Rapid DNA technologies at the crime scene
Mapes, A.A.

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Chapter 4

Knowledge on DNA Success Rates to Optimise the DNA Analysis Process: From Crime Scene to Laboratory

Abstract

DNA analysis has become an essential intelligence tool in the criminal justice system for the identification of possible offenders. However, it appears that about half of the processed DNA samples contains too little DNA for analysis. This study looks at DNA success rates within 28 different categories of trace exhibits and relates the DNA concentration to the characteristics of the DNA profile. Data from 2260 analysed crime samples show that cigarettes, bloodstains, and headwear have relatively high success rates. Cartridge cases, crowbars, and zip ties are on the other end of the spectrum. These objective data can assist forensics in their selection process. The DNA success probability shows a positive relation with the DNA concentration. This finding enables the laboratory to set an evidence-based threshold value in the DNA analysis process. For instance, 958 DNA extracts had a concentration value of 6 pg/µL or less. Only 46 of the 958 low-level extracts provided meaningful DNA profiling data.

1This chapter was published as: Mapes AA, Kloosterman AD, Marion van V, Poot de CJ. Knowledge on DNA success rates to optimise the DNA analysis process: from crime scene to laboratory. Journal of Forensic Sciences, 2016:61(4), 1055-1061. This study was designed, performed, analysed and published as an article by the first author. The co-authors advised on the set-up of the study and made suggestions and recommendations for the article.
4.1 Introduction

In the Netherlands, more than 100,000 forensic DNA analyses are performed annually. The analysed samples consist of reference samples and crime samples. This illustrates the confidence in DNA as a “silent witness” with which to identify suspects and to provide evidence in court. Furthermore, offender DNA databases have led to an exponential increase in the storage of both offender and crime trace profiles. Many countries have their own success stories on the use of offender DNA databases to identify suspects (1–4). This success story on forensic DNA typing has given the criminal justice system (CJS) the impression that the sky is the limit, so to speak. This has resulted in a steadily increasing number of requests for DNA analysis. In many countries, forensic laboratories are facing DNA backlogs (5,6). This is mainly due to the fact that Scene of Crime Officers (SoCOs) secure an increasing number of DNA samples at crime scenes, with the goal of solving more crimes. Although this policy has been successful in a number of cases, it also leads to growing backlogs both at the police forensic department and at the laboratory (7). Due to these backlogs, turnaround times are increasing (8,9), which does not benefit fast case solving and the identification of suspects. Further research into the circumstances pertaining to the backlog situation has shown that many secured DNA traces contain no or too little DNA for analysis (9–14). A recent evaluation of the DNA success story in the Netherlands has shown that 46% of analysed serious crime traces and 36% of analysed high volume crime traces produced no DNA profiling results (9). It should be noted that these traces were run through the complete analysis process, up to and including the forensic report. These results suggest that the criminal justice chain could benefit from more insight into DNA success rates. It takes time and money to secure, analyse, and report on DNA traces. Through an effective selection process, both at the sites of the police and the laboratory, the process can be made more efficient. It is expected that a thorough selection of DNA traces for analysis, based on DNA success rates, will lead to fewer unnecessary analysis activities and will therefore shorten turnaround times and reduce backlogs. To facilitate this selection process, knowledge on DNA success rates is necessary. This information could lead to creating a decision support system (15,16) for the SoCO to make evidence-based decisions on the selection of DNA traces for analysis. Research shows that knowledge-driven decisions can lead to efficient decision-taking on effective investigative actions (16). Currently, SoCOs are making decisions on the analysis of DNA traces under circumstances of uncertainty. To reduce this uncertainty, a thorough analysis on DNA success rates is the necessary first step toward creating a decision support system.

