<u>The Effectiveness of Low Copy Number DNA in</u> <u>Criminal Investigation.</u>

Jacquelyn Newman

June 2009

Acknowledgements

The author would like to acknowledge the support of Greater Manchester Police, in particular the Director of Forensic Services, Dr Hall, the staff within the Forensic Submissions Unit and the Crime Scene Investigators, without which this research would not have been possible. In addition the assistance of Mrs Jean Titchmarsh from Greater Manchester Police library services proved invaluable in obtaining reference documents.

The author would also like to thank her University supervisors, Dr A Campbell and Mrs S Marshall, for their advice throughout the period of research.

However the biggest debt of gratitude goes to my friends and family who have never doubted my ability to complete this work and have provided constant encouragement and support.

| Acknowledgements | ii |
|--------------------------------------|------|
| Contents | iii |
| Summary of Tables | vii |
| Summary of Figures | viii |
| Abbreviations / Explanation of Terms | xi |
| Abstract | xiii |

<u>Chapter 1 – Introduction</u>

| 1.1 | Introduction | 2 |
|-----|-----------------------------------|----|
| 1.2 | Crime Scene Investigation Units | 3 |
| 1.3 | The National DNA Database (NDNAD) | 7 |
| 1.4 | Overview of DNA | 9 |
| 1.5 | LCN DNA | 17 |

<u>Chapter 2 – Review of Current Literature and Publications</u>

| 2.1 | LCN DNA Technique | 20 |
|-----|---|----|
| 2.2 | The Shedder Factor | 21 |
| 2.3 | Contamination and Transfer of DNA | 22 |
| 2.4 | Laboratory Simulation of Crimes for LCN DNA | 24 |
| 2.5 | LCN DNA used within Criminal Investigation | 26 |
| 2.6 | Literature and Research Gaps | 30 |

Chapter 3 – Filling the Research Gap

| 3.1 | Why the Research is Needed | 33 |
|-----|--|----|
| 3.2 | Research for Crime Scene Investigation | 35 |
| 3.3 | Detections | 36 |
| 3.4 | Research Aims | 37 |
| 3.5 | Research Stages | 37 |

<u>Chapter 4 – Process and Methodology</u>

| 4.1 | Process and Methodology | 40 |
|-----|--|----|
| 4.2 | Reinforced Anti Contamination Measures | 40 |
| 4.3 | Standardisation of Swabbing Techniques | 41 |
| 4.4 | Examination Protocols | 42 |
| 4.5 | Submissions Policy | 44 |
| 4.6 | Laboratory Processes | 46 |
| 4.7 | Methodology | 46 |
| 4.8 | Statistical significance | 48 |

<u>Chapter 5 - Defining Useful Profiles & Matches and Categorising</u> <u>Samples</u>

| 5.1 | Defining a 'Useful Profile' | 51 |
|-----|--|----|
| 5.2 | Defining a 'Match' | 54 |
| 5.3 | Changes from Cell Type to Surface Type | 56 |

Chapter 6 - Phase 1 Results of Categories and Sub-Groups

| 6.1 | Succes | ss Rates | 59 |
|-----|---------|-----------------------|----|
| 6.2 | Overar | rching Categories | 60 |
| 6.3 | Individ | dual Category Results | 63 |
| | 6.3.1 | Body Fluids | 64 |
| | 6.3.2 | Body Samples | 66 |
| | 6.3.3 | Communication Items | 74 |
| | 6.3.4 | Firearms | 76 |
| | 6.3.5 | Ligatures | 81 |
| | 6.3.6 | Personal Belongings | 86 |
| | 6.3.7 | Premises | 90 |
| | 6.3.8 | Tools | 92 |
| | 6.3.9 | Vehicles | 94 |
| | 6.3.10 | Weapons | 99 |

| 6.3.11 | Worn Items | 102 |
|--------|------------|-----|
| 6.3.12 | Groups | 111 |

<u>Chapter 7 – Discussion of Phase 1 Results</u>

| 7.1 | Comparison of Sub-Groups | 115 |
|-----|--|-----|
| 7.2 | Discussion of Results and Early Findings | 121 |

