and different persons which are the result of that combination. Figure 2 shows an example of the visualization of such cluster of crimes and persons derived from DNA and fingerprint information.

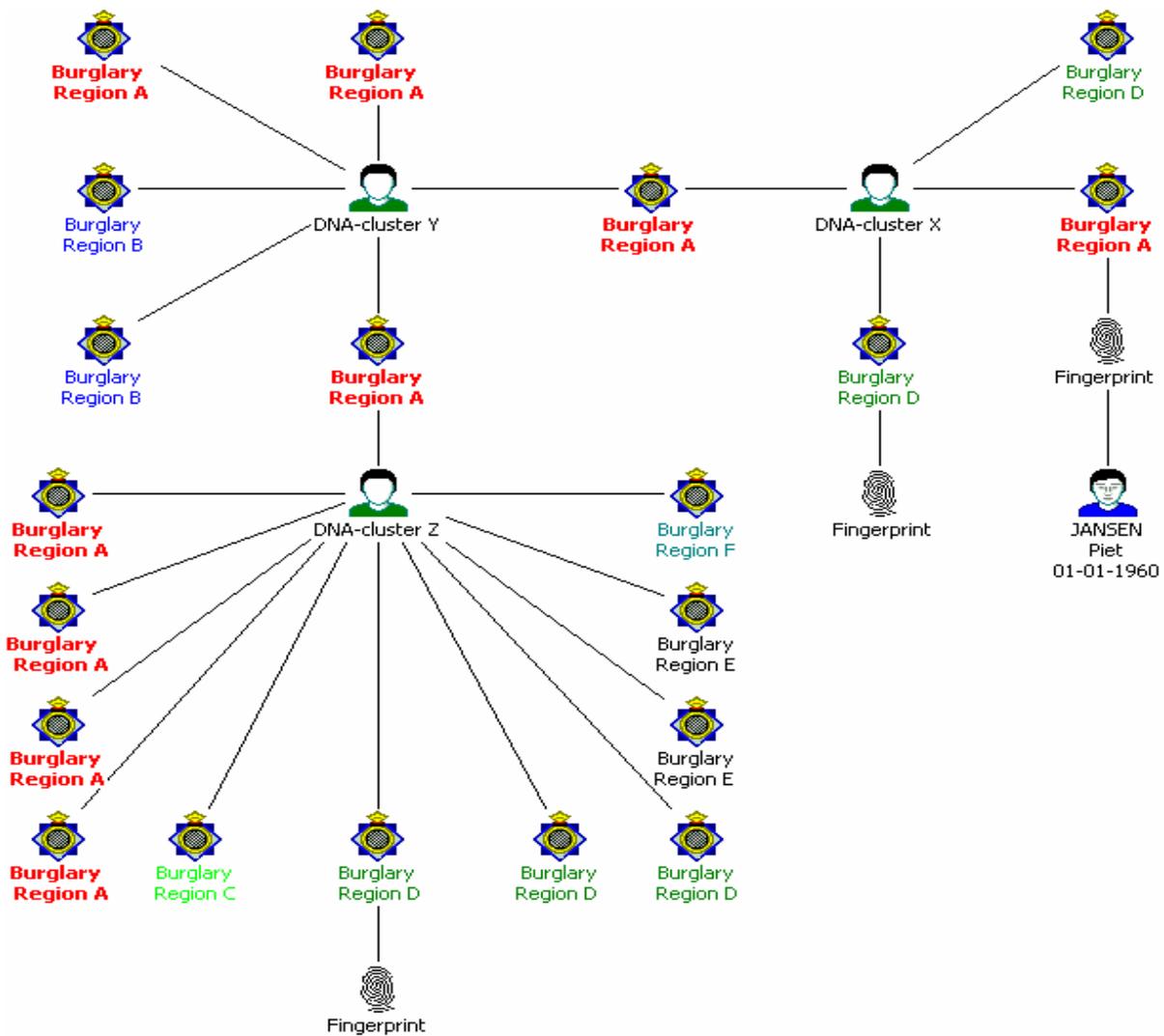


Figure 2: Three DNA-clusters (X, Y, Z) linked by 2 crime scenes where DNA-profiles from 2 clusters were found (X+Y and Y+Z) combined with two unidentified and one identified fingerprint.

#### ENFSI-recommendation 25

Information from a National DNA-database should be combined with other types of evidence to increase the number of crimes for which a lead can be identified.