Different studies have given some insight into DNA success rates (9–11,14). For example, in a previous study, blood stains and saliva traces from cigarette ends show a high success rate in providing the CJS with DNA typing results (9). This study also
showed that 42% of processed contact traces produced no typing results. Another study (10) showed that only 26% of the contact stains yielded DNA profiles suitable for comparison with the DNA database. DNA contact traces with prolonged contact such as clothing (61%) or car items (37%) showed relatively high success rates. Two other studies (11,14) concerning “handled items” demonstrated that approximately half of the samples from the handled items did not produce a DNA profile. It was hypothesized that DNA success rates not only depend on the nature of the cellular material (blood, saliva, or epithelium) but also on the type of the exhibit sampled for DNA. Knowledge of these DNA success rates will help SoCOs to decide which traces should be submitted to the laboratory. For instance, we expect the success rate of blood traces to be much higher than the success rate of several contact traces. This is possibly due to the low DNA concentration in extracts of these contact traces, which means that also on the part of the forensic laboratory there are opportunities to make a further selection. Samples with a high DNA concentration offer a much higher success probability of obtaining a profile than samples with a low DNA concentration. Objective knowledge on the success rate of the DNA typing process in relation to the DNA concentration can be used to introduce a threshold value in the DNA analysis process. This would mean that DNA extracts are only analysed if the amount of DNA in the extract is above the set threshold value.

To introduce an actual success rate model for the decision to analyse DNA traces from different types of exhibits, the following information is relevant:

- concentration of DNA present in extracts of samples from different categories.
- characteristics of the DNA profile (single, mixed, or complex DNA profile or no typing result).
- characteristics of the obtained DNA profiles (match with suspect, victim/witness, or DNA database).

These three parameters form the basis of a decision model based on DNA success rates, which can be used by police and the forensic laboratory in the trace selection process. Overall, we expect that knowledge of the actual DNA success rates can be used to make smart decisions on the selection of traces for further analysis, which will significantly reduce the number of “empty” traces that only encumber the DNA analysis processes. First, this knowledge can be used to guide the decision-making process of the SoCOs who select DNA traces and send them to the laboratory. Second, this knowledge will improve the DNA analysis process at the laboratory. The data for this DNA success rate study were obtained from 2260 analysed crime samples secured at the crime scene. These samples were collected and secured by police force SoCOs.
4.2 Materials and Methods

For this study, a dedicated set of DNA traces was selected. The DNA traces involved traces of blood that were directly secured from the crime scene, as well as exhibits that were secured from the crime scene and subsequently swabbed and sampled at the police station for DNA analysis. This dataset consists of 5754 crime samples that were analysed in the period of 1 January 2012 until 31 December 2013. These analysed samples were categorized (Table 1) in terms of 28 defined categories for evaluation, which make up the most frequent exhibit types. It was decided that for frequently sampled exhibits containing more than 100 samples, a random sample of 100 was selected for this study (17). In our study, for each trace exhibit $t$, we determined the percentage $p_t$ of cases that produced DNA profiling results. Let $N_t$ be the number of traces of exhibit $t$ in our material. The value of $p_t$ can be determined exactly by analysing all $N_t$ traces of a type $t$, but as this is rather wasteful for frequently occurring types (i.e., large $N_t$), we decided to estimate $p_t$ for frequent types using a random sample of 100 from all available traces of each exhibit (17). Sample size $n_t$ was chosen as the minimum of 100 and $N_t$. Notice that for types with $N_t \leq 100$, this procedure determines $p_t$ exactly. For very large $N_t$, a sample size of 100 would always result in a 95% two-sided confidence interval smaller than ± 0.1 (17). In our case, we have moderate $N_t$; hence, a multiplicative finiteness correction factor $(1-n_t/N_t)$ is in place, which entails that widths of confidence intervals shrink further. For the most frequent type $t = \text{“weapon grip”}$ ($N_t = 441$), the confidence interval is not larger than ± 0.08. Less frequent types have even smaller confidence intervals, for example, for $t = \text{“car items,” } N_t = 150$, the confidence interval is smaller than 0.03. In our opinion, this determines $p_t$ with sufficient accuracy. This selection process resulted in the 2260 samples used in this study.

From these selected samples, we evaluated i) the concentration of DNA present in extracts of samples from the 28 different categories (Table 1); ii) the characteristics of the DNA profiles; and iii) matching characteristics of the obtained DNA profiles (match with suspect, victim/witness or DNA database). The characteristics of the DNA profiles were further classified as i) single DNA profiles; ii) mixed DNA profiles that meet the criteria for storage in the Dutch national DNA database; iii) complex DNA profiles that do not meet the criteria for storage in the DNA database but contain typing data that can be used for exclusion; and iv) no typing result, when the profiling data contain too little information for a meaningful comparison.