<u>Chapter 8 – Phase 2 Results</u>

| 8.1 | Phase 2 Areas for Consideration | | 124 | |
|-----|---------------------------------|-----------------------|-----|--|
| 8.2 | Surface Materials | | | |
| | 8.2.1 | Plastics | 127 | |
| | 8.2.2 | Textiles | 128 | |
| 8.3 | Surfac | e Characteristics | 130 | |
| | 8.3.1 | Porosity | 130 | |
| | 8.3.2 | Surface Texture | 131 | |
| 8.4 | Recov | ery Factors | 132 | |
| | 8.4.1 | Environmental Factors | 132 | |
| | 8.4.2 | Recovery Decisions | 135 | |
| 8.5 | Submi | ssion Times | 138 | |
| 8.5 | Submi | ssion Times | 138 | |

<u>Chapter 9 – Conclusion & Recommendations for Further</u> <u>Research</u>

| 9.1 | Conclusion | 142 |
|-----|--|-----|
| 9.2 | Key Findings | 143 |
| 9.3 | Positive Factors | 145 |
| 9.4 | Neutral Factors | 146 |
| 9.5 | Negative Factors | 147 |
| 9.6 | Profiling and Anticipated Eliminations | 148 |
| 9.7 | Outstanding Profiles | 149 |
| 9.8 | Recovery of Samples | 150 |

| 9.9 | New Technology | 152 |
|------|--------------------------------------|-----|
| 9.10 | Summary | 153 |
| 9.11 | Recommendations for Further Research | 154 |

References

156

Appendices

| 1 | Allelic Ladders | 167 |
|----|-------------------------------------|-----|
| 2 | Elimination DNA Databases | 179 |
| 3 | DNA Swabbing Process | 182 |
| 4 | Submissions Policy for LCN DNA | 184 |
| 5 | Statistical Evaluation | 196 |
| 6 | Sample Categories and Sub-Groups | 205 |
| 7 | Firearms and Ammunition Terminology | 220 |
| 8 | Firearm Images | 224 |
| 9 | Street Robbery Initiative | 227 |
| 10 | Hook & Cane Burglaries | 232 |

Summary of Tables

| Table 1.1 | Example of full SGMplus DNA profile in numerical | |
|------------|--|-----|
| | form, as it would be loaded onto the NDNAD. | 16 |
| Table 5.1 | Example of a full male SGMplus DNA profile. | 51 |
| Table 5.2 | Example of a mixed SGMplus DNA profile, showing more than 2 alleles at several loci. | 52 |
| Table 5.3 | Example of a partial SGMplus DNA profile, showing missing alleles at several loci. | 53 |
| Table 9.1 | Top five items for generating a profile, generating a useful profile and anticipated eliminations. | 143 |
| Table 9.2 | Top five items for generating a useful profile and to generate a match. | 143 |
| Table 9.3 | Key findings that can affect LCN DNA analysis results. | 145 |
| Table A5.1 | Sample of the probability points of the chi-square distribution table. | 199 |
| Table A5.2 | Summary of phase 1 and phase 2 chi-test results. | 201 |
| Table A5.3 | Abridged sample of the chi-square distribution table. | 204 |

