GUIDELINE FOR DNA DATABASE MANAGEMENT REVIEW AND RECOMMENDATIONS

DOCUMENT TYPE:	REF. CODE:	ISSUE NO:	ISSUE DATE:
GUIDELINE	**DNA-GDL-004**	**001**	**05.10.2023**

TABLE OF CONTENTS

1. INTRODUCTION

This document discusses the different aspects of forensic DNA database management and makes recommendations, where deemed useful. Questions, remarks and additions in relation to this document can be sent to Emilia Lindberg (emilia.lindberg@poliisi.fi). The first (2008) version of this document was approved at the 28th ENFSI DNA Working Group meeting which was held on 23rd - 24th April 2008 in Prague. Every year until 2017 an updated version of the document was presented at the ENFSI DNA Working Group meeting and republished on the ENFSI website after the approval of the group, from 2017 updates occur every second year.

The initial version of the document was produced with financial support from the ISEC Program of the European Commission - Directorate General Justice and Home Affairs as part of the project JLS/2007/ISEC/506: “Improving the efficiency of European DNA data exchange”, authored by Kees van der Beek (NFI – Netherlands).

In 2019 additional feedback was obtained from 21 operational Databases using the audit trail contained in Appendix 2. Forensic Science Ireland as co-chair of the group co-ordinated this work and was supported by Dr. Siobhan Smith of FSI.

This document was extensively reviewed for 2022, with contributions from Christina Widén (Sweden), Séverine Steuve (Belgium), Igor Obleščuk (Croatia), Susan Hitchin (Interpol), Eusebio López Reyes (Spain), Maria José Farfan Espuny (Spain), Emilia Lindberg (Finland), Reinhard Schmid (Austria), representatives of the ICMP and feedback from the ENFSI DNA Working Group Subgroup C – DNA Database Management and Legislation, Lisbon, September 27, 2022.

2. ESTABLISHING A FORENSIC DNA DATABASE

A forensic DNA database can assist investigations of crimes by linking DNA profiles from crime-related biological trace material to each other and to the possible donors (or their relatives). Over the past 20 years, forensic DNA databases have 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 invited its member states to consider establishing DNA databases[1] back in 1997. In 2001, a European Standard Set (ESS) of loci was established to enable the comparison of DNA profiles from different countries[2] and in 2009, the ESS was expanded with 5 extra loci[3]. In June 2008, the Council of the European Union converted the Treaty of Prüm into EU legislation (The EU Prüm Decision)[4]. The new EU legislation requires every EU Member State 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, previously derived from the European Data Protection Directive 95/46 but, as of May 2018, derived from Regulation (EU) 2016/679 (General Data Protection Regulation) or, depending on the status of the institution conducting DNA analysis, Directive (EU) 2016/680 (Law Enforcement Directive), also applies to forensic DNA databases. This has certain consequences, which will be explained in chapter 14. It is therefore preferable to have specific DNA database legislation.

[1] EU Council Decision of 9 June 1997 on the exchange of DNA analysis results
[2] EU Council Resolution 9192/01
[3] EU Council Resolution 2009/C 296/01
[4] Decision 2008/615/JHA — cross-border cooperation, particularly in combating terrorism and cross-border crime

The DNA Working Group of the ENFSI strongly feels that every European country should have a forensic DNA database to enhance:
the possibility of solving crimes
the number of crimes that are solved
the speed with which crimes are solved
the time that 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 is usually 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 European country should establish a forensic DNA database and pass specific legislation for its implementation and management.

3. INCLUSION CRITERIA

There are several criteria to consider in order to 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 additionally require the 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 almost always present in a DNA database.

Crime-related stains

These are the DNA profiles which are assumed to originate from the perpetrators of crimes. It is the responsibility of the police to collect crime-related items. When the origin of the trace 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 specimens to prevent DNA profiles from innocent people being included in the DNA database. DNA testing in high-volume crime (burglaries, etc.) is often very standardized and automated, to increase the number of traces analyzed and to decrease the throughput time from crime scene to inclusion in the DNA database. Specimens taken at these types of crime scenes should be chosen in such a way that the possibility that they originate from a perpetrator is maximized. Examples of such “safe” traces are: bloodstains (e.g. on broken windows), saliva stains (e.g. on tins, cups, bottles), cigarette butts and chewing gum, which the residents of the burgled house can testify that they did not produce themselves.

Usually the types of crime from which stains originate correspond with the types of crime for which persons can be forced to provide a DNA sample. 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 individual 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 investigation of 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.

Reference profiles

Several categories of reference profiles from known 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 may not) be (conditionally) convicted to imprisonment, a penalty, labor, hospitalization or a combination of these. 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 as defined above.
- Volunteers, persons outside the above-mentioned categories who have agreed to give a DNA sample for investigative purposes. In some countries, volunteers can also be included in the national DNA database with 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 that the law allows for a crime.

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

- A person may first be asked to give a sample on a voluntary basis;
- An official police or judicial order may be served to provide a sample, either directly or upon refusal to give the sample on a voluntary 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 the person's cell material (a surrogate sample). 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 identification of the donor of a stain depends on the presence of the donor in the DNA database, more donors can be identified if more relevant persons are included in the DNA database. Moreover, the persons included in the DNA database should adhere to the scope of the DNA database. For instance, 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 identifying the donors of stains, the number of persons in a DNA database who are likely to be the donors of those stains should be as large as legally (and financially) possible.

Apart from nationally collected DNA profiles, DNA profiles originating from international legal comparison requests may also be included, to enable repeated comparisons against newly added DNA profiles. See also: chapter 22.

Victims

Some countries allow the inclusion of DNA profiles from the deceased victims of unsolved crimes in their DNA database. The purpose of this is to find matches which may help to solve the crime. If, for instance, the DNA profile of a dead victim who was stabbed to death later matches a blood stain on a knife, then the owner of the knife may become a murder or a manslaughter suspect.

There are two types of victims: identified and unidentified victims. Unidentified persons who are not apparent victims of a crime are usually included in a missing persons DNA database, but may be compared with the criminal DNA database in an attempt to identify them (see chapter 22). The "risk" of including victims is getting matches with other unsolved crimes, in which case the victim becomes a suspect. Therefore, victims who are still alive, like other volunteers, should be informed and asked to give their consent.

Missing persons

Some countries allow the inclusion of DNA profiles from missing persons if there is a suspicion that a crime is involved in their disappearance. The purpose of this is the same as for the inclusion of victims, namely, to find matches which may help to solve the crime.

Elimination profiles

The inclusion of DNA profiles in the DNA database for contamination detection purposes is dealt with in chapter 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 kits which are or have been commercially available, 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 the creation of the first DNA databases, but their discriminating power is insufficient to generate meaningful matches in relation to the millions of DNA profiles available for comparison today.

The EU Council resolutions 2001/C 187/01 and 2009/C 296/01 call upon European countries to use the European Standard Set (ESS) as a minimum to enable the international comparison of DNA profiles. In the USA, the required number of loci for the inclusion of a reference profile in the national DNA database of the USA (CODIS) used to be 13, but in 2015, the CODIS core locus set was expanded to 20 loci[5]. The INTERPOL Standard Set of Loci (ISSOL) is equal to the European Standard Set, plus the amelogenin locus. Until December 2009, the European Standard Set of Loci contained only 7 loci. This was 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 Decisions, 7 loci are generally insufficient, because the chance of adventitious matches becomes significant, and makes a routine process inefficient. In addition, each DNA database contains a significant portion of partial profiles with a much higher probability of matching randomly. This is why ENFSI has recommended that the European Standard Set of Loci should be expanded by 5 additional loci and the Council of the European Union adopted this recommendation on 30 November 2009. In the meantime, commercial companies have produced kits which contain these new loci to enable the implementation of the new ESS loci.

The locus D5S2500 is contained in the Investigator HDplex Kit of Qiagen, the 21+1 kit of AGCU Scien Tech and the Goldeneye DNA ID 22NC kit of Peoplespot. It has been shown however that the D5S2500 locus in the 21+1 kit of AGCU Scien Tech is incorrectly typed and actually is located 1643 nucleotides away from the correct D5S2500 locus and may be called D5S2800[6]. The D5S2500 locus in the Investigator HDplex Kit of Qiagen is correctly typed. For the D5S2500 locus in the Goldeneye DNA ID 22NC kit of Peoplespot no data were found to verify its typing.

[5] D.R. Hares (2015) Forensic Science International: Genetics 17 (2015) 33–34. Selection and implementation of expanded CODIS core loci in the United States

[6] C. Phillips et al (2016) Forensic Science International: Genetics 23 (2016) 19–24. D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age

The frequencies of the alleles of the different loci for different populations can be found in different sources, which are summarized in a publication of the DNA Commission of the ISFG[7].

[7] M. Dodner et al (2016) Forensic Science International: Genetics 24 (2015) 97–102. Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER)

	Company	Thermo Fischer													Promega														Qiagen										Gordiz			Peoplespot		AGCU Scien Tech							Biotype		Serac	Health Gene Technologies			Historic kits			Standard sets		
Chromosome	Locus	SGM Plus	Profiler	Profiler Plus (ID)	Cofiler	SE-filer (Plus)	Blue-kit	Identifiler (Direct) (Plus)	Minifiler	NGM	NGM Select/Detect (Express)	Sinofiler	Globalfiler (Express)	Verifiler	Powerplex 1.1 or 1.2	Powerplex 2.1	Powerplex 16	Powerplex ES	Powerplex ESX 16 (Fast)	Powerplex ESX 17 (Fast)	Powerplex ESI 16 (Fast)	Powerplex ESI 17 (Fast)	Powerplex 18D	Powerplex CS7	Powerplex S5	Powerplex 21	Powerplex Fusion	Powerplex Fusion 6C	Investigator ESSplex Plus Kit	Investigator ESSplex SE Plus/GO!/QS	Investigator Decaplex SE Kit	Investigator IDplex Plus (GO!)	Investigator Nonaplex ESS Kit	Investigator Hexaplex ESS Kit	Investigator TriplexDSF Kit	Investigator Triplex AFS QS Kit	Investigator HDplex Kit	Investigator 24plex	COrDIS-9	COrDIS-11	COrDIS Plus	Goldeneye DNA ID 20A	Goldeneye DNA ID 22NC	17 + 1	21 + 1	EX 16	Ex 20	Ex 22	Expressmarker 16+10Y	Expressmarker 16+18Y	Mentype Nonaplex I or QS	Mentype Pentaplex ESS	MPX II or MPX II-LF	SureID Compass	Locally prepared kit Austria	Locally prepared kit Belgium	FFFL	QUAD	SGM	ENFSI/European Union (ESS) Old	Interpol (acceptable)	USA (CODIS core-loci) Old
1	F13B																							+																																	+					
	D1S1627																																												+																	
	D1S1656									+	+		+	+					+	+	+	+				+	+	+	+	+			+	+				+			+		+									+								+	+	+
	D1S1677																																												+																	
	D1GATA113																																												+																	
2	D2S1338	+				+		+	+	+	+	+	+	+					+	+	+	+	+			+	+	+	+	+	+	+						+				+		+		+	+	+	+	+				+							+	+
	TPOX		+		+			+					+		+	+	+						+			+	+	+				+						+		+	+	+		+		+	+	+	+	+				+							+	+
	D2S441									+	+		+	+					+	+	+	+					+	+	+	+			+	+				+		+	+		+		+			+				+								+	+	+
	D2S1360																																				+																									
	D2S1776																																												+																	
3	D3S1358	+	+	+	+	+	+	+		+	+	+	+			+	+	+	+	+	+	+	+			+	+	+	+	+	+	+	+		+			+		+	+	+	+	+		+	+	+	+	+	+		+	+	+					+	+	+
	D3S1744																																				+						+																			
	D3S3045																																										+																			
	D3S4529																																												+																	
4	FIBRA (FGA)	+	+	+		+	+	+	+	+	+	+	+			+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+		+	+		+	+		+	+		+		+	+	+	+	+	+		+	+	+				+	+	+	+
	GABA																																																													
	D4S2366																																				+						+																			
	D4S2408																																												+																	
5	D5S818		+	+				+				+	+		+		+						+			+	+	+				+						+	+		+	+		+		+	+	+	+	+				+							+	+
	CSF1PO		+		+			+	+			+	+		+		+						+			+	+	+				+						+	+		+	+		+		+	+	+	+	+				+							+	+
	D5S2500																																				+						+		+																	
6	F13A																							+																																	+	+				
	ACTBP2 (SE33)					+					+		+					+		+		+						+		+	+		+		+	+	+	+	+		+										+		+		+	+					+	
	D6S1043											+		+												+																+		+		+	+	+														
	D6S474																																				+								+																	
	D6S477																																										+																			
	D6S1017																																												+																	
7	D7S820		+	+	+			+	+			+	+		+		+						+			+	+	+				+						+		+	+	+		+		+	+	+	+	+				+							+	+
	D7S1517																																				+						+																			
	D7S3048																																										+																			
8	D8S1179	+		+		+		+		+	+	+	+			+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+					+	+		+	+		+		+	+	+	+	+	+		+	+	+				+	+	+	+
	LPL																							+																																	+					
	D8S1132																																				+						+																			
9	Penta C																							+																																						
	D9S1122																																												+																	
10	D10S1248									+	+		+	+					+	+	+	+					+	+	+	+			+	+				+	+		+		+		+			+				+								+	+	+
	D10S2325																																				+																									
	D10S1435																																										+		+																	
11	TH01	+	+		+	+		+		+	+		+	+	+	+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+				+		+	+	+		+		+	+	+	+	+	+		+	+	+	+		+	+	+	+	+
	D11S2368																																										+																			
	D11S4463																																												+																	
12	vWA	+	+	+		+	+	+		+	+	+	+		+	+	+	+	+	+	+	+	+			+	+	+	+	+	+	+	+					+		+	+	+		+		+	+	+	+	+	+		+	+	+			+	+	+	+	+
	CD4																																																							+						
	D12S391									+	+	+	+	+					+	+	+	+				+	+	+	+	+			+	+			+	+	+	+	+	+					+	+				+								+	+	+
	D12ATA63																																												+																	
13	D13S317		+	+				+	+			+	+		+		+						+			+	+	+				+						+		+	+	+		+		+	+	+	+	+				+							+	+
	D13S325																																										+																			
14	D14S608																																										+																			
	D14S1434																																												+																	
15	FES/FPS																							+																																	+	+				
	Penta E															+	+						+	+		+	+	+														+		+			+	+													+	
	D15S659																																										+																			
16	D16S539	+			+	+		+	+	+	+	+	+		+		+		+	+	+	+	+			+	+	+	+	+	+	+						+	+		+	+		+		+	+	+	+	+				+							+	+
17	D17S1290																																										+																			
	D17S1301																																												+																	
18	D18S51	+		+		+		+	+	+	+	+	+			+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+				+	+		+	+	+		+		+	+	+	+	+	+		+	+	+				+	+	+	+
	D18S535																																										+																			
	D18S853																																												+																	
19	D19S433	+				+		+		+	+	+	+	+					+	+	+	+	+			+	+	+	+	+	+	+						+				+		+	+		+	+	+	+				+							+	+
	D19S253																																										+																			
20	D20S482																																												+																	
21	D21S11	+		+		+		+	+	+	+	+	+			+	+	+	+	+	+	+	+			+	+	+	+	+	+	+	+					+		+	+	+		+		+	+	+	+	+	+		+	+	+	+			+	+	+	+
	Penta D																+						+	+		+	+	+														+					+	+													+	
	D21S2055																																				+																									
22	D22S1045									+	+		+	+					+	+	+	+					+	+	+	+			+	+				+			+				+							+								+	+	+
	D22GATA198B05																																										+																			
X/Y	Amelogenin	+	+	+	+	+		+		+	+		+				+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+		+	+					+		+	+
Y	DYS19																																																	+				+								
	DYS385a/b																																																+	+				+								
	DYS389I																																																	+				+								
	DYS389II																																																	+				+								
	DYS390																																																+	+				+								
	DYS391												+														+	+										+											+	+				+								
	DYS392																																																+	+				+								
	DYS393																																																+	+				+								
	DYS437																																																					+								
	DYS438																																																+	+				+								
	DYS439																																																					+								
	DYS448																																																	+				+								
	DYS456																																																+	+				+								
	DYS458																																																+	+				+								
	DYS481																																																													
	DYS529a/b																																																	+												
	DYS570																											+																																		
	DYS576																											+																																		
	DYS635																																																+	+				+								
	DYS643																																																													
	GATA-H4																																																	+				+								
	Y Indel												+																																									+								
	Total nr of loci	11	10	10	7	12	3	16	8	16	17	15	24	9	8	9	16	9	16	17	16	17	18	7	5	21	24	27	16	17	12	16	14	7	3	3	13	23	9	11	20	20	22	18	22	16	20	22	25	31	9	5	9	33	8	4	4	4	7	12	24	21

3.3 Number of loci

For the comparison of DNA profiles between EU countries, DNA profiles must comply with the Prüm inclusion rules. For comparison of DNA profiles within a single country, however, national criteria may apply. DNA profiles from crime scene stains may not contain all loci present in the kit(s) used to produce DNA profiles in a specific country. These partial DNA profiles may be included in national DNA databases, provided they have a high enough evidential value and/or the chance of producing adventitious matches is not too high (see chapter 7). Two criteria commonly used for the inclusion of partial profiles are 1) minimum number of loci and 2) maximum random match probability. 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 the former includes one or more rare alleles.

A simulation study has been published, which shows 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[8].

ENFSI recommendation 4
Managers of national DNA databases should establish (together with other stake-holders) 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 the 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 is still searched against the national DNA database, accepting the fact that many of the matches found will be adventitious matches. Tactical police work is then necessary to find out if any of the matches lead to a potential suspect. If no potential suspect is found by the police, the search action may be repeated after some time or at regular intervals, because new reference profiles will have been added to the national DNA database. The CODIS autosearcher mode produces only new matches in these types of search actions, which saves work in sorting out old and new matches.

For historic reasons, the countries who started early with their DNA databases (like the United Kingdom 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 are often 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 is still available for further testing.

ENFSI recommendation 5
If possible, DNA profiles should be upgraded after a match in the national DNA database if it increases the evidential value of the match and decreases the possibility of an adventitious match.

[8] T. Hicks et al (2010) FSI Genetics 4(4) 232-238. Use of DNA profiles for investigation using a simulated national DNA database: Part I. Partial SGM Plus® profiles

The number of loci in reference samples should be the maximum number of loci present in the kit(s) used for the production of the DNA profiles of reference samples, to increase the chance of finding relevant matches with partial DNA profiles. However, sometimes this is not possible due to an allelic drop out or a true or apparent trisomy.

ENFSI recommendation 6
Reference sample profiles should preferentially be loaded to a database only if a complete profile (maximum number of loci) is obtained using the PCR chemistry of choice.

3.4 Suppliers 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 used in the match. A wrongly called allele may prevent a match and a sample mix-up may produce a false match. For these and other reasons, labs producing DNA profiles for DNA databases should be able to show objectively that they produce DNA profiles with quality-driven processes. This means, 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

Council Framework Decision 2009/905/JHA of 30 November 2009 “on the accreditation of forensic service providers carrying out laboratory activities” requires ISO 17025 accreditation for all forensic DNA laboratories.

ENFSI recommendation 7
Labs producing DNA profiles for a DNA database should, as a minimum, be ISO-17025 (and/or national equivalent) accredited and should participate in challenging proficiency tests.

In some countries, laboratories which supply DNA profiles to the national DNA database are audited by the custodian of the DNA database. In addition to this, the custodian of the DNA database should have regular contact with the suppliers of the DNA profiles to exchange information about legal and technical developments, changes in the inclusion and matching rules, incidents, etc.

ENFSI recommendation 8
The custodian of the DNA database should have regular contact with the suppliers of the DNA profiles to exchange information about legal and technical developments, changes in the inclusion and matching rules, incidents, etc.

