Swedish familial searches 2019 - 2024

An overview

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Summary

DNA analyses and law enforcement DNA databases, also often referred to as national DNA databases, have been used to help identify perpetrators for many years. Identifying a perpetrator through a relative in law enforcement DNA databases or in commercial genetic genealogy databases are newer methods that have received a lot of attention recently. However, many people are unaware that the DNA data used in traditional forensic casework at forensic laboratories differ substantially from the data required for searches in commercial genetic genealogy databases. Moreover, it seems that few people understand that familial searches, in law enforcement DNA databases, and investigative forensic genetic genealogical searches, in commercial genetic genealogy databases, are two distinct approaches to identify a perpetrator through relatives.

This report provides a brief overview of forensic DNA, forensic DNA analysis and the use of the law enforcement DNA database in Sweden. The difference between familial searches and investigative forensic genetic genealogy (iFGG) is also explained.

However, the primary focus of this report is to shed light on how familial searches are carried out in Sweden and in some other countries and highlight some differences. The Swedish familial search legislation, enacted in 2019, is explained, as well as how and when familial searches are carried out. Since the legislation gained force, 186 familial searches, involving 160 unique DNA profiles, have been carried out in Sweden. Seven of these profiles, belonging to previously unidentified individuals, have been identified thanks to a close relative present in the national DNA database, thus yielding a success rate of 4 %. The size of the DNA database as well as the proportion of the population registered are critical factors influencing the success of the tool. A familial search commonly results in a list of candidates who are potentially close relatives of the person of interest in the investigation. The ability to narrow down or specify the number of candidates, by expanding the DNA profile or using for example Y-STR data, are other important factors to address. In the report limitations, challenges and possibilities associated with familial searches are discussed.

Contents

1 Introduction

1.1 Background

For many years DNA, DNA analyses and law enforcement DNA databases, also often called national DNA databases, have been used to help identify perpetrators. The United Kingdom (UK) was the first country using DNA databases for this purpose in 1995 [1], followed by New Zealand in 1996 [2], the Netherlands and Austria in 1997 [3] and then the United States (US) and Germany in 1998 [3, 4]. The law enforcement DNA database in Sweden, was introduced in 1999 preceded by specific legislation [5].

Identifying a suspect and solving a serious crime via DNA from a relative, rather than through a direct match, is a newer approach. Such indirect searches, involves individuals who are not directly connected to the crime in question and can be carried out in either law enforcement DNA databases or in commercial genetic genealogy databases. Apart from being intriguing approaches they also raise ethical concerns regarding the use of sensitive personal (genetic) data.

Familial searches in a law enforcement DNA database was first introduced in the UK in 2002 [6], followed by some states in the US from 2008 [7] and the Netherlands in 2012 [8]. In Sweden, familial searches were allowed in January 2019 [9]. Finding perpetrators with the help of commercial genetic genealogy databases was first reported in the US 2018 [10] and in Sweden 2020 [11]. In 2023, Norway and Australia reported that they had solved cold cases using commercial genetic genealogy databases, and the Netherlands and New Zealand planned on performing pilot cases [12].

Identifying perpetrators via DNA from a relative is often highlighted by the media. It became big news in Sweden, when the rapist, who raped and almost killed a 9-year-old girl in Billdal in 1995, was found with the help of familial searches in 2019. Finding the Golden State killer in 2018 in the US, as well as the Linköping double murderer in Sweden in 2020 using commercial genetic genealogy databases, made big headlines as well [11]. Media is as keen on reporting about these cases and the use of novel approaches and techniques, as the public likes to read and listen about them [13, 14]. Most people, at least in Sweden, do not seem to be against the use of any of these methods [15-17]. On the contrary, most people seem to be in favour of using DNA and different kind of DNA database searches as means to find culprits and to solve crimes.

It is, however, unknown to the vast majority that the DNA data used in regular casework at forensic laboratories consists of much less information and in addition is completely different from the DNA data that is used in the commercial genetic genealogy databases. In regular forensic practice, a relatively small number of short tandem repeat (STR) markers are needed to fulfil the task whereas, in investigative forensic genetic genealogy (iFGG), a vast DNA data set analysing single nucleotide polymorphisms (SNPs) is required in order to obtain matches against distant relatives. Also, most people do not understand that familial searches and genetic genealogical searches are two completely different ways of searching for a perpetrator with the help of relatives and in totally different types of DNA databases.

1.2 Aim

In order to understand familial searches, one aim with this report is to provide a basic understanding of forensic DNA, forensic DNA analysis, the use of the national DNA database in Sweden, for both regular searches and familial searches. A second aim is to sort out and explain the difference between familial searches carried out in national DNA databases and investigative forensic genetic genealogy searches carried out in commercial genetic genealogy databases.

However, the main aim of this report, is to give the reader an insight into the familial search process in Sweden and in some other countries, present the results of the familial searches carried out in Sweden 2019-2024 and to discuss limitations, challenges and possibilities.

2 Forensic DNA

2.1 Forensic DNA STR analysis

When analysing DNA in criminal cases, the standard method is DNA profiling using a selected set of STR markers. These markers are located at various sites, called loci, in the genome of cell nuclei, mainly in the autosomal chromosomes but also in the sex chromosomes. The STRs are short regions of DNA usually in the size range of 100-500 base pairs, not coding for a protein, that vary between individuals. The variation seen, is the number of repeated sequences and thereby also its variation in length. The more repeats present, the longer the DNA fragment. STR DNA analysis means that the length of the DNA sequence is examined, at a number of certain loci (or markers). Our genome, including the STRs, is inherited from both parents and so the length, the number of repeats, are inherited in a predictable way. As an example, a specific STR loci located on chromosome 10, D10S1248, normally range from 8 to 13 repeats and if one individual shows the pattern 11 and 12, it means that the individual inherited these repeats from the mother and the father respectively. But the STR analysis will not tell if the variant (allele) 11 is inherited from the mother or the father, only that it is inherited from one parent and that variant 12 comes from the other one. In turn, if this individual has children, the children will inherit either 11 or 12 of these repeat variants at that specific locus [18].

There are thousands of STR regions in the human genome but only a limited number is used for forensic purposes. Therefore, the forensic community has agreed upon a standard sets of autosomal STR loci, to make comparisons between different laboratories and nations possible [19]. In the US, 20 so called core loci[1] are used throughout the whole country [4], and in Europe, 12 European Standard Set of loci (ESS), that were agreed upon in 2009, are used [19]. Combining certain STRs makes an STR pattern, called the DNA profile, that in principle is unique for an individual, apart from monozygotic twins that shares an identical DNA profile. How unique or rare a DNA profile is, can be calculated using a frequency database of the included allele values (relative frequency in a given population). A DNA profile obtained from a crime scene or recovered evidence items can be compared to DNA profiles from known individuals that might be of interest in the case, to find out who left DNA at the crime scene. If the DNA profile does not match the suspect or other individuals of interest in the case, it can be included and searched for in a national DNA database [18].

At the Swedish National Forensic Centre (NFC) different STR DNA analysis kits, analysing an increasing number of STR loci, have been used throughout the years. For example, 10 autosomal STRs were analysed 2001-2011. The same 10 STRs plus another 5 STRs were

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[1] From October 1998 to December 2016 the US had defined 13 core loci. Since January 2017, 20 core loci are defined.

analysed 2011-2023, including the 12 ESS loci. From 2023, 23 STRs are analysed, the old 15 STRs plus another 8 STRs, when the PowerPlex® Fusion 6C System was implemented [20, 21].

Most STR DNA analysis kits also investigate the so called amelogenin marker on the X and Y chromosomes thereby giving information regarding the genetic sex of individuals leaving crime scene samples [18]. In addition, STRs from the Y chromosome (male DNA) have started to be incorporated in newer kits.

2.2 Forensic DNA Y-STR analysis

The non-recombining region of the Y chromosome is inherited unchanged from father to son, except if mutations occur. The Y chromosome also carries STRs which can be useful to study, not only in kinship and migration cases and in historical studies, but also in contexts such as identifying missing persons or unidentified human remains (UHR). In addition, the Y-STR loci information can be useful when DNA profile mixtures consisting of one known female and an unknown male, as commonly encountered in sexual assault cases, are to be interpreted. Y-STR loci may also be valuable when interpreting mixtures with two or more male contributors.

There are commercial Y-STR kits which contain up to 27 Y-STR loci [22]. Modern STR kits often include several Y-STR loci as well. For example, the PowerPlex® Fusion 6C System kit used at the NFC includes 3 Y-STR loci in addition to the 23 autosomal STR loci. The 3 Y-STR loci are used routinely in casework at NFC for the evaluation and interpretation of complex male mixture DNA profiles.

2.3 Forensic mtDNA analysis

Mitochondrial DNA (mtDNA) is found in the mitochondria in the cell and, like the Y-STR, it is inherited unchanged, except when mutations occur. However, mtDNA is inherited from a mother to her children. MtDNA is commonly used when working with distant relationships and missing persons cases but also when analysing samples that lack DNA from the cell nuclei, such as in highly degraded nuclear samples as hair shafts without a hair root. A hair shaft usually contains intact mtDNA but highly degraded nuclear DNA, while the cells of a hair root usually contain both intact mtDNA and nuclear DNA [18, 23].

When analysing mtDNA, first hypervariable regions of the DNA are amplified and then, the product is sequenced. The sequence from a hair can be compared to an individual of interest to tell if the individual can be excluded from being the donor of the hair or if he or she cannot be excluded. With newer techniques the sequencing of the full length of the mtDNA is possible. At present, mtDNA analysis is not carried out at NFC but in cases where the mtDNA is considered useful, analysis is carried out by another laboratory on demand (behalf of the NFC). This only occurs in a couple of cases per year.

3 The law enforcement DNA database in Sweden

According to Swedish legislation, the law enforcement DNA database consists of three distinct databases; the crime scene samples database and the databases of suspects and convicted offenders [9, 24]. The original legislation began to apply in 1999 [5] and was amended to the current legislation in 2006 [9]. On July the 1st 2025, a further amended and improved legislation on DNA, “Biometrics in law enforcement” will come into force [25]. The coming legislation will, in many ways, stay the same (as now) regarding DNA, but some improvements have been proposed that hopefully will result in more DNA profiles in the DNA databases of suspects and convicted offenders[2].

NFC is the custodian of the national DNA database (and before 2015 its predecessor Statens kriminaltekniska laboratorium). All information regarding the database is stored in NFC's Laboratory Information Management System (LIMS); Forum.

According to Swedish law, both the current and upcoming, no information that may reveal personal characteristics can be registered. This means that neither genetic sex, as seen with amelogenin, nor Y-STR data can be included. As far as we know, Sweden is the only country that does not include information regarding genetic sex in their national DNA database. All other countries, having a national DNA database, include this information. The trend in other countries seems to be to include Y-STR information, when available. The US, for example, has been registering Y-STR information as well as mtDNA in their national DNA database for many years, when available, mainly to aid in searches related to missing persons [4]. Spain also began doing Y-STR analyses of male individuals with the purpose to include the information in their national DNA database already in 2000 [26].

3.1 The crime scene samples database

The crime scene samples database includes unknown DNA profiles obtained during an investigation. When a DNA profile from a crime scene sample matches a DNA profile from a suspect or a convicted offender in the DNA database, and if the match is approved and reported – thus no longer from an unknown – the DNA profile is automatically deleted from the crime scene samples database. Otherwise, the DNA profile will remain for 15, 30 or 70 years depending on the type of crime in which it was collected.

3.2 The DNA database of suspects

In Sweden suspects can, according to current law, be sampled for DNA and their DNA profile included in the DNA database of suspects if the crime may result in a prison sentence. Beside this, the person is also expected to be sentenced to anything but a fine, if convicted. The DNA profile from the suspect is deleted from this database if the person is sentenced to a fine or if charges are dropped and he or she is no longer a suspect. The police database of suspects ("Misstankeregistret") directs if an individual's DNA profile will remain in the DNA database of suspects or if it shall be deleted. This means, in order to work, that the DNA database of suspects communicates with the police database of suspects once every 24 hours to keep the information up to date. As suspicion of crime comes and goes it means that a high number of DNA profiles are included and deleted from the DNA database of suspects every year.