Summary of Figures

| Figure 1.1 | Basic cell structure, showing nucleus, chromosome and | 10 |
|-------------|---|----|
| | DNA structure. | |
| Figure 1.2 | Basic cell structure showing the mitochondria outside | 11 |
| | the nucleus. | |
| Figure 1.3 | DNA interlinking base pairs, adenine& thymine, cytosine | 12 |
| | & guanine. | |
| Figure 1.4 | Electropherogram showing full SGMplus DNA profile at | 16 |
| | 10 STR loci. | |
| Figure 4.1 | Full protective suit with hood, face mask, overshoes and | 40 |
| | gloves taped at wrists. | |
| Figure 4.2 | Cartridge case in wet muddy area. | 45 |
| Figure 6.1 | Example of how data will appear in research results. | 60 |
| Figure 6.2 | Results of all samples analysed. | 61 |
| Figure 6.3 | Total percent of samples generating a useful DNA profile | 62 |
| | within each category. | |
| Figure 6.4 | Total percent of samples that went on to generate a match | 62 |
| | within each category. | |
| Figure 6.5 | Total percent of samples that resulted in an anticipated | 63 |
| | elimination result within each category. | |
| Figure 6.6 | Results of profiling for the category body fluids and the | 65 |
| | Sub-groups. | |
| Figure 6.7 | Overall results for body samples. | 67 |
| Figure 6.8 | Results of profiling areas of the torso. | 68 |
| Figure 6.9 | Results of profiling areas with visible bruising. | 69 |
| Figure 6.10 | Results of profiling areas associated with kissing | 70 |
| | and sucking. | |
| Figure 6.11 | Results of profiling for different areas of the arm. | 72 |
| Figure 6.12 | Results of profiling from genitalia. | 73 |
| Figure 6.13 | Overall results for communication items, mobile | 75 |
| | phones and mobile phone sub-groups. | |
| Figure 6.14 | Overall results for firearms and ammunition. | 77 |

| Figure 6.15 | Results for handgun sub-group. | 78 |
|-------------|--|-----|
| Figure 6.16 | Results for shotgun sub-group. | 79 |
| Figure 6.17 | Results for general areas of firearms. | 81 |
| Figure 6.18 | Results for ligatures. | 83 |
| Figure 6.19 | Wrists bound with cable tie showing target area. | 84 |
| Figure 6.20 | Ankles bound with adhesive tape showing target area. | 84 |
| Figure 6.21 | Overall results for personal belongings. | 88 |
| Figure 6.22 | Results for fasteners on bags. | 89 |
| Figure 6.23 | Overall results for premises. | 91 |
| Figure 6.24 | Results for tools. | 93 |
| Figure 6.25 | Overall results for vehicle samples. | 95 |
| Figure 6.26 | Results for vehicle sub-groups. | 96 |
| Figure 6.27 | Result for number plates and screws. | 98 |
| Figure 6.28 | Results for weapons. | 101 |
| Figure 6.29 | Results for worn items. | 103 |
| Figure 6.30 | Results for headwear. | 104 |
| Figure 6.31 | Results for footwear – shoe type. | 105 |
| Figure 6.32 | Results for footwear – aim of profiling. | 106 |
| Figure 6.33 | Results for sub-group underwear. | 107 |
| Figure 6.34 | Results for upper clothing. | 108 |
| Figure 6.35 | Results for jewellery. | 110 |
| Figure 6.36 | Results for groups. | 113 |
| Figure 7.1 | Screwdriver and knife handle comparison. | 116 |
| Figure 7.2 | Handgrip of handgun showing textured grip. | 116 |
| Figure 7.3 | Mobile phone and handgun grip comparison. | 117 |
| Figure 7.4 | Mobile Phone in use showing close proximity to | 118 |
| | persons mouth. | |
| Figure 7.5 | Comparison of small items which require fiddly | 119 |
| | finger manipulation. | |
| Figure 7.6 | Comparison of similar surfaces in vehicles. | 120 |
| Figure 8.1 | Results of surface materials. | 126 |
| Figure 8.2 | Results of hard and soft plastics. | 127 |
| Figure 8.3 | Results of textile types. | 129 |
| Figure 8.4 | Results of porous v non porous surfaces. | 131 |

| Figure 8.5 | Results of rough v smooth textures. | 132 |
|--------------|---|-----|
| Figure 8.6 | Sample results by month recovered (all years/samples). | 133 |
| Figure 8.7 | Sample results by seasonal periods (all years/samples). | 134 |
| Figure 8.8 | Results by location, inside v outside. | 135 |
| Figure 8.9 | Sample target areas. | 136 |
| Figure 8.10 | Item v swab results. | 137 |
| Figure 8.11 | Time trend for DNA profiling. | 138 |
| Figure 8.12 | Useful profile time trend for swabs and items. | 140 |
| Figure 9.1 | Showing revised target area for swabbing in hook & | 149 |
| | cane burglaries. | |
| Figure A9.1 | Results for street robbery. | 231 |
| Figure A10.1 | Results for hook and cane burglaries. | 235 |