For all selected crime samples, the measured DNA concentrations, the characteristics of the DNA profiles, and the matching characteristics were obtained from the case file and the testimonies of the reporting scientists.
traces of exhibit

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interval is smaller than 0.03. In our opinion, this determines
from all available traces of each exhibit (17). Sample size
smaller confidence intervals, for example, for

= 441), the confidence interval is not larger than ± 0.08. Less frequent types have even

percentage

sampled exhibits containing more than 100 samples, a random sample of 100 was

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analysed in the period of 1 January 2012 until 31 December 2013. These analysed

station for DNA analysis. This dataset consists of 5754 crime samples that were

traces of blood that were directly secured from the crime scene, as well as exhibits that

4.2 Materials and Methods

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knowledge on DNA success rates

Table 1. Categories and Number (Total and Selected) of Samples Evaluated in this Study for a Decision
Model Based on DNA Success Rates

<table>
<thead>
<tr>
<th>Exhibit</th>
<th>N total</th>
<th>N selected</th>
<th>Exhibit</th>
<th>N total</th>
<th>N selected</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Fire) weapon grip</td>
<td>441</td>
<td>100</td>
<td>Crowbar</td>
<td>78</td>
<td>78</td>
</tr>
<tr>
<td>Blood</td>
<td>354</td>
<td>100</td>
<td>Collar</td>
<td>77</td>
<td>77</td>
</tr>
<tr>
<td>Fabric gloves</td>
<td>273</td>
<td>100</td>
<td>Torch</td>
<td>77</td>
<td>77</td>
</tr>
<tr>
<td>Cigarette end</td>
<td>182</td>
<td>100</td>
<td>Sleeve cuff</td>
<td>70</td>
<td>70</td>
</tr>
<tr>
<td>Screwdriver</td>
<td>163</td>
<td>100</td>
<td>Handle motor/bike</td>
<td>67</td>
<td>67</td>
</tr>
<tr>
<td>Car items</td>
<td>150</td>
<td>100</td>
<td>Sock</td>
<td>64</td>
<td>64</td>
</tr>
<tr>
<td>Tools (other)</td>
<td>139</td>
<td>100</td>
<td>Gas cylinder</td>
<td>53</td>
<td>53</td>
</tr>
<tr>
<td>Cartridge case</td>
<td>137</td>
<td>100</td>
<td>Shoe</td>
<td>48</td>
<td>48</td>
</tr>
<tr>
<td>Drinking items</td>
<td>134</td>
<td>100</td>
<td>Tape</td>
<td>44</td>
<td>44</td>
</tr>
<tr>
<td>Cap</td>
<td>123</td>
<td>100</td>
<td>Keys</td>
<td>43</td>
<td>43</td>
</tr>
<tr>
<td>Handbag grip</td>
<td>118</td>
<td>100</td>
<td>Glasses</td>
<td>32</td>
<td>32</td>
</tr>
<tr>
<td>Balaclava</td>
<td>108</td>
<td>100</td>
<td>Lighter</td>
<td>23</td>
<td>23</td>
</tr>
<tr>
<td>Knife grip</td>
<td>104</td>
<td>100</td>
<td>Undefined gloves</td>
<td>350</td>
<td>0</td>
</tr>
<tr>
<td>Zip tie</td>
<td>99</td>
<td>99</td>
<td>Undefined*</td>
<td>853</td>
<td>0</td>
</tr>
<tr>
<td>Headwear</td>
<td>98</td>
<td>98</td>
<td>Other†</td>
<td>1165</td>
<td>0</td>
</tr>
<tr>
<td>Latex gloves</td>
<td>87</td>
<td>87</td>
<td>Total</td>
<td>5754</td>
<td>2260</td>
</tr>
</tbody>
</table>

*Exhibit unknown
†Infrequently sampled exhibits

4.2.1 DNA Analysis Process of the Selected Samples

DNA Sample Preparation

The traces used in this study were secured from the crime scenes by SoCOs and sampled
for DNA analysis at the police laboratories (18). The sampling was performed by the
police laboratories using NFI standards and protocols. Most samples were secured by
swabbing the exhibit using a dry cotton swab. At the police laboratories, the swabs were
transferred to special containers and sent to the NFI. Cigarette ends were cut from the
cigarette and placed in the container. Exhibits such as balaclavas and fabric gloves were
sampled using the stubbing procedure (19).

