Evaluation of the 4-year test period of the Swiss DNA database

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Abstract. With reference date 31st December 2004 the 4-year test period of the Swiss DNA database ended. An evaluation of this test period was performed. The database holds DNA profiles of suspects, single stains and also mixed stains. The success rate was excellent: almost every second stain that was entered into the database resulted in a hit. The main crime category was burglary and theft, but also 285 homicides/bodily harm and 161 sexual offence cases could be assigned to a suspect. © 2005 Elsevier B.V. All rights reserved.

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1. Introduction

The Swiss federal DNA profile information system (EDNA) has been operational since July 2000 [1]. After a test period of 4 years, routine operation started in January 2005. Currently, Switzerland has the fifth largest database in Europe, behind England, Germany, Scotland and Austria.

EDNA is based on the CODIS (Combined DNA Index System) software provided by the FBI (Federal Bureau of Investigation). CODIS consists of 3 main subprograms: one handling the profiles (Specimen Manager), another handling the hits (Match Manager) and the third for conducting database searches. During the test period the CODIS software was upgraded once to version 5.6.

This study reports the results of the 4-year test period of the database that ended on 31st December 2004.

2. Profiles in the database

The database holds DNA profiles of suspects, single stains and also mixed stains (presumably consisting of not more than two people). The criteria for entering profiles into the database are the 10
SGMplus loci for suspects, at least 6 SGMplus loci for single stains and at least 8 SGMplus loci for mixtures. At the end of the 4-year test period the database contained 61,954 DNA profiles, 53,400 profiles from suspects (89% male, 11% female) and 8554 profiles from stains (90.7% single profiles, 9.3% mixtures) (Fig. 1). 518 profiles had been analyzed in foreign countries. 75% of the single stain profiles and 57% of the mixed profiles in the database were complete with all the 10 SGMplus loci. Stains that were assigned to a suspect were removed from the database on a day-by-day basis, so only unsolved profiles stayed in the database. During the test period 461 profiles from suspects were removed; 93 because the suspect had died, 368 because the investigation had been closed.

3. Hits

During the 4-year test period the database provided excellent results. 6830 stains were assigned to a suspect (so-called ‘offender hits’) and 3043 connections between individual crime-sites were established (so-called ‘forensic hits’). Among the suspects, 35 monozygotic twin-pairs were identified.

3.1. From the view of the suspects

Most of the people listed in the database (68.71%) were linked to no more than one crime in the database, another 16.56% of the people were linked to two crimes and 14.73% were linked to more than 2 crimes (Table 1). One person’s DNA marks were found at 62 different crime-sites all over Switzerland in the time-period 2001–2003. In June 2003 that person was arrested after being identified through DNA analysis.

Table 1
Number of persons and database hit count

<table>
<thead>
<tr>
<th>Persons</th>
<th>Hit count</th>
<th>% of persons</th>
</tr>
</thead>
<tbody>
<tr>
<td>2664</td>
<td>1</td>
<td>68.71</td>
</tr>
<tr>
<td>642</td>
<td>2</td>
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<td>239</td>
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</tr>
<tr>
<td>31</td>
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</tr>
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<td>29</td>
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<tr>
<td>15</td>
<td>8</td>
<td>0.39</td>
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<td>0.34</td>
</tr>
<tr>
<td>43</td>
<td>&gt;10</td>
<td>1.11</td>
</tr>
</tbody>
</table>
3.2. From the view of the stains

44.3% of the single stains were matched to a suspect, allowing the identification of the previously unknown perpetrator. 13.3% of the single stains caused a match with other stains (forensic hits), thus connecting different crime-sites. 42.3% of the single stains did not cause a match in the database, representing the total of unsolved cases (Fig. 2). 48.9% of the mixtures were matched to one suspect and another 14.9% were linked to two people. Only 36.2% of the mixtures did not match in the database (Fig. 2).

3.3. Crime categories

The 6830 hits identifying suspects can be subdivided into the following crime categories: the major group with 85.2% was burglary/theft/wilful damage, followed by homicide/bodily harm with 4.2%, robbery with 4%, sexual offenses with 2.4% and 4.2% other crimes (e.g. illicit drug offenses, arson, fraud). The spectrum of crime categories expanded for the DNA laboratories since the implementation of the database. Previously, only severe crimes with an identified suspect could be investigated using DNA samples.

4. Quality control

The DNA profiles of laboratory staff and involved police can be entered into a separate ‘staff’ index in the database in order to detect contamination. Until 31st December 2004, 76 profiles of laboratory staff and police members were registered in the database. The staff profiles are matched regularly against all stains. DNA profiles from 36 stains were matched to staff or police and thus identified as contamination.

A special search mode, which is less stringent, helps finding incorrect profiles. This search is performed once per month. 33 additional hits were discovered during the test period using this search mode.

5. Conclusions

The database showed an excellent success rate during the test period: almost every second stain that was entered into the database resulted in a hit (46%). The stain mixtures provided valuable data, as they showed a hit with one or two people in 63.8% of the cases. It cannot be predicted whether the success rate will increase further or if a plateau is reached.

The criteria that were employed for entering profiles into the database proved to be helpful for the routine searches. In particular, incomplete mixed stains can reveal several hundreds of improbable hits that have to be interpreted carefully by the DNA laboratory that analyzed the stain.

The ‘staff’ index in the database is used to separate contamination from true hits. Increasingly, police officers agree to have their DNA profiles added to the database.

Reference