3.5 DNA profiles produced from low levels of DNA

DNA profiles produced from low levels of DNA, whether by a standard or enhanced number of PCR-cycles or by signal enhancing techniques like increased injection settings or post-PCR clean-up, can contain allele drop-ins and allele drop-outs, even if a consensus profile is produced from repeated determinations[9]. Hence, they may never produce matches when included in a DNA database, if all alleles are required to match. If DNA profiles produced from low levels of DNA are included in a DNA database, they should be recognizable and/or a

[9] C.C.G. Benschop et al. (2011) Forensic Sci Int Genet. 5, 316-328. Low template STR typing: Effect of replicate number and consensus method on genotyping reliability and DNA database search results.

dedicated match strategy (allowing one or more mismatches) should be used to detect possible allelic drop-ins and drop-outs (as will be discussed in § 5.4). For a discussion on mixed profiles from low levels of DNA, see § 3.9

ENFSI recommendation 9
If a laboratory uses enhanced techniques to produce DNA profiles, they should be searched using a dedicated (near) match strategy.

3.6 Composite DNA profiles

The smaller PCR products of DNA profiles from stains regularly show higher peak heights than larger PCR products. This is due to partial breakdown of the DNA. It can even occur that the larger PCR products disappear below the detection threshold, while the smaller PCR products still show good peaks. Sometimes the peak heights of the larger PCR products can be improved by increasing the input of the PCR reaction, but this can often result in the overloaded peaks of smaller PCR fragments. By using low as well as high input during the PCR reaction, two DNA profiles may be obtained, one with clear, legible peaks of the smaller fragments and the other with clear, legible peaks of the larger fragments. These can then be combined into a composite DNA profile. This should, however, only be done with DNA profiles obtained from the same DNA extract and not with DNA profiles obtained from different DNA extracts (even if they come from the same sample), because it cannot be excluded that different samples (or different parts of a sample) contain DNA from different individuals.

ENFSI recommendation 10
Composite DNA profiles should only be created from DNA profiles generated from the same DNA extract because it cannot be excluded that different extracts, even from the same sample, contain DNA from different individuals.

3.7 Rare alleles/chromosomal anomalies

For each commercial kit, the known alleles of each locus and their relative 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 it is important to consider whether these new alleles should be included in the DNA database, and which frequency they should be assigned in order to calculate the probability of the particular DNA profile in the population of interest (i.e. the so-called random match probability). When a new allele is observed, its appearance should first be confirmed by repeated DNA extraction, 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[10]. If a new allele has not been sequenced yet, it can be sent to NIST for sequencing. Only new alleles whose 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 relative frequency attributed to a new allele may be one divided by the size of the reference database used to estimate allelic proportions, a predetermined (low) relative frequency or a proportion calculated according to alternative statistical estimation procedures. Allelic relative

[10] http://www.cstl.nist.gov/biotech/strbase/index.htm

frequencies can be estimated using methods like the Balding[11] size correction formula (i.e. a Bayesian estimator).

STRidER (**STR**s for **Id**entity **E**NFSI **R**eference Database) is the expanded and enhanced version of the ENFSI STRbASE (2004-2016). This curated online high quality STR allele frequency population database enables scientifically reliable **STR genotype probability estimates** and provides **quality control** of autosomal STR data. A suite of software tools has been developed at the Institute of Legal Medicine, Medical University of Innsbruck to scrutinize STR population data and thus increase the quality of datasets to ensure reliable allele frequency estimates. STRidER acts as **frequency database and software platform** for the development of novel tools for STR data QC and other forensic analyses, https://strider.online/.

ENFSI recommendation 11
When a new allele is observed in a DNA profile, its presence should be confirmed by repeated DNA extraction, PCR, capillary electrophoresis and allele calling of the entire DNA profile. Only new alleles whose 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. A well-known example of this is trisomy 21, which causes Down's syndrome. 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 be included in the DNA database. However, extra peaks can also be caused by somatic mutations, which may appear only in certain tissues/body fluids. This means that DNA profiles from different sample types (e.g. buccal swab and blood) may appear to be from different donors and might be dismissed as a match. This can, of course, contribute to the evidential value after the match has been found in the DNA database. However, if the default search strategy is moderate, a profile containing a trisomy will match a profile without the trisomy[12].

ENFSI recommendation 12
Alleles from loci with chromosomal anomalies may be included in a DNA database if the default search strategy allows at least one mismatch. If the default search strategy does not allow any mismatches, wildcards may be used, as long as an agreed set of wildcards is determined to permit meaningful international exchange.

Sometimes an apparent trisomy can occur when an unusually long or short allele of a locus falls out of its own bin and falls into a neighboring bin in the electropherogram. The allele calling software then calls three peaks in one bin and only one in the neighboring bin. This situation can be clarified by using a monoplex PCR or by using a different kit where the two loci involved are not adjacent on the electropherogram.

A regularly observed tri-allelic pattern for TPOX has been analyzed[13]. The results showed that some of these tri-allelic patterns are caused by a translocation of allele 10 of the TPOX locus to the X-chromosome.

[11] Balding, DJ (1995) J. Am. Stat. Assoc. 90:839-844. Estimating products in forensic identification.
[12] An inventory of tri-allelic pattern observations for the commonly used STR markers can be found at: http://www.cstl.nist.gov/biotech/strbase/tri_tab.htm
[13] Picanço, J.B. et al (2015) Forensic Science International Genetics 16, 88–93. Identification of the third/extra allele for forensic application in cases with TPOX tri-allelic pattern.

The inclusion rules for DNA profiles which are compared on the basis of the EU Prüm Council Decisions state that a tri-allelic locus should be converted into the first allelic value, plus a wildcard. This is in contrast with recommendation 12, but cannot be changed at this moment because Council Decision 2008/616/JHA, which contains the inclusion rules, will not be amended until all EU countries are operational.

3.8 Wildcards

If there is uncertainty about the presence or absence of an allele in a DNA profile, a so-called "wildcard" may be included in the DNA profile. This may be the case with low peaks, where the DNA analyst cannot determine whether it is a homozygote peak or a locus where one allele has dropped out.

In some countries, a wildcard is used to replace a rare allele which is not in the ladder-range of the DNA kit used. In this case, the wildcard represents a designated allele which can be used to verify a match with a DNA profile containing the same wildcard. Searching with wildcards means that any allele is accepted as a match for the wildcard allele. Different countries use different designations for their wildcards. For the purposes of 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 presently use "*" as a wildcard. There has been a proposal to use "*" for a wildcard that represents a designated allele, and to use "B" for a wildcard that represents an unknown allele, but this proposal has not yet been implemented. The use of wildcards increases the chance of finding adventitious matches in the DNA database[14], but if the wildcard represents a rare allele and both profiles prove to contain this rare allele, the evidential value of the match greatly increases.

3.9 Mixed profiles

Mixed profiles can occur when two or more individuals have left cell material on the same object (e.g. smoking from the same cigarette or drinking from the same bottle), or when, for example, cells of a perpetrator are mixed with cells of a victim (which often occurs in rape cases). If possible, mixed DNA profiles should be interpreted and separated into their contributing DNA profiles. Mixed profiles from (known) victims and (unknown) donors occasionally can be resolved, because the alleles of the victim's DNA profile can be subtracted from the mixed profile. The remaining alleles must belong to the unknown donor. Mixed DNA profiles from two donors, however, can often only be completely designated into separate contributors if there is a significant difference in contribution between the two donors (Major/Minor contributors). A working group of the IFSG has produced a document with guidelines for the analysis of mixed profiles[15], although technological developments (such as increased sensitivity and improved computational power) have led to the development of specialized programs for mixture analysis. Several software tools, both commercial and open-source, have become available that can resolve mixtures and produce possible combinations of donor profiles (see the website of the ISFG http://www.isfg.org/software for open-source software). Such tools may be used, provided they are properly validated.

ENFSI recommendation 13

[14] Tvedebrink, T. et al (2015) Forensic Sci Int Genet 16, 98-104. The effect of wild card designations and rare alleles in forensic DNA database searches.

[15] Gill, P. et al (2006), Forensic Sci Int. 160, 90-101. DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures

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. Software tools may also be used, provided they are properly validated.

In some DNA databases (like CODIS), mixed DNA profiles can be included and searched. This is very useful when a mixed DNA profile cannot be reliably resolved into its contributing components. In CODIS, it is even possible to designate the 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 electropherograms of the DNA profile, because a numerical match may not be a true match, as shown in figure 1. For this reason, mixed profiles cannot currently be used in the automated international comparison of DNA profiles, like the comparisons which are performed under the terms of the EU Prüm Council Decision, and those conducted in the INTERPOL DNA database.

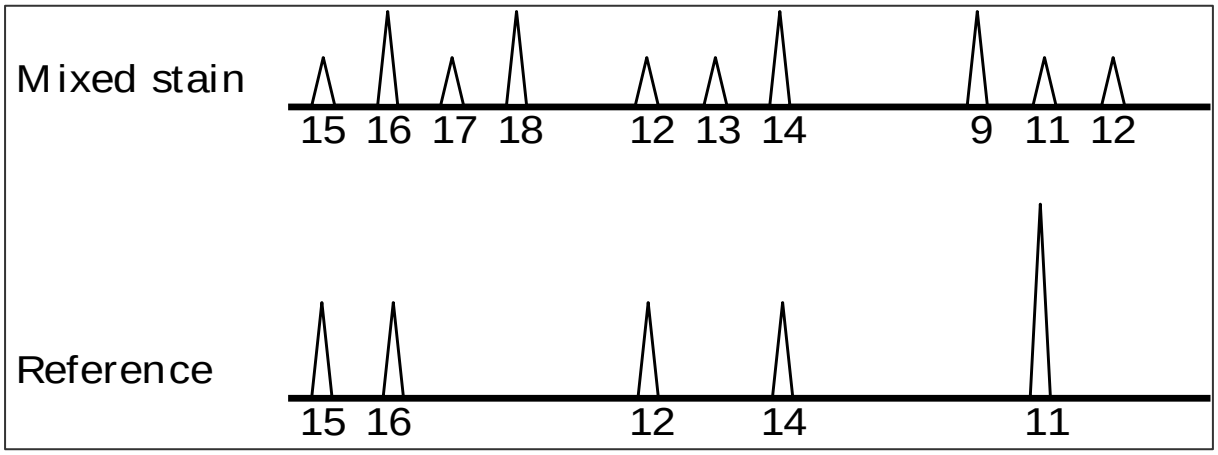

Figure 1: Three loci of a mixed stain and a reference sample which match on a numerical basis but are an unlikely combination when peak heights are taken into account

ENFSI recommendation 14
A numerical match between a reference profile and a mixed profile must always be checked against the electropherogram of the mixed profile.

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

ENFSI recommendation 15
Mixed profiles of more than 2 individuals should not be systematically included in a DNA database because they will generally produce too many adventitious matches.

Special software exists to resolve mixed DNA profiles into possible contributors (see above). These possible contributors can then be searched against the national DNA database of a country. Some people have expressed their concern that this will lead to an increase in false positive matches. Compared to the situation where mixed profiles themselves are included in a DNA database (which can, for instance, be done by countries using CODIS), conducting a

search using the possible contributors of a mixed DNA profile will not lead to more false positive matches, provided that any resulting matches are interpreted with caution.

In rare cases, a mixed profile can be obtained from a single individual. This can happen when a buccal swab is taken from an individual who has received a bone-marrow or blood stem cell transplant in the context of medical therapy. As a result, the blood has the DNA profile of the tissue donor, whereas other body tissues still have the original profile of the individual. However, when taking a buccal swab, very small superficial blood vessels may be damaged, causing a mixed profile.

Mixed profiles obtained from low levels of DNA can contain allelic drop-in and drop-out peaks and are even more difficult to analyse than single-source profiles obtained from low levels of DNA. The use of consensus and composite profiles may assist in the analysis and interpretation of these profiles[16]. Special software has been developed to compare these profiles to reference samples, resulting in a likelihood ratio expressing the ratio of the probability of the results, given that the trace came from the person who is the source of the reference profile and one or more unknown persons; and the probability of the results, given that the trace originates from two (or more) unknown persons. LRmix Studio is an open-source example of such a software program[17]. SmartRank is a program that links LRmix Studio to a DNA database for the comparison of complex mixed profiles to all reference profiles in the DNA database[18]. This will result in a list of likelihood ratios for each reference profile in the DNA database. The names of the persons associated with the reference profiles with the highest likelihood ratios can then be used by the police as an investigative tool. Additional DNA testing may be necessary to confirm/reject that a candidate obtained in this way could be a true contributor to the mixed profile. SmartRank, developed with the support of an ENFSI Monopoly Grant, has been validated in 2017[19]. Many other programs, both commercial and open source (such as True Allele, STRMix, EuroForMix – this is not an exhaustive list) are now available. SmartRank, STRMix[20] and EuroForMix[21] can now compare mixed profiles to DNA databases[22].

3.10 Sequence variation between STR alleles of similar size

The present designation of STR alleles is based on the 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)[23], or massive parallel sequencing[24], have shown, however, that STR alleles in general display considerable sequence variability, resulting in additional discrimination for alleles of identical size. In addition, the flanking sequences between the STR

[16] C. Benschop et al (2013) Int. J. Legal Med. 127, 11-23. Consensus and pool profiles to assist in the analysis and interpretation of complex low template DNA mixtures.
[17] https://github.com/smartrank/lrmixstudio
[18] https://github.com/smartrank/smartrank
[19] C.Benschop et al (2017) Forensic Sci Int Genet. 2017 Jul;29:145-153. Validation of SmartRank: A likelihood ratio software for searching national DNA databases with complex DNA profiles.
[20] https://www.strmix.com/news/dblr-discussion-with-dr-maarten-kruijver/
[21] http://www.euroformix.com/?q=dnamatch2
[22] The mentioning of trade names does not mean that ENFSI recommends or endorses any of these programs. The aim of ENFSI is to provide insight into what is available on the market.
[23] 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
[24] Børsting C, Morling N. N Forensic Sci Int Genet. (2015) Feb 14. ext generation sequencing and its applications in forensic genetics. DOI: http://dx.doi.org/10.1016/j.fsigen.2015.02.002

and the primer binding site show sequence variability. These findings will have significant consequences for forensic DNA typing:

- Alleles determined as similar by capillary electrophoresis will be differentiated due to sequence variability.
- Match probabilities will be lower than presently calculated, because allelic proportions will be smaller, resulting in the enhanced discrimination power of DNA typing, which is especially important for mixtures and partial DNA profiles.
- The established DNA databases can still be used, but the nomenclature of the alleles will have to be adjusted to deal with different alleles of similar size. The DNA commission of the International Society for Forensic Genetics (ISFG) has published considerations on minimal nomenclature requirements for massively parallel sequencing of forensic STRs[25].

3.11 Non-autosomal STR markers

In the previous paragraphs, only autosomal STR markers have been discussed. However, the X- and Y-chromosomes also contain STR markers. Y-chromosomal markers are especially important and are frequently used in forensic DNA testing because they can be used to reveal the presence of male DNA amongst an excess of female DNA. They can also help establish male familial relationships because they segregate unchanged as a haplotype from a father to his sons (provided there is no mutation). X- and Y-chromosomal markers can easily be stored in DNA database software programs like CODIS. The difference with other STR markers is that most Y-chromosomal STR markers contain only one allele due to their haploid nature. Searching with Y-chromosomal STR markers is also possible, but this implies a familial search which may need special permission from the competent authorities. With rapidly mutating Y-STRs, males of the same male lineage may still be distinguished from each other[26].

3.11.1 Y-chromosomal STR markers

Y-chromosomal markers belong to the lineage (or haploid) markers. Due to the lack of recombination and the linear mode of inheritance, both the sampling strategy and the reporting of frequencies differs from autosomal DNA markers, but follows the same principles based on theories in population genetics and the laws of probability. Because of full linkage between markers within a Y-STR profile (haplotype), the product rule cannot be applied, and instead large haplotype reference databases are mandatory to perform calculations. The YHRD (Y-Chromosome Haplotype Reference Database, https://yhrd.org) is the largest, annotated, strongly curated and quality-controlled forensic database[27]. It is designed to store haplotypes from hundreds of population samples from around the globe and to rapidly disseminate haplotype frequency data via the internet to forensic analysts. The databases also include several tools to analyze population substructure effects, to interpret matches between Y-STR profiles, to attach likelihood ratios in mixture analyses, and to formulate valid forensic testimonies. YHRD is built by direct submissions of population data from individual certified laboratories. Upon receipt of a submission, the YHRD staff examines the originality of the data, assigns an accession number to the population sample and performs quality assurance

[25] W. Parson et al. (2016) Forensic Science International: Genetics, Volume 22, May 2016, Pages 54-63. Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements.

[26] Alghafri, R. et al. (2015) Single multiplex assay for simultaneously analyzing 13 rapidly mutating Y-STRs. Forensic Sci Int Genet. (2015) 17, 91-98

[27] Willuweit S, Roewer L (2007) Y-chromosome haplotype reference database (YHRD): update. Forensic Sci Int Genet. 1(2): 83-7

checks. The submissions are then released to the public database, where the entries are retrievable by search for haplotypes, populations, contributors or accession numbers. Currently the YHRD presents 343 932 minimal haplotypes in 1398 different populations (https://yhrd.org/pages/resources/stats, June 2022). All population data published in forensic journals such as Forensic Science International Genetics (FSI Genetics) or the International Journal of Legal Medicine are required to be validated by the YHRD custodians and are subsequently included in the YHRD[28].

3.11.2 X-chromosomal STR markers

X-chromosomal STR markers can be useful in analyzing specific kinship cases. Like Y-chromosomal markers, they can be stored and searched in DNA database programs like CODIS but familial search restrictions may also apply here. Furthermore, the particular linkage situation of the STR markers on the X-chromosome has to be taken into consideration in the case of biostatistical calculations[29].

3.12 Amelogenin

Most commercial kits contain the amelogenin marker, which is present on both the X- and Y-chromosome. The amelogenin gene on the X-chromosome contains a 6 base-pair deletion, which results in different PCR fragment lengths and thus the ability to distinguish male and female DNA profiles. In rare cases, a mutation or a deletion in the amelogenin gene can result in the inability to produce a PCR-fragment which then gives a wrong impression about the sex of the DNA profile donor[30]. Because the amelogenin marker does not give foolproof results, some companies have added additional Y-chromosomal markers to their newest kits (e.g. GlobalFiler, PowerPlex Fusion).

3.13 Mitochondrial DNA (mtDNA) information

Mitochondrial DNA (mtDNA) information is frequently used in forensic DNA testing. The information is sequence-based and typically covers the mtDNA control region approx. 1 kb in length on the D-loop from positions 16024 to 576 (comprised of the hypervariable regions HV I-III). In contrast to autosomal DNA, of which only two copies are present in each cell, mtDNA is present in many hundreds of copies. For this reason, traces that fail to give an autosomal DNA result may still give an mtDNA result. Just like Y-chromosomal DNA results can be used to help establish male familial relationships, mtDNA results can be used to help confirm (or disprove) a relationship in the female lineage, as mtDNA is transmitted unchanged from a female parent to all (male and female) children. It is common practice in forensic genetics to determine the rarity of a mtDNA haplotype by searching the profile in question in dedicated mtDNA haplotype databases.

The largest and highest quality, freely available mtDNA database is the EDNAP Mitochondrial DNA Population Database EMPOP (http://empop.online), which offers the following features:
a) EMPOP offers tools and help for quality control of population datasets and individual sequences deriving from evidentiary samples. EMPOP is conducting quality control in scientific

[28] Carracedo A. et al. (2014) Update of the guidelines for the publication of genetic population data. Forensic Sci Int Genet. 10, A1-A2
[29] Nothnagel M, et al., (2012) Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome. Forensic Sci Int Genet. 6: 778-84
[30] For more information about amelogenin anomalies see: http://www.cstl.nist.gov/biotech/strbase/Amelogenin.htm

studies on mtDNA for the leading forensic genetic journals as a requirement before manuscript submission actually takes place.
b) EMPOP uses alignment-free haplotype searches to guarantee that matches are found in the database, regardless of the alignment used.
c) EMPOP v4/R13 is designed to offer haplogroup determination of mtDNA sequences based on a maximum likelihood concept.