Abbreviations / Explanation of Terms

| ACPO | Association of Chief Police Officers. | | | |
|---------------|---|--|--|--|
| Allele | One part of the gene, inherited from one parent, found at a | | | |
| | specific part of the chromosome. | | | |
| Casework | Relating to a real crime scene or event, not simulated. | | | |
| CPS | Crown Prosecution Service. | | | |
| CSI | Crime Scene Investigator also known as Scenes of Crime | | | |
| | Officer (SOCO). | | | |
| DNA | Deoxyribo-Nucleic Acid. | | | |
| DNA Profile | The characteristics of DNA at target regions that can be | | | |
| | used for identification purposes. Historically referred to as | | | |
| | DNA fingerprinting. | | | |
| FSS | Forensic Science Service. | | | |
| GMP | Greater Manchester Police. | | | |
| HMIC | Her Majesty's Inspectorate of Constabulary. | | | |
| LCN | Low Copy Number. | | | |
| LCN DNA | Low Copy Number Deoxyribo-Nucleic Acid – The | | | |
| | analysis of small amounts of cellular material, sometimes | | | |
| | referred to as 'trace DNA' or 'touch DNA'. | | | |
| Locus/Loci | Area of the DNA molecule analysed. | | | |
| LTDNA | Low Template DNA, when amounts of DNA $<$ 200pg are | | | |
| | submitted for analysis. | | | |
| Match | When the part of the DNA profile available matches | | | |
| | another, usually 'person to scene' or 'scene to scene'. Also | | | |
| | known as a 'DNA hit'. | | | |
| NDNAD | National DNA database. | | | |
| Nanogram (ng) | One thousand millionth of a gram. 10^{-9} grams. | | | |
| PACE | Police and Criminal Evidence Act 1984. | | | |
| PCR | Polymerase chain reaction – Also known as amplification, | | | |
| | is where the DNA is replicated many times. | | | |
| PED | Police Elimination Database. | | | |
| Picogram (pg) | A million million th of a gram. 10^{-12} grams. | | | |

| Police Incident | An event that is dealt with by the police that does not | | | |
|----------------------------------|--|--|--|--|
| | constitute a crime. For example, a fatal fire (accidental | | | |
| | ignition) or suspicious death that turns out to be natural | | | |
| | causes. | | | |
| PPE | Personal Protective Equipment. This can include gloves, | | | |
| | facemasks, goggles, hardhats etc. | | | |
| Profile | See DNA profile. | | | |
| SGM | Second Generation Multiplex – examines 6 areas of the | | | |
| | nuclear DNA molecule and a gender marker, amelogenin. | | | |
| $\mathbf{SGMplus}^{\mathrm{TM}}$ | Second Generation Multiplex plus – examines 10 areas of | | | |
| | the nuclear DNA molecule and a gender marker, | | | |
| | amelogenin. | | | |
| SIO | Senior Investigating Officer – Person in overall charge of | | | |
| | a criminal investigation. | | | |
| SSM | Scientific Support Manager – Person in charge of the | | | |
| | scientific services, including crime scene investigators, | | | |
| | within a Police Force. | | | |
| STR | Short tandem repeat – short sequences of repeated DNA. | | | |
| UK | United Kingdom. | | | |
| Volume Crime | Crimes against property such as burglary, theft of motor | | | |
| | vehicles, theft from a motor vehicle, criminal damage. | | | |
| | | | | |

<u>Abstract</u>

When offenders commit crime there is the potential that they may leave behind trace amounts of their DNA, even when there has been no apparent body fluid spill. During the examination of crime scenes, scene investigators try to identify areas that may be sampled to locate these traces. Specialist techniques are then required within the laboratory to enable such small amounts to be analysed to obtain a profile. These techniques are referred to as Low Template DNA analysis (LTDNA), of which Low Copy Number DNA (LCN DNA) is one instance.

In 2008, following the Omagh Bombing trial, and comments made by Judge Weir, the UK Forensic Regulator commissioned a review of the science of LTDNA analysis. The subsequent report made specific mention of the fact that there was no available information on the success rate of the use of such DNA techniques and that there seemed to be confusion over what constituted a success. The report went on to state that there was no information on where such trace amounts of DNA were likely to be found, or what factors could influence the likelihood of obtaining a trace DNA profile (Caddy, 2008).