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[2] The new law will make it clearer when DNA samples can be collected for registration in the national DNA database. Currently, this can only be done if a person is reasonably suspected of a crime that includes imprisonment in its penalty scale. Besides this, the person is also expected to be sentenced to prison if convicted (and not merely fines). Under the new law, DNA samples may be collected if a person is reasonably suspected of a crime that includes imprisonment in its penalty scale. Furthermore, currently a person can only be sampled for registration in the national DNA database while reasonably suspected of a crime. Under the new law convicted individuals who were not sampled when they were reasonably suspected may also be sampled afterwards, once they have been convicted. Finally, a larger number of convictions will serve as a basis for registering a person's DNA profile in the DNA database. Currently, only DNA from individuals sentenced to a penalty other than fines can be registered in the DNA database. Under the new law, DNA from any convicted individual will be eligible for registration in the DNA database. This means that if a person is sentenced to prison, a fine, a suspended sentence, or receives a penalty order that corresponds to a conviction, the person's DNA profile may be registered in the DNA database.

According to the legislation, the physical (DNA) sample must be destroyed within six months after collection or sooner if charges are dropped. Usually, it is not a significant issue, but not being able to conduct additional analyses can sometimes be challenging.

3.3 The DNA database of convicted offenders

If a suspect is convicted to anything but a fine, the DNA profile is transferred and included in the DNA database of convicted offenders. The DNA profile is deleted from the database of convicted offenders 3, 5 or 10 years after the sentence is served. To achieve this, the DNA database of convicted offenders communicates with the police database of criminal records ("Belastningsregistret") every 24 hours. Before deleting a DNA profile from the DNA database of convicted offenders, the system checks in the police database of suspects if the individual is suspected of a(nother) crime that may result in a prison sentence. If the answer is no, the DNA profile is deleted. If the answer is yes, the DNA profile is transferred to the DNA database of suspects. As for the DNA database of suspects, this means that a lot of DNA profiles from convicted offenders are included and deleted from the DNA database of convicted offenders every year.

To be clear, in Sweden, a DNA sample can only be taken from a suspect, if the crime may result in a prison sentence. In addition, no DNA samples can be taken retroactively from convicted offenders. However, the new legislation, which will start to apply on the 1st of July 2025, will make it possible to take DNA samples also from convicted offenders who for any reason were not sampled as suspected.

3.4 Statistics

The number of DNA profiles in the national DNA database at the end of 2024 was 231 000. The DNA database of crime scene samples included 50 000 DNA profiles, the DNA database of suspects 19 000 profiles and the DNA database of convicted offenders about 162 000 profiles [27].

During 2024, 45 000 DNA samples were taken from suspected criminals[3] and sent to NFC. The net increase in DNA profiles from suspects in the DNA database of suspects was 600 and the net increase in DNA profiles in the DNA database of convicted offenders was 5 200 [27]. Unfortunately, it is not possible to obtain data on the number of DNA profiles that were transferred from the DNA database of suspects to the DNA database of convicted offenders and vice versa during the year.

The size of the national DNA database is comparable to other countries in Europe with a similar population size [28]. With a population in Sweden of approximately 10.6 million and the number of individuals in the DNA database being 180 000, the equivalent of 1.7 % of the population is included in the database.

3.5 National searches

All searches between the three DNA databases are carried out in the software CODIS (Combined DNA Index System) [29, 30]. CODIS was originally developed in 1990 by the US Federal Bureau of Investigation (FBI) to share DNA information within the states and at a national level. Through a clear strategy of generously sharing CODIS outside the US, its use has quickly expanded and today 63 countries around the world use CODIS for their daily DNA

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[3] This number includes both new samples taken from suspects who have never been sampled before and new samples taken from suspects already included in the DNA database but whose DNA data needs to be updated with the latest DNA analysis kit in order to get the full set of STRs used.

database searches [4]. Sweden has been using CODIS since 2003 and before that an in-house Microsoft Access solution was used.

Every weekday, new DNA profiles are imported to CODIS and DNA profiles are deleted, in accordance with to the Swedish legislation. Thereafter, so called incremental identity autosearches[4] [4] are carried out and the obtained matches are transferred to Forum (LIMS) to be reported to the clients. In CODIS, only the DNA profile itself, its reference ID number and information about the specimen category (forensic unknown, forensic mixture, suspected and/or convicted individuals) are stored.

In Sweden, single source (one person) DNA profiles are routinely autosearched with *high stringency search mode*[5] and mixture DNA profiles with *moderate stringency search mode*[6]. In the US, and in some other countries, single source DNA profiles are searched using *moderate stringency* which, in addition to exact matches, also may provide so-called partial matches which is further discussed later on [4].

3.6 Prüm searches

All single source DNA profiles in the three databases are also automatically searched, "Prüm searched", against the national DNA databases of currently 27 countries[7] in Europe, and vice versa, according to the Prüm Decision [31, 32]. Matches between the countries can be obtained thanks to the extension of the European standard set of markers (ESS) into 12 STR markers, as decided by the EU in 2009 [33], alongside a decision making accreditation according to ISO 17025 mandatory in order to share DNA profiles and search in other EU countries DNA databases [31, 32].

4 Finding a perpetrator via relatives

4.1 Lineage markers

As mentioned in section 2.2 and 2.3, the Y chromosome is passed unchanged from a father to his sons and mtDNA is inherited unchanged from a mother to her children, except when mutations occur. The DNA found on the Y chromosome and in the mitochondria is called lineage markers since it can be traced through many generations back in time.

The DNA, found on the Y chromosome and in the mitochondria, is in criminal cases not by itself useful to identify a specific individual but can be used to identify relationships between individuals or to exclude a person as a trace donor.

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[4] In the CODIS module Identity Autosearcher, index versus index is searched. A full identity autosearch, means that all profiles, which meet the complete profile requirements for the indexes, are searched against each other. Incremental identity autosearch, on the other hand, means that only previously not searched DNA profiles, new and updated DNA profiles, are searched.

[5] *A high stringency match* is defined as a match that requires all alleles to match between two DNA profiles. An example of a *high stringency* match is when alleles 11,12 match alleles 11,12.

[6] *A moderate stringency* is defined as a match where the target and the candidate may have different number of alleles but the one with fewest alleles must match. An example of a *moderate stringency* match is when alleles 11,12 match 11,11 or 12,12. Another example, is when 11,12,13 match 11,11; 11,12; 11,13; 12,12; 12,13 or 13,13.

[7] Austria (2015), Belgium (2017), Croatia (2019), Cyprus (2023), Denmark (2017), Estonia (2014), Finland (2014), France (2017), Germany (2016), Greece (2022), Hungary (2016), Ireland (2020), Italy (2025), Latvia (2016), Lithuania (2014), Luxembourg (2018), Malta (2016), Norway (2024), Poland (2014), Portugal (2016), Romania (2015), Slovakia (2014), Slovenia (2016), Spain (2015), the Czech Republic (2015), the Netherlands (2013), the UK (2020).

4.2 Familial searches using forensic STR DNA

Familial search means that an unknown STR DNA profile, from a crime scene sample, following a no-match in regular database searches is searched against the DNA from suspects and convicted offenders with the goal to find partial matches. A partial match may indicate close biological relatives - such as parents, children or siblings - thereby, providing investigative leads that can help identify the perpetrator.

Familial searches can be successful because close biological relatives, as parent-child, share about 50 % of their DNA, including the STR loci in the forensic DNA profile. It is important, though, to remember that the approach is blunt as also unrelated individuals by chance may have similarities in their DNA, especially common STR alleles. Thus, a partial match from a familial search is most likely caused by pure chance. The lists of candidates obtained by familial searches will therefore mainly consist of persons with random similarities. However, the list can be reduced as well as refined with for example Y-STR data, if available.

The method is primarily used in cases when traditional investigative methods have not led to the identification of a perpetrator. The first documented familial search was carried out by the Forensic Science Service (FSS) in the UK, in 2002 [6]. Since then, several countries have started to use familial searches as a tool to combat crimes [7, 18], but it is not a generally accepted tool and is for instance not permitted in Norway [34].

4.3 Familial searches using Y-STR

Y-STR familial searches means that an unknown Y-STR DNA profile, from a crime scene sample, is searched with the goal to obtain exact matches against Y-STR DNA of suspects and convicted offenders in the law enforcement DNA database. The Y-STR search will find any male relatives included in the database, unlike STR familial searches that first and foremost may find parents, children and siblings.

Spain, for example, have had Y-STR data registered in their national DNA database since 2000 although this was of minor magnitude in the beginning [26]. In 2013, Spain started to increase the Y-STR data in their DNA database more decisively. Spain usually analyses and register fourteen Y-STR loci. Nowadays, thanks to the extensive Y-STR data in their national DNA database, unknown male perpetrators can, under certain conditions, be found if there are male relatives in the DNA database.

4.4 Investigative forensic genetic genealogy

Genetic genealogy means that traditional genealogy is combined with the use of genetic information from DNA analysis. DNA testing kits to study familial relationships and ancestry is provided by several commercial companies and a DNA testing kit can easily be ordered by anyone at a reasonable cost[8]. The DNA testing companies use microarray chip analysis and/or massive parallel sequencing (MPS) to characterize so called single nucleotide polymorphisms (SNPs) of the genome. SNP is the difference of a single nucleotide at the same position in the DNA and normally, a variation with a frequency greater than 1% is called an SNP. Generally, 600 000 – 1 000 000 SNPs are analysed to explore genetic heritage [18].

Investigative genetic genealogy (IGG), forensic genetic genealogy (FGG), forensic investigative genetic genealogy (FIGG) and even investigative forensic genetic genealogy (iFGG) [12], are variants of expressing that law enforcement agencies use commercial genetic genealogy

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[8] The cost of utilizing this service is of relevance for law enforcement use. Lower consumer cost means larger databases which in turn leads to a better tool for law enforcement use.

databases - open for law enforcement - to find a perpetrator of a crime, or to identify unknown human remains in combination with traditional genealogy.

It is important to understand that SNP data is not equal to the STR data registered in law enforcement DNA databases. In order to match distant relatives using SNP data, much more genetic information is needed than that found in an STR profile. To search a crime scene sample, or DNA data generated from UHR, in a commercial genetic genealogy database, the law enforcement must first perform a SNP analysis. If the DNA data meets quality and quantity requirements, it is uploaded to a genetic genealogy database to find both distant and close relatives. Investigators or genealogists then build a pedigree by combining genealogy database information with traditional genealogy thereby encircling a potential suspect that can be further scrutinized in the criminal investigation [11]. Thus, iFGG is carried out in commercial genetic genealogy databases using large SNP datasets.

5 Familial searches in Sweden 2019-2024

5.1 Legal basis for familial searches

When the act 2018:1693, regulating the Police processing of personal data under the Criminal Data Act, came into effect on the 1st of January 2019, familial searches could begin to be carried out in Sweden [9].

The act 2018:1693, Chapter 6, Paragraph 5 states that the search ban, previously established in the Criminal Data Act 2018:1177, Chapter 2, Paragraph 14 - which prohibited searches with the aim of obtaining a selection or list of individuals based on sensitive personal data - does not apply to searches in DNA, fingerprint and description databases [24, 9]. Thus, the act 2018:1693 made it possible to carry out familial searches in the Police's DNA databases.

Interestingly, since familial search means an extended use of the DNA data, including making lists of potential relatives, the law does neither limit its use, nor specify which categories of crime it is allowed for [9]. This compared to coming legislation on the use of iFGG being strict and clear in limiting the use to cases of murder, serious rape and serious rape against children [25].

5.2 Spreading the news

Information about the new tool was communicated to crime investigators across Sweden in 2019, mainly through the police web forum and a fact sheet but also via a national information “tour”. During this information campaign, presentations provided clear information about both possibilities and limitations of familial searches to investigators, cold case investigators and national detectives, both in person and through video. The media also showed interest in the new tool. After several interviews, articles were published for example in Svenska Dagbladet, one of Sweden’s most popular morning newspaper [35], and interviews were broadcasted on Swedish radio and television [14].

5.3 Familias

Familial searches are carried out using Familias [36, 37] which is a software that can be downloaded free of charge [38]. CODIS can be used as well, but it was not until July 2018 that FBI published a manual on how to use CODIS for familial searches [39]. By then, Sweden had already decided to use Familias for familial searches and started to validate the software for that purpose.

Familias was initially developed by scientists in Norway to solve paternity and other kinship cases. By using autosomal STR DNA profiles from putative family members, Familias computes the probabilities for different given family relationships. In a later version, a module was added allowing searches for close relatives, such as parent-child and siblings, using databases with many individuals [40].

Familial searches in Familias are clearly described and follow a straightforward process [41]. The main steps included are as follows:

- Define a frequency database to be used.
- Import the DNA profiles from suspects and convicted offenders.
- Import the DNA profile to be searched.
- Set the search options:
    - likelihood ratio[9] (LR) threshold,
    - relationship to search for,
    - alternative hypothesis and
    - the fixation index[10] (FST) value, usually set between 0 and 0,02 [42, 43].
- Perform the search.
- Sort the lists of candidates.