## 12 Automation of working processes

Automation of DNA-database working processes can take place at different levels:

- Import of DNA-profiles as already discussed in § 4.3
- Comparison of DNA-profiles using saved sets of matching rules
- Comparison of DNA-profiles at scheduled points in time (e.g. overnight)
- Reporting unambiguous results

- Sending out the unambiguous results

As automated processes reduce the possibility of human errors, they should be introduced for those processes that are straight forward like the production of DNA-profiles from reference samples

**ENFSI-recommendation 26**

As automated processes reduce the possibility of human errors, they should be introduced for those processes that are straight forward.

As already stated in § 2.7 candidate matches with mixed profiles should always be checked by a DNA-specialist to determine whether the numerical match could be a real match. This is also the reason why mixed DNA-profiles are not included in the automated DNA-comparisons between countries operating under the terms of the EU-Prüm-decision.

### 13 Storage of cell material

The cell material of crime scene stains from which a DNA-profile has been generated usually is stored. With regards to the storage of cell material of reference samples however countries have different policies. Some countries allow the storage of the reference samples for later reuse if this becomes technically or legally necessary and in other countries the reference samples have to be destroyed as soon as the DNA-profile has been generated and included in the DNA-database. In two examples it will be shown that from a forensic point of view it is better to store the cell material.

Example 1

In the recent past several improved DNA-typing technologies have been developed. Multiplex kits with more loci to get a higher evidential value, as well as mini STR-kits and SNP-kits to obtain DNA-profiles from degraded DNA are good examples. It has become possible to re-examine stains from (c)old cases which could not be examined in the past. But if the stain has been retyped with a new technology, the reference sample must also be retyped to enable comparison between the two. If the reference sample has been destroyed, the police or the judiciary have to obtain a new reference sample from the suspect which may not always be possible.

Example 2

A Prüm-treaty-member-country sends a SGM+ DNA-profile of a crime scene stain to another Prüm-treaty-member-country. A match with a reference DNA-profile is reported but it is only a 7 locus match due to the fact that the other country uses a different kit. To exclude the possibility of an adventitious match the SGM+ country then asks the other country to upgrade its reference DNA-profile. If the reference sample has been destroyed this upgrade is not possible without obtaining a new reference sample from the person involved which may not always be possible.

The ENFSI DNA-working group realizes that the storage of cell material from reference samples is a politically very delicate subject. Although the European personal data-protection directive clearly states that personal data (which includes DNA-profiles and the cell material from which the DNA-profiles were derived) can only be used for the purpose for which they were obtained, there are

people who fear that they could be misused in the future and hence choose for the “better safe than sorry” principle.

**ENFSI-recommendation 27**

From a forensic point of view the cell material of reference samples should be stored as long as their corresponding DNA-profiles.

## 14 Legislative matters

As the compulsory taking of a DNA-sample is a breach of someone’s privacy and bodily integrity, article 8 of the European Convention on Human Rights demands a justification and legislation. For arrestees and suspects the justification can be found in the fact that DNA-testing can help solving the case by either finding a match (resulting in incriminating evidence) or no match (resulting in exclusion of the suspect) with a DNA-profile from a crime scene which is thought to be left behind by the culprit of the crime. This means however that crime scene DNA must be present for this type of justification. The inclusion of someone’s DNA in a DNA-database is justified by the fact that it can help solving old and future crimes committed by the same person and that it may prevent new crimes because the person involved may fear to be detected when he/she commits new crimes. The continued inclusion in a DNA-database of persons who are not prosecuted or convicted has been condemned by the European Court of Human Rights<sup>14</sup>

Every EU-country is supposed to have data protection legislation derived from the European Data Protection Directive 95/46. Because DNA-profiles and the cell-material from which they are derived are also regarded as personal data, they fall under the umbrella of this legislation unless the data protection legislation is overruled by specific DNA-legislation containing other provisions. (Lex Specialis precludes Lex Generalis). Some examples are given below to illustrate why it is useful to have specific DNA-legislation in addition to data protection legislation:

- According to the data protection legislation personal data must not be stored longer than necessary for the purpose for which they were collected. It is practically impossible to determine this necessity for all the DNA-profiles in a DNA-database at regular intervals. So the DNA-legislation should say something about storage times (see also: § 3.1)
- According to the data protection legislation persons have certain rights with regard to their own data (access/modification/removal). For investigative reasons this is usually not desirable. So the DNA-legislation should say something about who has access to information present in and generated by the DNA-database.
- In some countries the data protection legislation states that genetic information can only be used in relation to the person from whom this information is derived. If such a country wants to allow familial searching in the DNA-database there should be rules for this in the DNA-legislation.