Additionally, mtDNA information is included in DNA databases as differences between the investigated DNA sequence and the Revised Cambridge Reference Sequence (rCRS). As with Y-chromosomal markers, searching is also possible but as this implies a familial search, special permission from the competent authorities may be required. Depending on local legislation, storing such data may not be permissible. Because differences between a mtDNA sequence or haplotype and the rCRS can sometimes be labelled in different ways, clear rules to indicate these differences should be implemented to avoid false exclusions. A better alternative could be a sequence-based comparison[31].

ENFSI recommendation 16
Databases may contain autosomal STR profiles only. For those databases containing profiles from non-autosomal STR profiles or mitochondrial DNA sequences, specific operating procedures must be in place to avoid unintended familial searches. To avoid false exclusions, clear rules should be in place to indicate differences between a mtDNA sequence and the rCRS when comparing mtDNA results.

3.14 Universal DNA database

From time to time, politicians initiate discussions regarding the establishment of a DNA database for all inhabitants (and visitors) of a country. The reasoning behind this is to solve more crimes and identify more unidentified human remains. Several years ago, there were plans in the United Arab Emirates to do this and, more recently, Kuwait announced a law to make this possible[32]. In Europe, however, this is not very likely to happen, as it violates Article 8 of the European Convention on Human Rights. In the United Kingdom, about 1.7 million DNA profiles were removed from the national DNA database, because a verdict from the European Court on Human Rights determined that their unlimited storage was in conflict with this article.

Most recently, in the USA, the idea of a universal DNA database has been raised in conjunction with the growing popularity (and therefore utility to law enforcement authorities) of commercial DNA databases[33]. Even in the context of specific crimes, there are many arguments regarding privacy and consent against the creation of such a database[34].

[31] Parson W, Gusmão L, Hares DR, Irwin JA, Mayr WR, Morling N, Pokorak E, Prinz M, Salas A, Schneider PM, Parsons TJ (2014) DNA Commission of the International Society for Forensic Genetics: revised and extended guidelines for mitochondrial DNA typing. Forensic Sci Int Genet. 13: 134-42; Just RS, et al. (2015) Full mtGenome reference data: development and characterization of 588 forensic-quality haplotypes representing three U.S. populations. Forensic Sci Int Genet. 14: 141-55.
[32] http://news.kuwaittimes.net/website/kuwait-to-enforce-dna-testing-law-on-citizens-expats-visitors-tests-wont-be-used-to-determine-genealogy-affect-freedoms/
[33] https://www.genengnews.com/news/universal-dna-database-could-keep-police-investigations-in-bounds/
[34] https://www.nextgov.com/ideas/2019/02/dangers-mandatory-dna-database/155028/

4. DELETION CRITERIA

In this chapter, the reasons to remove a DNA profile from the DNA database are discussed. Regardless of the reason for deletion, the removal 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 as well as hard copies of the DNA profiles and their electropherograms. Deletion of DNA profiles from back-ups or analytical data files is usually 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 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
- Fixed time after the completion of sentence
- Variable time after the completion of sentence, depending on the type of sentence or sentence history
- 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 to determine the deletion date of a DNA profile. In these cases, the custodian should have access to this information, preferably by means of automated messages, delivered following the event which influences the deletion date of a DNA profile.

ENFSI recommendation 17
If the removal of a DNA profile from the DNA database is dependent on external instruction from an authorized agent, a process should be in place to inform the custodian of the DNA database of this instruction, preferably by means of an automated message.

For non-matching DNA profiles of stains, the storage time is fixed or variable, depending on the type of crime or the statute of limitation for the crime. For matching DNA profiles of stains, see § 4.3.

4.2 Non-conviction of a person

Suspects, arrestees and convicted persons who have successfully appealed their conviction may have to be removed from the DNA database. If this is prescribed by law, the custodian of the DNA database must receive or have access to information regarding convictions or acquittals of any persons included in the DNA database. Experience in several countries has shown 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 matches a DNA profile from a crime scene stain in the DNA database and the match has been processed 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 sometimes called a "benchwork match", although some countries, like Belgium, further differentiate between a match with a Suspect profile, and a match with a Convicted Offender profile. In other countries, like the Netherlands, a crime scene DNA profile cannot 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 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 recommended this in their 2007 Bioethics report, to verify possible future doubts about a match[35].

4.4 Duplication

Persons may or may not be sampled repeatedly for inclusion in the DNA database, depending on the legislation of the country, although sometimes this may also occur inadvertently. An inadvertent duplicate is a waste of resources, therefore a system that can be consulted by those responsible for sampling should be implemented, through which they can verify whether a person is already present in the DNA database.

ENFSI recommendation 18
There should be a system that can be consulted by those responsible for taking reference samples, to verify whether a person is already present in the DNA database.

Sometimes people use a false identity, and for this 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.

The analysis of unintentional and (low level) intentional duplicates, however, is a useful quality control instrument. When taking a duplicate sample, the sample with the least chance of being removed in the future should be kept (if legally possible). Duplicates produced with partially non-overlapping sets of loci are, of course, also useful to keep (e.g. PowerPlex 16 and Identifiler); DNA profiles obtained using two different kits may be combined into a single extended DNA profile when entered into the database. It can also be useful to analyze a duplicate from the same person in order to expand the existing DNA profile with new loci, especially since DNA analysis and the number of useful loci is constantly evolving.

4.5 Match with elimination database

Any DNA database should have an associated so-called elimination DNA database (or databases), containing the DNA profiles of persons who could introduce cross-contamination to the investigated traces. Such elimination databases should include anybody handling the DNA samples in the DNA lab, as well as those cleaning the labs or performing any other kind of maintenance. Also, those involved earlier in the chain of custody, such as investigating officers, crime scene experts and technicians, and other persons present at the crime scene,

[35] http://nuffieldbioethics.org/project/bioinformation/

should be included. In addition, unidentified DNA profiles found in negative controls, which may come from people involved in the manufacturing of 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 be deleted because it is not meant to be included. However, this should not be done before the contamination incident has been analyzed thoroughly, the presumed cause of the match (contamination) has been confirmed, and actions to prevent this (and similar) accidents occurring in the future have been formulated. 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. In most countries, there is no specific legal basis for the establishment of an elimination database. However, because personal data are involved, laboratories, which, for quality control reasons, have decided to establish an elimination database, are bound by the data protection law of their country. These laws usually require the explicit written consent of the persons to be included into the elimination DNA database. In addition, employers may include willingness to be included in the elimination database as a job requirement.

ENFSI recommendation 19
DNA databases should contain an associated elimination DNA database (or databases). This should include laboratory staff of all categories, as well as visitors and maintenance personnel and profiles from those with access to traces (e.g. police, crime scene technicians).

Manufacturers of disposables and/or chemicals should follow the joint recommendations of ENFSI, SWGDAM and SMANZL[36], which have been converted into the ISO18385 standard, to prevent the contamination of their products.

The ICMP[37] has developed a manufacturers' elimination database (MED)[38], which was devised in concert with the forensic DNA community, based on ICMP's independent status and data protection capabilities. The application has been successfully tested and launched in 2018. It is intended to provide forensic DNA laboratories with the ability to query a database of DNA profiles of individuals, acquired from the staff of participating companies involved in the forensic DNA supply chain, to avoid the inadvertent inclusion of manufacturers' staff profiles in either forensic DNA databases or investigations. Countries wishing to upload profiles can email **tmpusr@icmp.int** to set up an account.

ENFSI recommendation 20
Because elimination databases are not shared with other EU/ENFSI countries, unidentified DNA profiles found in negative controls, which may originate during the manufacture of disposables and/or chemicals should be uploaded to the ICMP Manufacturers Exclusion Database, MED

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

[36] Manufacturer contamination of disposable plastic-ware and other reagents—An agreed position statement by ENFSI, SWGDAM and BSAG. Forensic Science International: Genetics, Volume 4, Issue 4, July 2010, Pages 269-270.
[37] See paragraph 23.7.1 for more information about ICMP
[38] http://www.icmp.int See https://www.icmp.int/press-releases/dna-exclusion-database-anonymous-secure-and-searchable/

Occasionally, during a police investigation, new information becomes available showing that a trace, which was thought to be relevant to the crime, has an origin that is not relevant to the crime. Additionally, a person may accidentally have been asked or ordered to give a buccal swab related to a crime illegally (for reasons not permitted by law). If such a DNA profile has already been included in the DNA database, it must be removed as soon as possible to prevent the presence of unauthorized DNA profiles in the DNA database.

ENFSI recommendation 21
Policies and procedures should be in place to ensure that DNA profiles deemed no longer relevant by the authorizing agent are deleted.

5. MATCHING RULES

This chapter describes the criteria which are used to determine whether two similar DNA profiles are 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 the DNA profiles of crime-related stains are correspondent, and the word “hit” if the DNA profile from a crime-related stain corresponds to the 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. The Council Decisions 2008/615/JHA and 2008/616/JHA (Prüm Decision), as well as the Proposal for a REGULATION OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL on automated data exchange for police cooperation (“Prüm II”), amending Council Decisions 2008/615/JHA and 2008/616/JHA and Regulations (EU) 2018/1726, 2019/817 and 2019/818 of the European Parliament and of the Council[39] use the term “match” exclusively. This document does not differentiate between a hit and a match, which are defined as follows:

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.[40]

In this document, the word ‘match’ will be used.

5.2 Search modes

DNA profiles can be compared in different ways. For example, in CODIS, these are called search stringencies:

- “High stringency” means that all alleles of every locus present in one DNA profile must also be present in the matching DNA profile in exactly the same amount;
- “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 homozygotes are designated by a single allele value in CODIS, searching at moderate stringency with single DNA profiles also detects an allele drop-out in one of the DNA profiles compared (e.g. 12/13 will also match the apparent homozygotes 12/ or 13/);
- “Low stringency” means that, in each locus 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.

Table 2 provides some examples of match results when a target[41] profile (15,16) is searched against different candidate profiles using the basic CODIS stringencies.

		Match stringency

[39] https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=celex%3A52021PC0784

[40] Formerly found at http://enfsi.eu/sites/default/files/documents/enfsi_dna_wg_terms_and_abbreviations_0.pdf, this document no longer exists on the ENFSI website.

[41] In CODIS, the profile with which the search is conducted, is called the target profile

Target profile	15,16	High	Moderate	Low
Candidate profile	15,16	Match	Match	Match
	15[42]	No match	Match	Match
	15,17	No match	No match	Match
	17,18	No match	No match	No match
	15,16,17	No match	Match	Match
	15,16,17,18	No match	Match	Match

Table 2: Examples of match results when a target profile (15,16) is searched against different candidate profiles in CODIS

In CODIS, mixed profiles cannot be compared to each other to find common donors. Recently, however, a program was developed which can be used to find common donors in mixed profiles exported from CODIS[43].

In some countries, a search strategy called "familial searching" is allowed. This means that, apart from searching for full matches, a search for matches with possible relatives of the donor of a crime scene associated DNA profile can also be conducted.

This search strategy may use the above-mentioned "low stringency" search mode to find possible parent-child relationships but may also search for profiles which:

1. share higher than the average number of alleles in random unrelated DNA profiles (which may indicate a possible sibling),
2. contain rare alleles (which may indicate a possible family member),
3. have a high likelihood ratio and therefore provide, for example, very strong support for the proposition that the persons are related (e.g. are siblings) rather than for the proposition that the persons are unrelated.

From a statistical point of view, the 3rd approach is the preferred strategy[44]. The programs mentioned in §22.6 Table 10 may be used to perform a familial search against a national DNA database. This requires, however, that all DNA profiles of persons from a national DNA database are present in or can be exported to this program. The outcome of the search is a starting point to find the true owner of the crime scene stain via tactical police work. This police work may be preceded or accompanied by Y-chromosomal and/or mitochondrial DNA testing, to decrease the number of candidates and/or their priority order. Simulation studies have been published showing the number of candidates a familial search in a DNA database may yield[45,46,47,48].

[42] In CODIS a homozygote is designated with a single allele value.

[43] K. Slooten (2017) Forensic Science International: Genetics 26,40-47

[44] D.J. Balding et al (2013) Decision-making in familial database searching: KI alone or not alone? Forensic Science International Genetics 7, 52-54.

[45] Hicks et al. (2010) Forensic Science International: Genetics 4 (5), pp. 316-322. Use of DNA profiles for investigation using a simulated national DNA database: Part II. Statistical and ethical considerations on familial searching.

[46] C. van Kooten et al. (2010) Poster nr 9 presented at the 21st International Symposium on Human Identification. It's all relative(s): Familial Searching in the Netherlands.

[47] Ge et al (2011) Journal of Forensic Sciences Volume 56, Issue 6, pages 1448–1456, November 2011 Comparisons of familial DNA database searching strategies.

[48] K. Slooten, and R. Meester (2014). "Probabilistic strategies for familial DNA searching." Journal of the Royal Statistical Society: Series C (Applied Statistics) Volume 63, Issue 3, pages 361–384, April 2014

The outcome of the search may point in the wrong direction, in the same way that a match may turn out to be an adventitious match. The search results should therefore be reported with a warning similar to the warning mentioned in Recommendations 25 and 26. Several extensive reviews of the ethical aspects of familial searching have been written by Professor Sonia Suter[49], Professor Erica Haimes[50], Dr Rafaela Granja[51] and many other researchers; several can be found at the Euroforgen website[52].

In recent years a growing trend has emerged where commercially available genealogy databases have been used by investigating police in the USA to identify the relatives of suspects in crime. However, this practice raises many ethical issues surrounding data protection, privacy and consent, since most people do not expect to participate in a criminal investigation when submitting their biological sample to commercial databases[53],[54]. In September of 2019, the US Department of Justice published their guidelines for the use of such databases in criminal investigations[55]: "The policy says "forensic genetic genealogy" should generally be used only for violent crimes such as murder and rape, as well as to identify human remains. The policy permits broader use if the ancestry database's policy allows such searches.[56]) Police should first exhaust traditional crime solving methods, including searching their own criminal DNA databases"[57].

More recently, some services like GEDmatch have separated their database into a "research" database, to be used for personal needs but not for law enforcement purposes[58], and a dedicated "forensic" database, developed specifically as an opt-in choice for customers and dedicated to support police and forensic teams[59].

5.3 Number of matching loci/match probability

The number of matching loci depends on the number of loci present in the DNA profiles to be compared and the number of loci the two DNA profiles have in common. The lower the number

[49] S M Suter (2010) Harvard Journal of Law & Technology Volume 23, Number 2. All in the Family: Privacy and DNA Familial Searching (https://www.euroforgen.eu/fileadmin/websites/euroforgen/media/Ethical_documents/Folder_5/Suter__2010_.pdf)

[50] E Haimes (2006) J Law Med Ethics 34 (2): 263-76 Social and ethical issues in the use of familial searching in forensic investigations: insights from family and kinship studies

[51] R Granja and H Machado 2019. Ethical Controversies of Familial Searching: The Views of Stakeholders in the United Kingdom and in Poland. Science, Technology & Human Values Vol.44(6) 1068-1092

[52] https://www.euroforgen.eu/dissemination-activities/ethical-legal-and-social-aspects-of-forensic-genetics/folder-5/

[53] https://www.theatlantic.com/science/archive/2019/10/genetic-genealogy-dna-database-criminal-investigations/599005/

[54] https://www.sciencenews.org/article/forensic-genetic-genealogy-companies-police-privacy

[55] https://www.sciencemag.org/news/2019/09/new-federal-rules-limit-police-searches-family-tree-dna-databases

[56] Initially, the US police used the database of GEDmatch secretly. When GEDmatch found out about this unexpected use of its database, it told its customers that their DNA data could also be used only for the investigation of rape and murder cases and advised people to opt-out if they did not want their data to be used for this purpose. However, when the police uploaded a DNA profile from a case which did not fulfil these criteria, it reversed its policy and opted everybody out and required an active opt-in from people to allow the police to use their DNA data to identify relatives of suspects. Very recently, however, the Florida police obtained a warrant to search the whole GEDmatch database, including all those who had opted out (https://futurism.com/cops-warrant-entire-dna-websites). 23andMe, another DNA genealogy company, has indicated that if they were to receive such a warrant, they would use every legal remedy possible to challenge it (https://blog.23andme.com/news/our-stance-on-protecting-customers-data/).

[57] https://www.sciencemag.org/news/2019/09/new-federal-rules-limit-police-searches-family-tree-dna-databases

[58] https://www.gedmatch.com/terms-of-service-privacy-policy

[59] https://pro.gedmatch.com/

of loci or overlapping loci, the higher the match probability of the DNA profile, and the higher the chance of an adventitious match, especially with large DNA databases. For this reason, DNA profiles included in the DNA database on a permanent basis should have a minimum number of loci, or, better yet, a maximum random match probability, as indicated in § 3.3. For reference samples, the number of loci is usually 10 or more, 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 in this case, the DNA profile should have a low match probability. The matching rules of the EU Prüm implementation decision as well as the INTERPOL DNA database in Lyon require a minimum number of 6 fully matching loci. For DNA profiles with more than 6 loci, a maximum of one (1) mismatch is permitted, provided all other loci match at high stringency.

5.4 Near matches

Several situations may lead to a near match (where one locus does not match or does not match completely) between two DNA profiles of the same person:

- A human error made during the production of one of the profiles. This may, for instance, happen when an allele is incorrectly called, a mixed profile is incorrectly split up into one or more of its contributors, or a typographical error is made while the DNA profile is entered manually into the DNA database. 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 the DNA database has been shown to be the greatest source of errors, hence this should be conducted using a process that detects typographical errors, such as the double-blind method (entering a DNA profile twice without seeing the first one and the database software checking if both entries are identical).

ENFSI recommendation 22
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. Automated processes reduce the possibility of human error, however, when DNA profiles are entered manually into the DNA database, a process that detects typing errors, for example the double-blind method of entry, should be used.

- An allele drop-in or drop-out due to low-level DNA profiling of one of the DNA profiles (see §3.5)
- The occurrence of so-called “null alleles”. These are alleles which are not amplified during the PCR reaction due to a mutation in the primer binding-site region. When two STR-typing kits use different primers for the same heterozygous locus, and the DNA of a person contains a mutation in the primer binding region used in one kit but does not contain a mutation in the primer region 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 unexpected low peak height of the apparent homozygote, but this requires an attentive DNA analyst or intelligent allele-calling software[60]. A special case of a null allele, not caused by a primer binding-site mutation but by a deletion instead, is the disappearance of the Y-amelogenin allele, which makes the DNA profile of a male look female.
- The occurrence of shifted allele size in one of the DNA profiles. When 2 kits use different primers for the same heterozygous locus and the DNA of a person contains a deletion or an insertion after the primer region used in one kit but before the primer region used in the

[60] More information about the occurrence of null alleles can be found at: https://strbase.nist.gov//NullAlleles.htm.

other kit, there will be a shift in the size of an allele in one DNA profile compared to the other (e.g. 10.3 and 11).

Given the above-mentioned phenomena, only searching a DNA database for full matches (high stringency) may lead to missed matches (false negative matches). To find false negative matches, a “less stringent” search strategy must be used, either permanently or occasionally. Some countries already perform this kind of regular quality control check, by searching for near matches, which are then checked for possible errors. Searching for near matches may lead to matches with close relatives, hence the pros and cons of this strategy should be evaluated in advance (see also chapter 9). The software used for the international comparison of DNA profiles under the terms of the EU Prüm decision also allows for one mismatch, to detect near matches[61][62]. After finding such a match, both countries may contact each other to verify the original data and the processing methods. Near matches involving 8 loci or less often prove to be adventitious (false positive), but it may be worth investigating further, if this can assist in the investigation of a serious case (see also chapter 9).