5.4 Criteria, settings, searches and reporting

Since the legislation does not regulate which categories of crime that could be relevant for familial searches, NFC specified some recommended criteria [44]. The searches should mainly be carried out in serious crimes such as murder, aggravated rape and serial rape or equivalent. The unknown DNA profile to be searched, shall originate from a relevant crime scene sample and not match a known individual in the specific case, in the national DNA database or in any databases in the European countries under the Prüm Decisions. When applicable, the unknown profile should also be searched in relevant countries not operational under the Prüm Decision beforehand.

The investigator in a case, in which a familial search is considered, is expected to contact a case reporting officer at the NFC before submitting a request. The reporting officer at NFC will make an initial assessment on whether the DNA profile is suitable for a familial search or not, with or without additional DNA analyses. In brief, the DNA profile is considered suitable if analysed with PowerPlex ESX 16 Fast and/or PowerPlex Fusion 6C, or any other equivalent DNA analysis kit including the 15 to 23 autosomal STR loci, respectively. However, over the years, DNA profiles with fewer number than 15 STR loci have been searched in a few occasional cases.

The search can be carried out with single source DNA profiles or mixture DNA profiles with two contributors where, preferably, one of the contributors is known.

Usually once a month, all DNA profiles from suspects and convicted offenders included in the DNA database, are exported from CODIS to Familias, using the CMF 3.3 format[11], together with the crime scene DNA profiles requested to be searched.

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[9] Likelihood ratio (LR) is a concept used in statistics to compare how well a result is explained by two different hypotheses.

[10] The fixation index (FST), also called the ϴ value, is a measure of population differentiation. It is frequently estimated from data, and corrects for differences of frequency values occurring within a population. FST ranges from 0 to 1 where 0 means no differentiation and 1 means complete differentiation.

[11] The CMF defines the packaging of information for import to and export from CODIS and is based on the Extensible Markup Language (XML) industry standard.

The LR threshold for matches is set to 300 [45, 46][12] and is chosen to get a good balance between the chance of identifying close relatives without getting too many unrelated candidates [47]. In other words, the candidate list will not be too long and the risk of missing a close relative is low.

Simulations using PowerPlex ESX 16 Fast results have shown that if a parent or a child is present in the database, the LR value will most often be higher than 1 000 and the parent or child will appears among the top 20 candidates [47]. However, simulations also indicate that identifying a full sibling is more challenging as the LR value may be less than 10 and a true full sibling could appear far down on the candidate list. Nevertheless, a full sibling will appear among the top 30 of the candidates in most cases, [47], but one true exception is discussed later (in Section 7).

Corresponding simulations using the PowerPlex Fusion 6C System show that if a parent or a child is present in the database, the LR value will be higher than 1 600 and the parent or child will appear as the top number one candidate [46]. Also, if any sibling is present in the database he or she will appear as the top number one candidate in 27 cases of 30. These simulations showed that in three cases, siblings appeared on rank 19-33 with an LR between 4 and 130 [46]. The more suspects and convicted offenders analysed with PowerPlex Fusion 6C System the better the familial search result, but finding siblings present in the database will in some cases still be a challenge.

A Swedish normal population is used to calculate the allele frequencies [45] and the FST value of 0.01 is used since it is the standard value normally used at NFC [46].

First, a parent-child search is carried out and the resulting list, consisting of the reference ID number of the DNA profiles, is sorted by the LR values and saved. Then, a search for possible siblings is carried out and the resulting list is sorted on given LR's and saved as well. The alternative hypothesis for both calculations is set to "unrelated".

When Y-STR data is available and when applicable, the information can be used manually to narrow down the lists of candidates and/or to pin-point potential brothers that do not appear as top candidates. Due to legislation, no cell material from sampled individuals can be stored over time, meaning no additional DNA analyses of the candidates' DNA, such as Y-STR analyses, can be done afterwards. If Y-STRs could be used to a larger extent it would minimize the risk of missing full-siblings presented far down on the candidate list.

The lists of parent-child and sibling candidates are manually supplemented with given names, surnames and social security number or date of birth. The candidate lists are reported in a forensic intelligence report "*forensiskt uppslag*" to the investigator who requested the search (an example is included in the Appendix).

During 2019-2024, the average number of candidates in the parent-child and siblings lists were 17 and 25, respectively.

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[12] In January to September 2019, the LR threshold 100 was used, but in October 2019 the LR value was adjusted to 300 where it has remained.

5.5 Capacity

Initially, NFC committed to carry out five familial searches per month, with the goal of increasing the number of searches as needed and after getting procedures in place. But the demand from investigators has never reached five searches per month.

The time spent for a familial search case is relatively limited. Usually, it takes a day or two to conduct the search, write the forensic intelligence report and issue the report. However, the actual average processing time in calendar days is 18, from request to reporting the forensic intelligence report. The reason behind is simply because the searches are normally carried out in batch, once a month, which means that requests have been queued up awaiting a run date.

5.6 How the result is used in investigations

It is up to the investigator to investigate if and how the candidates, from the top to bottom of each list, could be of interest for the case inquiry. Normally the top candidate should be the candidate of greatest interest and the first one to be further investigated. However, one needs to keep in mind that, especially regarding siblings, true siblings can be positioned far down on the list [46].

Obvious questions to consider should be whether if and how an individual on the list has any parent, child or sibling with a criminal record being of relevant age, but also, if this relative at the time of the crime was situated on a geographical location of relevance. This together with other investigative measures may then end up with the police deciding to take an ordinary DNA sample from that individual for comparison and find out if the DNA profile matches the profile from the crime scene sample or not.

The Police Region Syd has recruited an investigator who is skilled in traditional genealogy research, thus being experienced in performing searches for information about family members in a variety of public as well as genealogy specific databases. This competence can be used in several different parts of a crime investigation and, apart from making the job more efficient, have other obvious benefits when exploring the candidate lists from a familial search.

5.7 Number of familial searches

Since the start in 2019, familial search has been performed on 160 unique DNA profiles (Table 1). A few of these DNA profiles have been searched repeatedly during the years, following renewed requests. As a result, a total of 186 familial searches have been carried out 2019-2024 [48-53].

Table 1*. The number of familial searches carried out 2019-2024, separated on the seven police regions (certain DNA profiles have been searched repeatedly).*

Police Region	2019	2020	2021	2022	2023	2024	Total
Bergslagen	1	3	2	0	1	5	12
Mitt	1	0	4	1	1	0	7
Nord	2	2	0	1	0	1	6
Stockholm	10	8	6	8	12	6	50
Syd	29	15	2	10	6	6	68
Väst	6	3	10	9	3	1	32
Öst	2	2	1	3	1	1	10
Total number of searches	**51**	**33**	**25**	**32**	**24**	**21**	**186**
Total number of unique DNA profiles searched	**49**	**28**	**23**	**25**	**18**	**17**	**160**

All Police Regions in Sweden requested familial searches during this period of time. Region Syd requested the most, 68 searches, followed by Region Stockholm and Väst who requested 50 and 32 searches, respectively.

A majority of the 160 searched DNA profiles were from various serious crimes such as murder, attempted murder, rapes, arson, explosions and devastations causing public danger as well as cases concerning serious weapons offences. Also, a few DNA profiles from less serious crime were searched during the period. For example, three different DNA profiles from three different cases concerning series of threatening letters. The reason why these DNA profiles were familial searched was because there were no other leads in these cases and the writers wrote numerous letters to many different victims. Two of the writers wrote “common” threatening letters, and the third one sexually harassed women with his letters. None of the DNA profiles would normally have been familial searched, but due to the high number of threats and repeated crimes, it was considered proportional and appropriate to try and bring the cases to an end. Unfortunately, none of these three perpetrators were found using familial searches. However, one of the perpetrators was found later thanks to other investigative efforts.

5.8 Cases solved by familial searches

Totally seven previously unknown and unmatched DNA profiles have matched a person thanks to familial searches, which gives a success rate of 4 %.

During the first year, 2019, three unknown DNA profiles could be identified. The first case, the so called Billdal case from 1995 which was a serious rape against a child, could be solved thanks to the presence of the perpetrator’s son in the DNA database [15]. The perpetrator was found, swabbed and already later that year sentenced to prison. The case was front page news when it was finally solved with the use of familial searches and has continued to receive a lot of media attention over the years[13] [54]. In the second case, an unknown body in a murder

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[13] This case is special in that sense that it is an example showing the importance of taking DNA samples from suspects of crime whenever possible. In retrospect, it has been found that the Billdal case could have been solved 11 years earlier if that person had been swabbed when he was suspected on probable cause in another rather serious crime. This would have provided justice to the victim earlier, but also avoided misuse of police resources as well as putting the culprit behind bars earlier. It has never been clarified why a DNA sample was not collected in the first instance.

investigation in Region Syd, could be identified thanks to a son present in the DNA database. The murder investigation gained new momentum as the victim could be identified, but as far as known the case has not yet been solved. In the third case, also a murder case in Region Syd, an unknown person could be identified thanks to a brother being present in the DNA database. However despite that the DNA matched an individual, the preliminary investigation did not sum up for a trial, the charges were withdrawn and the case was later closed by the prosecutor [48].

Since 2020, four other DNA profiles have been identified thanks to familial searches, through the presence of a brother in three of the cases, and a father in one of the cases [50-52]. Despite requesting more information, it is unclear how these four identified DNA profiles affected the investigations and the outcomes of these cases.

Also, in a few cases a familial search was requested, carried out and reported at the same time as the investigation leader in parallel closed the case, before anyone had the chance to investigate the lists of candidates. Therefore, it is not clear if the familial search was or would have been successful or not.

6 Familial searches in other countries

6.1 United Kingdom

As the first country, UK started to carry out familial searches using STR DNA profiles in 2002 [6, 8].

The UK law neither supports nor prevents familial searches [8], but the Forensic Information Databases Service (FINDS) Strategy Board[14] [55] controls the searches and must follow current guidelines and policies [56]. This means that all searches must follow the DNA Familial Searching Policy for the National DNA Database (NDNAD) [57]. This, in turn, means that legal requirements relating to the creation, operation and maintenance of the NDNAD must be taken into consideration. Ethical and moral obligations with respect to the use of the DNA data and samples taken under Police and Criminal Evidence Act 1984, in particular the Human Rights Act 1998 and the Data Protection Act 2018, must be taken into account as well [56].

The familial search process in the UK starts with the identification of a potential case where DNA from the perpetrator is available but no match to a person has been obtained. Any relevant DNA profile from any serious offences can be a good candidate. In the UK it is also possible to search DNA from unidentified human remains to find a close relative which can help identifying the body [56].

Firstly, the familial search must be approved by a force National Police Chiefs' Council (NPCC) officer, or equivalent or above, and receive budgetary approval from the Force Forensic budget holder. Then, the search must be agreed and supported by the Forensic Service Provider. Finally, the National Crime Agency Major Crime Investigative Support against the Familial Tactical Guide must assess and support the search and the Chair (or nominee) of FIND Strategy Board also have to give his or her approval [56].

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[14] The Forensic Information Databases (FINDS) Strategy Board provides governance and oversight over the operation of the National DNA Database and the National Fingerprint Database. The Board includes representatives of the: National Police Chiefs' Council (NPCC), Home Office, Association of Police and Crime Commissioners, Biometrics and Forensics Ethics Group, Forensic Science Regulator, Information Commissioner's Office, Biometrics Commissioner, Scottish Biometrics Commissioner, Police and devolved administrations of Scotland and Northern Ireland.

When a familial search is approved, the current DNA profile is loaded into the familial search software used by the provider and two different search algorithms, based on the number of shared alleles, are ran. The first search algorithm searches for parents or children in the DNA database and the second searches for siblings. Thus, the software generates two lists of candidates, each sorted by the LR. Only the reference ID of the DNA profiles of the candidates are included in the lists. The DNA information itself is not included. Information about geography, age, gender and ethnic appearance of the individuals on the lists are added afterwards and this information is also used to rearrange the lists. Finally, the lists are completed with names and delivered to the investigation.

During 2021-2022, 27 familial searches were carried out [58], while 13 searches were carried out 2022-2023 [59]. The success rate for these time periods are not stated on the homepages but earlier, between 2002 and 2014, the success rate has been reported to be about 17 % [8].

In the UK there are about 5 900 000 DNA profiles from unique individuals in the NDNAD as of March 2023. To be included, an individual must have been arrested and detained in a police station and if convicted the profile is retained indefinitely [60]. The number of inhabitants in the UK is 67 million which means that an equivalent of 9 % of the population is included in the NDNAD.