DNA Extraction and Quantification

DNA extraction and profiling were performed at the NFI. At the time of this study, the
DNA quantification method for DNA extracts was the Quantifiler" Duo DNA
quantification kit using the 7500 Real-Time PCR System (Applied BiosystemsTM—
AB). The manufacturer of the quantification kit reports a DNA concentration range of
50 ng/μL to 23 pg/μL (20). However, much lower sensitivities – even as low as 2 pg/μL
– have been reported (21–23) for this quantification system. Therefore, for this study,
we took all DNA concentration data into account, including the data that fell below the
minimum value of the indicated concentration range of 23 pg/IL.
**DNA Profiling**

All short tandem repeat (STR) DNA profiles included in this study were obtained with the Next Generation Multiplex (NGM) DNA analysis system (AB). The NGM DNA analysis system determines the genetic information on 15 polymorphic DNA loci and the sex-specific locus amelogenin (24). DNA amplification (29 PCR cycles) and fragment analysis were performed according to the manufacturers’ instruction. If necessary, post-PCR samples were reanalysed under enhanced conditions for the detection of the amplified STR fragments. Validated in-house adaptations involved either enhanced electrophoresis settings or post-PCR clean up of the amplified STR fragments. The clean up removes salts and primers that compete with amplified DNA fragments for injection into the capillary during electrophoresis and allows for increasing the signal strength of the amplified STR fragments (25).

The reporting scientist performed the interpretation and statistical evaluation of the DNA profile comparisons. DNA profiles for entry, comparison, and storage in the DNA database must meet minimal criteria (26). The Netherlands uses the CODIS DNA database software. For automated comparison, the DNA profile of the crime sample should contain the typing results of at least 6 loci. The random match probability of partial profiles to be searched should exceed the figure of 1 in 10 million (9,26). In some instances, intelligence-based database searches on complex profiles were performed as indicated by the reporting scientist.

### 4.3 Results

**DNA Quantification**

As stated above, the Quantifiler® Duo DNA quantification kit reported a DNA concentration down to 23 pg/μL. However, sensitivities as low as 2 pg/μL have been reported in the literature. Moreover, the combined DNA data from the extracts of the crime samples in this study show a continuous function for the DNA concentration in the extract down to 2 pg/μL. Although the interpretation of the quantification values of low-level DNA samples should be approached with caution, the data at least support that meaningful concentration estimates can be obtained from DNA samples that contain less than 23 pg/μL. Of 2260 samples, 641 (28%) samples had concentration values between 2 pg/μL and 23 pg/μL, and 700 (31%) extracts had values below 2 pg/μL.

**DNA Profiling**

We evaluated the DNA profiling results of 2260 samples. From 1120 (50%) of the traces, no DNA profiling results were obtained; 290 traces (13%) resulted in complex DNA profiles that did not meet the quality criteria for DNA database storage; and 850 traces (38%) yielded profiling results that met the quality criteria (26) for DNA database storage.
knowledge on DNA success rates

Table 2. Characteristics of the Obtained DNA Profiling Results

<table>
<thead>
<tr>
<th>DNA profiling results</th>
<th>Number</th>
<th>%</th>
<th>Mean (pg/μL)</th>
<th>St.dev</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single</td>
<td>573</td>
<td>25</td>
<td>628.4</td>
<td>1462.5</td>
</tr>
<tr>
<td>Mixed</td>
<td>277</td>
<td>12</td>
<td>186.4</td>
<td>213.2</td>
</tr>
<tr>
<td>Complex</td>
<td>290</td>
<td>13</td>
<td>52.0</td>
<td>62.6</td>
</tr>
<tr>
<td>No result</td>
<td>1120</td>
<td>50</td>
<td>3.1</td>
<td>5.0</td>
</tr>
<tr>
<td>Total</td>
<td>2260</td>
<td>100</td>
<td>170.7</td>
<td>0.6</td>
</tr>
</tbody>
</table>

*The concentration data of outliers with more than 3 times the original st.dev were not taken into consideration for calculating the mean concentration.