The above-mentioned stringencies in CODIS can be adapted and combined to create more robust searches that can take into account allele drop-in and drop-out in a more flexible manner, thus increasing the chances of a match being returned. For example:

- A “Partial loci” search can be initiated by marking all loci to High stringency, with the exception of those loci marked as partial when inputting the data – these should be set to Moderate stringency. This setting guarantees that all known (complete) loci will be evaluated as such, but will find more potential matches for the partial loci. Matches otherwise missed will be included in search results and can be reviewed accordingly.
- The “Floating moderate” search can be initiated by setting all loci to High stringency, while configuring the search to allow for a specific number of loci to match at Moderate stringency.

Other dedicated search strategies can be developed and adapted for different situations to return the best possible results, which can then be reviewed accordingly to determine if they are true, investigatively useful matches or not.

ENFSI recommendation 23
To prevent and detect false exclusions (e.g. true matches that are not found due to an error in one of the DNA profiles), DNA profiles should be searched using a full Database search allowing at least one mismatch or other dedicated search strategy. The original data of DNA profiles involved in such near matches should be checked for possible errors during their production and processing.

5.5 Match validation

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

- Confirmation of the original DNA analysis:
  - Many states have the legal option of retaining the collected biological material after analysis, as long as the DNA profile is also stored. This allows repeated re-analyses and quality improvement of the DNA profiles through upgrades at any time.
  - Some countries require a new sample to be taken from the person of interest, if this person is available for repeated sampling, and have that new sample re-analyzed.

[61] https://eur-lex.europa.eu/legal-content/en/TXT/?uri=CELEX:32008D0616, 1.2 Matching Rules

[62] Forensic DNA Profiles Crossing Borders in Europe (Implementation of the Treaty of Prüm). Profiles in DNA 2011. (https://worldwide.promega.com/resources/profiles-in-dna/2011/forensic-dna-profiles-crossing-borders-in-europe/)

- 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 analyzed to decrease the possibility of an adventitious 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 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 true match (see § 3.8). This type of match should be validated and explained by a qualified forensic DNA expert.

6. DISPOSITIONING

After finding a candidate match in the DNA database, this match must be confirmed. When a match is found between two full DNA profiles, this confirmation can be done by specially qualified DNA database personnel or using an automated process. However, matches with partial and/or mixed profiles must be examined and assigned a final disposition by a DNA expert. Usually, the final disposition of a match can also be registered in the DNA database to prevent the same match from being reported again after a new search action.

6.1 Match counting

One of the parameters to determine the efficiency of a DNA database is the number of matches it generates. Counting the matches between two DNA profiles is easy. In serial crimes committed over a period of time, however, different approaches are possible. Table 3 shows the number of matches that will be found when a single (unknown) individual commits a series of 8 crimes over time and leaves DNA at each crime scene.

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 3. Number of matches that will be found when a single (unknown) individual commits a series of 8 crimes over time and leaves DNA at all 8 crime scenes.

For a series of X crimes, the number of matches is (X-1)X/2. For high volume crime cases, this manner of counting leads to match counts which may not representative when compared to the number of cases involved. This is why ENFSI counts matches in serial crimes in a different manner. The following definition is taken from the document “ENFSI DNA Working Group Terms and Abbreviations”[63]:

For statistical purposes, matches with multiple identical profiles from the same case will be counted as one match, but as separate matches if they originate from different cases. In serial crimes, the total number of 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 matches). If subsequently the DNA profile of a person matches the series, it yields 8 stain-to-person 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.

[63] Online reference no longer available.

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

6.2 Output/efficiency measurement

The output of a DNA database is the number of matches it generates, either at the national level or at the international level. The output measurement will be different for each country even if they have the same number of matches due to the different number of DNA profiles included in their respective DNA database. Simon Walsh et al.[64] have published a formula 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 in the 'offender' database
M = active criminal population
C = number of crimes in the '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: $\alpha\omega = HM/NC$.

Walsh et al. propose an efficiency measurement parameter, the return index (RI), where RI=H/NC. As this parameter is inversely proportional to the size of the database, it wrongly suggests that large DNA databases are less efficient than smaller DNA databases. The ENFSI DNA Working Group proposes the use of two different DNA database performance parameters, which express two different types of efficiencies:

1) H/C: the number of stain-to-person matches, relative to the number of stains included in the DNA database (also known as the match rate). This parameter expresses the chance that a stain profile included in the DNA database will match a reference profile. This is a very important parameter, because it shows the crime-solving capacity of the DNA database and whether the right items were collected by the crime scene officers. It is self-evident that more stains will be matched to a person as more members of the (criminal) population are included in the DNA database. So, as the size of the DNA database increases, H/C will increase. One can determine the match rate at a certain point in time (including all stains that have ever been included) or during a certain time interval. The UK for instance determines the match rate per month so they measure how many matches were found with the stains that were uploaded in a certain month. This approach also includes matches which were found after stains that initially did not match a person, match a person that was included at a later date.
2) H/N: the number of stain-to-person matches relative to the number of persons included in the DNA database (the percentage of persons in the database that are involved in matches). This parameter indicates whether the right people have been sampled for inclusion in the DNA database. This parameter is also important, because it does not make sense to allocate resources for including people into the DNA database who will never be involved in matches

[64] S.J. Walsh et al (2010) Modeling Forensic DNA Database Performance; J. For. Sci. 55(5) 1174-1183

(even though it is a one-time process). To properly calculate this parameter, duplicate person profiles and additional matches with the same person should be excluded.

Also this parameter can be followed over time, and 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).

Because the policies for keeping or removing DNA profiles from stains and persons in a DNA database are different in different countries, table 4 cannot be used to compare the DNA database performance of the different ENFSI countries using the parameters H/C and H/N.

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).

European DNA databases*	Population size	Persons						Stains			Matches				Date Update	Remarks
		A	S	CO	T	Prum	Duplicate	T	Prum	Remarks	Person-Stain	Stain-Stain	Person matches per person	Person matches per stain		
													#DIV/0!	#DIV/0!		
Albania													#DIV/0!	#DIV/0!		
Armenia													#DIV/0!	#DIV/0!		
Austria	8,980,000		260 739		260 739	260 739	No	137 922	46 282		37 034	16 075	0,14	0,27	01.08.2022	Matches to persons national DNA database without Prüm hits
Belgium	11 569 034	0	3 430	62 264	65 694	65 694	No	65 213	47 473	More than one stain profile per crime scene	13 665	25 948	0,21	0,21	31.12.2021	Matches to persons national DNA database without Prüm hits
Bosnia & Herzegovina										More than one stain profile per crime scene			#DIV/0!	#DIV/0!	05.04.2022	no DNA DB - DNA law in draft version
Bulgaria													#DIV/0!	#DIV/0!		
Croatia	3 888 529	/	4 285	494	4 902	4 902	Yes	6 838	6 185	Only one stain profile per crime scene/ All identified stain	603	N/A	0,12	0,09	31.12.2021	Matches to persons national DNA database without Prüm hits
Cyprus	800 000	0	309	1 434	1 743	517	Yes	17 689	3 959	Persons Prum only unique all others duplicates allowed	357	119	0,20	0,02	31.12.2021	
Czech Republic	10 700 000				262 218	262 204	No	29 909	26 544	Identified stains processed by the authorities removed,Only one stain profile per crime scene	544	76	0,0021	0,02	21.02.2022	
Denmark													#DIV/0!	#DIV/0!		
Estonia	1 328 439				65 087	46 388	No	13 787	6 274	All identified stain profiles removed ; Only one stain profile per crime scene	554	83	0,01	0,04	31.12.2021	
Finland	5 550 000				198 307	198 307	Yes	14 105	14 105	All identidied stain profiles removed. More than one stain profile per crime scene. Stain profiles removed when consideration of charges for the crime has expired.	39 960	na	0,20	2,83	31.12.2021	
France	67 813 396	168 860	4 590 812	629 135	5 219 947	5 219 947	Yes	805 998	475 757	Identified stain profiles removed only on request of the authorities More than one stain profile per crime scene	354 865	85 291	0,07	0,44	31.12.2021	S/S FR/FR = 83 557 (national hit checked by DB operator and report sent to the investigator) S/P FR/FR = 351 341 (national hit checked by DB operator and report sent to the investigator) S/S FR/EM = 14 103 prum hit checked by DB operator – including 1734 prum hit report sent to the investigator S/P FR/EM = 24 686 prum hit checked by DB operator – including 3524 prum hit report sent to the investigator
Georgia													#DIV/0!	#DIV/0!		
Germany	83 700 000				838 429	828 206	No	380 538	368 881	All identified stain profiles removed	282 890	77 335	0,34	0,74	31.12.2021	
Greece	10 678 632				19 544	19 537	Yes	22 470	10 285	Only one identical stain profile per crime scene	2 746	3 222	0,14	0,12	31.12.2021	
Hungary	9 769 000				228 141	154 694		11 799	6 612	All identified stain profiles removed, Only one identical stain profile per crime scene	5 245	439	0,02	0,44	31.12.2020	
Iceland													#DIV/0!	#DIV/0!		
Ireland	4 980 000		30 255	13 180	43 435	43 435	Yes	9 727	4 442	All stain profiles ever added	4 709	324	0,11	0,48	01.01.2022	
Italy	59 236 000	0	0	41 700	41 700	41 700	No	27 629	11 200		1 300	2 137	0,03	0,05	31.12.2021	
Kosovo**													#DIV/0!	#DIV/0!		
Latvia	1 920 000		59 541	10 565	70 106	70 106	Yes	12 474	7 049	All identified stain profiles removed	3 854	284	0,05	0,31	31.12.2021	
Liechtenstein	38 500				420		No	407		All identified stain profiles removed	345	103	0,82	0,85	31.12.2021	
Lithuania	2 800 000		129 993		129 993	129 993	Yes	8 136	7 586	All identified stain profiles removed	5 521	673	0,04	0,68	31.12.2021	
Luxembourg													#DIV/0!	#DIV/0!		
North Macedonia	2,082,658				27 582		Yes	13 959		More than one stain profile per crime scene	3 882	512	0,14	0,28	31.12.2021	
Malta													#DIV/0!	#DIV/0!		
Montenegro													#DIV/0!	#DIV/0!		
Netherlands	17 700 000		23 045	331 388	354 433	354 433	Yes	69 529	41 556	Identified stains processed by the authorities removed	38 222	/	0,11	0,55	07.07.2022	
Northern Ireland													#DIV/0!	#DIV/0!		
Norway	5,385,000		2760	116 760	119 520		No	12981		All identified stain profiles removed	29965	2173	0,25	2,31	31.12.2021	
Poland													#DIV/0!	#DIV/0!		
Portugal													#DIV/0!	#DIV/0!		
Romania	22 000 000		4 970	60 055	65 025	65 025	Yes	2 782	2 453	All stain profiles ever added	2 307	461	0,04	0,83	31.12.2021	
Scotland													#DIV/0!	#DIV/0!		
Serbia	7 000 000				13 385			800		All identified stain profiles removed, Only one stain profile per crime scene	135	23	0,01	0,17	31.12.2020	
Slovakia	5 500 000	0	24 957	54 201	79 158	81 203	No	14 752	13 397	All identified stain profiles removed	8 360	2 834	0,11	0,57	21.01.2021	
Slovenia	2 111 461				25 127	1 714	Yes	8 960	694	All identified stain profiles removed. We include in DNA database more than one stain profile per crime scene if stains have different profiles.	167	21	0,01	0,02	31.12.2021	
Spain	46 552 504		408 407	35	408 442	405 328	Yes	122 778	57 355	All stain profiles ever added. Only one stain profile per crime scene	67 184	76 004	0,16	0,55	01.03.2022	
Sweden	10 350 000		16 300	152 900	169 200	169 200		43 100	42 800	All identified stain profiles are removed. Only one stain/person per crime scene is included in the database.	66 200	20 100	0,39	1,54	31.12.2021	
Switzerland	8 637 000				184 285		No	101 550		All identified stain profiles removed	87 079	22 276	0,47	0,86	31.12.2021	
Turkey													#DIV/0!	#DIV/0!		
UK (England & Wales)					6 212 725	6 174 815		648 260	251 263				0,00	0,00	31.12.2021	
Ukraine	41 167 336		10 964	300	20 239		No	24 191		All identified stain profiles removed. More than one identical stain profiles per crime scene.	1 297	2 604	0,06	0,05	01.01.2022	
													#DIV/0!	#DIV/0!		
Total	**435 789 831**				**15 129 526**			**2 628 283**			**1 058 990**			**#DIV/0!**		

A = Arrestees S = Suspects CO = Convicted offenders T = Totals (or when no distinction can be made)

When using these data one should realize that:
 # There are countries that add more than one DNA-profile of a person to their DNA-database
 # There are countries that add more than one unique DNA-profile of a stain per crime scene to their DNA-database
 # Counties use different removal regimes for DNA-profiles of stains: never or immediately after a match with a person or after the authorities have dealt with the match with the person
 # Counties use different removal regimes for DNA-profiles of persons: After some storage time and/or if a person is not prosecuted or convicted
 # Stain-to-person matches can be so-called "cold hits" (matches for which no suspect was known) or matches where both a stain and a suspect were added to the DNA-database
 # One person can match more than one stain

***This survey is organized and updated by the DNA DB & legislation subgroup of the ENFSI DNA expert WG and by the CODIS EU users group**
**** This designation is without prejudice to positions on status, and is in line with UNSC 1244 and the ICJ opinion on the Kosovo Declaration of Independence.**

Table 4. Annual ENFSI overview of European DNA databases for 2021.

As a national DNA database is regularly 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 24
As a national DNA database is regularly subject to attention from the public, politicians and the media, a DNA database manager should consider establishing tools to monitor the effectiveness of their DNA database and communicating this objective information publicly.

The above-mentioned performance parameters only apply to the performance of the DNA database itself. The efficiency of a DNA database as a tool to investigate and solve crimes also depends on many other factors, which have been reviewed by Bieber[65]. The fate of 625 international matches reported to the Dutch authorities in 2010 was investigated during the ISEC-PIES project[66]. Only 37 of those matches were used in court. Jennifer Doleac has investigated the effects of DNA databases on crime in the USA[67], and in 2021 an in-depth study by Tegner Anker, Doleac and Landersø on the effect of the expansion of the Danish national DNA database with regard to crime and other socio-economic factors was published[68]. Amankwaa and McCartney have examined the effectiveness of the UK national DNA database from a more financial point of view[69]. Additionally, the efficiency of DNA databases in the context of cross-border exchange of data has also been examined within the scope of the EU Prüm Decisions[70].

[65] F.R. Bieber (2006) Turning base hits into earned runs: Improving the effectiveness of forensic databank programs. Journal of Law, Medicine & Ethics 34(2) p 222-233.
[66] https://nicc.fgov.be/pies
[67] Doleac, Jennifer (2016) The effect of DNA databases on crime. American Economic Journal; Applied Economics 9(1): 165-201
[68] Anker, Anne Sofie Tegner, Doleac, Jennifer L., & Landersø, Rasmus (2021). The Effects of DNA Databases on the Deterrence and Detection of Offenders. AEJ: Applied Economics
[69] Amankwaa, Aaron Opoku and Carole McCartney (2019) The effectiveness of the UK national DNA database. Forensic Science International: Synergy, Vol.1, 45 – 55.
[70] http://www.europarl.europa.eu/RegData/etudes/STUD/2018/604971/IPOL_STU(2018)604971_EN.pdf

7. ADVENTITIOUS MATCHES

As DNA databases become larger, the chance of adventitious matches occurring also increases, especially with partial and mixed profiles and the 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 their DNA database. Table 5 may be helpful in this respect. This table gives the expected number of adventitious matches when a DNA database of a given size is searched using a DNA profile with a given match probability.

		Size of the DNA database			
		10.000	**100.000**	**1.000.000**	**10.000.000**
RandomMatch 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 5: Expected number of adventitious matches when searching a DNA database of a given size using a DNA profile with a given random match probability

The expected numbers of adventitious matches in Table 5 are the expected numbers for one search using a DNA profile with a given random match probability in a DNA database of a given size. On an annual basis, the number of searches is usually 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 multiplied by the annual number of those searches. So a DNA database in which many crime scene DNA profiles are compared can expect more adventitious matches on an annual basis than a DNA database of similar size in which fewer crime scene DNA profiles are compared per year. An estimation of the annual expected number of adventitious matches can be made by separating the crime-related DNA profiles into match probability classes, and estimating how many of each class are compared to the reference samples in the DNA database.

Table 6 gives a theoretical example of a DNA database containing 4 million reference DNA profiles, with 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 (but there may be more or less than the expected number).

DNA-database size	RMP crime related stain	Number of searches	Expected Number of Adventitious 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
Total		70.000	

Table 6: Theoretical example of a DNA database containing 4 million reference DNA profiles, with which 70,000 crime-related DNA profiles of different random match probabilities are compared.

Another factor that 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 7 lists the theoretically calculated mean approximate match probabilities between various kinds of relatives, as compared to a random match probability of 1 in 10^{12}.

Relationship	**Match Probability**
No relationship (random match probability)	1 in 10^{12}
First cousin	1 in 10^{11}
Half-sib or uncle/nephew	1 in 10^{10}
Parent or child	1 in 10^{8}
Full-sib	1 in 10^{5}

Table 7: Approximate match probabilities[71] between various kinds of relatives, as compared to a random match probability of 1 in 10^{12}.

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 have a sibling in the DNA database, 5,000 DNA profiles will have a match probability of 1:10,000 instead of 1:10,000,000,000. The extra expected number of adventitious matches caused by the DNA profiles of these 5,000 persons with a sibling in the DNA database is 5,000 x 1/10,000 = 0.5. This is only a small extra number, when 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 who 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, a next generation of relatives may also be present. In addition, a recent study of the Danish DNA database indicated that the effect of relatives must not be ignored[72].

Because the risk of adventitious DNA database matches cannot 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. An example of such a warning can be found in Appendix 3.

[71] A.J. Hopwood et al (2012) Science and Justice 52, 185-190. Consideration of the probative value of single donor 15-plex STR profiles in United Kingdom populations and its presentation in United Kingdom courts.
[72] Tvedebrink T, Eriksen PS, Curran JM, Mogensen HS, Morling N. (2012) Analysis of matches and partial-matches in a Danish STR data set. Forensic Sci Int Genet. 6(3): 387-92.

ENFSI recommendation 25
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. (A warning can be included in a report, indicating the factors that increase the possibility of an adventitious match such as size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members, etc.).

To compare theoretical numbers of adventitious matches with actual 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, as Tvedebrink et al. have done[73].

Special attention must be paid to the occurrence of false positive matches when performing large-scale international comparisons of DNA profiles, such as those based on the EU Prüm decision[74]. As some countries have expressed discontent with the 6 loci rule (a minimum of 6 loci must be matching)[75], the Next Generation Prüm project, among other goals, aims to discuss the necessity for changes to the matching rules (increase the lower limit to 8 matching loci) in order to decrease the frequency of false positive matches[76]. However, because there are also true 6 and 7 locus matches (which can be found by additional DNA testing), it is being recommended that the matching rules remain as they are, and let each country decide what to do with 6 and 7 locus matches according to their own internal criminal justice requirements and processes.

8. REPORTING RESULTS

Matches in DNA databases are often so-called “cold hits”, which means that there was no prior evidence suggesting that the match would occur. Even in cases where there is prior evidence, this is not usually known to the DNA database manager. This means that reporting should be done in such a way that does not create misconceptions 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 or the likelihood ratio of the corresponding loci/alleles should be reported, to provide the person receiving the report with an idea of the evidential value of the match. Because the present kits produce DNA profiles with random match probabilities which are difficult to comprehend for lay people, Hopwood et al.[77] have recommended the use of maximum likelihood ratios for reporting the weight of the evidence for a fully matching 15-plex DNA profile, shown in Table 8.