If one compares familial searches in the UK with those carried out in Sweden, the following is noted. The system(s) used for familial searches in the UK is not public information. However, the software(s) used by the Forensic Service Provider in the UK and Familias used in Sweden both use shared alleles to search for candidates and LR to sort the candidates. Familial searches are not covered by legislation in the UK as they are in Sweden. On the other hand, familial searches are far more strictly regulated and handled in UK as compared to Sweden. The regulations in the UK decides which categories of crimes familial searches can be relevant in, and a formal approval from an independent board is needed.

6.2 The Netherlands

In the Netherlands, familial searches using STR DNA profiles have been carried out since 2012 following the introduction of a legislation covering the use of DNA kinship investigations in criminal cases, including familial searches. The legislation allows familial searches in police investigations of serious, unsolved criminal cases with eight years of imprisonment in the penalty scale, including violent deaths and sexual assaults [8].

In order for a familial search to be carried out, a pre-assessment is needed as well as an approval from an investigative judge and a mandate from a local prosecutor.

The DNA profile needs to be a single source DNA profile or a single DNA profile deduced from a mixture DNA profile [61]. The pre-assessment needed is basically to evaluate technically if the DNA profile in question is or can be made suitable for familial searches. The following checks and actions are done: Firstly, a minimum of 15 STR loci are required. Secondly, there must be enough DNA extract left so that a supplementary autosomal STR analysis, Y-STR analysis and/or mtDNA analysis of the sample can be performed. Thirdly, if the DNA profile has not been analysed with the latest DNA kit, an upgrade of the DNA profile is usually also performed, but this is not mandatory. Finally, a familial search simulation is carried out to get an idea of the number of candidates and of the chance of finding the relative if the relative is present in the database[15]. If the DNA profile meets all technical requirements, legal permission involving the investigative judge and the local prosecutor could be granted [61].

The familial searches are carried out using the Bonaparte software which was initially developed for kinship analysis in disaster victim identifications but is also used to help identify missing persons and unidentified human remains [62]. In the Netherlands, CODIS is used for storing and searching all DNA profiles in the national DNA database [28, 61] and Bonaparte contains a copy of the information present in CODIS, being updated and synchronised every night. ProbRank, a new search tool developed at the Netherlands Forensic Institute [63], is currently being tested for familial searches and is expected to replace Bonaparte in the future [61].

In the Netherlands, the search strategy is to do a parent-child search as well as a sibling search with the DNA profile from the actual crime scene sample. A likelihood ratio threshold of 50 000 is used for the initial search. The candidates, usually 0-2 individuals, are investigated further and supplementary autosomal STR, Y-STR and/or mtDNA analyses are performed [61]. The DNA samples themselves, from all individuals included in the DNA database, are stored as long as the DNA profiles are registered, which means that any DNA sample from a convicted offender can be re-analysed whenever needed. After analysing the autosomal STR, Y-STR and/or mtDNA of the candidate(s) and the sample, usually there is 0-1 candidate left in the final list. The turnaround time for a case, after the legal permit has been obtained, is usually less than two weeks.

A likelihood ratio threshold of 1 000 can also be used for familial searches when the search with the LR threshold 50 000 did not give a reportable candidate and the prosecutor wishes to search again with a slightly higher chance of finding a relative (if the relative is present in the database) and at the same time increasing the number of candidates not being a true relative. Then, obviously the initial list of candidates will be longer, normally about 50 candidates, and the turnaround time is three months due to supplementary autosomal STR, Y-STR and/or mtDNA analyses of the candidates on the list. The final list is short and usually contains 0-1 candidates [61].

Besides parent-child and sibling searches, so called pedigree searches can be carried out as well, for example in cases with an abandoned child. In such cases, the DNA profile from the child is used together with the DNA profile from the putative mother, whose DNA often can be found on the child’s clothes, to search for the father [61].

In the Netherlands, Y-STR is analysed if needed for a case, such as sexual assault cases with low amount of male DNA or cases including male and female mixture DNA profiles. The Y-STR data for the convicted offenders is registered in the DNA database in addition to the autosomal STR DNA profile. Currently, there is Y-STR data registered for about 80 000 (20 %) of the convicted offenders in the database. Y-STR familial searches are allowed and may be used to find for example male relatives, as cousins and uncles, of someone who left a crime scene sample [61].

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[15] The simulations are carried out in Wolfram Mathematica (https://www.wolfram.com/mathematica/) using an in-house script. The input values are the database size, including information about the proportion of the profiles having information in 10, 16 or 23 loci, the actual DNA profile to be familial searched and the LR threshold chosen for the search. The number of estimated candidates indicates the expected workload for upgrading the candidates, mainly autosomal STR and Y-STR upgrades but also a small number of mtDNA upgrades. The result of the simulation can help prioritizing searches, if needed.

Moreover, if a DNA profile from a crime scene sample contains a “rare allele”, this allele alone can be used to search for individuals in the database who have the same allele in their DNA profile. Individuals sharing the same “rare allele” may be close relatives and such matches can be investigated further [61].

Since 2012, familial searches have been carried out in 140 cases in the Netherlands. Twelve potential relatives have been found so far thanks to these searches, which gives a success rate of 9 %.

There are about 400 000 DNA profiles from convicted offenders registered in the Dutch DNA database. To be included an individual must have been convicted for a crime with at least 2 years of imprisonment in the penalty scale. The offence determines how long the DNA profile is kept. If the offence carries a maximum sentence of at least six years, the DNA profile will be kept for 30 years. If the offence carries a maximum sentence of fewer than six years, the DNA profile can be kept for up to 20 years [64]. The number of inhabitants in the Netherlands is 17.7 million which means that an equivalent of 2 % of the population is included in their national DNA database.

If one compares familial searches in the Netherlands with searches in Sweden, there are some differences. The first is the use of different software, Bonaparte and Familias, both initially developed for another purpose: kinship analyses. The second difference is that searches are more strictly regulated in the Netherlands, for examples in terms of the categories of crimes accepted for the search and the formal acceptance to perform it. A third difference is that in the Netherlands all DNA samples taken from individuals are saved as long as the DNA profile remains in the database, whereas in Sweden the sample can be kept only for a restricted period of time. Consequently, in contrast to the Swedish situation, the Dutch approach provides a high degree of flexibility for future needs, including supplementary DNA analyses of the candidates from a familial search - such as Y-STR analyses – and thus generates a more precise and shorter list of match candidates to the crime investigation.

6.3 Spain

In Spain, legislation regulating their national DNA database dates from 2007 [26]. The law states in which crime categories DNA sampling can be carried out, that DNA profiling can be useful in the identification of unidentified human remains and missing persons, which institutions that are authorized to analyse genetic profiles, as well as when the DNA profiles must be removed from the database [26].

The legislation states that it is non-coding regions of DNA that can be registered and used. As a consequence, Spain has since the beginning registered both autosomal STR DNA and Y-STR DNA in their database [26]. The analysis and registration of Y-STR DNA was a rare event from the start. In 2013, however, Y-STR analyses became more common and since the year 2020 Y-STR analyses are carried out for all male DNA samples from suspects and convicted individuals and when applicable also regarding crime scene samples.

In Spain, familial searches have been carried out since 2012, when the National Commission for the Forensic Use of DNA (CNUFADN)[16] [65], proposed that the national DNA database could be used to carry out familial searches, using both autosomal STR DNA and Y-STR DNA [66, 67]. The Commission concluded in their report that familial search is advisable and a valuable tool for finding perpetrators of serious crimes. They also noted that the new generation analysis systems of autosomal STR DNA and Y-STR DNA offer high discrimination power. However, the Commission stated that a judge must give authorization and that familial searches can only be carried out in serious crimes such as acts of terrorism, murders and sexual assaults. Furthermore, such searches may only be carried out when all other investigative actions have been taken and that the impact on human rights is minimal [66, 67].

A new DNA database legislation is expected in Spain. According to a draft legal bill, the legislation will mainly follow the suggestions and conclusions previously stated by the CNUFAD in 2012 [26].

Familial searches with autosomal STR DNA are used for example when searching for a perpetrator of sex-related crimes using abortive remains or to find the parents in cases with abandoned and dead infants [61]. The success rate of Spanish autosomal-based STR familial searches is unclear.

Thanks to the extensive number of Y-STR data in the Spanish DNA database, Spain also carries out Y-STR familial searches, mainly to help find perpetrators in sexual assault cases [26]. Spain has reported a success rate of 28 % when doing Y-STR familial searches to find a male criminal via his male relatives and so far, they have been able to solve more than 30 crimes [26].

The familial searches in Spain are carried out in CODIS using the Pedigree Tree Search tool. The tool in CODIS was originally developed for kinship analysis for unidentified victim identification and missing persons, but can be used to carry out familial searches using specific settings [39, 26]. The Y-STR familial searches are carried out in CODIS as well, using the Identity Search function [26].

The Spanish DNA database contains more than 460 000 DNA profiles from suspects and convicted offenders and more than 70 000 (15 %) of these profiles contains data in at least 14 Y-STR loci besides the usual autosomal STR loci. The DNA profiles from suspected criminals are deleted upon acquittal and normally the DNA profile from convicted offenders is deleted after 20 years. The number of inhabitants in Spain is 48,3 million which means an equivalent of 1 % of the population is included in their national DNA database [26].

If one compares familial searches in Spain with those carried out in Sweden, there are some differences. The first difference is the use of different software, CODIS and Familias. The second difference is that familial searches are not yet regulated in the Spanish legislation.

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[16] The National Commission for the Forensic Use of DNA (CNUFADN) acts in plenary sessions or through a Technical Steering Committee: The ***plenary session*** comprises a chairperson (the head of the Department for Relations with the Justice Administration), two deputy chairs (the director of the National Institute of Toxicology and Forensic Sciences and a representative from the office of the Spanish Secretary of State for Security) and as voting members, a judge, a public prosecutor, representatives from the National Institute of Toxicology and Forensic Sciences, the Spanish forensic police service, the criminal investigation department of the Spanish Civil Guard and the police forces of the autonomous regions (with DNA laboratories integrated into the police database), as well as experts on bioethics and genetics. The *Technical Steering Committee* is chaired by the director of the National Institute of Toxicology and Forensic Sciences and have representatives from the laboratories of the security forces, and a representative of the Institute, who will function as secretary. Different working groups can be created to focus on different tasks.

However, familial searches are harmonized by the CNUFAD that has specified how and when they can be carried out, for example within which categories of crimes searches are allowed, as well as the required judicial authorization. A third difference is that in Spain, Y-STR is routinely analysed for male DNA and, when available, the Y-STR data is used to refine and narrow down the lists of candidates. Thanks to extensive Y-STR data present in the Spanish national DNA database, Y-STR familial searches can be carried out as well, obviously with a high success rate. Since the success rate of autosomal STR familial searches in Spain is unclear, it is impossible to make the comparison with Sweden.

The data presented in previous sections is summarised below (Table 2).

***Table 2**. Summarized data from Sweden, UK, the Netherlands and Spain on population size, the number of suspected and/or convicted individuals in the national database, the proportion of individuals in the database and the success rate of familial searches.*

	SE	UK	NL	ES
Year of first familial search	2019	2002	2012	2012
Legislation	Yes	No	Yes	No
Population size (million)	10,6	67	17,7	48,3
Persons (suspects and convicted) in National DNA database (million)	0,18	5,9	0,4	0,46
Proportion of the population in the national DNA database (%)	1,7	8,8	2,3	1,0
Success rate of familial searches (%)	4	17	9	-

6.4 The US

In the US, the Scientific Working Group on DNA Analysis Methods (SWGDAM)[17] [68] stated in 2018 that routine familial search at national level is not recommended [39]. The reason was, and still is, that SWGDAM consider it difficult to establish a threshold ranking for the review of a ranked candidate list, when searching a database of more than 10 million records. This, since additional filters such as geography and Y-STR testing may not be possible. Nevertheless, SWGDAM have also stated that there is nothing preventing the states from carrying our familial searches in their own state DNA databases. At the same time, SWGDAM published for the first time a familial search manual to assist states carrying out familial searches in their databases using the Pedigree Manager function in CODIS [39]. Therefore, familial searches are not carried out on a federal level in the US, but in some states. The legislation in the states that allow familial searches varies to some extent. Currently Arkansas, California, Colorado, Florida, Michigan, Texas, Utah, Virginia, Wisconsin and Wyoming has legislation permitting familial searches [69].