DNA-profiles are not only very specific for an individual but they also contain information about relatives of that individual. That means that when people

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<sup>14</sup> <http://www.bailii.org/eu/cases/ECHR/2008/1581.html>

voluntarily give their DNA-profile (e.g. in a mass screen) they should be informed that this may possibly also incriminate a relative. In this way a person can decide whether he/she will make use of his/her right not to testify against relatives.

Most countries also allow the inclusion of DNA-profiles of minors in their DNA-database. The legitimacy of this is being questioned in some countries amongst others by referring to the international convention on the rights of the child. Several appeal court cases are ongoing to develop jurisprudence on this. The Supreme Court of the Netherlands has ruled that there are no reasons to differentiate between minors and adults.

## 15 Financing

In most countries the costs of establishing and maintaining a National DNA-database are financed by a dedicated annual budget of the Ministry of Justice or the Ministry of the Interior. In England however (parts of) the budget are managed by the Police which pays for the production and the storage of the DNA-profiles.

## 16 Personnel requirements

It goes without saying that persons working on a DNA-database should be properly trained to use the DNA-database software. If the program is self-developed this will be an in house training. If the DNA-database software is commercially obtained the company selling the software will usually also offer training in the use of the software. As stated already in § 8 CODIS has been developed by a company called SAIC for the FBI and this company also provides 1-week-training courses free of charge.

Apart from being properly trained DNA-database personnel must at least have the following personal skills:

- Being able to work very conscientiously
- Being able to keep confidential information confidential
- Being able to accept to be checked by colleagues
- Being able to report own mistakes to enable further process improvement

Apart from the abovementioned requirements a “proof of good conduct” may be required or even a positive outcome of an investigation by the police or the secret service into somebody’s reliability.

## 17 Governance

When a DNA-database is established in a country its custody is either assigned to an existing organization or to a newly established organization. In some countries (like the UK) a special supervisory board has been established with representatives of different stake-holders. Also in the UK a special ethics group

has been established<sup>15</sup> to provide independent advice on the ethical aspects of DNA-database management. If there is no dedicated supervisory board, the data-protection authority of a country usually has the power to audit the organization managing the DNA-database to check its compliance with the data-protection legislation of that country.

## 18 External Communication

Because DNA-databases usually are publicly funded, politicians, the public and the media have a right to know how the DNA-database is managed and what results are obtained.

### 18.1 Annual report

A good way to do so is to produce an official annual report. Such a report can either be part of an annual report of an organization which is responsible for the management of the National DNA-database or it can be a separate annual report only dedicated to the DNA-database. In Europe the United Kingdom and the Netherlands have already produced such dedicated annual reports. Outside Europe The Royal Canadian Mounted Police also produces an annual report about their DNA-database. Below are the locations where the most recent issues of these annual reports can be downloaded:

- United Kingdom: <http://www.npia.police.uk/en/11403.htm>
- Netherlands: <http://www.dnasporen.nl/docs/literatuur/dna-jaarverslag%202008%20definitief%20lr.pdf>
- Canada: [http://www.nddb-bndg.org/an\\_report\\_e.htm](http://www.nddb-bndg.org/an_report_e.htm)

### 18.2 Internet site

Whereas annual reports are milestones in a written form, websites provide a continuous way of providing information to those interested. Below is a list of internet sites devoted to DNA-databases or containing information about DNA-databases:

#### Europe

- United Kingdom: <http://www.npia.police.uk/en/8934.htm>
- Germany: <http://bka.de/profil/faq/dna01.html>
- Ireland: [http://www.lawreform.ie/files/Consultation%20Paper%20\(1\).pdf](http://www.lawreform.ie/files/Consultation%20Paper%20(1).pdf)  
(comprehensive thoughts on setting up a DNA-database in Ireland)
- Netherlands: [http://www.dnasporen.nl/content/thema\\_detail.asp?id=9](http://www.dnasporen.nl/content/thema_detail.asp?id=9)