Storage (Table 2). Table 2 shows that samples that yielded profiling results contained higher concentrations of DNA than samples that did not lead to profile results. To form a complete picture, all traces were plotted from lowest to highest measured concentration (Fig. 1), giving more insight into the pattern of concentrations toward obtaining certain DNA profile results. Figure 1 indicates that samples with higher DNA concentrations have a higher success probability than samples with a low DNA concentration. The data from Fig. 1 and Table 2 show a positive relation between DNA concentration and the success probability. When the mean concentration increases, the DNA profiling results improve.

This relation was not dependent on the category of the sampled exhibit. Between the different categories of exhibits, the proportion of samples with a DNA concentration of less than 10 pg/μL that yielded no DNA profiles was comparable. For high-level DNA with a concentration of 10 pg/μL or more, the same trend was observed. Based on these results, we can conclude that the obtained profile result of the DNA typing process depends on the amount of DNA, independent of the nature of the sampled exhibits.

Practically, all traces with a concentration higher than 100 pg/μL yield DNA profiles that meet the quality criteria for DNA database storage. In our study, 23% of the extracts (Fig. 1) contained more than 100 pg/μL of DNA. Only 4 traces with a concentration higher than 100 pg/μL (Fig. 1) resulted in a profile that did not meet the quality criteria for DNA database storage, due to the fact that they were too complex (mixed) and therefore had insufficient discriminative factors to perform a DNA comparison study. At the other end of the spectrum, Fig. 1 shows that practically all traces that had a measured concentration of 2 pg/μL or less resulted in no DNA profiling results; this applied for 31% of all traces.

Between these extremes, the success rates are harder to predict. This applied for 46% of the traces. Setting a threshold value within that range will therefore always result in a loss of DNA profiling data. For example, setting a conservatively low threshold at 2 pg/μL would mean that 31% (700/2260) of the samples can be set aside after the quantification step (Fig. 1). A DNA profiling result was obtained from only 13 of these 700 samples, of which 9 were complex profiles. Above the 2 pg/μL threshold, 72% of
the traces produced a DNA profiling result. This must be compared to the no-threshold situation where only 50% of the traces produced a DNA profiling result.

A less conservative threshold (i.e., 6 pg/μL) would mean that 42% (958/2260) of the traces would not need further analysis (Fig. 1). In this case, we would lose profiling results in about 5% (46/958) of the cases.

At the other extreme, if the threshold was to be set at a value of 100 pg/μL, this would mean that practically all traces would yield a DNA profiling result. This high threshold would however result in a much higher loss of samples that could potentially produce a DNA profiling result. In our study, 36% (621/1737) of the samples contained less than 100 pg/μL of DNA but still produced a DNA profiling result.

**Different Type of Exhibits**

Table 3 shows the obtained DNA profile success rates for a range of different exhibits. Successful exhibits can be understood as having a high DNA concentration (average ≥ 100 pg/μL) or a high success probability (≥ 80%). The DNA success probabilities in Table 3 show that cigarette ends, blood, balaclava, headwear (other), ball caps, collars, sleeve cuffs, and socks are the exhibits with the highest success rate. Unsuccessful exhibits have a low DNA concentration (average ≤ 5.0 pg/μL) or a low success ≤ 5.0 probability (≤ 20%), and these include cartridge cases, crowbars, keys, tape, zip ties, and gas cylinders.
Samples secured from ball caps show the highest success probability (94%) in obtaining DNA profiling results. It was also observed that a large proportion of the sampled ball caps yielded mixed DNA profiles. Cigarette ends also have a high success probability (87%). However, practically all these DNA profiles were single DNA profiles (84%). Although ball caps show the highest success probability in obtaining a DNA profiling result, we observed higher concentrations of DNA in extracts from cigarette ends, bloodstains, balaclavas, and headwear (other).