Relationship	Likelihood ratio
No relationship (random match probability)	1 in 10^9

[73] Ibid.
[74] Forensic DNA Profiles Crossing Borders in Europe (Implementation of the Treaty of Prüm). Profiles in DNA 2011. (https://worldwide.promega.com/resources/profiles-in-dna/2011/forensic-dna-profiles-crossing-borders-in-europe/)
[75] http://www.europarl.europa.eu/RegData/etudes/STUD/2018/604971/IPOL_STU(2018)604971_EN.pdf, Section 4.3
[76] http://data.consilium.europa.eu/doc/document/ST-12275-2018-INIT/en/pdf
[77] A.J. Hopwood et al (2012) Science and Justice 52, 185-190. Consideration of the probative value of single donor 15-plex STR pro-files in United Kingdom populations and its presentation in United Kingdom courts.

First cousin	1 in 10^9
Half-sibling or uncle/nephew	1 in 10^9
Parent or child	1 in 10^7
Full-sibling	1 in 10^5

Table 8: Proposed maximum likelihood ratios for reporting the weight of the evidence for a fully matching 15-plex DNA profile

The evidential value of matches with mixed profiles should be reported as a likelihood ratio, which is the ratio of the probability of the results given two alternative propositions: 1) the crime stain contains DNA from the suspect and an unknown unrelated person and 2) the crime stain contains DNA from two unknown, unrelated persons (see also § 3.9 and recommendation 12). The reported LR is only valid for the evaluated propositions and should be recalculated if alternative propositions are put forward.

There has been discussion in the literature and in courts about the appropriate way to report the evidential value of DNA database search results[78,79,80]. In essence, the difference between the evidential value of a DNA match obtained through a DNA database search and a DNA match obtained through comparison with a single suspect lies in other evidence available in the case: with a "cold hit", other incriminating evidence against the matched person may be completely missing, whereas the comparison of a single suspect is necessarily based on other incriminating evidence. As argued in Sjerps and Meester[81], the report should therefore contain a warning concerning the possibility of adventitious matches, as mentioned in recommendation 21. This warning should make clear that adventitious matches are possible, and that this possibility should be taken into account, especially when the database match was obtained from a search with a partial DNA profile and in situations where other incriminating evidence is missing or weak. Meester and Sjerps[82] have suggested the inclusion of 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 determine the evidential value of the match. An alternative option, which is currently used by the Netherlands Forensic Institute, is to include a special textbox in the match report, which explains the possibility of adventitious matches (see Appendix 3).

ENFSI recommendation 26
A DNA database match report of a crime scene-related DNA profile with a person should be informative. It may include an indication of the evidential value of the match (RMP/LR), a warning indicating the possibility of adventitious matches (as mentioned in recommendation 25), and the implication that the match should be considered together with other evidence.

[78] Kaye, DH. (2009) Rounding up the usual suspects: a legal and logical analysis of DNA database trawls, North Carolina Law Review 87: 425-503.
[79] Gittelson S. et al. (2012) The database search problem: A question of rational decision making. Forensic Sci Int. 222, 186-199
[80] Biedermann A. et al. (2012) A Bayesian network approach to the database search problem in criminal proceedings. Investigative Genetics 3, 16
[81] Sjerps, M. & R. Meester (2009). Selection effects and database screening in forensic science. Forensic Sci Int. 192 (2009), 56–61.
[82] Meester, R. and Sjerps, M. (2004) Why the effect of prior odds should accompany the likelihood ratio when reporting DNA evidence; Law, Probability and Risk, 3, 51-62.

9. DNA DATABASE SOFTWARE[83]

Software programs designed for the storage and comparison of DNA profiles are referred to as DNA database software. Some programs also have other functions. DNA database software can either be internally developed by a country to meet its own specific needs, or it can be obtained from a developer, who provides it without cost or offers it on a commercial basis. Examples of DNA database programs which can be obtained without cost are:

- CODIS, which has been developed by the FBI for the USA, but which is also available for non-USA law enforcement organizations. A private company (ECS Tech, formerly Leidos) runs a well-organized and skillful helpdesk and computer-based training is available. 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).
- Argentina has developed its own DNA database program called GENis, as an open source system developed to run forensic DNA database at local, regional and national levels[84]

Programs which are or have been commercially available are[85]:

- FSS-iD™, afrom the former Forensic Science Service in the United Kingdom
- Dimensions, from the Austrian company Ysselbach Security Systems
- eQMS::DNA, from the Croatian company Pardus (www.Pardus.hr)
- *f*DMS-STRdb, distributed by the Czech Republic company Forensic DNA Service (http://dna.com.cz/files/file/fdms-strdb.pdf)
- *Rapid**DNA*** from the Australian company Forensics International (http://www.rapiddna.biz)
- SmallPond (http://www.smallpondllc.com/)
- Bode Match (http://www.bodecellmark.com/pages/bode-match)

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

One company has launched a cloud-based DNA database specifically for local law enforcement agencies to archive, search and reference DNA profiles from crime scene samples[86] more easily. It remains to be seen if this storage method will be acceptable to the authorities responsible for DNA testing and/or the data protection authorities.

Table 9 shows which DNA database programs are used by different European countries and some international organizations.

[83] The mentioning of trade names does not mean that ENFSI recommends or endorses any of these programs. The aim of ENFSI is to provide insight into what is available on the market.

[84] Ariel Chernomoretz et al. (2020) GENis, an open-source multi-tier forensic DNA information system. Forensic Science International: Reports 2

[85] Some of these links might no longer be functional.

[86] http://www.sorensonforensics.com/

Country, regional entity or international organization	DNA database program
Albania	CODIS
Armenia	No DNA database yet
Austria	Self-developed program
Belgium	CODIS
Bosnia & Herzegovina	CODIS
Bulgaria	Self-developed program
Croatia	CODIS
Cyprus	Self-developed program
Czech Republic	CODIS
Denmark	Self-developed program + CODIS
Estonia	CODIS
Finland	CODIS
North Macedonia	eQMS::DNA
France	CODIS + Self-developed program
Germany	Self-developed program
Georgia	CODIS
Greece	CODIS
Hungary	CODIS
Iceland	CODIS
Ireland	CODIS
Italy	CODIS
Kosovo*[87]	CODIS
Latvia	CODIS
Liechtenstein	Included in the Swiss DNA database
Lithuania	CODIS
Luxembourg	Self-developed program
Malta	CODIS
Montenegro	CODIS
Netherlands	CODIS
Northern Ireland	Self-developed program
Norway	CODIS
Poland	CODIS
Portugal	CODIS
Romania	CODIS
Russia	Self-developed program
Scotland	Self-developed program
Serbia	Self-developed program
Slovakia	CODIS
Slovenia	Self-developed program
Spain	CODIS
Sweden	CODIS
Switzerland	CODIS
Turkey	No DNA database yet
Ukraine	Self-developed program
United Kingdom (England, Wales, Scotland, North	Self-developed program

[87] This designation is without prejudice to positions on status, and is in line with UNSC 1244 and the ICJ opinion on the Kosovo Declaration of Independence.

Ireland)[88]	
INTERPOL	Self-developed program
Prüm Treaty countries (exchange database)	Self-developed program or CODIS
ICMP	Self-developed program

Table 9: DNA database programs used by different European countries, regional entities and some international organizations.

[88] Northern Ireland and Scotland have their own DNA databases, even though their profiles are also loaded to the UK National DNA Database.

10. DATA INTEGRITY CONTROL MEASURES

For forensic reasons, and in accordance with personal data protection legislation, DNA profiles and their associated information should be entered and stored correctly. For this reason, the manual entry of DNA profiles should be avoided. If this is not possible, DNA profiles should be entered using the double-blind method[89]. 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 require access for various reasons (data entry, searching, etc.). Regular back-ups should be made, stored in a safe place and recovered at regular intervals to simulate recovery from a disaster. If the DNA profiles and/or the information associated with DNA profiles are also registered in another system, like a LIMS or a judicial or police system, the contents of these systems should be regularly compared to verify whether the systems are properly synchronized.
Official recognition of compliance with personal data protection legislation may be sought by submitting the organization and its work procedures to an independent, external audit.

ENFSI recommendation 27

- DNA profiles should be entered into a database in a way that guarantees correct entry.
- Access to the DNA database should be limited to those persons who require access, by physical and organizational measures.
- Regular back-ups should be made, stored in a safe place, and recovered 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 verify whether they are properly synchronized.

The above-mentioned recommendations are made to maximize the reduction of errors. It has been shown, however, that despite all of these measures, DNA profiles may still 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 appear 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 or false exclusions (e.g., true matches that are not found due to an error in one of the DNA profiles), regular full DNA database searches, allowing one or more mismatches, should be performed, as indicated and recommended in §5.2. The software used by countries exchanging DNA profiles under the terms of the EU Prüm Decision allows for one mismatch. When a match between two DNA profiles contains a mismatch at one of the loci, the original data of both DNA profiles should be checked for any errors.

If no error is found in either profile, it must be concluded that the mismatch is a true mismatch. During the international exchange of DNA profiles based on the EU Prüm Council decisions, many 6 and 7 locus matches plus a mismatch are found. Nearly all of these mismatches have proven to be true mismatches, and statistical calculations also show that these high numbers of

[89] 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.

6 and 7 locus matches plus a mismatch are to be expected. Some countries, therefore, have chosen to ignore these matches, except for those which may assist in solving serious cases.

11. 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 information associated with the DNA profile. As indicated in the previous chapter, regular comparisons of the systems are then required to verify 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.

12. 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 to an unknown person and one of the crime scenes has a fingerprint matching a known person, the combined information may solve the whole series of cases. Countries like the United Kingdom[90], Switzerland[91] and others are working on systems to combine the contents of different forensic databases and to visualize the links between different cases and different persons which result from that combination. Figure 2 shows an example of how the visualization of the links between a cluster (or clusters) of crimes and persons derived from DNA and fingerprint information can be charted.

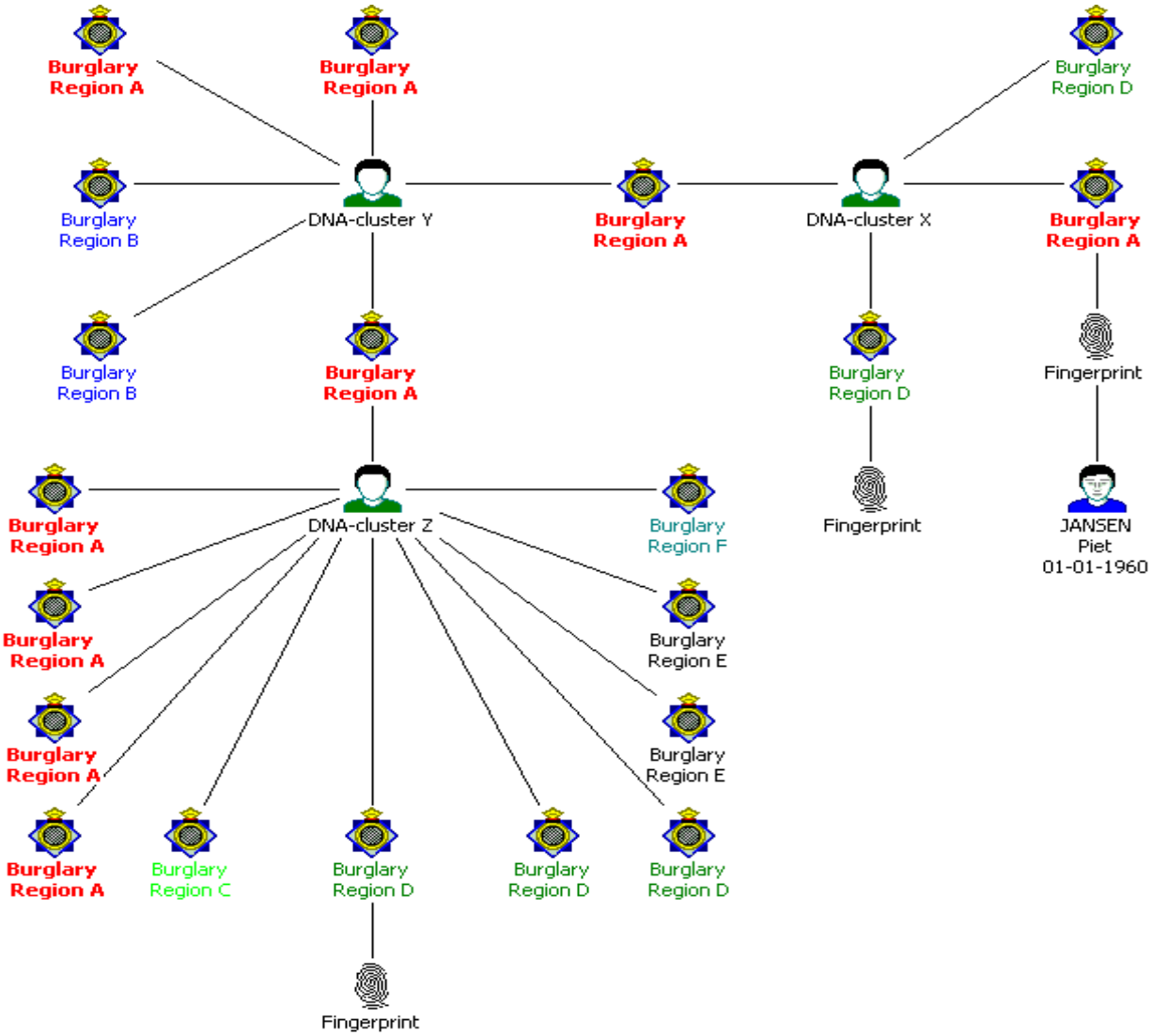

Figure 2: Three DNA clusters (X, Y, Z) linked by 2 crime scenes where DNA profiles from 2 clusters were found (X+Y and Y+Z) combined with two unidentified and one identified fingermarks.

90 http://webarchive.nationalarchives.gov.uk/+/http://www.homeoffice.gov.uk/docs2/resconf2002/richardlearyrolenimflints.pdf

91 Ribaux et al. (2010) Intelligence-led crime scene processing. Part II: Intelligence and crime scene examination. Forensic Science International 199 (1-3) 63-71

ENFSI recommendation 28 Investigating authorities should consider combining the information from a national DNA database with other types of evidence to increase the likelihood of identifying leads in other crimes.

13. AUTOMATION OF WORK PROCESSES

Automation of DNA database work 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 error, they should be introduced for those processes that are straightforward, like the production of DNA profiles from reference samples.

As already stated in § 2.7, candidate matches with mixed profiles should always be checked by a DNA expert to determine whether the numerical match could be a true 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.

Recently, Rapid DNA instruments has been developed, for the fully automated production of DNA profiles from reference samples without human intervention. These systems allow for immediate searching of qualifying arrestee DNA profiles against unsolved crimes of special concern (sexual assault/rape, homicide, kidnapping and terrorism cases), while the arrestee is in police custody during the booking process.[92] It can also be used for rapid identification in case of mass fatalities[93],[94]. Currently, the USA have progressed furthest in the implementation of rapid DNA, although evaluation studies have and are being conducted in Europe[95],[96].

However, some concerns have been raised in the implementation of this technology[97],[98]. The field is evolving quickly, and efforts are being made into the development of crime-stain-appropriate rapid DNA machines as well, with varied success[99]. Nevertheless, it should be noted that in Europe, for example, there are binding quality assurance requirements in regular DNA laboratories (EN/ISO 17025), as well as country-specific legislation, that may prohibit the use of this technology in the forensic area. The use of this rapid DNA technology for crime scene stain analyses is currently not recommended, as it could lead to the destruction of irretrievable important biological stain material[100].

[92] FBI.gov, National Rapid DNA Booking Operational Procedures Manual

[93] Bowman et al. (2022) Rapid DNA from a disaster victim identification perspective: Is it a game changer? FSI: Genetics Volume 58

[94] Watherston et al. (2022) An in-field evaluation of rapid DNA isntruments for disaster victim identification. Int J Legal Med 136 (2): 493-499

[95] Rapid DNA: A summary of available Rapid DNA systems, NFC Report 2022:02

[96] https://www.brightlands.com/en/brightlands-maastricht-health-campus/news/trial-starts-rapid-dna-testing-system

[97] https://www.latimes.com/california/story/2019-09-24/rapid-dna-forensics-crime-police

[98] L. Wilson-Wilde, F. Pitman, Legislative and policy implications for the use of Rapid DNA technology in the Australian context, Forensic Sci. Policy Manage. (2017), http://dx.doi.org/10.1080/19409044.2017.1335809

[99] Boiso et al. (2017) RapidHIT for the purpse of stain analyses – An interrupted implementation. Forensic Science International: Genetics Supplement Series 6 e589–e590

[100] Hares, Kneppers, Onorato, Khan (2020) Rapid DNA for crime scene use: Enhancements and data needed to consider use on forensic evidence for State and National DNA Databasing - An agreed position statement by ENFSI, SWGDAM and the Rapid DNA Crime Scene Technology Advancement Task Group Forensic Sci Int Genet 48:102340

14. STORAGE OF CELL MATERIAL

The cell material of crime scene stains from which a DNA profile has been generated is usually stored. Regarding the storage of cell material from reference samples, however, different countries have different policies. Some countries allow the storage of reference samples for later reuse, if this becomes technically or legally necessary, while in other countries, the reference samples must be destroyed as soon as the DNA profile has been generated and included in the DNA database. The following three examples show 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 for higher evidential value and higher sensitivity, 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 that could not be examined in the past. But if the stain has been retyped with new technology, the reference sample must also be retyped, to enable a more stringent comparison between the two. If the reference sample has been destroyed, the police or the judiciary must obtain a new reference sample from the suspect, which may not always be possible.

Example 2
A Prüm Treaty member country sends an SGM+ DNA profile of a crime scene stain to another Prüm Treaty member country. A match with a reference DNA profile is reported for 7 loci due to the fact that the matching country uses a different kit. To exclude the possibility of an adventitious match, the SGM+ country first tries to improve its own DNA profile, but if this is not possible, it requests that the matching country 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.

Example 3
Countries which are allowed to perform familial searching in their DNA database usually get many possible candidates after an initial DNA database search. False positives can be eliminated from this possible candidate list by additional Y-chromosomal or mitochondrial DNA testing. However, this is only possible if the samples from which the DNA profiles were generated are still available.

The ENFSI DNA Working Group realizes that the storage of cell material from reference samples is politically a 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 are 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 the “better safe than sorry” principle and choose to destroy the sample after a profile has been included in the DNA database. These concerns have not been reduced with the implementation of GDPR and LED legislation in May of 2018.

On the other hand, one could also argue that keeping the samples enhances privacy, because there is no need for resampling if additional DNA testing is necessary to investigate a possible false positive match to determine whether it is a true match.

ENFSI recommendation 29
If possible, the cell material of reference samples should be stored to permit further processing, such as a loci upgrade, depending on internal laboratory procedures or national legislation.

15. LEGISLATIVE MATTERS

As the compulsory taking of a DNA sample is a breach of an individual's privacy and bodily integrity, Article 8 of the European Convention on Human Rights demands justification and legislation. For arrestees and suspects, justification is found in the fact that DNA testing can help solve a case by either finding a match (resulting in possible incriminating evidence) or an exclusion (resulting in possible exonerating evidence) with a DNA profile from a crime scene 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 an individual's DNA in a DNA database is justified by the fact that it can help solve old and future crimes committed by the same person, and that it may prevent new crimes because the person involved may fear being detected. The indefinite retention of a person's DNA profile in a DNA database without prosecution or conviction has been condemned by the European Court of Human Rights[101]. The Court has explicitly approved the retention of the DNA of innocent people in appropriate circumstances by praising the Scottish retention system. Also, in the Netherlands, suspects can be kept in the DNA database until their case has been dealt with by the public prosecution office. Similarly, in Latvia, the data of a person with the status of suspect in a specific case must be deleted from the DNA database if the case against them has been closed on rehabilitative grounds, or if they have been found not guilty in court, but only if there are no other active cases against them. Their data will also be retained if they have been convicted in the past.