This research considered the outcomes of LCN DNA analysis from 3,552 samples to try to establish where trace amounts of DNA could be found, whether some areas sampled were more successful in generating profiles than others, and the likelihood of the profiles obtained being of use to a criminal investigation. Analysis of results identified areas that were more successful in generating profiles of use to an investigation and highlighted significant differences in results across a variety of items from which samples were taken. DNA samples taken from items associated with communication such as mobile phones were much more likely to produce a profile useful to a criminal investigation than those taken from fixed surfaces within premises.

The results obtained showed that obtaining a DNA profile did not necessarily correlate with the profile being of use to a criminal investigation. This was due

xiii

to the fact that a large number of these profiles were anticipated eliminations from legitimate sources. Items that produced high numbers of profiles but were anticipated eliminations, and therefore of no value to an investigation, came from items associated with skin samples and clothing.

The research went further to identify key factors that affected the profiling rates. Factors that had a positive influence on the ability to obtain a profile included: any area that had been in close proximity to saliva (direct contact was not required); samples that had been recovered from the inside of premises or vehicles and therefore protected from the elements; those that were dry; items that were of a porous nature; and those that had a rough texture. No differences were found between the actual surface materials (plastic, glass, wood, metal), as all showed a propensity to generate profiles. Other factors that were considered but proved to have no effect on the profiling rates included seasonal differences and whether the area targeted for sampling was clearly defined. Items that had had high contact with a victim, were recovered from outside or had been wet, all proved to be less useful to an investigation. A further finding of the research was that swabs that had been recovered and stored frozen appeared to deteriorate in their ability to profile. This was particularly notable if they were submitted later than 5 months after recovery. Items stored in dry conditions did not deteriorate in this way.

Overall the research can be used to provide investigators with the knowledge of what areas of crime scenes are most likely to yield trace DNA material, the key factors that can affect the likelihood of obtaining a profile, and those areas that are more likely to produce profiles useful to criminal investigations.

Chapter 1

Introduction

1.1 Introduction

' although used for a number of years we do not yet have any reliable measure of the success rate of LTDNA analysis and this needs to be corrected'

Caddy 2008

The use of Low Copy Number DNA (LCN DNA) was recently challenged at the trial of Sean Hoey, which included the Omagh bombing that occurred on the 15th August 1998. The judgement that was delivered at the conclusion of the trial, on 20th December 2007, questioned the reliability of LCN DNA with regard to the science and methodology and its ability to produce results of a validated evidential quality (Weir, 2007).

As a result of this judgement the Home Office Forensic Science Regulator ordered a review of LCN DNA and its use within criminal investigation. A temporary withdrawal of the use of LCN DNA was ordered for all current criminal investigations and those, which were going through the judicial process, were reviewed.

Professor Brian Caddy of Strathelyde University was appointed to carry out the review and Dr Graham Taylor and Dr Adrian Linacre assisted him as DNA experts. The review included processes which analyse samples with less than 200 pg of material, referred to as low template DNA (LT DNA) profiling techniques, of which LCN DNA is one. The overall findings of the review were that the science and processes involved in LCN DNA reporting were fully validated and acceptable. The report made many recommendations to improve forensic services and scientific / police knowledge including an education programme to set out the advantages and limitations of low template DNA techniques. Specific comment is made within their executive summary that there is currently no measure of the success rates of low template DNA (Caddy, 2008).

2

Without a measure of the success rates Crime Scene Investigators (CSIs) do not know where to recover trace DNA samples from. This research, which was ongoing at the time of the Caddy report, aims to address this fundamental knowledge gap by identifying areas that can be sampled to obtain low template DNA by establishing the success rates of profiling using the Low Copy Number DNA technique.

A major factor for the CSI is that it is not possible to visualise trace amounts of DNA material at the scene, neither is it possible to identify the source of the cell from such minute amounts of cellular material. Ultimately, for criminal investigations, the success or failure of DNA profiling is dependent on the DNA material submitted for laboratory analysis. If the CSI does not sample the most suitable areas, the analysis will fail due to a lack of material recovered. Even after the most appropriate samples have been obtained it is essential that the scientific techniques utilised in the laboratories that follow recovery are fully recognised and accepted within the judicial arena (Rennison, 2008).