In some cases, similar categories of exhibits show comparable success rates, for instance, the sleeve cuff and collar. This suggests that it might be sufficient to sample either the sleeve cuff or the collar of a clothing item when seeking to identify the wearer of this item. Screwdrivers, crowbars, and other tools belong to roughly the same category (hand-tools). However, there was a significant difference between the type of tool and the DNA concentration obtained at the p < 0.01 level (one-way ANOVA: F(2, 262 = 5.717, p = 0.004). Post hoc comparison using the LSD Fisher test revealed that screwdrivers showed a significantly higher DNA concentration than crowbars and hand-tools (other). Crowbars and hand-tools (other) did not significantly differ from each other. The same trend was observed for the success probabilities.

Other similar exhibits like gloves of latex and gloves of fabric show a significant difference at the p < 0.01 level in measured DNA concentrations (one-way ANOVA: F(1, 180) = 14.095, p < 0.001). The same trend was observed for the success probabilities.

The lowest DNA concentrations were observed in the exhibit categories of gas cylinder, zip tie, keys, and tape. Although we obtained a DNA profiling result from 15% of the samples from zip ties, in half of the cases theses profiles match the victim. Samples from tapes show the same picture. Profiles fit for comparison were also evaluated for their matching features (Table 3). Whether a DNA profile from a crime sample has an added value for the criminal investigation depends on the circumstances of the case. In most cases, the goal is to identify a suspect or to find evidence to link the suspect with the crime. However, in some cases, it can be important to obtain a match with a victim, for instance to find DNA traces of the victim on the clothes or in the car of the suspect.

When a balaclava was sent in for DNA analysis, a DNA profile was obtained in 92% of the cases. In 37% of these cases, a match was obtained with a person in the DNA database, and in 21%, a match with a known suspect. Samples from the grip of (fire) weapons have a 26% success probability in obtaining DNA profiling data. In only 12% of the cases, these profiles matched a person in the DNA database, but in 38% of the cases, a match with a known suspect was obtained. At 62%, DNA profiles from ball caps have the highest success probability of obtaining a DNA match with a person; most of these matches are DNA database matches.
The overall DNA profiling results from 2260 samples showed that 50% of the samples entering, searching, and storing in the DNA database. The DNA concentration obtained (50% of total) that did yield a DNA profiling result, 75% met the quality criteria for crime traces analysed at the NFI did not yield a DNA profile (9). Of the 1140 samples with the success probability of obtaining a DNA profile, differed between the different types of sampled exhibits (Table 3). Cigarette ends, blood, balaclava, headwear (other), ball caps, collars, sleeve cuffs, and socks show the highest DNA success rates, while traces exhibit with the number of samples that gave DNA profiling results. A total of 62 DNA success rates ranked from highest to lowest mean concentration