#### Rest of the world

- USA (CODIS) <http://www.fbi.gov/hq/lab/html/codis1.htm>
- USA (Florida): [http://www.fdle.state.fl.us/Content/getdoc/6835b26c-ae3f-49c5-845e-0c697bb86001/DNA\\_Investigative.aspx](http://www.fdle.state.fl.us/Content/getdoc/6835b26c-ae3f-49c5-845e-0c697bb86001/DNA_Investigative.aspx)
- USA (NewYork): [http://www.troopers.state.ny.us/Forensic\\_Science/DNA/](http://www.troopers.state.ny.us/Forensic_Science/DNA/)
- USA (Legislation): <http://www.dnaresource.com/>
- Canada: [http://www.nddb-bndg.org/main\\_e.htm](http://www.nddb-bndg.org/main_e.htm)

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<sup>15</sup> See: <http://police.homeoffice.gov.uk/operational-policing/forensic-science-regulator/ndnad-ethics-group/>

- Australia:  
[http://www.crimtrac.gov.au/systems\\_projects/NationalCriminalInvestigationDNADatabaseNCIDD.html](http://www.crimtrac.gov.au/systems_projects/NationalCriminalInvestigationDNADatabaseNCIDD.html)
- New Zealand:  
<http://www.esr.cri.nz/competencies/forensicscience/dna/Pages/DNAdatabank.aspx>
- Hong Kong: [http://www.govtlab.gov.hk/english/abt\\_fsd\\_dds.htm](http://www.govtlab.gov.hk/english/abt_fsd_dds.htm)
- South Africa: <http://strlab.co.za/>

#### **ENFSI-recommendation 28**

Because DNA-databases have a very important but also very delicate role in society, the custodian of a DNA-database should develop tools to make objective information about the DNA-database available to politicians, the public and the media.

## **19 International overviews**

Several documents have already been published which contain overviews of different aspects of DNA-database legislation and DNA-database management:

- The EU has sent out a questionnaire about these subjects and has distributed the outcome in 2005. This document can be obtained by sending a request to Kees van der Beek.
- The ENFSI has produced and regularly updates a document on DNA-legislation in its member state countries (see: <http://www.enfsi.org/ewg/dnawg/db/UpdatedENFSILegislationFinalReport>)

## **20 International comparison of DNA-profiles**

As crimes committed in one country may be committed by a person from another country it is very useful to have means for international comparisons of DNA-profiles. In § 2.2 it was already described that a European Standard Set of Loci has been agreed upon to enable such comparisons. In addition to common loci, DNA-profile exchanging countries should of course also use the same quality standards for the production of their DNA-profiles as already described in § 3.5.

There are different channels through which international comparison of DNA-profiles can take place:

- Individual legal assistance requests on paper  
Until recently this was the most commonly used channel. Depending on the legal embedding of the DNA-legislation in a country either police channels or judicial channels are used for this way of exchanging DNA-information. Before the advent of XML to communicate DNA profiles, Interpol developed a special form to standardize and facilitate this way of exchanging DNA-information (<http://www.interpol.int/Public/Forensic/dna/form/form.pdf>). A great disadvantage of this way of information exchange is that it is very time consuming.

- Interpol DNA-database and DNA-gateway  
Interpol has a central DNA database in Lyon in which DNA profiles and their sample codes can be included by its member states for comparison. The database is an autonomous database and does not keep any nominal data linking a DNA profile to any individual. Member states retain the ownership of their profile data and control its submission, access by other countries and destruction in accordance with their national laws. As soon as a match is found a message is sent to the countries contributing to the match. This message contains the basic case information that was provided and can optionally provide the sample codes. Member countries then decide if they wish to pursue this forensic intelligence link. A central DNA-database is most effective when all participating countries submit all their crime-scene DNA-profiles and all their reference sample DNA-profiles. Some countries have already done so and others have indicated that they will do so. The DNA Gateway provides for the transfer of DNA-profiles between two or more countries and for the management of a country's own DNA-profiles in the central DNA-database. Access to the DNA-gateway is provided directly to a country via the Interpol National Central Bureau's (NCB's) using Interpol's secure communications system I-24/7. For more information about the DNA-gateway of Interpol see:  
<http://www.interpol.int/Public/ICPO/FactSheets/FS01.pdf>.

Interpol's secure communications system I-24/7 has recently also been successfully tested for the exchange of DNA-profile comparison requests between the G8-countries (USA, Russia, Japan, Canada, UK, France, Germany and Italy). A special G8-request form has been developed which, when received by an Interpol National Central Bureau (NCB) of a G8-country will be forwarded directly to a person associated with the national DNA-database who will carry out the comparison and will return the result back to the Interpol NCB which will send the result to the requesting country.