In the US, the *moderate search mode* in CODIS is the regular search mode for single source DNA database searches, unlike in Sweden were *high search mode* is used [30]. Therefore, so called “partial matches” can be obtained in the US, between a single-source and non-degraded DNA profiles sharing at least one allele at each locus with individuals in the database. Since

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[17] The Scientific Working Group on DNA Analysis Methods (SWGDAM), is a forum to discuss, share, and evaluate forensic biology methods, protocols, training, and research. The responsibilities of SWGDAM are: 1) to recommend revisions to the Quality Assurance Standards for Forensic DNA Testing Laboratories and the Quality Assurance Standards for DNA Databasing Laboratories; 2) to serve as a forum to discuss, share, and evaluate forensic biology methods, protocols, training, and research to enhance forensic biology services; and 3) to recommend and conduct research to develop and/or validate forensic biology methods.

sharing one allele at each locus indicates a potential familial relationship, as for parent-child, this information may be used to solve cases. In the US, familial searches are defined as *intentional* searches for parent-child or siblings and can only be done if the state law allows it, while on the other hand "partial matching", as achieved using the *moderate search mode*, is regarded as a type of excess information obtained when doing regular searches. This information can be disclosed and used further in the investigation depending on whether or not it is allowed by the legislation and/or procedures [69]. In Maryland and Washington D.C. familial searches are prohibited. In Alaska, Georgia, Massachusetts, New Mexico, Nevada and Vermont neither "partial matches" are reported, nor are familial searches carried out, although there are no specific laws by which it is either allowed or prohibited. Meanwhile, Minnesota, Pennsylvania and Tennessee are reviewing the possibility of including familial searches in their respective legislation [70].

It would be too extensive for the purpose of this report to compare familial searches in the US with familial searches in Sweden. Mostly because familial searches are not allowed on the national level in the US but also because the states allowing for familial searches have different legislations and different ways of carrying out their searches.

6.5 Familial searches in other countries

In addition to the countries and states already mentioned, several other countries also carry out familial searches, to varying degrees and with varying levels of regularity. The approach to familial searches also varies, as does the reporting. While working on this report, some information about familial searching in other countries was found. For those interested, a selection of the information gathered is presented below, along with references for further reading.

In Australia and New Zealand, there is no specific legislation that either allows or prohibits familial searches and in practise the process in both countries resembles that in the UK [70, 71].

In Hungary, familial searches have been carried out since 2016 using Familias [40]. In Hungary, there is no legislation regulating these searches although specific regulations have been requested to formally legalise its use. The main argument is to prevent violations of personal autonomy and genetic privacy [72].

Israel recently reported that they have started to carry out familial searches using the CODIS Pedigree Tree Search tool, mainly in high profile cases where no more investigational leads are to be found [73].

France has reported the use of the *low stringency search strategy*[18] in CODIS for familial searches [74, 28].

In Belgium, new legislation was adopted in 2023, that allows for familial searches using both STR- and Y- STR DNA profiles [75].

Austria and Romania have reported that they carry out familial searches on a regular basis, whereas the Czech Republic, Estonia, Finland have reported that they carry out familial searches albeit to a very limited extent [28].

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[18] *Low stringency* is defined as a match where a target and a candidate must share at least one allele. An example of a *low stringency* match is when 11,12,13 match 11,14.

The current legislation in Canada does not allow for familial searches. However, the National DNA Data Bank (NDDB) Advisory Committee concluded that using familial searching in the NDDB is consistent with its purpose, solving crimes using the convicted offender index [76]. So far, and to our knowledge, there is no legislation that enables familial searches in Canada, even if familial searches have been reported to be carried out on at least one occasion, in 2002 [77].

Finally, in Norway the legislation does not allow familial searches in the law enforcement DNA database [34]. However, in 2023 Norway solved its first case using commercial genetic genealogy databases [78]. The reason behind why iFGG is deemed possible but not familial searches, is that the users sending their DNA data to the commercial genetic genealogy databases can voluntarily choose to allow their DNA data to be used by law enforcement to solve crimes via the so called “opt-in” function [34], set in contrast to persons having their DNA profile in a law enforcement DNA database due to a conviction or suspicion of crime.

7 Limitations, challenges, potential use and future perspectives

Familial searches can only help identify unknown criminals who have criminal relatives in law enforcement DNA databases. From a general perspective, most individuals who leave their DNA at a crime scene have no criminal relatives, or at least no criminal relatives found in a law enforcement DNA database.

Even if a close relative is included in a national DNA database, he or she might still not be identified through familial search. Siblings, in particular, can be found far down the ranked list or even be missed entirely, if their forensic STR DNA profiles are limited in number of loci, too dissimilar or if the shared STR allele values are too common. This was found to be the case in a murder case from 2005, the so called “*Stuvkällarmordet*”. When the murderer finally was identified in 2023, after 18 years and thanks to standard DNA sampling following a minor offence, it was revealed that at least one of the murderer’s siblings was included in the national DNA database when the DNA profile from the murder case was familial searched in the beginning of 2019. The actual brother appeared on the siblings’ list but in the lower part. In this case, the murderer was missed, partly due to the low ranking but partly also because the investigators were looking for an older perpetrator than the actual sister of the (brother) candidate on the list [79, 80].

Due to current legislation, Sweden has a relatively high turnover of both suspects and convicted individuals in the DNA database compared to other countries such as the UK, the Netherlands and Spain. As a result, the DNA profile of a criminal’s close family member may have been included in the DNA database at an earlier stage but subsequently deleted by the time a familial search is carried out. In that perspective, countries such as the UK, the Netherlands and Spain have an advantage in terms of database retention since DNA from convicted individual usually remain in the DNA database for a longer period of time than in Sweden, in the UK for an indefinite time period. But on the other hand, the Netherlands for example, do not permit DNA from suspected individuals to be added in the DNA database, until after conviction and for more severe crimes. From this perspective, despite turnaround times and availability in the database, the Swedish legislation allowing for DNA collection and registration from suspects in the database, provides a distinct advantage despite the shorter sample retention time. This approach enables the resolution of crimes committed by suspects before they are eventually convicted for another crime. The effectiveness of both regular database searches and familial searches depends on several factors: the conditions under which a sample can be collected, the duration for which the physical DNA sample can be stored, and the retention period of the DNA profile within the database.

Since Sweden started using the PowerPlex® Fusion 6C System during spring 2023, the proportion of the DNA profiles in the databases of suspects and convicted offenders containing data from 23 autosomal STR loci, instead of 15, is steadily increasing and will continue to do so[19]. As the proportion of DNA profiles with data from 23 STR loci increases, the number of familial search candidates decreases due to the improved stringency provided by the additional information. At the end of 2024, approximately 33 % of the suspect and convicted offender DNA profiles in the database were based on 23 STR loci. By that time, six familial searches had been carried out using crime scene samples containing data for 21-23 STR loci. These searches produced parent-child lists with an average of three candidates and sibling lists with an average of 12 candidates. This marks a significant reduction compared to the period from 2019 to 2023, when the average number of candidates was 20 for the parent-child lists and 31 for the sibling lists. Shorter and more precise lists are beneficial for the police investigation by narrowing the pool of candidates, thereby making the investigative process more efficient. Also, shorter and more precise candidate lists enhance privacy protection, reducing unnecessary investigation of unrelated and thus irrelevant individuals.

In Sweden, familial searches are carried out only upon request from case investigators who should contact NFC before submitting a formal request. If a case investigator is unaware of this tool, or does not receive a recommendation from a reporting officer at NFC to use this tool, the tool will not be utilized. From this perspective, it would be straightforward to introduce a standard procedure to carry out familial searches on selected crime scene profiles from certain categories of crime without the need for a formal case-specific request. In such cases, one could consider reporting only top candidates with an LR value of, let's say, greater than 500 000. Such a high LR value would strongly indicate a close relationship and could be reported to case investigators. However, a first and simpler measure to make investigators more aware of this tool is to ensure that information about familial searches is available on all relevant police information portals.

Familial searches could be carried out either once or repeatedly, and over the years, some DNA profiles have been searched multiple times following new requests. However, the frequency of repeated searches raises an important question: how often should these searches be carried out, considering the possibility that a relative may enter or leave the database? Should it be performed once every year or even more frequently, or less frequent? There is no definitive answer to this question. Nevertheless, the current recommendation given is to request a repeated search once every year.

In the Netherlands and Spain, Y-STR data is used to narrow down the candidate lists obtained with familial searches. In both countries any available Y-STR data is included in their DNA databases. In the Netherlands, under certain conditions, Y-STR analysis of male DNA samples is carried out and the Y-STR DNA profile is included in the database together with the autosomal STR DNA profile. In addition to this, the DNA samples themselves, from convicted offenders, are stored as long as the DNA profiles are included in the database. Therefore, Y-STR analyses can always be carried out afterwards if and when needed. In Spain, the Y-STR loci are always analysed for male DNA and the Y-STR data is included in their DNA

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[19] It is easy for a police officer to check whether a suspected individual is already registered in the DNA database. If the individual is already included, there is no need to take a new sample. However, when the NFC started using PowerPlex® Fusion 6C System, the police were encouraged to collect new samples from suspects whose DNA was already registered in the database. Therefore, when a police officer checks if a suspect is registered in the DNA database, the system indicates whether the individual is registered but also if a new sample is needed, to update the DNA profile with PowerPlex® Fusion 6C System. Before 2023, when PowerPlex® Fusion 6C System was introduced, approximately 32 000 DNA samples were collected annually. In 2023 and 2024, about 51 000 (45 000 from suspects) DNA samples were collected each year, thanks to both new and updated samples.

database routinely. In both the Netherlands and Spain, available Y-STR data can be used right away to narrow down the candidate lists from familial searches, when applicable. Obviously, such an approach will refine the searches and narrow the candidate list(s) significantly. Also, the risk of missing a brother far down the list as described earlier with the situation in Sweden, will not happen. Since creating lists with individuals in general is a legal concern due to privacy perspectives, a short and stringent list can be seen as beneficial from that view. However, on such a list there may still be candidates who are not related to the person who is of interest in the case.

Countries such as Spain and the Netherlands, having registered Y-STR DNA profiles in their DNA databases, can also carry out searches using only the Y-STR DNA profile. The Y-STR familial searches are easily carried out using for example the Identity Search function in CODIS. A search of the Y-STR from an unknown male perpetrator will identify any male, paternally related, registered in the database. Spain has reported a success rate of 30 % when carrying out Y-STR searches. Thus, Y-STR familial search is a very valuable tool for solving serious crimes in those countries that allow Y-STR DNA in their DNA databases.

In Sweden, according to our current and coming new DNA database legislation expected to gain force in July 2025, it is not, and will not be, allowed to include Y-STR data in the database. Not even data regarding XX (female) or XY (male) as revealed by the amelogenin marker can be registered, even though all forensic STR amplification kits since long include this marker. If Y-STR data could be included in the Swedish national DNA database, it would open up for the routine analysis of more than three Y-STR loci. This data could also be used to carry out Y-STR familial searches on crime scene samples left by a male, as done in Spain and the Netherlands today. Clearly, some of the STR kits available today come very handy in this perspective, as for examples the "PowerPlex® 35GY System" from Promega including 23 autosomal STR loci and 11 Y-STR loci [81], allowing for simultaneous generation of both autosomal STR and Y-STR data to be registered, if allowed.

8 Discussion

Totally seven, previously unknown, DNA profiles have been identified in Sweden thanks to familial searches. That gives a success rate of 4 % which is just under half of the success rate of 9 % reported in the Netherlands [61]. However, the Dutch DNA database is twice as large as the one in Sweden and also includes a slightly larger proportion of the population compared to Sweden. Overall, this may in part explain the difference in success rate. Hopefully, the new Swedish biometric legislation [25] will lead to an increasing number of DNA profiles in the database, which in turn can lead to a higher success rate for familial searches in the future.

However, it is bit of a shame that familial searches are not used more often in Sweden. Especially as the process is straightforward and the tool easy to use, as compared to the situation in the UK, the Netherlands and Spain, having more or less complicated procedures including approvals at different hierarchy levels by different decisionmakers. In Sweden, investigators can request the search after verifying with NFC that a DNA profile of interest is good enough to search. Despite this, the number of familial searched DNA profiles has declined over the years, from 49 searches in 2019 to 17 searches in 2024. To increase the number of familial searched DNA profiles, NFC may communicate the tool better, both internally among the reporting officers but also to crime investigators. Perhaps a new "information tour" similar to the one done in 2019 could be considered. NFC could also consider a strategy to include familial searches of important and relevant DNA profiles as a standard procedure in certain categories of crimes, such as murder cases, without requiring a request. Since December 2024, NFC offers DNA analyses on appearance (eye-, hair- and skin colour) and biogeographical ancestry of a perpetrator whose DNA has been found at a crime scene. Familial search shall precede such analysis, according to best practice saying that available DNA data should be investigated with tools available before retrieving more data by performing additional (sensitive) DNA analyses [82]. The interest in these analyses is expected to increase having the tools available in-house and, subsequently, the more this tool is used, the more familial searches will be carried out as well.