<table>
<thead>
<tr>
<th>Trace exhibit</th>
<th>N (E=2420)</th>
<th>Single profile</th>
<th>Mixed profile</th>
<th>Complex profile</th>
<th>Mean concentration (pg/µL)*</th>
<th>Stdev</th>
<th>Observed profile results (%)</th>
<th>Observed (%) matches†</th>
<th>Suspect</th>
<th>Database</th>
<th>Victim/Witness</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cigarette end</td>
<td>100</td>
<td>84</td>
<td>3</td>
<td>0</td>
<td>1692.4</td>
<td>17</td>
<td>10</td>
<td>10</td>
<td>36</td>
<td>10</td>
<td>26</td>
</tr>
<tr>
<td>Blood</td>
<td>100</td>
<td>68</td>
<td>6</td>
<td>7</td>
<td>920.2</td>
<td>19</td>
<td>10</td>
<td>10</td>
<td>27</td>
<td>10</td>
<td>37</td>
</tr>
<tr>
<td>Balaclava</td>
<td>100</td>
<td>46</td>
<td>29</td>
<td>17</td>
<td>386.3</td>
<td>8</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Headwear (other)</td>
<td>100</td>
<td>27</td>
<td>34</td>
<td>29</td>
<td>265.8</td>
<td>6</td>
<td>10</td>
<td>10</td>
<td>37</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Ball cap</td>
<td>100</td>
<td>42</td>
<td>34</td>
<td>20</td>
<td>224.8</td>
<td>20</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Collar</td>
<td>100</td>
<td>34</td>
<td>26</td>
<td>19</td>
<td>147.5</td>
<td>17</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Sleeve cuff</td>
<td>100</td>
<td>70</td>
<td>64</td>
<td>25</td>
<td>126.7</td>
<td>17</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Handglove (inside)</td>
<td>100</td>
<td>64</td>
<td>38</td>
<td>15</td>
<td>77.0</td>
<td>9</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
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<td>Torch</td>
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<td>27</td>
<td>33</td>
<td>24</td>
<td>64</td>
<td>9</td>
<td>10</td>
<td>10</td>
<td>32</td>
<td>10</td>
<td>21</td>
</tr>
<tr>
<td>Drinking items</td>
<td>100</td>
<td>87</td>
<td>21</td>
<td>17</td>
<td>29</td>
<td>8</td>
<td>10</td>
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<td>21</td>
</tr>
<tr>
<td>Shoe</td>
<td>100</td>
<td>57</td>
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*On average 2 outliers (Table 1) per exhibit were removed (min = 1, max = 6). For example secured bloodstains had a mean concentration of 1459.3 pg/µL, after removing 1 outlier with a concentration of 54.8 ng/µL the mean concentration was 920.2 pg/µL.
†The success probabilities in obtaining a match (with the database, suspect or victim/witness) were calculated on the basis of the number of samples that gave DNA profiling results. A total of 1459.3 pg/µL after removing 1 outlier with a concentration of 54.8 ng/µL.
4.4 Conclusions and Discussion

This study was performed to gain more insight into forensic DNA success rates and to help build an objective decision model for the analysis of DNA traces based on these DNA success rates. First, it was hypothesized that DNA success rates vary across different types of exhibits that are sampled for DNA, so that a model that incorporates this factor can assist the SoCOs in their selection process when examining crime scenes for biological trace evidence. Second, it was hypothesized that DNA success rates depend on the concentration of DNA, so that a carefully chosen threshold value may lead to a more efficient DNA profiling process at the laboratory.

The overall DNA profiling results from 2260 samples showed that 50% of the samples that were sampled and sent in by SoCOs for DNA analysis at the NFI did not yield a DNA typing result. The high number of negative profiling results from this study concurs with the results from our previous study which showed that 46% of the serious crime traces analysed at the NFI did not yield a DNA profile (9). Of the 1140 samples (50% of total) that did yield a DNA profiling result, 75% met the quality criteria for entering, searching, and storing in the DNA database. The DNA concentration obtained and the DNA profiling results from the crime scene samples relate to each other, and this is in agreement with the expectation that the DNA concentration value is a key factor to obtain successful DNA profiling results. With increasing DNA concentrations, the number of DNA profiles that meet the criteria for DNA database storage increases (Fig. 1). This finding appears to be independent of the exhibit sampled and therefore implies that any threshold set in the DNA profiling process only depends on the quantification result.

The observed pattern of average DNA concentrations of the different exhibits, combined with the success probability of obtaining a DNA profile, differed between the different types of sampled exhibits (Table 3). Cigarette ends, blood, balaclava, headwear (other), ball caps, collars, sleeve cuffs, and socks show the highest DNA success rates, while cartridge cases, crowbars, keys, tape, zip ties, and gas cylinders show the lowest DNA success rates. This information can assist the SoCO in prioritising traces for DNA profiling.

Samples from gas cylinders show extremely low quantification measures, and none of the analysed gas cylinder samples produced a DNA profiling result. The same applies to samples from the tape and zip tie exhibits, with very low DNA quantities measured and, respectively, 11% and 15% producing a DNA profile. It is worth asking whether these traces should still be collected by SoCOs and submitted for the DNA profiling process. In robberies, the perpetrator often uses tape and zip ties to immobilize the victim. In these cases, the exhibits are secured by the SoCOs for DNA analysis to identify the perpetrator. However, 50% of the obtained profiles from the tape and 47%
of the obtained profiles from the zip tie matched the victim. The actual success rate to obtain the DNA profile from a suspect is therefore even lower.