(<http://www.interpol.int/Public/ICPO/PressReleases/PR2007/PR200729.asp>)

- The EU-Prüm-Decision (derived from the Treaty of Prüm)  
The EU-Prüm-Decision deals with the exchange of judicial and police information between the EU-member states and some associated countries (Norway, Switzerland, Liechtenstein and Iceland). With regards to DNA countries are allowed to search in each other's DNA-database. To enable this each country creates a copy of its DNA-database with a standardized table structure which can be accessed by common data-exchange and DNA-comparison software which is present in each country. The DNA data exchange and matching system used by the EU member states is similar to DNA data exchange and matching system of the Interpol DNA Gateway. When this ENFSI-document was approved the following countries were already exchanging DNA-profiles on a day-to-day-basis under the terms of the EU-Prüm-Decision: Austria, Germany, Spain, Luxembourg, Slovenia and The Netherlands.

The EU-Prüm-decision and the EU-Prüm-implementation-decision can be found at the following internet locations:

<http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:L:2008:210:0001:0011:EN:PDF>  
<http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:L:2008:210:0012:0072:EN:PDF>

Chapter 2 of the Annex to the EU-Prüm-implementation-decision contains the DNA-inclusion, -matching, and -reporting rules. Like the Interpol DNA-database, the Prüm DNA-profile exchange system is a hit-no-hit-system meaning that only DNA-profiles are compared. After finding a match, countries can obtain the personal and/or case information associated with the DNA-profile via existing police or judicial channels.

A national DNA-database always contains DNA-profiles from national crime-related stains. However as already mentioned in § 3.1, if the national law of both countries allows it, crime-related stains from other countries may also be included if an international legal request for comparison from another country has not resulted in a match. By including the DNA-profile from the other country, there is no need for a regular repeat of the often lengthy legal request. This is of course not necessary for countries which can already search each other's DNA-database under the terms of the EU-Prüm-Decision because they can repeat the request as frequently as they wish.

## **Annex 1: Summary of ENFSI-recommendations**

- 1) Every EU/ENFSI-country should establish a forensic DNA-database and specific legislation for its implementation and management.
- 2) The type of crime-related stain DNA-profiles which can be included in a DNA-database should not be restricted.
- 3) To increase the chance of DNA-profiles of stains to match a person, the number of persons in a DNA-database who are likely to cause matches with those stains should be as high as legally (and financially) possible
- 4) Managers of national DNA-databases should establish (together with other stakeholders) criteria for the inclusion of partial DNA-profiles to obtain an acceptable balance between the minimum allowable level of evidential value (maximum random match probability) of a DNA-profile and maximum number of adventitious matches a partial DNA-profile is expected to generate
- 5) DNA-profiles produced by older commercial kits should be upgraded (if possible) after a match in the National DNA-database to increase the evidential value of the match and also to fulfill the criteria for international comparison if a country wants to include DNA-profiles produced by older commercial kits in international search actions.
- 6) The number of loci in reference samples should be the maximum of the number of loci present in the kit(s) used for the production of the DNA-profiles of the reference samples to enhance the chance of finding relevant matches with partial DNA-profiles.
- 7) Labs producing DNA-profiles for a DNA-database should, as a minimum, be ISO-17025 (and/or nationally equivalent) accredited and should participate in challenging proficiency tests (for Europe: e.g. GEDNAP).
- 8) When DNA-profiles produced from low levels of DNA are included in a DNA-database they should be recognizable and a dedicated (near) match strategy should be used for them
- 9) When a new allele is observed in a DNA-profile, its presence should be confirmed by repeated DNA-isolation, PCR, Capillary Electrophoresis and allele calling of the DNA-profile. Only new alleles of which the size can be accurately determined using the internal DNA-size-standard, should be included in the DNA-database.
- 10) Alleles from loci with chromosomal anomalies should not be included in a DNA-database as they may be caused by somatic mutations which may only occur in certain tissues/body fluids.
- 11) Wild cards that do not represent a designated allele should not be part of the minimum number of loci/alleles required by the Prüm-matching rules.
- 12) The guidelines in the document of the ISFG-working group on the analysis of mixed profiles should be used for the analysis of mixed profiles
- 13) A numerical match between a reference sample and a mixed profile must always be checked against the plot of the mixed profile.
- 14) Mixed profiles of more than 2 persons should not systematically be included in a DNA-database because they generally will produce many adventitious matches.
- 15) If the removal of a DNA-profile from the DNA-database is dependent on external information, a process should be in place to give the custodian of the DNA-database access to this information preferably by means of an automated message after an event which influences the deletion date of a DNA-profile.
- 16) There should be a system that can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA-database.