The legislation in many countries covers neither familial search nor the use of iFGG. In this perspective, Sweden was quite early to establish legislation on familial searches in 2019. Some countries, like the UK and Spain, lack legislation about familial searches but have recommendations that allow the use of familial searches anyway. New legislation is expected to gain force in Spain within the next few years, allowing familial searches using both autosomal STR and Y-STR data [26]. Norway has concluded that it is not allowed to use law enforcement DNA databases to do familial searches in order to protect privacy rights but, on the other hand, they allow the use of iFGG in commercial genetic genealogy databases. The motif is that the users of such databases actively choose to make their DNA information available to be used by law enforcement to solve crimes using iFGG [34]. The trend seems to be that an increasing number of countries are legislating to allow the police and law enforcement authorities to use familial searches, Y-STR familial searches and sometimes also iFGG. Belgium is an example where new legislation recently has come into force that enables familial searches and registration of (already available) Y-STR data in their national DNA database which in turns also enables Y-STR familial searches [75].

In the new, upcoming Swedish biometric legislation, iFGG will be allowed to be used in certain cases. That is good news for law enforcement authorities as well as for relatives in unsolved murder and serious rape cases, and society as a whole. However, the new legislation still does not provide the provision for registering amelogenin and non-coding Y-STR data in the DNA databases. In the perspective of strengthening law enforcement in solving serious crime, which in fact was one of the aims when modifying the biometric legislation, it is desirable and eligible to look into the changes needed to include Y-STR data in the national DNA database. Perhaps, the background proceedings and legal text in Spain, which allows non-coding regions of DNA to be registered in their DNA database, could be useful also for Swedish legislators. If Y-STR could be included in the DNA databases, it would open for the possibility to routinely carry out more extensive Y-STR analysis of crime scene samples from males and all suspected male individuals. Then, Y-STR DNA profiles of a crime scene sample could be used to do Y-STR familial searches, when applicable.

Solving crimes using Y-STR data only, means that only male criminals can be identified using their male relatives. However, according to recent statistics published by the Swedish National Council for Crime Prevention (Brottsförebyggande rådet), 82 % of all prosecuted individuals in 2023 were men and 18 % were women [83]. These numbers clearly state that a large percentage of criminals are men, although the proportion of prosecuted women are slowly increasing [83]. Unfortunately, since amelogenin data is not registered in Sweden, there is no data available neither on how many crime scene samples that have been left by a male criminal nor the number of males in the DNA databases of suspect or convicted offenders. Solving crimes using Y-STR data only, means that only male criminals can be identified using their male relatives. However, the possibility to help solve more crimes committed by males using Y-STR data is valuable.

Obviously, Y-STR familial searches cannot be used to solve crimes committed by a female criminal. Also, an unknown male criminal might have female relatives in the DNA database which will not help solving the crime if only Y-STR familial searches are used. Autosomal STR-based searches and Y-STR based familial searches are therefore to be regarded as two different approaches that could be used separately or as a complement to each other when no direct match is obtained in the DNA databases.

The development and possibilities of solving crimes with DNA are constantly moving forward and it is sometimes difficult for the legislators to keep pace. It is particularly good that Sweden by law, since 2019, allows familial searches to solve crimes and that the upcoming legislation will allow the use of iFGG to solve crimes. However, since the legislature so far has not allowed the Y-STR data to be included in the national DNA database, Sweden cannot use that kind of information to solve crimes.

9 Conclusions

The following conclusions can be drawn:

- Using relatives to find a perpetrator can be achieved in law enforcement databases using familial searches, as well as in commercial genetic genealogy databases using iFGG.

- Familial searches using STR DNA profiles is a valuable tool that can be used to help solve serious crimes when standard investigative measures and regular DNA database searches have not been successful in finding a perpetrator.

- In Sweden, seven unknown DNA profiles were identified during the period 2019-2024 using STR familial searches, resulting in a success rate of about 4 %. The success rate is comparable with that of other countries if consideration is taken to how large proportion of the population that is included in the national DNA databases.

- The candidate lists from familial searches of a DNA profile, left by an unknown perpetrator, can be narrowed down by increasing the number of autosomal STR loci used and/or by using Y-STR data when applicable. Y-STR data can also reveal true brothers that have ended up far down the list.

- With Y-STR DNA profiles registered in a database, Y-STR familial searches can be carried out to find paternal male relatives, as done in Spain, the Netherlands and in Belgium, usually with a greater success rate than STR familial searches. To be able to register and use Y-STR data and Y-STR familial searches in the Swedish national DNA database, new legislation is required.

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11 References

[1] Amankwaa Aaron Opoku, McCartney Carole (2019) The effectiveness of the UK national DNA database. Forensic Science International: Synergy **1**, 45-55.

[2] Harbison Sally Ann, Hamilton Jacqueline, Walsh Simon Joseph (2001) The New Zealand DNA databank: its development and significance as a crime solving tool. Science & Justice **41**, 33-37.

[3] Schneider Peter M., Martin Peter D. (2001) Criminal DNA databases: the European situation. Forensic Science International **119**, 232-238.

[4] Federal Bureau of Investigation. https://www.fbi.gov/how-we-can-help-you/dna-fingerprint-act-of-2005-expungement-policy/codis-and-ndis-fact-sheet. Accessed 2025-03-03.

[5] Polisdatalag (1998:622). https://www.riksdagen.se/sv/dokument-och-lagar/dokument/svensk-forfattningssamling/polisdatalag-1998622_sfs-1998-622/ . Accessed 2025-06-07

[6] Bieber Frederick R., Brenner Charles H., Lazer David (2006) Finding criminals through DNA of their relatives. Science **312**, 1315-1316.

[7] Miller Greg (2010) Familial DNA testing scores a win in serial killer case. Science **329**, 262-262.

[8] Maguire Christopher N., McCallum L. A., Storey C., Whitaker Jonathan P. (2014) Familial searching: A specialist forensic DNA profiling service utilising the National DNA Database® to identify unknown offenders via their relatives—The UK experience. Forensic Science International: Genetics **8**, 1-9.

[9] Lag (2018:1693) om polisens behandling av personuppgifter inom brottsdatalagens område. https://www.riksdagen.se/sv/dokument-och-lagar/dokument/svensk-forfattningssamling/lag-20181693-om-polisens-behandling-av_sfs-2018-1693/. Accessed 2025-06-07.

[10] Wickenheiser Ray A. (2019) Forensic genealogy, bioethics and the Golden State Killer case. Forensic Science International: Synergy **1**, 114-125.

[11] Tillmar Andreas, Fagerholm Siri Aili, Staaf Jan, Sjölund Peter, Ansell Ricky (2021) Getting the conclusive lead with investigative genetic genealogy – A successful case study of a 16 year old double murder in Sweden. Forensic Science International: Genetics **53**, 102525.

[12] Tuazon Oliver M., Wickenheiser Ray A., Ansell Ricky, Guerrini Christi J., Zwenne Gerrit-Jan, Custers Bart (2024) Law enforcement use of genetic genealogy databases in criminal investigations: Nomenclature, definition and scope. Forensic Science International: Synergy **8**, 100460.

[13] Omni. Ahmadi Isabella. https://omni.se/tva-okanda-garningsman-hittades-med-dna-sokning/a/dO0bXO. Accessed 2025-02-05.

[14] Sveriges Radio. Pierrou Martina https://sverigesradio.se/avsnitt/1417554. Accessed 2025-01-15.

[15] Göteborgs-Posten. https://www.gp.se/nyheter/goteborg/har-ar-domen-mot-sonen-som-ledde-polisen-till-billdalsmannen.5db118f2-9389-4568-8043-0e5326458b8e. Accessed 2025-02-03.

[16] Forskning & Framsteg. Snaprud Per https://fof.se/tidning/2019/4/artikel/mordare-fangad-av-slaktforskare. Accessed 2025-03-03.

[17] Guerrini Christi J., Robinson Jill O., Elsaid Mohamed I., Brooks Whitney Bash, Levchenko Ariel, Fullerton Stephanie M., Huston Sara, Crossnohere Norah L., Bridges John F. P., Dahlquist Jacklyn M., Kalokairinou Louiza, Madden Diana, Moore CeCe, McGuire Amy L. (2025) FIGG at 5: An update on U.S. public perspectives on forensic investigative genetic genealogy five years after its introduction to criminal investigations. Forensic Science International **367**, 112372.

[18] Bell Suzanne, Butler John M. (2022) Understanding forensic DNA. Cambridge University Press, Cambridge, United Kingdom.

[19] Welch Lindsy, Gill Peter, Phillips Christopher, Ansell Ricky, Morling Nils, Parson Walter, Palo Jukka, Bastisch Ingo (2012) European Network of Forensic Science Institutes (ENFSI): Evaluation of new commercial STR multiplexes that include the European Standard Set (ESS) of markers. Forensic Science International: Genetics **6**, 819-826.

[20] (2023) Driftsättningsbeslut STR-analys av DNA-extrakt för personprov med PowerPlex Fusion 6C System 2113-04. Biologisektionen.

[21] (2023) Driftsättningsbeslut för STR-analys av DNA-extrakt för spårprov med PowerPlex Fusion 6C System 2113-09. Biologisektionen.

[22] Thermo Fisher Scientific. https://www.thermofisher.com/se/en/home/industrial/forensics/human-identification/forensic-dna-analysis/pcr-amplification-forensic-dna-profiling/y-str-analysis.html. Accessed 2025-02-03.

[23] Faktablad Forensisk mitokondriell DNA-analys (2023) Nationellt forensiskt centrum.

[24] Brottsdatalag (2018:1177). https://www.riksdagen.se/sv/dokument-och-lagar/dokument/svensk-forfattningssamling/brottsdatalag-20181177_sfs-2018-1177/. Accessed 2025-06-07.

[25] Biometri i brottsbekämpningen, Proposition (2024/25:37). https://www.regeringen.se/rattsliga-dokument/proposition/2024/10/prop.-20242537. Accessed 2025-06-07.

[26] Personal communication: Reyes Eusebio López, National Police Chief Inspector, Custodian of The National DNA and ABIS Database (2024) Security Technology Center of the Ministry of Interior, Madrid, Spain.

[27] Andersson Lars (2024) Statistik dna-register 2024. DNA-register 2025:01.

[28] European Network of Forensic Science Institutes (ENFSI) (2022) Survey regarding the use of DNA database.

[29] Biometrics Analysis Section Laboratory Division, CODIS Unit, Federal Bureau of Investigation (2021) Combined DNA Index System (CODIS) 9.0 International Release Notes.

[30] Widén Christina (2024) Handhavandebeskrivning för CODIS (414). Biologisektionen.

[31] Council Decision 2008/615/JHA of 23 June 2008 on the stepping up of cross-border cooperation, particularly in combating terrorism and cross-border crime. https://eur-lex.europa.eu/eli/dec/2008/615/oj/eng. Accessed 2025-06-07.

[32] Council Decision 2008/616/JHA of 23 June 2008 on the implementation of Decision 2008/615/JHA on the stepping up of cross-border cooperation, particularly in combating terrorism and cross-border crime. https://eur-lex.europa.eu/eli/dec/2008/616/oj/eng. Accessed 2025-06-07.

[33] Council resolution on the exchange of results of DNA analysis result, 2009/C 296/01. https://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ%3AC%3A2009%3A296%3A0001%3A0003%3AEN%3APDF. Accessed 2025-06-07.

[34] Personal communication: Thor Turid Haugen, Seniorrådgiver (2023) Avdeling for kriminalteknikk og ID, Seksjon for DNA og saknet, Politiet, Norge.

[35] Svensson Frida (2019) Nytt polishopp: Dubbelmördaren kan hittas med släktsökning. Svenska Dagbladet **30 juni**. https://www.svd.se/a/vQx1q4/okand-dubbelmordare-jagas-med-ny-slaktsokning. Accessed 2025-06-09.