1.2 Crime Scene Investigation Units

Crime Scene Investigation Units and the specialist forensic and technical services that these units provide, which contribute to the forensic investigative element of criminal enquiries, are found worldwide.

A large variation can be found in what these Units are called not only worldwide but also within the UK. The title 'CSI' has been made popular by the media but titles such as 'Scenes of Crime Unit' or 'Forensic Investigation Unit' are not uncommon. The personnel employed within the units often come from a varied background and can include scientists, police officers and police staff with the employing body being a government agency, independent laboratory or police service. Regardless of the terminology used the role essentially remains the same whether a specialist Crime Scene Investigator (CSI), trained Police Officer or Scientist carries it out. In the United Kingdom (UK), CSI Units are mainly found within police organisations. Smaller units can also be found within forensic service providers and military organisations. The primary aim of these departments and their staff is to collect forensic evidence to aid the detection or prevention of criminal acts. The majority of evidence supplements the wider investigation in proving or disproving a person's involvement in a specific criminal activity. This may be by placing a person directly at a crime scene or by showing association by having the tools and methods to carry out the crime. The role is not exclusive to criminal investigation as these units also have a part to play in the identification of persons following mass disasters and in the event of other incidents that may not be criminal in nature but require an investigation to ascertain the facts of what has happened. For instance, before an investigation it may not be known if a large fire is caused by a criminal act and the same can be said of multiple vehicle road traffic collisions. Suicides and special procedure deaths for example, child deaths, drug overdoses, vulnerable persons, deaths in custody etc. are also areas that are covered by CSIs to ensure the facts of what has happened are available to the Coroner or Procurator Fiscal.

There are several forensic methods, based on intelligence databases that can directly implicate a suspect in a crime when there have been no witnesses. These include fingerprints, DNA, facial recognition and footwear pattern analysis. At present only two of these methods are based on invariable factors that can directly provide the name of an offender, suspect or donor of the material being examined, without any other clues or evidence being available; these are fingerprints and DNA. In addition fingerprints and DNA are the only ones currently held on National Databases accessible to all Police Forces and Law enforcement agencies within the UK, for the use in criminal investigations (Nuffield Council on Bioethics, 2007).

Footwear, although it can be useful, is less consistent as wear occurs on shoes progressively and is therefore constantly changing, shoes can also be discarded or worn by different people (Bodziak, 2000). The majority of information relating to footwear mark intelligence is usually held on locally based systems. Facial recognition systems can also provide a potential match to a name,

4

however, facial features can be altered through surgery, weight gain or loss and aging all have an effect (Albert, *et al.*, 2007). These changes are complicated by the many different angles photographs and images can be taken from. Identification using this method remains under development and is unlikely to be conclusive.

A widespread belief is that fingerprints are fixed whilst the foetus develops in the womb (Kucken, 2007). Fingerprints remain consistent throughout life unless there is mutilation of the hands either deliberate, accidental or through disease (warts) or occupation, which can affect the fine ridge detail of fingerprints (Shetty, *et al.*, 2009). DNA is fixed at conception from the combination of the female egg and sperm and remains consistent although it may show some irregularities if a person has undergone bone marrow transplant (Dauber, *et al.*, 2004). Most countries hold databases with fingerprint and DNA information for criminal, identification or immigration purposes. The size and use of these databases vary depending on the different legal systems within each country. The ethics of such a database are often hotly debated with points of view ranging from calls to DNA profile the whole population to a desire to see the databases outlawed as they may infringe civil liberties (Guillen, *et al.*, 2000).

CSIs have a tendency to focus their attention on the recovery of material, which can be searched against intelligence databases and may provide a police investigator with the name of a suspect. Primarily these are usually the fingerprint and DNA databases, and footwear if databases are held locally. Although this is not to the exclusion of other evidence types, which will be recovered, such as broken glass and tool marks, for direct comparison against any samples taken from potential suspects or items they may have been in contact with.