Every EU country should have data protection legislation derived from Regulation (EU) 2016/679 (General Data Protection Regulation) or, depending on the status of the institution conduction DNA analysis, Directive (EU) 2016/680 (Law Enforcement Directive). 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 data protection legislation, personal data must not be stored longer than is necessary for the purpose for which it was collected. It is practically impossible to determine this necessity at regular intervals for all the DNA profiles in a DNA database. Therefore, DNA legislation provide guidelines on storage times (see also: § 3.1).
- According to data protection legislation, individuals have certain rights with regard to their own data (access/modification/removal). For investigative reasons, this is usually not desirable. Therefore, DNA legislation state who has access to information present in, and generated by, the DNA database.
- In some countries, 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 would allow familial searching in the DNA database, appropriate rules for this should be provided in the DNA legislation.

DNA profiles are not only very specific for an individual, but they also contain information about the relatives of that individual. This means that, when people voluntarily give their DNA profile (e.g. in a mass screen), they should be informed that this may possibly incriminate a relative. In this way, a person can decide whether they will make use of their right not to testify against relatives.

Most countries also allow the inclusion of DNA profiles from minors in their DNA database. The legitimacy of this is under question in some countries, with reference to the international convention on the rights of the child. Several appeal court cases are ongoing to develop

[101] http://www.bailii.org/eu/cases/ECHR/2008/1581.html

jurisprudence on this. The Supreme Court of the Netherlands has ruled that there is no reason to differentiate between minors and adults. Additionally, the European Court of Human Rights does not regard minority as a reason to exclude a person from the Dutch DNA database[102].

[102] European Court on Human Rights 20689/08.

16. FINANCING

In most countries, the costs of establishing and maintaining a National DNA database are financed by a dedicated annual budget under the Ministry of Justice or the Ministry of the Interior. In the United Kingdom, however, (part of) the budget is managed by the police, who pay for the production and the storage of the DNA profiles.

17. PERSONNEL REQUIREMENTS

It goes without saying that personnel working with any DNA database should be properly trained to use the DNA database software. If the program is self-developed, this will be in-house training. If the DNA database software is commercially obtained, the company selling the software will usually offer training in the use of the software. CODIS can be obtained from the FBI by law enforcement organizations, and computer-based training is available.

Apart from undergoing proper training, DNA database personnel must have the following personal skills as a minimum:

- Ability to work very conscientiously
- Ability to keep confidential information confidential
- Ability to accept verification by colleagues
- Ability to report own mistakes to enable further process improvement

Apart from the above-mentioned requirements, a “proof of good conduct” may be required, sometimes even a positive outcome in an investigation by the police or the secret service into a candidate’s reliability.

18. 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, a special supervisory board has been established, staffed with the representatives of different stake-holders.[103] In the United Kingdom, a special ethics group has been established[104] 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 verify its compliance with the data protection legislation of that country.

[103] Nina Amelung et al. (2021) Modes of Bio-Bordering, The Hidden (Dis)integration of Europe. Book, Palgrave-MacMillan

[104] See: https://www.gov.uk/government/organisations/national-dna-database-ethics-group

19. RESEARCH AND DEVELOPMENT

Studies on the statistics, performance and different search strategies of DNA databases are usually done using simulated DNA databases. Some scientists, however, have asked for disclosure of the actual DNA profiles contained in DNA databases, to allow them to evaluate some of the assumptions in population genetics underlying DNA testing[105]. Of course, this should be done under strict conditions and by removing any links to the identity of the owner of the DNA profile. Some countries already allow this in the interest of quality assurance and/or process improvement[106,107,108]. Additional ethical issues have been raised in relation to the submission of samples to the YHRD database, turning attention to the possible coercive or uninformed collection of the DNA profiles submitted[109].

A major issue for DNA database managers is that they cannot distinguish matches between monozygotic twins. Both epigenetic[110] as well as next generation sequencing[111] research is occurring, but the amounts of DNA which are necessary for these analyses must be reduced to enable analysis of forensic traces containing low amounts of DNA.

Social scientists also study DNA databases. A recent review was produced by the EUFORGEN project[112], and the European Horizon 2020 project “EXCHANGE” has also been examining the sociological aspects of forensic genetics, DNA databases, and information exchange[113].

[105] Krane et al. (2009) Science 326,1631-1632. Time for DNA-disclosure.
[106] Sjerps et al (2009) Oral presentation at the European Academy of Forensic Science (EAFS) 2009 conference in Glasgow. Observed and expected numbers of (partially) randomly matching profiles in the Dutch DNA-database and in international searches.
[107] Tvedebrink et al (2012) Forensic Science International: Genetics Volume 6, Issue 3 , Pages 387-392, May 2012. Analysis of matches and partial matches in a Danish STR data set.
[108] Hedell et al. (2011) Forensic Science International: Genetics Supplement Series Volume 3, Issue 1, Pages e135-e136, December 2011.
[109] Schiermeier. Forensic database challenged over ethics of DNA holdings (https://www.nature.com/articles/d41586-021-01584-w)
[110] Li et al (2011) Forensic Science International: Genetics Supplement Series Volume 3, Issue 1 , Pages e337-e338, December 2011. Identical but not the same: The value of DNA methylation profiling in forensic discrimination within monozygotic twins.
[111] J. Weber-Lehmann et al (2014) Forensic Science International: Genetics 9, 42-46. Finding the needle in the haystack: Differentiating “identical” twins in paternity testing and forensics by ultra-deep next generation sequencing
[112] http://www.euroforgen.eu/fileadmin/websites/euroforgen/images/Dissemination_Documents/WP4/Williams_and_Wienroth_-_2013_-_Systematic_Review.pdf
[113] For example: https://www.researchgate.net/publication/338879980_Forensic_Genetics_in_the_Governance_of_Crime, https://link.springer.com/book/10.1007/978-981-15-8183-0

20. EXTERNAL COMMUNICATION

DNA databases are usually publicly funded, therefore, in the interests of transparency, politicians, the public and the media should be allowed to know how the DNA database is managed and what results are obtained.

20.1 Annual report

A good way to make this information publicly available is to produce an official annual report. Such a report can either be part of the annual report of the organization responsible for the management of the national DNA database, or it can be a separate annual report dedicated solely to the DNA database. In Europe, dedicated annual reports have already been produced by the United Kingdom, Belgium and the Netherlands. Outside Europe, the Royal Canadian Mounted Police also produces an annual report for their DNA database. Below are the locations where the most recent issues of these annual reports can be downloaded:

- United Kingdom: https://www.gov.uk/government/collections/dna-database-documents
- Netherlands: https://dnadatabank.forensischinstituut.nl/
- Canada: https://www.rcmp-grc.gc.ca/en/forensics/annual-reports-national-dna-data-bank
- Belgium: https://incc.fgov.be/banques-nationales-de-donnees-adn
- Spain: https://www.interior.gob.es/opencms/es/archivos-y-documentacion/documentacion-y-publicaciones/publicaciones-descargables/publicaciones-periodicas-anuarios-y-revistas/base-de-datos-policial-de-identificadores-obtenidos-a-partir-de-adn-memoria/
- Sweden: https://polisen.se/siteassets/dokument/ovriga_rapporter/nfc-rapport-2022-05---arsrapport-dna-register.pdf
- Ireland: https://www.justice.ie/en/JELR/FSI_Annual_Report_2021.pdf/Files/FSI_Annual_Report_2021.pdf

20.2 Internet site

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

Europe

- United Kingdom: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1071384/Forensic_Information_Databases_Strategy_Board_AR_20-21_Web_Accessible.pdf; https://www.gov.uk/government/collections/dna-database-documents
- Germany: https://www.bka.de/DE/UnsereAufgaben/Ermittlungsunterstuetzung/Kriminaltechnik/Biometrie/DNAAnalytik/dnaAnalytik.html
- Ireland: http://www.lawreform.ie/_fileupload/Reports/Report%20DNA%20Database.pdf (comprehensive thoughts on setting up a DNA database in Ireland)
- Netherlands: https://dnadatabank.forensischinstituut.nl/dna-dossier/jaarverslagen-dna-databank
- Belgium: https://nicc.fgov.be/nationale-dna-databanken and https://incc.fgov.be/banques-nationales-de-donnees-adn

Rest of the world

- USA (CODIS) https://www.fbi.gov/services/laboratory/biometric-analysis/codis/codis-and-ndis-fact-sheet#CODIS
- GTH (global): https://www.dnaresource.com/
- Canada: https://www.rcmp-grc.gc.ca/en/forensics/annual-reports-national-dna-data-bank
- New Zealand: https://www.esr.cri.nz/home/about-esr/our-science-in-action/about-the-dna-databank/
- INTERPOL: https://www.interpol.int/How-we-work/Forensics/DNA

20.3 International overviews

Several documents have been published in the past containing country-specific overviews on the different aspects of DNA database legislation and DNA database management. However, most of these documents are significantly older than 5 years. In 2011, the Council of Responsible Genetics produced a world map of DNA databases[114]; however, the organization appears to have shifted its focus away from forensic DNA since then. The Euroforgen project produced an international (European) overview in 2014, with an update in 2016[115] and it is anticipated that another update might soon be released.

[114] http://www.councilforresponsiblegenetics.org/dnadata/world_map.html - link no longer functional
[115] Reed and Syndercombe-Court, 2016, A comparative audit of legislative frameworks within the European Union for the collection, retention and use of forensic DNA profiles. Available at: https://www.euroforgen.eu/fileadmin/websites/euroforgen/images/Dissemination_Documents/WP4/

21. INTERNATIONAL COMPARISON OF DNA PROFILES

Crimes committed in one country may be committed by a person whose DNA profile is stored in another country's DNA database, therefore it is very useful to have the means for the international comparison of DNA profiles. Chapter 2 contains descriptions of how a European Standard Set of Loci has been agreed upon to enable such comparisons. In addition to common loci, countries exchanging DNA profile information should, of course, also use the same quality standards for the production of their DNA profiles, as described in § 3.5.

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

- Individual legal assistance requests

For the majority of countries outside of the Prüm network (see below), this is still the most commonly used channel. Depending on the legal embedding of the DNA legislation of a country, either police channels or judicial channels are used for this method of exchanging single search requests of DNA information. Before the advent of XML to communicate DNA profiles, INTERPOL developed a special form, the INTERPOL DNA Search Request Form, to standardize and facilitate this manner of exchanging DNA information. Since 2012, an electronic version has been available in all countries, where applicants complete the form (either typing in data or by XML upload) and send the request to their choice of selected countries, and/or to the INTERPOL DNA database. National administrations can contact their INTERPOL National Central Bureau (NCB) to request an international DNA search request using this form. A new and updated version of this form was released in 2021.

- INTERPOL DNA Database and DNA Gateway

In 2002, INTERPOL created a central DNA database, in which DNA profiles can be included for comparison by its 195 member countries. The database is an autonomous database and does not keep any nominal data linking a DNA profile to any individual. Member Countries retain the ownership of their profile data and control its submission, comparison with other countries' data stored in the database, and destruction in accordance with their national laws. The database currently host 4 types of indexes: references (from suspected or convicted individuals), crime stain, missing person and unidentified human remains. INTERPOL also has a separate DNA database, called I-Familia, for international kinship matching for missing persons (see section 22.7.2). When a match is found, a message is immediately sent within 15 minutes to the countries contributing to the match. This message contains the basic case information that was provided, and can optionally provide the DNA profile itself. 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. There are currently 86 participating countries providing DNA profiles in accordance with their national laws. To encourage further participation, an INTERPOL resolution was adopted by all countries at the 78th INTERPOL General Assembly for National Central Bureaus to facilitate the submission of DNA profiles from unsolved crime scenes and foreign national offenders by national law enforcement agencies to the INTERPOL DNA database[116].

The INTERPOL DNA Gateway is a medium 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 INTERPOL National Central Bureaus (NCBs), using INTERPOL's secure communications system, I-24/7[117]. The results of the 2019 Global Survey can also be viewed from their DNA information page.

[116] https://www.interpol.int/fr/Actualites-et-evenements/Evenements/2009/78th-INTERPOL-General-Assembly
[117] https://www.interpol.int/en/How-we-work/Forensics/DNA

- Europol

Formerly, Europol was authorized to process DNA profiles within the framework of Council Decisions 2009/9343/JHA and 2009/371/JHA. In the context of the first Decision, DNA profiles could be used together with other intelligence for criminal analysis purposes in order to fight serious international crime. The second Decision allowed Europol to process DNA profiles in the Europol Information System (EIS). Non-EU states which have signed a co-operation agreement with Europol can also provide DNA profiles to Europol for insertion into the EIS. However, in 2016 a new Regulation was accepted that repealed and essentially replaced the two previous Decisions (Regulation (EU) 2016/794 on the European Union Agency for Law Enforcement Cooperation (Europol) and replacing and repealing Council Decisions 2009/371/JHA, 2009/934/JHA, 2009/935/JHA, 2009/936/JHA and 2009/968/JHA).

- The EU Prüm Decisions (derived from the Treaty of Prüm)

The EU Prüm Decisions deal with the exchange of judicial and police information between EU Member States. Some associated countries (Norway, Switzerland, Liechtenstein and Iceland) have also been permitted to join this undertaking. With regards to DNA, countries can search each other's' DNA databases in an automated way. 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, present in each country. The DNA data exchange and matching system used by EU Member States is similar to the DNA data exchange and matching system of the INTERPOL DNA Gateway.

The EU Prüm Decision (2008/615/JHA) and the EU Prüm Implementation Decision (2008/616/JHA) 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

In 2022, the following countries are already exchanging DNA profiles on a day-to-day basis with one or more of the other countries, under the terms of the EU Prüm Decisions, with Norway expected to join the growing list before the end of the year:

Austria,	Estonia,	Italy,	Portugal,
Belgium,	Finland,	Latvia,	Romania,
Bulgaria,	France,	Lithuania,	Slovakia,
Croatia,	Germany,	Luxembourg,	Slovenia,
Cyprus,	Greece,	Malta,	Spain,
Czech Republic,	Hungary,	Netherlands,	Sweden,
Denmark,	Ireland,	Poland,	United Kingdom.

Chapter 2 of the Appendix to the EU Prüm Implementation Decision contains the DNA inclusion, matching and reporting rules. However, due to the advances and developments in the field of forensic DNA analysis, these rules are undergoing review[118]. Discussion over the proposal for a new regulation (Proposal for a Regulation of the European Parliament and of the Council on automated data exchange for police cooperation ("Prüm II"), amending Council Decisions 2008/615/JHA and 2008/616/JHA and Regulations (EU) 2018/1726, 2019/817 and 2019/818 of the European Parliament and of the Council) was begun at the end of 2021, with an amended second draft made public in 2022 (ST 10350/2022). The new Prüm II regulation will expand the data categories to be exchanged over the network, and will also update and streamline the processes devised in 2008, including for DNA.

[118] http://data.consilium.europa.eu/doc/document/ST-12275-2018-INIT/en/pdf

Like the INTERPOL DNA database, the Prüm DNA profile exchange system is a match/no-match system, meaning that only DNA profiles are compared. After verifying a match, countries can request the personal and/or case information associated with the DNA profile via existing police or judicial channels. The minimum number of matching loci under the terms of the Prüm system is six, with one mismatch permitted for matches between DNA profiles of more than 6 loci. However, it can be calculated, and it has been shown in daily practice, that six and seven locus matches have a non-negligible chance of being false positive[119]. Therefore, it is recommended that these matches are analysed further by additional DNA testing before any legal action is undertaken against any matching person. Other countries set more stringent matching rules at the national level that must be met before personal information can be released.

ENFSI recommendation 30
If a Prüm-related information request is received from another country, the quality of the corresponding match should be verified before providing the requested information to the other country.

ENFSI recommendation 31
If possible, when operational under the Prüm treaty, international matches near or below the laboratory threshold should be further analyzed by additional DNA testing or statistical analysis before requesting information from another country. This threshold can be set individually in each laboratory in accordance with national legislation or guidelines.

The minimum number of loci for a DNA profile to participate in the Prüm system is six, and the required minimum number of matching loci is also six. One should realize, however, that two profiles which both fulfil the inclusion rule may not match if there is not enough overlap to produce the minimum number of six matching loci. This is especially true for over 600.000 “old” German reference profiles which consist of the old 7 ESS loci + SE33.

To improve the evidential value of a match by additional DNA testing, one must know which loci are present in the DNA profile of the other country. Therefore, those loci that are not used by the receiving country should be configured in the DNA database of the receiving country. If this is not done, those loci will not be visible in the DNA profile received from the sending country.

ENFSI recommendation 32
All regularly-used loci (in addition to those not used by the receiving country) should be configured in the DNA databases of countries participating in the international exchange of DNA profiles under the terms of the Prüm system in order to see the full composition of the DNA profile of the sending country.

Countries that compare DNA profiles under the terms of the EU Prüm decisions should regularly perform 3 checks:

- Check if all profiles that comply with the Prüm inclusion rules are Prüm-marked
- Check if all Prüm-marked profiles have been sent to all active Prüm labs
- Check if an answer was received and processed from all active Prüm labs for every profile that was sent out

A Power Point presentation on how to perform these checks in CODIS can be downloaded from the European CODIS Users Platform at Europol

[119] Forensic DNA Profiles Crossing Borders in Europe (Implementation of the Treaty of Prüm). Profiles in DNA 2011 (http://www.promega.com/resources/articles/profiles-in-dna/2011/forensic-dna-profiles-crossing-borders-in-europe/).

- The PCSC Agreements

The USA has negotiated so called PCSC (Prevention and Combatting Serious Crime) agreements with several European countries. A PCSC agreement resembles the Prüm agreement and provides for the reciprocal exchange of biometric and biographic data and any relevant underlying information for law enforcement purposes. Some countries already compare fingerprints with the USA on the basis of such a treaty but the DNA exchange has not yet come into force because the federal DNA law of the USA has to be adjusted to give other countries access to the DNA database of the USA.

- PCC SEE and PCC SEE Prüm (Police Cooperation Convention for South East Europe)

PCC SEE is a multilateral state agreement cooperation (international law) between Albania, Austria, Bosnia and Herzegovina, Bulgaria, Hungary, North Macedonia, Moldavia, Montenegro, Romania, Serbia, Slovenia and Croatia. The PCC SEE agreement content covers classical international Police Cooperation with European legal and data protection standards (mainly with identical content of multilateral DACH Police Cooperation Agreement and parts of Schengen acquis and the target for preparation of EU Standards and EU Membership in the Western Balkan area). This PCC SEE was signed in 2006 in Vienna and is in force since 2007.

These PCC SEE countries have decided in 2013 to set up a Prüm-like system[120] and therefore drafted an additional multilateral PCC SEE Prüm agreement. Content of this agreement is Prüm-like online cooperation in all three Prüm data categories (DNA, Dactyloscopic data and Vehicle registration data) and also contains parts of enhanced EU police cooperation tasks in line with EU Framework Decision “Swedish Initiative” as e.g. binding usage of SPOCs in this cooperation. This PCC SEE Prüm agreement was signed in 2018 in Vienna and is in force since 2019. As of January 21, parties to the agreement are the 9 states of those PCC SEE parties (AL, AT, BG, HU, ME, MD, MK, RO, RS). Currently, all Western Balkan partner states are working on the national implementation of this Prüm-like cooperation with the support of the EU PCC SEE partner states and the European Commission.