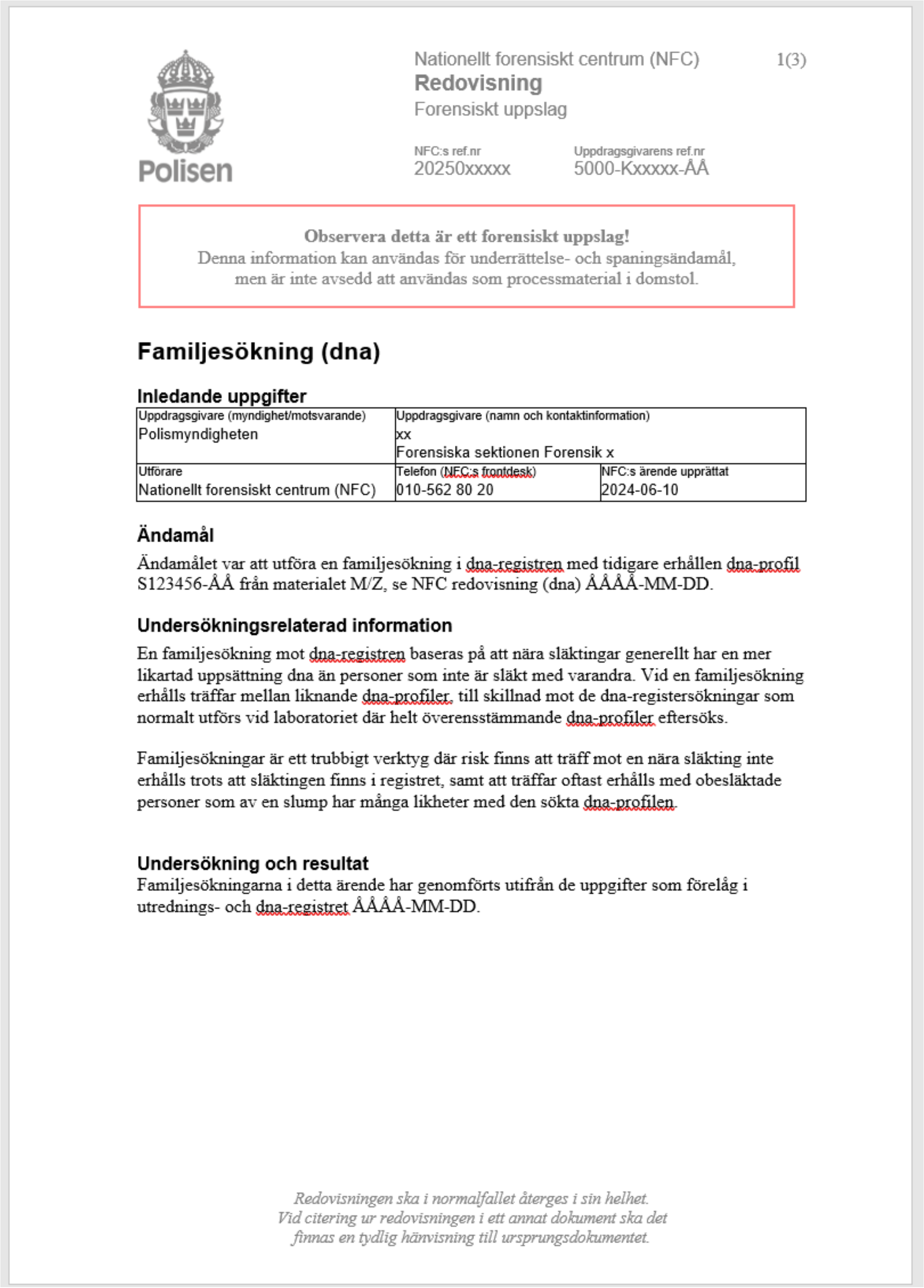
[36] Egeland Thore, Mostad Petter F., Mevåg Bente, Stenersen M. (2000) Beyond traditional paternity and identification cases: Selecting the most probable pedigree. Forensic Science International **110**, 47-59.

[37] Kling Daniel, Tillmar Andreas O., Egeland Thore (2014) Familias 3 – Extensions and new functionality. Forensic Science International: Genetics **13**, 121-127.
[38] Department of Forensic Sciences, Oslo University Hospital. Kling Daniel, Egeland Thore, Mostad Petter https://familias.no/. Accessed 2025-03-03
[39] Federal Bureau of Investigation (2018) Familial Searching Manual for CODIS 8.0.
[40] Kling Daniel, Füredi Sándor (2016) The successful use of familial searching in six Hungarian high profile cases by applying a new module in Familias 3. Forensic Science International: Genetics **24**, 24-32.
[41] Egeland Thore, Kling Daniel, Mostad Petter (2016) Relationship interference with Familias and R statistical methods in forensic genetics. Elsevier Inc, United States.
[42] EEB Articles. Holsinger Kent E., Weir Bruce S. https://digitalcommons.lib.uconn.edu/eeb_articles/22/?utm_source=opencommons.uconn.edu%2Feeb_articles%2F22&utm_medium=PDF&utm_campaign=PDFCoverPages. Accessed 2024-12-18.
[43] Ansell Ricky, Nilsson Anders, Hedman Johannes, Ansell Carina (2010) Uttryck, begrepp och definitioner inom DNA-verksamheten på SKL. Intern rapport, Biologienheten 2010:02.
[44] Faktablad Familjesökning av brottsplatsspår (2023) Nationellt forensiskt centrum.
[45] Hedell Ronny (2023) Instruktion för familjesökningar (1374). Biologisektionen.
[46] Hedell Ronny (2023) Verifieringsrapport för Familias med PowerPlex Fusion 6C System 2288. Biologisektionen.
[47] Hedell Ronny (2019) Fördelning av resultatvärden vid familjesökningar. NFC Notat, Biologisektionen 2019:26.
[48] Widén Christina (2020) Familjesökningar 2019. NFC Notat, Biologisektionen 2020:16.
[49] Widén Christina (2021) Familjesökningar 2020. NFC Notat, Biologisektionen 2021:18.
[50] Widén Christina (2022) Familjesökningar 2021. NFC Notat, Biologisektionen 2022:11.
[51] Widén Christina (2023) Familjesökningar 2022. NFC Notat, Biologisektionen 2023:04.
[52] Widén Christina (2024) Familjesökningar 2023. NFC Notat, Biologisektionen 2024:01.
[53] Widén Christina (2025) Familjesökningar 2024. NFC Notat, Biologisektionen 2025:04.
[54] Expressen. https://www.expressen.se/gt/billdalsmannen-kunde-ha-gripits-for-elva-ar-sedan/. Accessed 2025-01-17.
[55] Government UK. https://www.gov.uk/government/groups/national-dna-database-strategy-board. Accessed 2025-02-03.
[56] Personal communication: Boniface Annette, Scientific DNA Leader (2024) Forensic Information Databases Service (FINDS), United Kingdom.
[57] Forensic Information Databases Service (2021) The Forensic Information Databases Strategy Board policy for access and use of DNA samples, DNA profiles, fingerprint images, and associated data. https://assets.publishing.service.gov.uk/media/61fcf00e8fa8f5388cafdb39/FIND_Strategy_Board_Policy_Access_and_Use.pdf. Accessed 2025-02-03.
[58] Forensic Information Databases (FIND) Strategy Board, Home Office, UK. https://www.gov.uk/government/publications/forensic-information-databases-annual-report-2021-to-2022/forensic-information-databases-annual-report-2021-to-2022-accessible-version. Accessed 2025-03-03.
[59] Forensic Information Databases (FIND) Strategy Board Home Office, UK. https://www.gov.uk/government/publications/forensic-information-databases-annual-report-2022-to-2023/forensic-information-databases-annual-report-2022-to-2023-accessible. Accessed 2025-03-03.
[60] Protection of Freedoms Act 2012: DNA and fingerprint provisions. https://www.gov.uk/government/publications/protection-of-freedoms-act-2012-dna-and-fingerprint-provisions--2/protection-of-freedoms-act-2012-dna-and-fingerprint-provisions-january-2019. Accessed 2025-06-07.

[61] Personal communication: Kal Arnoud, Doctor of Philosophy (2023) Department of Biological Traces and DNA at the Netherlands Forensic Institute (NFI), the Netherlands.
[62] SMART Research BV. https://www.bonaparte-dvi.com/. Accessed 2025-03-03.
[63] Hoogenboom Jerry, Sijen Titia, Benschop Corina (2023) ProbRank: An efficient DNA database search method for complex mixtures per a quantitative likelihood ratio model. Forensic Science International: Genetics **65**, 102884.
[64] DNA Testing (Convicted Persons) Act (2019) Public Prosecution Service. https://www.prosecutionservice.nl/documents/publications/openbaar-ministerie/algemeen/alles/dna-testing-convicted-persons-act. Accessed 2025-06-07.
[65] Comisión Nacional para el Uso Forense del AND (2014) National Commission for the Forensic Use of DNA. https://www.mjusticia.gob.es/es/ElMinisterio/OrganismosMinisterio/Documents/1292428320857-Annual_report._National_Commission_for_the_forensic_use_of_DNA._Activities_2014.PDF. Accessed 2025-06-07.
[66] Comisión Nacional para el Uso Forense del AND (2012) Actividades 2012. https://www.mjusticia.gob.es/es/ElMinisterio/OrganismosMinisterio/Documents/1292428320905-Memoria_de_la_Comision_Nacional_para_el_Uso_Forense_del_ADN._Actividades_2012.PDF. Accessed 2025-06-07.
[67] Comisión Nacional para el Uso Forense del AND (2023) Recomendaciones de la Comisión Técnica Permanente (CTP) de la Comisión Nacional para el Uso Forense del ADN (CNUFADN) sobre valoración de coincidencias mediante el empleo de STR de cromosoma Y. https://www.mjusticia.gob.es/es/ElMinisterio/OrganismosMinisterio/Documents/Evaluacio%CC%81n%20estadi%CC%81stica%20CrY_aprobado%20el%20PLENO_111223.pdf. Accessed 2025-06-07.
[68] Scientific Working Group on DNA Analysis Methods. https://www.swgdam.org/. Accessed 2025-02-03.
[69] Federal Bureau of Investigation. https://le.fbi.gov/science-and-lab/biometrics-and-fingerprints/codis-2#CODIS-Unit. Accessed 2025-03-03.
[70] García Óscar, Crespillo Manuel, Yurrebaso Iñaki (2017) Suspects identification through “familial searching” in DNA databases of criminal interest. Social, ethical and scientific implications. Spanish Journal of Legal Medicine **43**, 26-34.
[71] Fact Sheet Familial DNA Searching (2018) Australia New Zealand Policing Advisory Agency. https://www.anzpaa.org.au/. Accessed 2025-06-07.
[72] Nogel Mónika (2022) How to regulate forensic familial DNA searching in Hungary? Forensic Science International: Genetics Supplement Series **8**, 136-137.
[73] Ram Tanya, Starinsky-Elbaz Sigal, Avlas Orna, Issan Yossi (2023) A new search tool for familial searches in the Israel Criminal DNA database. Forensic Science International **346**, 111639.
[74] Pham-Hoai Emmanuel, Crispino Frank, Hampikian Greg (2014) The first successful use of a low stringency familial match in a French criminal investigation. Journal of Forensic Sciences **59**, 816-819.
[75] The Brussels Times. https://www.brusselstimes.com/363948/belgium-to-expand-use-of-dna-databases-in-criminal-investigations. Accessed 2025-02-03.
[76] National DNA Data Bank Advisory Committee (2019) Annual Report 2018/2019. https://www.rcmp-grc.gc.ca/en/the-national-dna-data-bank-canada-annual-report-20182019. Accessed 2025-02-03.
[77] Conroy Amy (2014) Combining familial searching and abandoned DNA: Potential privacy outcomes and the future of Canada's National DNA Data Bank Canadian Journal of Law and Technology **12**, 171-188.

[78] Forensic. https://www.forensicmag.com/594329-Oslo-Police-Use-Genetic-Genealogy-for-the-First-Time-to-ID-Murder-Suspect/. Accessed 2025-03-03.
[79] Dagens nyheter. Cato Carl https://www.dn.se/sverige/misstankta-mordarens-slakting-pa-lista-over-mojliga-dna-traffar/. Accessed 2025-03-03.
[80] Dagens Nyheter. Ferhatovic Marina https://www.dn.se/sverige/tre-syskon-topsades-anda-hittades-inte-stuvkallarkvinnan/. Accessed 2025-03-01.
[81] Promega. https://se.promega.com/products/forensic-dna-analysis-ce/str-amplification/powerplex-35gy-system/?catNum=DC3520. Accessed 2025-02-03.
[82] Faktablad Forensiskt uppslag: DNA-baserad bedömning av utseende och ursprung (2024) Nationellt forensiskt centrum.
[83] Brottsförebyggande rådet (2024) 2023 Personer lagförda för brott, slutlig statistik. https://bra.se/statistik/statistikpubliceringar/statistik---publicering/2024-10-24-personer-lagforda-for-brott-2023. Accessed 2025-03-03.

12 Appendix



Polisen

Nationellt forensiskt centrum (NFC)
Redovisning
Forensiskt uppslag

NFC:s ref.nr
20250xxxxx

Uppdragsgivarens ref.nr
5000-Kxxxxx-ÅÅ

Observera detta är ett forensiskt uppslag!
Denna information kan användas för underrättelse- och spaningsändamål,
men är inte avsedd att användas som processmaterial i domstol.