- 17) The system which can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA-database should be combined with a rapid biometric identification system like fingerprints to verify whether a person is already present in the DNA-database.
- 18) Any DNA-database should have an associated elimination DNA-database (or databases). This should include laboratory staff of all categories as well as visiting maintenance personnel. Profiles from those with access to samples (e.g. police) should also be included in addition to unidentified DNA-profiles found in negative control samples which may originate in manufacturing disposables and/or chemicals. The latter category of DNA-profiles should be shared with other ENFSI-countries
- 19) The occurrence of errors in DNA-profiles as a result of human mistakes associated with data entry should be avoided as much as possible by automating the allele calling and the DNA-database import process. When DNA-profiles are entered manually into the DNA-database this should be done by a process which detects typing errors, for example by double (blind) entry of data.
- 20) As a national DNA-database regularly is subject to attention from the public, politicians and the media, a DNA-database manager should consider establishing performance parameters and making these publicly available.
- 21) DNA-database managers should be aware of the possibility of adventitious matches and be able to calculate their expected numbers for the matches they report. When reporting a DNA-database match, a warning should be included indicating the factors that increase the possibility of finding an adventitious match (size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members)
- 22) A DNA-database match report of a crime scene related DNA-profile with a person should be informative and apart from the usual indication of the evidential value of the match (RMP) it should also contain a warning indicating the possibility of finding adventitious matches (as mentioned in recommendation 21) and its implication that the match should be considered together with other information.
- 23) DNA-profiles should be entered into a database in a way that guarantees their correct import.  
Access to the DNA-database should be limited to those persons who need to have access, by physical and organizational measures.  
Regular back-ups should be made, stored in a safe place, and put back at regular intervals to simulate recovery from a disaster.  
When DNA-profiles and their associated information are present in different systems, these systems should be regularly compared to check whether they are still properly synchronized.
- 24) To detect false negative matches (e.g. matches which should be found but are not found because one of the DNA-profiles contains an error) regular full DNA-database searches allowing one or more mismatches should be performed.  
When a match between two DNA-profiles contains a mismatch in one of the loci, the original data of both DNA-profiles should be checked to see if one of the DNA-profiles contains an error.
- 25) Information from a National DNA-database should be combined with other types of evidence to increase the number of crimes for which a lead can be identified
- 26) As automated processes reduce the possibility of human errors, they should be introduced for those processes that are straight forward
- 27) From a forensic point of view the cell material of reference samples should be stored as long as their corresponding DNA-profiles

**28)** Because DNA-databases have a very important but also very delicate role in society, the custodian of a DNA-database should develop tools to make objective information about the DNA-database available to politicians, the public and the media.

## **Annex 2: Changes in the 2009 document relative to the 2008 document**

- New info has been added to table 1 (kits and loci)
- A reference to a Swiss simulation study on the minimum nr of loci required for the inclusion of a DNA-profile in a database has been added
- An explanation about different types of wildcards has been added
- The wording of several recommendations (9, 11,14, 22, 23, 27) has been adapted
- A new chapter on sequence variation between STR alleles of similar length has been added
- The chapter on match validation has been restructured and extended
- Table 2 on match counting has been made more explicit
- A paragraph on stain-to-stain counting has been added
- The old recommendation 27 has been removed because it was more or less equal to recommendation 13
- References have been made to judgments of the European Court on Human Rights and the Dutch Supreme Court
- The chapter on data integrity control measures has been extended with a paragraph about error detection and a new recommendation replacing recommendation 20
- The links mentioned in the chapter on internet sites have been checked
- The Prüm-paragraph has been updated
- Several minor text adaptations have been made to improve the readability of the document
- The footnote on mixture analysis software has been converted into a paragraph
- Reference is made to the fact that deleting a profile from a DNA-database may also require the destruction of the cell material and hard copies of the DNA-profile and a remark that deleting a profile from backups or analytical files may be difficult
- The origin of table 6 has been added (relative RMP's of different types of family members)
- A reference to the Ethics Group in the UK has been added