[120] https://www.pccseesecretariat.si/libs/download.php?file=/8dba58dc1687894a70673cbc0122ff11; https://www.pccseesecretariat.si/libs/download.php?file=/8a621f1388a219ba63188c9a1e2bd620

22. MISSING PERSONS

22.1 Introduction

The main purpose of a DNA database for missing persons is to see whether the DNA profiles of unidentified human remains can be linked to DNA profiles of missing persons or their family members. In this way, the family members of missing persons can be made aware of the fact that their missing relative is no longer alive and can start coming to terms with their loss. A second purpose is to link the body parts of a single person, which may be found in different locations (e.g. two feet washed ashore at different places and at different times), or in situations where more than one person has been killed and unidentified body parts cannot be reliably attributed to one person (e.g. airplane crash or secondary mass grave). Missing persons DNA databases are usually operated together with, or as part of, a system where other important attributes of missing persons and unidentified bodies/body parts can also be included and compared (e.g. dental records, fingerprints, externally visible traits, medical data, etc.). Samples obtained from the personal items of missing persons or samples obtained from their family members are indicated as *ante mortem* samples, and a sample from an unidentified body (or body part) is indicated as a *post mortem* sample.

22.2 Different missing person situations

A person can become a missing person either as an individual or as part of a mass fatality. Mass fatalities may have a natural cause (e.g. tsunami, earthquake) or a human-induced cause (e.g. war situation, terrorist attack). In mass fatalities, a distinction can also be made between closed systems, where the number, names and mutual relationships of the missing persons are known (e.g. airplane crash) and open systems, where the number of missing persons cannot be properly accessed (e.g. tsunami or earthquake).

22.3 Different types of matches

In the DNA databases of missing persons, a distinction can be made between direct and indirect comparisons.

➢ A direct match is either a full match between the DNA profile of a missing person and the DNA profile of an unidentified body(part), or a full match between different body parts.

- A direct match between the DNA profile of a missing person and the DNA profile of an unidentified body(part) is the most reliable type of match, but it requires that the DNA profile of the missing person be available – that it was obtained, for instance, from a personal item or a medical specimen of the missing person. Care should be taken to ensure that the personal item was used only by the missing person. To verify this, DNA profiles should also be obtained from the parents or children of the missing person, for comparison with the DNA profile obtained from the personal item. The strength of a direct match is usually expressed as the random match probability of the matching loci between the DNA profile of the missing person and the DNA profile of the unidentified body(part), or as a likelihood ratio expressing the probability of the results, given the following two propositions: either the DNA is from the missing person, or it is from an unknown person.
- Sometimes different body parts of an unidentified person are found. These can then be linked to each other by direct matches. DNA database programs may include the possibility to combine these profiles into one so-called representative specimen without losing the original data. This should only be done if the Likelihood Ratio of the individual profiles is high enough to allow for this kind of clustering.

➢ An indirect comparison is a comparison between the DNA profiles of persons that are possibly related to the missing person. For instance, to investigate whether an unidentified body-(part) of a particular missing person, the DNA profile can be compared to the DNA profiles of the missing person's relatives. This approach is used when the DNA profile of the missing person is not available for direct comparison. In this case, the strength of the match is usually expressed as a likelihood ratio (e.g. assuming that X is indeed the biological child of Y and Z, the result of the DNA analysis is x times more likely if the unidentified body(part) is X than if it is a random unrelated person). Specialized software is available to perform these calculations (see § 22.6). Some of these programs (like CODIS and Bonaparte) have the possibility to build pedigrees and add DNA data to the nodes of a pedigree by the drag-and-drop principle. The use of prior odds for missing persons identifications has been discussed by Budowle et al.[121] and Thompson et al. [122]. International DNA kinship matching, based on autosomal STR profiles obtained through sharing international data, requires the use of allele frequencies from reference populations. National or continental datasets can be used depending on data availability, and the accessibility information regarding the ancestry of the individuals whose biological relationships will be tested. In case the information on the genetic ancestry in unknown or thought to be inaccurately reported, worldwide allele frequencies can be primarily used to evaluate the strength of the DNA evidence and confirmed using the correct reference population once the identification is confirmed**Fehler! Textmarke nicht definiert.**.

Compared to forensic DNA testing, the identification of missing persons or the victims of disasters is even more complex. There may be inconsistencies in the reference pedigree due to unknown relationships. Additionally, mutations and partial profiles may cause problems and/or false positive and false negative matches. Also, the statistics are more complex when compared to forensic DNA testing. Therefore, additional training is necessary for DNA experts involved in kinship testing. This has been confirmed by a collaborative exercise of the Spanish- and Portuguese-speaking Working Group of the ISFG[123].

Kinship (pedigree) searches can be conducted in CODIS as well as other database programs.

22.4 Markers

A comparison between the DNA profiles in a missing persons DNA database usually starts with 10-15 autosomal STR markers. In the case of a direct match, the evidential value of the match will usually be sufficient for the decision-maker to identify the person, but in the case of an indirect match, additional autosomal markers may have to be determined, as well as Y-STR markers and/or mtDNA, to verify or falsify the match.

22.5 Relationship between criminal and missing persons DNA databases

In some countries, DNA profiles of missing persons (and/or their relatives) and unidentified human remains are kept in the same DNA database as the DNA profiles used for solving crimes, while in other countries a separate DNA database is used for missing persons (and/or their relatives) and unidentified human remains. There may be several reasons for this:

[121] Budowle et al (2011) Investigative Genetics 2: 15. Use of prior odds for missing persons Identifications

[122] Thompson et al. (2013) Frontiers in Statistical Genetics and Methodology 4(220), pp. e1-e3, 10-2013. The role of prior probability in forensic assessments.

[123] Vullo et al. (2016) GHEP-ISFG collaborative simulated exercise for DVI/MPI: lessons learned about large scale profile database comparisons. Forensic Sci. Int. Genet. 21: 45-53

- Data protection considerations. By keeping DNA profiles of missing persons and their relatives separate from the DNA profiles in the criminal DNA database, they cannot be accidentally compared with profiles with which they should not be compared;
- Both DNA databases may be managed by different organizations (e.g. Ministry of Justice versus the Police);
- Specialized software is needed to find and evaluate matches between unidentified human remains and multiple relatives in pedigrees of missing persons.

If two separate DNA databases are used, it must be kept in mind that it can be useful to compare the DNA profiles of unidentified human remains with the DNA profiles of the criminal DNA database:

- DNA profiles of unidentified human remains found in one location may match with stains found at a crime scene at another location, indicating that the unidentified person may have been the victim of a crime (if this was not yet obvious) and has been transported to another location;
- DNA profiles of unidentified human remains may match with a reference sample, which may assist an identification. This comparison needs to be done only once, as the unidentified person is dead and hence cannot be added to the DNA database as a reference sample in the future.

22.6 Software

Specialized software is available to search for relatedness between (a series of) DNA profiles and/or to calculate the likelihood ratio of the relatedness of a person and their putative family member(s). This type of software is also used in forensic and civilian cases to verify or falsify the biological relationship between known persons. Table 10 lists the different programs that are known to the editors of this document[124],[125].

[124] The mentioning of trade names does not mean that ENFSI recommends or endorses any of these programs. The aim of ENFSI is to provide insight into what is available on the market.
[125] Morimoto et al. 2020 DOI: https://doi.org/10.1016/j.fsigen.2020.102279

Program	Developer	Country	Website	Price	Remarks
Bloodhound	Ananomouse Corporation	USA	http://www.ananomouse.com/products/bloodhound.asp	Unknown	URL does not refer to the software
Bonaparte Disaster Victim Identification System	SMART Research	Netherlands	http://www.bonaparte-dvi.com/	Not free	
CODIS 7.0	FBI	USA	https://www.fbi.gov/about-us/lab/biometric-analysis/codis	Free	Only for Law enforcement organizations
DNAStat	Jaroslaw Berent	Poland	http://www.umed.lodz.pl/ou/zms/	Unknown	URL does not refer to the software
DNA-View	Charles Brenner	USA	http://dna-view.com/index.html	Not free	
EasyDNA	Wing Kam Fung	Hong Kong	http://www.hku.hk/statistics/EasyDNA/	Free	Accompanying book is essential
EasyPat	Michael Krawczak	Germany	http://www.uni-kiel.de/medinfo/mitarbeiter/krawczak/download/	Free	
familias	Petter Mostad	Norway	http://www.familias.name/	Free	
FSS DNA Lineage	Forensic Science Service	UK	http://www.forensic.gov.uk/html/services/analytical-solutions/software/fssibd/	Unknown	URL does not refer to the software
GeneMarker HID	SoftGenetics	USA	http://www.softgenetics.com/GeneMarkerHID.html	Not free	
GenomiCalc	Genomic	Brazil	http://www.genomicalc.com.br	Unknown	URL does not refer to the software
GenoProof2	Qualitype	Germany	http://qualitype.de/genoproof/	Not free	
Genolab	Qualitype	Germany	http://www.genolab.eu	Not free	
Genotype	Kvant	Slovakia	http://www.dip.sk/typo3/dip.sk/index.php?id=9&no_cache=1&L=1	Unknown	URL does not refer to the software
Grape	DNA-SOFT	USA	http://www.dna-soft.com	Not free	
Hugin	Hugin Expert	Denmark	http://www.hugin.com/productsservices/demo/hugin-lite	Not free	URL does not refer to the software
KIn CALc	California DOJ/Steven Myers	USA	Steven.Myers@doj.ca.gov	Unknown	No URL
KINGROUP	Dmitry A. Konovalov	Australia	http://www.kingroup.org/	Unknown	URL does not refer to the software
LISA	Future Technologies, Inc.	USA	http://www.ftechi.com/dna_biometric.shtml	Not free	
M-FISys	Gene Codes Forensics	USA	http://www.genecodesforensics.com/software/	Not free	
PatCan	Jose Antonio Riancho	Spain	jose.riancho@unican.es	Unknown	No URL
Patern	Michael Krawczak	Germany	http://www.uni-kiel.de/medinfo/mitarbeiter/krawczak/download/	Free	
Paternity Index	Michael Jung	Germany	http://www.paternityindex.com/	Not free	
PatPCR	Juan Antonio Luque	Spain	vestad@telepolis.com	Unknown	No URL
PedExpert	Sérgio Danilo Junho Pena	Brazil	spena@dcc.ufmg.br	Unknown	No URL
RELPAIR	William L. Duren, Michael Epstein, Mingyao Li, and Michael Boehnke	USA	http://csg.sph.umich.edu/boehnke/relpair.php	Free	
SmallPond	SmallPond LLC	USA	http://www.smallpondllc.com/	Not free	
VAT	Max Baur, Rolf Fimmers, W. Spitz	Germany	http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4025154/	Not free	URL does not refer to the software

Table 10: Software programs to search for relatedness between (a series of) DNA profiles and/or to calculate the likelihood ratio of the relatedness of a person and their putative family member(s).

Depending on the required application of the software, different program properties will be more or less important to have. Table 11 lists some program parameters which should be considered when choosing (buying) a missing persons software program.

Parameter category	Parameter
Data which can be compared	Autosomal STRs
	Y-STRs
	mtDNA
	SNPs
	Metadata
Search strategies	UHR against UHRs
	UHRs against UHRs to find relations
	UHR against MPs
	UHR against pedigrees of MP
	UHRs against pedigrees of MP
	Familial searching (shared alleles)
	Familial searching (LR-ranking)
Calculations	Pedigree likelihood ratio calculation
	Fst correction
	Size-bias correction
	Mutation correction[126]
	Allele drop-out correction
	Multiple allele relative frequency tables
	Minimum allele relative frequency substitution for rare alleles
	Datafilters
	Resultfilters
Other features	Graphical pedigree manager
	Combining DNA profiles of the same person
	Incestuous relationships
	Reporting module
	Simulations module
	Import module
	Replacing MP by IP in pedigree

Table 11: Program parameters which may be considered when choosing (buying) a missing persons software program (UHR: Unidentified Human Remains; MP: Missing Person; IP: Identified Person; LR: Likelihood Ratio)

Because software programs are continuously adapted and improved, interested persons should refer to the producer of the program to find out the latest properties.

[126] A discussion about different mutation models can be found in: Chakraborty et al (2011) Investigative Genetics 2:8. Response to: DNA identification by pedigree likelihood ratio accommodating population substructure and mutations-authors' reply.

22.7 International Organisations

22.7.1 International Commission on Missing Persons (ICMP)[127]

The International Commission on Missing Persons was established at the initiative of U.S. President Bill Clinton in 1996 at the G-7 Summit in Lyon, France. It spearheaded the regional effort that has made it possible to account for more than 75 percent of the 40,000 people who were missing at the end of the conflicts in former Yugoslavia. In 2003 its mandate and sphere of activity were extended by supporting governments, to address the global issue of missing persons, including cases arising from natural disasters. On 15 December 2014, the Foreign Ministers of the Netherlands, the United Kingdom, Sweden, Belgium and Luxembourg signed the ICMP Agreement, constituting ICMP as a treaty-based international organization with its own system of governance and international capacities. ICMP moved its Heaquarters to The Hague, the Netherlands, in 2015. Its mandate is to secure the cooperation of governments and others in locating missing persons from conflict, human rights abuses, disasters, organized crime, irregular migration and other causes and to assist them in doing so. It also supports the work of other organizations, encourages public involvement in its activities and contributes to the development of appropriate expressions of commemoration and tribute to the missing.

Since November 2001, ICMP has led the way in using DNA as a first step in the identification of large numbers of persons missing from armed conflict and other causes. ICMP's DNA laboratory in The Hague is based on an integrated system that delivers a highly developed capacity to obtain DNA profiles from very difficult cases of unidentified human remains, such as bone samples from decades-old mass graves. ICMP has conducted the world's largest missing persons DNA testing program, having successfully tested more than 50,000 bone samples and established a database of almost 100,000 family reference DNA profiles to support the identification of almost 20,000 missing persons.

ICMP has been involved in a number of large-scale DVI efforts, including the 2004 SE Asian tsunami, the 2006 Hurricane Katrina in the United States and the 2010 earthquake in Haiti. ICMP has also been involved in DVI responses in Cuba, Cameroon, Namibia, Kenya and Ukraine among others. In addition to DNA testing, ICMP delivers rapid assessment, online information sharing, training and long-term strategies to develop domestic institutions that can address the issue of missing persons in the wake of disasters.

In 2007, in light of lessons learned from the 2004 Tsunami regarding preparedness and DNA standing capacity, ICMP and INTERPOL formalized their DVI cooperation with an agreement that was invoked for the first time in 2008, to respond to Typhoon Frank in the Philippines. ICMP provides DNA testing and matching capabilities and participates in INTERPOL's Incident Response Teams (IRTs) that are deployed at the invitation of relevant national authorities to assess and help guide DVI response activities.

ICMP has developed a comprehensive Integrated Data Management System (iDMS), a set of powerful applications that support the process of storing, viewing and analyzing very large amounts of data on missing persons, investigations, and identifications. The iDMS and its associated Online Inquiry Center (OIC) have been designed to deliver a high degree of control over access to sensitive information, such as DNA and family data. Each user has access only to authorized portions of the database, and sensitive data is stored and analyzed in an

[127] The text of this paragraph was supplied by ICMP

anonymous, coded form. ICMP's data protection policies and recognized privileges and immunities ensure data protection both in policy and practice.

22.7.2 INTERPOL

INTERPOL member countries can call for assistance in disaster victim identification (DVI).
The services offered by INTERPOL include:

- A downloadable DVI guide with Ante Mortem and Post Mortem report forms available on the INTERPOL public website;
- Assistance from the Command and Co-ordination Centre at the INTERPOL General Secretariat in Lyon, France, to send messages between National Central Bureaus 24 hours a day in Arabic, English, French or Spanish;
- An Incident Response Team to provide further assistance upon request, such as on-site investigative support or connection to INTERPOL's databases.
- International collection of Ante-Mortem data from the countries of victims to be provided to the authority in charge of the comparison with the Post-Mortem data.

INTERPOL also has two central DNA databases (the INTERPOL DNA Database and I-Familia) at its General Secretariat in Lyon, which is described in chapter 21 of this document. The INTERPOL DNA database allows the comparison between the DNA profiles of missing persons and unidentified bodies. The missing persons index is only compared against the unidentified human remains index. In I-Familia, the DNA from biological relatives of a missing person are compared with unidentified bodies through international DNA kinship matching. Seventy INTERPOL member countries representing all regions of the world, have submitted missing persons profiles and/or unidentified human remains profiles to the INTERPOL DNA Database.

I-FAMILIA

In 2021, INTERPOL launched I-FAMILIA (which stands for INTERPOL Family Associated Matching to Identify Lost Individuals Abroad), a new DNA database dedicated to the identification of missing persons through family DNA kinship matching. The aim of the database is to provide an additional opportunity to identify a missing person when a direct DNA match is not possible because the DNA profile of the missing person of themselves is unavailable. This database is completely separated from any criminal DNA data and the kinship calculations are performed using the DNA software BONAPARTE (Smart Research BV). A comparison between family pedigrees and DNA profiles from unidentified human remains is performed by computing a likelihood ratio using worldwide allele frequencies and potential matches are evaluated using published LR interpretation guidelines[128]. When the strength of the DNA evidence is not sufficient, additional information (DNA profile from another relative or additional STR loci) can be requested before issuing a potential biological association report. Further information on I-Familia can be found here : https://www.interpol.int/How-we-work/Forensics/I-Familia.

22.8 European missing persons DNA databases

The table below, which is based on the INTERPOL Global DNA profiling 2019 Survey, the Use of DNA Database survey disseminated by the European CODIS Users Group and on directly obtained information, contains an inventory of countries in Europe which have a separate missing

[128] Laurent et al (2021) Streamlining the decision-making process for international DNA kinship matching using Worldwide allele frequencies and tailored cutoff log10LR thresholds. Forensic Sci. Int. Genet. 57. DOI:https://doi.org/10.1016/j.fsigen.2021.102634

persons database or which include the DNA profiles of missing persons and unidentified human remains in their DNA databases.

Country, regional entity or international organization	Missing persons database	Missing Persons	Unidentified Human Remains	Separated from (S) or included (I) in the criminal DNA database	Software
Albania	Unknown	Yes	Yes	x	x
Andorra	No	Yes	Yes	x	x
Austria	Yes	Yes	Yes	I	National design
Belarus	Yes	Yes	Yes	x	x
Belgium	Yes	Yes	Yes	I	n/a
Bosnia & Herzegovina	No	x	x	x	x
Bulgaria	x	Yes	Yes	I	National Design
Croatia	x	Yes	Yes	I	CODIS
Cyprus	Yes	Yes	Yes	I	National Design
Czech Republic	x	Yes	Yes	I	CODIS
Denmark	No	Yes	Yes	I+S	CODIS + Plassdata
Estonia	No	Yes	Yes	I	CODIS
Finland	Yes	Yes	Yes	I	CODIS
France	Yes	Yes	Yes	S	CODIS + FNAEG
Germany	Yes	Yes	Yes	S	National design
Georgia	x	Yes	Yes	x	x
Greece	Yes	Yes	Yes	S	CODIS
Hungary	Planned	Yes	Yes	I	CODIS
Iceland	x	No	No	n/a	n/a
Ireland	Yes	Yes	Yes	S	CODIS
Italy	Yes	Yes	Yes	I	National Design
Kosovo*[129]	No	Yes	Yes	I	CODIS
Latvia	No	Yes	Yes	I	CODIS
Liechtenstein	x	Yes	Yes	I	CODIS
Lithuania	x	Yes	Yes	I	CODIS
Luxembourg	No	Yes	Yes	x	x
Malta	x	Yes	Yes	x	x
Moldova	Planned	n/a	n/a	x	x
Montenegro	Yes	Yes	Yes	x	x
Netherlands	Yes	Yes	Yes	S	Bonaparte; CODIS; DNAView
North Macedonia	x	No	No	n/a	n/a
Northern Ireland	x	x	x	x	x
Norway	Yes	Yes	Yes	I	CODIS
Poland	Yes	Yes	Yes	I	CODIS
Portugal	Yes	Yes	Yes	n/a	n/a

[129] See footnote 87.