Such information should be considered when traces are collected at the crime scene or when they are selected for further analysis at the forensic laboratory. In serious crime cases, a success rate of 15% or lower can probably justify the selection and processing of such traces for DNA analysis. This might not be true for less serious crimes, however. It should be noted that the actual decision on whether or not to analyse a DNA trace might therefore be case dependent. For instance, a low success rate trace such as a zip tie could still be selected for DNA profiling in a murder case, but not in a burglary case. We expect that the introduction of a decision model based on DNA success rates will lead to evidence-based selection of traces and exhibits by the police and a better use of the DNA profiling capacity at the forensic laboratory. In addition, the forensic laboratory can improve the efficiency of the DNA profiling process by introducing a threshold value for the minimum amount of DNA in a sample. When profiling DNA samples, the procedure starts with quantifying the amount of DNA in the sample. If the estimated DNA concentration does not exceed a set threshold value, no DNA profiling will be performed on the sample extract.

For decisions on setting the threshold value, the method of quantification is essential. In this study, the samples were quantified with the Quantifiler® Duo. The lowest reported sensitivity of this quantification system is 2 pg/μL, which would allow the threshold value to be set at 2 pg/μL. Furthermore, there is a clear positive relation between the measured DNA concentration in the extract and the DNA profiling result. The data from this study can therefore be used to objectively justify the decision on the height of the threshold value.

The data from this study showed that 98% of the samples with an estimated DNA concentration of 2 pg/μL or less produced no profiling result. Of the 2260 samples, 31% had a concentration of less than 2 pg/μL (Fig. 1). Setting the threshold at this value in routine DNA analysis would thus imply that 31% of the samples could be rejected for analysis after quantification of the extract. The probability that any of these samples would produce a meaningful profiling result is low (less than 2%), and of the profiles that were obtained, most proved too complex to use.

Setting a less conservative threshold (i.e., 6 pg/μL) would expedite the laboratory process even further: in that case, some 42% of the extracts would likely be rejected for further processing. Using the higher threshold value, we observed that DNA profiling data were obtained in less than 5% of the samples with a concentration value of less than 6 pg/μL (Fig. 1). In more than half of the cases, however, the profiling data obtained from these low-level DNA samples did not meet the quality criteria for searching and storing in the DNA database. This shows that introducing a threshold value in the forensic DNA analysis process can be very effective, saving capacity, time, and money for the forensic laboratories and the CJS. If forensic laboratories perform their own study
to obtain a threshold value, we expect similar results. However, the laboratory-specific value will likely be codetermined by their specific protocols for sample collection and the systems used for DNA analysis. The quantification method used is another key issue. The data in this study were obtained with a relatively less sensitive quantification method. Recently, more sensitive quantification methods have become available such as the AluQuant (27). The new quantification methods will allow for a more precise determination of the threshold value, reducing the risk that low-level DNA samples are set aside for analysis.

A decision model based on DNA success rates can be used by the police and the laboratory to reduce the number of “empty” traces that encumber the DNA analysis processes: on the one hand by enabling SoCOs to make knowledge-based judgments in their trace selection process for DNA analysis and on the other hand by introducing a threshold value for the quantification step of DNA analysis at the laboratory. It is expected that SoCOs will be more aware of what to sample at the crime scene, thereby reducing backlogs and turnaround times, as “empty” DNA traces will be rejected for the complete DNA analysis process at the forensic laboratory. Information on DNA success rates can thus form the basis for such evidence-based decisions and may result in an actual decision support system for the SoCOs for the selection of DNA traces for analysis. Although using such systems during the intelligence phase of a crime case within the police and forensic field is still explorative (15,16,28,29), we do expect this to offer a way forward in optimising crime scene investigations.

The data of this study can furthermore serve to create evidence-based decision models for the use of new and mobile DNA technologies for future crime scene work. Several manufacturers are marketing mobile DNA technologies to further optimise forensic DNA testing as an investigative tool (30–35). To make optimal use of these mobile technologies, knowledge of the properties of biological traces that allow for fast mobile analysis or that require the expertise of a fully equipped forensic DNA typing laboratory is then essential.

**4.5 References**