Familjesökning (dna)

Inledande uppgifter

Uppdragsgivare (myndighet/motsvarande) Polismyndigheten	Uppdragsgivare (namn och kontaktinformation) xx Forensiska sektionen Forensik x	
Utförare Nationellt forensiskt centrum (NFC)	Telefon (NFC:s frontdesk) 010-562 80 20	NFC:s ärende upprättat 2024-06-10

Ändamål

Ändamålet var att utföra en familjesökning i dna-registren med tidigare erhållen dna-profil S123456-ÅÅ från materialet M/Z, se NFC redovisning (dna) ÅÅÅÅ-MM-DD.

Undersökningsrelaterad information

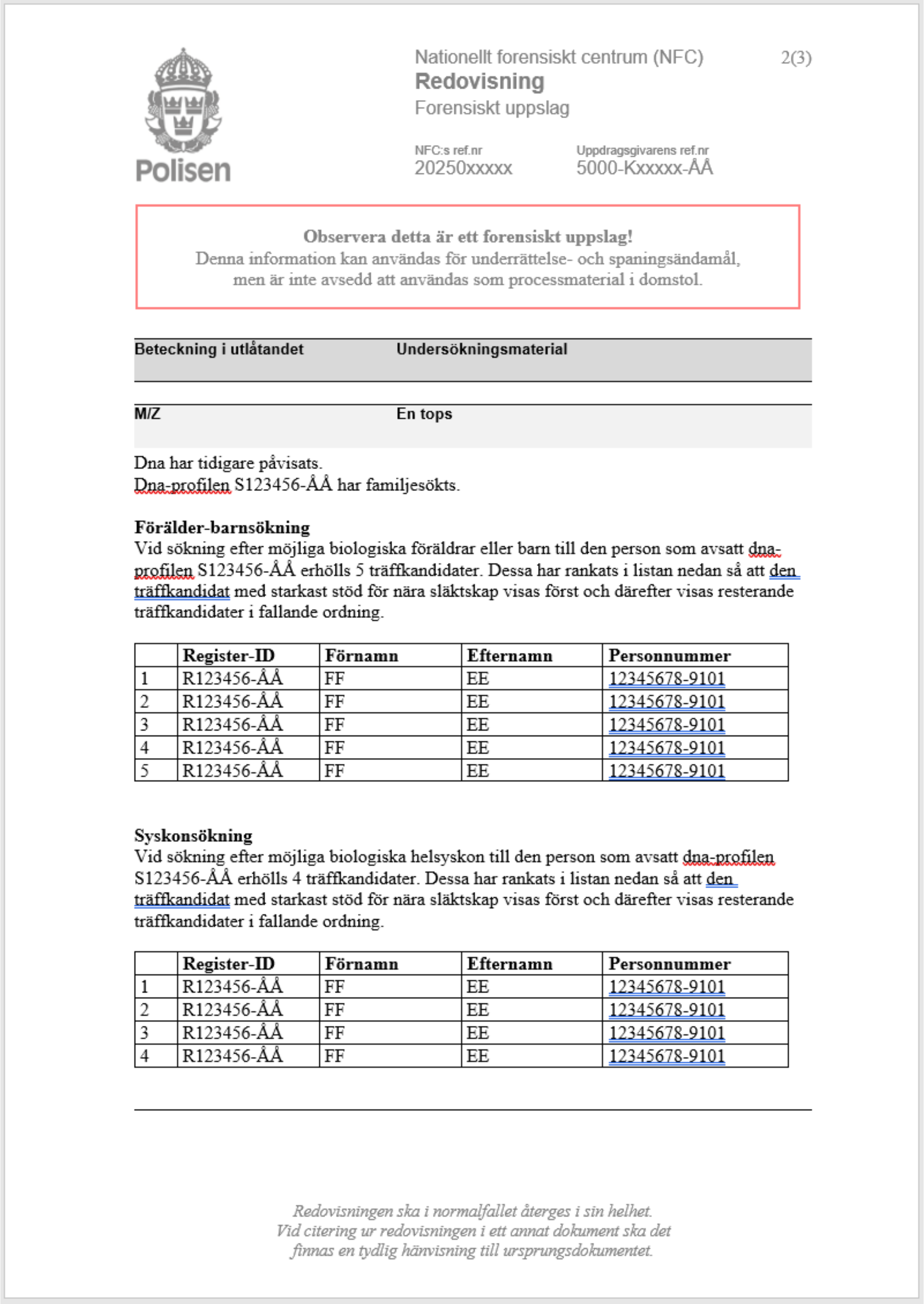
En familjesökning mot dna-registren baseras på att nära släktingar generellt har en mer likartad uppsättning dna än personer som inte är släkt med varandra. Vid en familjesökning erhålls träffar mellan liknande dna-profiler, till skillnad mot de dna-registersökningar som normalt utförs vid laboratoriet där helt överensstämmande dna-profiler eftersöks.

Familjesökningar är ett trubbigt verktyg där risk finns att träff mot en nära släkting inte erhålls trots att släktingen finns i registret, samt att träffar oftast erhålls med obesläktade personer som av en slump har många likheter med den sökta dna-profilen.

Undersökning och resultat

Familjesökningarna i detta ärende har genomförts utifrån de uppgifter som förelåg i utrednings- och dna-registret ÅÅÅÅ-MM-DD.

Redovisningen ska i normalfallet återges i sin helhet.
Vid citering ur redovisningen i ett annat dokument ska det
finnas en tydlig hänvisning till ursprungsdokumentet.



Polisen

Nationellt forensiskt centrum (NFC) 2(3)

Redovisning

Forensiskt uppslag

NFC:s ref.nr
20250xxxxx

Uppdragsgivarens ref.nr
5000-Kxxxxx-ÅÅ

Observera detta är ett forensiskt uppslag!
Denna information kan användas för underrättelse- och spaningsändamål,
men är inte avsedd att användas som processmaterial i domstol.

Beteckning i utlåtandet	**Undersökningsmaterial**
M/Z	**En tops**

Dna har tidigare påvisats.
Dna-profilen S123456-ÅÅ har familjesökts.

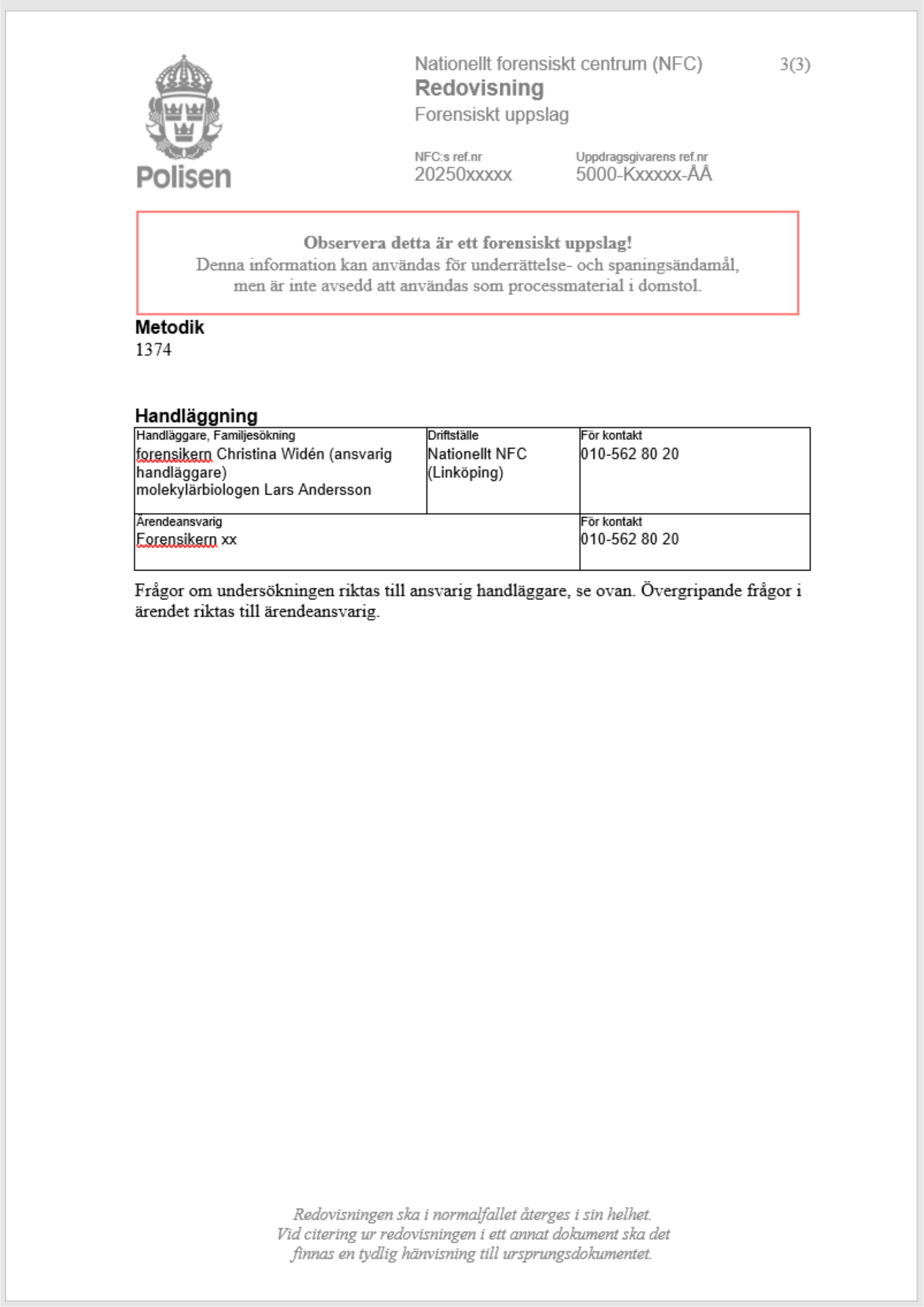
Förälder-barnsökning
Vid sökning efter möjliga biologiska föräldrar eller barn till den person som avsatt dna-profilen S123456-ÅÅ erhölls 5 träffkandidater. Dessa har rankats i listan nedan så att den träffkandidat med starkast stöd för nära släktskap visas först och därefter visas resterande träffkandidater i fallande ordning.

	Register-ID	**Förnamn**	**Efternamn**	**Personnummer**
1	R123456-ÅÅ	FF	EE	12345678-9101
2	R123456-ÅÅ	FF	EE	12345678-9101
3	R123456-ÅÅ	FF	EE	12345678-9101
4	R123456-ÅÅ	FF	EE	12345678-9101
5	R123456-ÅÅ	FF	EE	12345678-9101

Syskonsökning
Vid sökning efter möjliga biologiska helsyskon till den person som avsatt dna-profilen S123456-ÅÅ erhölls 4 träffkandidater. Dessa har rankats i listan nedan så att den träffkandidat med starkast stöd för nära släktskap visas först och därefter visas resterande träffkandidater i fallande ordning.

	Register-ID	**Förnamn**	**Efternamn**	**Personnummer**
1	R123456-ÅÅ	FF	EE	12345678-9101
2	R123456-ÅÅ	FF	EE	12345678-9101
3	R123456-ÅÅ	FF	EE	12345678-9101
4	R123456-ÅÅ	FF	EE	12345678-9101

*Redovisningen ska i normalfallet återges i sin helhet.
Vid citering ur redovisningen i ett annat dokument ska det
finnas en tydlig hänvisning till ursprungsdokumentet.*



Polisen

Nationellt forensiskt centrum (NFC) 3(3)

Redovisning

Forensiskt uppslag

NFC:s ref.nr
20250xxxxx

Uppdragsgivarens ref.nr
5000-Kxxxxx-ÅÅ

Observera detta är ett forensiskt uppslag!
Denna information kan användas för underrättelse- och spaningsändamål,
men är inte avsedd att användas som processmaterial i domstol.

Metodik

1374

Handläggning

Handläggare, Familjesökning forensikern Christina Widén (ansvarig handläggare) molekylärbiologen Lars Andersson	Driftställe Nationellt NFC (Linköping)	För kontakt 010-562 80 20
Ärendeansvarig Forensikern xx		För kontakt 010-562 80 20

Frågor om undersökningen riktas till ansvarig handläggare, se ovan. Övergripande frågor i ärendet riktas till ärendeansvarig.

Redovisningen ska i normalfallet återges i sin helhet.
Vid citering ur redovisningen i ett annat dokument ska det
finnas en tydlig hänvisning till ursprungsdokumentet.

nfc.polisen.se

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e-mail registrator.nfc@polisen.se

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