Romania	Yes	Yes	Yes	I	CODIS
Russia	x	Yes	Yes	I	National Design
San Marino	No	Yes	x	x	x
Scotland	x	x	x	x	x
Serbia	x	Yes	Yes	x	x
Slovakia	Yes	Yes	Yes	I	CODIS
Slovenia	Yes	Yes	Yes	I	National Design
Spain	Yes	Yes	Yes	S	CODIS
Sweden	No	No	No	n/a	n/a
Switzerland	Yes	Yes	Yes	x	CODIS
Turkey	x	Yes	Yes	x	x
Ukraine	x	No	No	n/a	n/a
United Kingdom (England + Wales)	Yes	Yes	Yes	S	x

Table 12: Missing persons DNA databases in Europe (x = not known; n/a = not applicable)

APPENDIX 1: SUMMARY OF ENFSI RECOMMENDATIONS ON DNA DATABASE MANAGEMENT

1) Every European country should establish a forensic DNA database and pass 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 identifying the donors of stains, the number of persons in a DNA database who are likely to be the donors of those stains should be as large as legally (and financially) possible.
4) Managers of national DNA databases should establish (together with other stake-holders) 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 the maximum number of adventitious matches a partial DNA profile is expected to generate.
5) If possible, DNA profiles should be upgraded after a match in the national DNA database if it increases the evidential value of the match and decreases the possibility of an adventitious match.
6) Reference sample profiles should preferentially be loaded to a database only if a complete profile (maximum number of loci) is obtained using the PCR chemistry of choice.
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.
8) The custodian of the DNA database should have regular contacts with the suppliers of the DNA profiles to exchange information about legal and technical developments, changes in the inclusion and matching rules, incidents, etc.
9) If a laboratory uses enhanced techniques to produce DNA profiles they should be searched using a dedicated (near) match strategy.
10) Composite DNA profiles should only be created from DNA profiles generated from the same DNA extract because it cannot be excluded that different extracts, even from the same sample, contain DNA from different individuals.
11) When a new allele is observed in a DNA profile, its presence should be confirmed by repeated DNA extraction, PCR, capillary electrophoresis and allele calling of the entire DNA profile. Only new alleles whose size can be accurately determined using the internal DNA size-standard should be included in the DNA database.
12) Alleles from loci with chromosomal anomalies may be included in a DNA database if the default search strategy allows at least one mismatch. If the default search strategy does not allow any mismatches, wildcards may be used, as long as an agreed set of wildcards is determined to permit meaningful international exchange.
13) 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. Software tools may also be used, provided they are properly validated.
14) A numerical match between a reference sample and a mixed profile must always be checked against the electropherogram of the mixed profile.
15) Mixed profiles of more than 2 individuals should not be systematically included in a DNA database because they will generally produce too many adventitious matches.
16) Databases may contain autosomal STR profiles only. For those databases containing profiles from non-autosomal STR profiles or mitochondrial DNA sequences, specific operating procedures must be in place to avoid unintended familial searches. To avoid false exclusions, clear rules should be in place to indicate differences between a mtDNA sequence and the rCRS when comparing mtDNA results.

17) If the removal of a DNA profile from the DNA database is dependent on external instruction from an authorized agent, a process should be in place to inform the custodian of the DNA database of this instruction, preferably by means of an automated message.
18) There should be a system that can be consulted by those responsible for taking reference samples, to verify whether a person is already present in the DNA database.
19) DNA databases should contain an associated elimination DNA database (or databases). This should include laboratory staff of all categories, as well as visitors and maintenance personnel and profiles from those with access to traces (e.g. police, crime scene technicians).
20) Because elimination databases are not shared with other EU/ENFSI countries, unidentified DNA profiles found in negative controls, which may originate during the manufacture of dis-posables and/or chemicals should be uploaded to the ICMP Manufacturers Exclusion Data-base, MED.
21) Policies and procedures should be in place to ensure that DNA-profiles deemed no longer relevant by the authorizing agent are deleted.
22) 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. Automated processes reduce the possibility of human error, however, when DNA profiles are entered manually into the DNA database, a process that detects typing errors, for example the double-blind method of entry, should be used.
23) To prevent and detect false exclusions (e.g. true matches that are not found due to an error in one of the DNA profiles), DNA profiles should be searched using a full Database search allowing at least one mismatch. The original data of DNA profiles involved in such near matches should be checked for possible errors during their production and processing.
24) As a national DNA database is regularly subject to attention from the public, politicians and the media, a DNA database manager should consider establishing tools to monitor the effectiveness of their DNA database and communicating this objective information publicly.
25) 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. (A warning can be included in a report, indicating the factors that increase the possibility of an adventitious match such as size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members, etc.).
26) A DNA database match report of a crime scene-related DNA profile with a person should be informative. It may include an indication of the evidential value of the match (RMP/LR), a warning indicating the possibility of adventitious matches (as mentioned in recommendation 25), and the implication that the match should be considered together with other evidence.
27) DNA profiles should be entered into a database in a way that guarantees correct entry. Access to the DNA database should be limited to those persons who require access, by physical and organizational measures. Regular back-ups should be made, stored in a safe place, and recovered 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 verify whether they are properly synchronized.
28) Investigating authorities should consider combining the information from a national DNA database with other types of evidence to increase the likelihood of identifying leads in other crimes.
29) If possible, the cell material of reference samples should be stored to permit further processing, such as a loci upgrade, depending on internal laboratory procedures or national legislation.
30) If a Prüm-related information request is received from another country, the quality of the corresponding match should be verified before providing the requested information to the other country.

31) If possible, when operational under the Prüm treaty, international matches near or below the laboratory threshold should be further analyzed by additional DNA testing or statistical analysis before requesting information from another country. This threshold can be set individually in each laboratory in accordance with national legislation or guidelines.
32) All regularly-used loci (also those not used by the receiving country) should be configured in the DNA databases of countries participating in the international exchange of DNA profiles under the terms of the Prüm system in order to see the full composition of the DNA profile of the sending country.

APPENDIX 2: ENFSI GUIDELINES FOR AUDITING DNA DATABASES

This appendix document aims to provide practical guidelines for teams auditing a DNA database with the intention of verifying its compliance with the ENFSI DNA Working Group recommendations. The document also aims to provide a reporting format for the auditing team, which can be filled out at the auditing site and can be presented to the person(s) requesting the audit. The recommendations of the ENFSI DNA Working Group, as listed in Appendix 1, have been taken as the foundation of the auditing operation, and the opinion of the auditor can be added to each item.

In 2008, the Council of the European Union agreed on converting major parts of the Treaty of Prüm into two EU Council decisions (2008/615/JHA and 2008/616/JHA). These decisions describe the obligation for EU Member States to establish a DNA database, and to make it available for automated searches by other Member States.
Any Member State initiating data exchange after 13 October 2009 must also pass an evaluation procedure (6661/2/09 Rev 2) consisting of:

- Filling out a questionnaire on data protection (6661/1/09 Rev 1 Add 1 Rev 1);
- Filling out a questionnaire on the exchange of DNA profiles (6661/1/09 Rev 1 Add 2 Rev 1);
- A pilot run to test and validate the IT environment;
- An evaluation visit by an external evaluation team to verify all the information provided;
- The approval of the EU Council based on the report of the evaluation team.

The EU Working Party on JHA Information Exchange (IXIM) – formerly DAPIX – has developed guidelines and a reporting format for the evaluation teams. Although there is some overlap between the guidelines of the EU and ENFSI, their focus is quite different. The ENFSI guidelines focus on the proper functioning and management of a DNA database in a national environment, while the EU guidelines focus on the interaction of a DNA database with other DNA databases and on their compliance with the contents of the two EU Council decisions (2008/615/JHA and 2008/616/JHA). Together, they offer an instrument to determine proper management in a national, as well as an international, environment.

It should be noted that ENFSI has established its recommendations based on forensic optimization criteria. Sometimes the national legislation is in contradiction with the ENFSI recommendations. In such cases, the auditor can indicate a Noncompliance with ENFSI guidelines, but that this Noncompliance is acceptable because national law supersedes the ENFSI guidelines.

GENERAL INFORMATION

Country	
Audit date(s)	
Audit requested by	
Hierarchy of the database	national/sub-national
Organizational position of the database	
Auditing persons (function)	
Database manager(s)	
Database user(s)	
Database IT personnel	
Sources of DNA profiles	

AUDIT QUESTIONS

ENFSI recommendation 1	Every European country should establish a forensic DNA database and pass specific legislation for its implementation and management.
Audit question(s)	Are copies of the legislation available (or internet sources where they can be found available)?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 2	The type of crime-related stain DNA profiles which can be included in a DNA database should not be restricted.
Audit question(s)	What are the criteria for the inclusion of stains?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 3	To increase the chance of identifying the donors of stains, the number of persons in a DNA database who are likely to be the donors of those stains should be as large as legally (and financially) possible.
Audit question(s)	What are the criteria for the inclusion of individuals?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 4	Managers of national DNA databases should establish (together with other stake-holders) 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 the maximum number of adventitious matches a partial DNA profile is expected to generate.
Audit question(s)	What are the criteria for the inclusion of partial profiles?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 5	If possible, DNA profiles should be upgraded after a

	match in the national DNA database if it increases the evidential value of the match and decreases the possibility of an adventitious match.
Audit question(s)	Is it possible to upgrade older/partial profiles? If so what is the reason to update the older/partial profiles?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 6	Reference sample profiles should preferentially be loaded to a database only if a complete profile (maximum number of loci) is obtained using the PCR chemistry of choice.
Audit question(s)	What are the criteria for the inclusion of reference samples?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 7	Labs producing DNA profiles for a DNA database should, as a minimum, be ISO17025 (and/or national equivalent) accredited and should participate in challenging proficiency tests.
Audit question(s)	Which labs produce DNA profiles for the DNA database and are they (in the process of being) accredited?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 8	The custodian of the DNA database should have regular contacts with the suppliers of the DNA profiles to exchange information about legal and technical developments, changes in the inclusion and matching rules, incidents, etc.
Audit question(s)	Does the custodian have regular contacts with the suppliers of the DNA profiles?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 9	If a laboratory uses enhanced techniques to produce DNA profiles they should be searched using a dedicated (near) match strategy.
Audit question(s)	If the lab uses enhancement techniques to produce DNA profiles (do you use a near match search strategy?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 10	Composite DNA profiles should only be created from DNA profiles generated from the same DNA extract because it can not be excluded that different extracts, even from the same sample, contain DNA from different sources.
Audit question(s)	Does the DNA database contain composite DNA profiles and if so, how were they created?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 11	When a new allele is observed in a DNA profile, its presence should be confirmed by repeated DNA extraction, PCR, capillary electrophoresis and allele calling of the entire DNA profile. Only new alleles whose size can be accurately determined using the internal DNA size standard, should be included in the DNA database.
Audit question(s)	Is there a written procedure for the inclusion of new/rare alleles?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 12	Alleles from loci with chromosomal anomalies may be included in a DNA database if the default search strategy allows at least one mismatch. If the default search strategy does not allow any mismatches, wildcards may be used, as long as an agreed set of wildcards is determined to permit meaningful international exchange.
Audit question(s)	Is there a written procedure for the handling of chromosomal anomalies?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 13	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. Software tools may also be used, provided they are properly validated.
Audit question(s)	Is there a written procedure for the processing of mixed DNA profiles (both in the lab and in the DNA database)?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 14	A numerical match between a reference sample and a mixed profile must always be checked against the electropherogram of the mixed profile.
Audit question(s)	See the question associated with recommendation 12.
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 15	Mixed profiles of more than 2 individuals should not be systematically included in a DNA database because they will generally produce many adventitious matches.
Audit question(s)	See the question associated with recommendation 12.
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 16	Databases may contain autosomal STR profiles only. For those databases containing profiles from non-autosomal STR profiles or mitochondrial DNA sequences, specific operating procedures must be in place to avoid unintended familial searches. To avoid false exclusions, clear rules should be in place to indicate differences between a mtDNA sequence and the rCRS when comparing mtDNA results.
Audit question(s)	Are non-autosomal STR profiles or mitochondrial profiles added to the criminal DNA database? If yes, are specific operating procedures in place to avoid unintended familial searches? Are clear rules in place to indicate differences between a mtDNA sequence and the rCRS when comparing mtDNA profiles?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 17	If the removal of a DNA profile from the DNA database

	is dependent on external instruction from an authorized agent, a process should be in place to inform the custodian of the DNA database of this instruction, preferably by means of an automated message.
Audit question(s)	What are the rules and procedures for informing the removal of DNA profiles from the DNA database?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 18	There should be a system that can be consulted by those responsible for taking reference samples, to verify whether a person is already present in the DNA database.
Audit question(s)	Is there a system that can be consulted by those responsible for sampling persons to see whether a person is already present in the DNA database?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 19	DNA databases should contain an associated elimination DNA database (or databases). This should

	include laboratory staff of all categories, as well as visitors and maintenance personnel and profiles from those with access to traces (e.g. police, crime scene technicians).
Audit question(s)	Do you have an elimination database in place?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 20	Because elimination databases are not shared with other EU/ENFSI countries, unidentified DNA profiles found in negative controls, which may originate during the manufacture of disposables and/or chemicals should be uploaded to the ICMP Manufacturers Exclusion Database, MED.
Audit question(s)	Are the DNA profiles detected in negative controls shared with the MED?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 21	Policies and procedures should be in place to ensure that DNA-profiles deemed no longer relevant by the authorizing agent are deleted.
Audit question(s)	Are there policies and procedures in place?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 22	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. Automated processes reduce the possibility of human error, however, when DNA profiles are entered manually into the DNA database, a process that detects typing errors, for example the double-blind method of entry, should be used.
Audit question(s)	Describe the allele calling and DNA database inclusion process. If not fully automated, which measures have been put in place to avoid human error?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 23	To prevent and detect false exclusions (e.g. true matches that are not found due to an error in one of the DNA profiles), DNA profiles should be searched using

	a full Database search allowing at least one mismatch. The original data of DNA profiles involved in such near matches should be checked for possible errors during their production and processing.
Audit question(s)	Are DNA profiles checked for mistakes using a near match approach in a whole of database approach?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 24	As a national DNA database is regularly subject to attention from the public, politicians and the media, a DNA database manager should consider establishing tools to monitor the effectiveness of their DNA database and communicating this objective information publicly.
Audit question(s)	Is the performance of the DNA database monitored and communicated to the public?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 25	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. (A warning can be included in a report, indicating the factors that increase the possibility of an adventitious match such as size of the database, number of searches, mixed and partial profiles/random match probability, presence of family members, etc.).
Audit question(s)	Can the database manager/laboratory calculate the expected number of adventitious matches?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 26	A DNA database match report of a crime scene-related DNA profile with a person should be informative. It may include an indication of the evidential value of the match (RMP/LR), a warning indicating the possibility of adventitious matches (as mentioned in recommendation 25), and the implication that the match should be considered together with other evidence.
Audit question(s)	What does the Database match report include?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 27	DNA profiles should be entered into a database in a way that guarantees correct entry. Access to the DNA database should be limited to those persons who require access, by physical and organizational

	measures. Regular back-ups should be made, stored in a safe place, and recovered 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 verify whether they are properly synchronized.
Audit question(s)	Does the laboratory implement these management strategies?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 28	Investigating authorities should consider combining the information from a national DNA database with other types of evidence to increase the likelihood of identifying leads in other crimes.
Audit question(s)	Are you aware of this investigative strategy in your country?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 29	If possible, the cell material of reference samples should be stored to permit further processing, such as a loci upgrade, depending on internal laboratory procedures or national legislation.
Audit question(s)	What are the rules and procedures under the legislation

	for the destruction of the cell material of reference samples?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 30	If a Prüm-related information request is received from another country, the quality of the corresponding match should be verified before providing the requested information to the other country.
Audit question(s)	Is the match verified before providing the requested information?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 31	If possible, when operational under the Prüm treaty, international matches near or below the laboratory threshold should be further analyzed by additional DNA testing or statistical analysis before requesting information from another country. This threshold can be

	set individually in each laboratory in accordance with national legislation or guidelines.
Audit question(s)	Are six and seven locus matches further analyzed before requesting information?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

ENFSI recommendation 32	All regularly-used loci (also those not used by the receiving country) should be configured in the DNA databases of countries participating in the international exchange of DNA profiles under the terms of the Prüm system in order to see the full composition of the DNA profile of the sending country.
Audit question(s)	Is it possible to show which loci have been configured in your DNA database?
Audit result	
Compliance? If not, why?	Yes / No
Noncompliance acceptable? If yes, why?	Yes / No
Remark(s)/recommendation(s)	

APPENDIX 3: ENGLISH TRANSLATION OF THE TEXTBOX INCLUDED IN DUTCH MATCH REPORTS

POINT OF ATTENTION WITH REGARDS TO A DNA DATABASE MATCH

DNA databases contain large numbers of DNA profiles of known persons and of biological traces related to unsolved crimes.

As the number of DNA profiles in a DNA database increases, so does the chance of obtaining an adventitious match with a person who is not the actual donor of the trace.

This is especially true for partial DNA profiles and mixed DNA profiles, because the chance that they would match with a randomly chosen person is greater than the chance that a full, single DNA profile would match a randomly chosen person.

If there are doubts as to whether the matching person is the donor of the trace, for instance - because there is no other tactical or technical evidence which links the person to the crime, the possibility for additional DNA testing should be considered.

This point of attention applies particularly to matches found as the result of large-scale international DNA profile comparisons based on the EU Prüm decisions.

23. AMENDMENTS TO PREVIOUS VERSION

- Introduction updated to reflect contributions, updated contact information.
- Chapter 2: reference to Prüm Decision added.
- Section name “Persons” changed to “Reference profiles”.
- Amelogenin uncapitalized throughout document, where appropriate.
- Caption added for Table 1.
- Links updated throughout document.
- Section 4.3: added alternate use of term “benchwork match”.
- Section 4.4: added comment regarding combining DNA profiles from same source but obtained with different, overlapping kits, and benefits of collecting duplicate samples.
- Section 5.1: definition of match/hit updated, reference to Prüm Decision included.
- Section 5.2: §23.6 updated to §22.6; added reference to several studies on ethical aspects of familial searching; comment and references on GEDmatch opt-in/opt-out policies added.
- Section 5.3: included comment on overlapping loci between two DNA profiles; reference to Germany and locus SE33 removed; added mention of one-mismatch rule.
- Section 5.4: reference to specific countries removed;
- Section 5.6: added comment that matches with mixtures should be verified and explained by an expert.
- Section 6.1: 7 corrected to 8; “are” changed to “may” to better reflect real situation.
- Section 6.2: added comment on differing output measurements for each country; updated table 4 with data from 2021 included; added reference to study on effect of DNA databases on deterrence of crime.
- Chapter 9: reference to STR-lab removed (no information available); comment removed on program GENis, reference maintained.
- Chapter 12: reference to Netherlands removed, as reference could no longer be confirmed.
- Chapter 13: paragraph on Rapid DNA updated with new developments, reference to opinions and recommendations added.
- Chapter 18: link for list of governing bodies removed, could not be confirmed.
- Chapter 19: reference to European Horizon 2020 project “EXCHANGE” updated; reference to footnotes 5 and 24 deleted.
- Chapter 20: references to annual reports and national websites, as well as international overviews, updated.
- Chapter 21: paragraphs on Interpol and Europol updated; list of Prüm countries updated with Italy, comment on Norway; explanatory note on Prüm II proposal added; comment on national matching rules added; paragraphs on PCC SEE updated with relevant information.
- Section 22.3: explanatory comment on international DNA kinship matching added;
- Section 22.6: new reference for kinship software added.
- Section 22.7.1: information updated by ICMP representatives.
- Section 22.7.2: information updated by INTERPOL representatives; paragraph on I-FAMILIA added; table of INTERPOL countries with DNA database deleted (reference to survey results of 2019 added).
- Section 22.8: column “Missing Persons and Unidentified Human Remains” separated into “Missing Persons” and “Unidentified Human Remains”; added column “Missing persons database”; “?” changed to “x” to signify unknown; table updated from various sources;
- Addition of asterisk and footnote in Table 9 for Kosovo;
- Recommendations 12 and 31 updated to reflect current situation;
- Various spelling, grammar and formatting changes that do not alter the meaning of the text.

###