A standard element in CSIs training is the assessment, preservation, recognition and recovery techniques for the majority of forensic evidence types, such as fingerprints, DNA, particulate traces, footwear marks, other impressions, soils, accelerants, and any transferred material. Training is also provided in maintaining the continuity and integrity of material once it is collected, all the

5

way through to the court and during any processes. The assessment of scenes under investigation commences ahead of arrival at any incident with the gathering of intelligence and all information available as to the crime type and modus operandi (Pepper, 2004). On arrival at the scene or incident the CSI will informally interview any witnesses or aggrieved parties to gain more information as to what has happened, before commencing a visual assessment. Preservation techniques may be employed to ensure fragile evidence is maintained prior to recovery and then the CSI will determine the course of action required to maximise the recovery of all the forensic evidence. The process usually follows the order of photographically recording the scene, recovery of trace forensic evidence, which includes DNA, and then lastly fingerprinting the scene. However, a flexible approach needs to be taken when faced with different environmental and circumstantial situations and as the layers of the crime scene are deconstructed the process of recording and recovery is repeated many times. The majority of evidence types can be visualised using a variety of techniques including lighting, fingerprint powders or chemical enhancement whether this be at the scene or later within a laboratory. The examination procedure can take from several minutes to several weeks depending on the complexity and size of the crime being investigated.

On occasion, in addition to the CSIs and photographers, specialists such as entomologists or ballistic experts may be deployed at a scene for the recovery of particular evidence types, such as insects or firearm trace residues (Townley & Ede, 2004).

The use of forensic evidence within the criminal justice system is not new, fingerprints have been used evidentially for over 100 years (Cole, 2001) however, the application of DNA to criminal investigation is relatively new with the first criminal case being that of Colin Pitchfork in 1986 who was convicted of a double murder in Leicestershire (Aronson, 2005). This case undoubtedly assisted in the recognition of DNA as a tool for criminal detection and in the development of the National DNA database (NDNAD), which opened in 1995 (Werrett, 1997), following a change in the law that allowed samples to be taken from suspects for inclusion on the database (Home Office, 1995).

1.3 The National DNA Database (NDNAD)

The UK's National DNA Database is currently populated with DNA from known offenders, arrestees, volunteers and crime scene stains. During the case of S. and Marper 'V' The United Kingdom, the legalities of arrestees and those who are acquitted in court, remaining on the NDNAD, has recently been challenged in the European Courts of Human Rights where it was found to infringe Article 8. It is therefore anticipated that these samples may be removed in the near future (ECHR, 2008). Within the UK DNA profiles that originate from crime scenes or mass disasters can be searched against this database, which may result in a match to a named suspect, volunteer or to another crime scene.

The American CODIS database is the largest in the world (Nuffield Council of Bioethics, 2007), however, the United Kingdom has the largest DNA database per capita (Jobling & Gill, 2004). As of the 31st March 2006, 3.8 million DNA profiles were held on the database mainly belonging to known criminal offenders. On the same date 270 thousand crime scene samples, referred to as scene stains, were also held on the database awaiting a match to a suspect (Home Office, 2006).

The technology to analyse DNA for criminal investigations has been around since the early 1980's prior to the inception of the NDNAD in 1995, but such testing required a large scene stain and a blood sample from an offender to directly compare it against. Blood samples were and still are considered an intimate sample under the Police and Criminal Evidence Act (Home Office, 2005)¹ as such they require a medical practitioner to take the sample and they also require consent from the suspect or donor. With these conditions, the time to arrange doctors and take the sample, cost implications and obtaining consent issues made a National database impractical. As technology advanced it became possible to obtain sufficient DNA to profile from a swab wiped against the inside of the cheek of the mouth and therefore the need for a blood sample was removed. These samples are known as buccal swabs or scrapes, and up to 1995

they were still considered an intimate sample as they invaded a body cavity, therefore still carrying the same time, cost and consent issues of blood samples.

The practicalities of establishing the NDNAD required legislation to be changed with regard to reclassifying certain intimate samples. In 1995 the Criminal Justice and Public Order Act amended the Police and Criminal Evidence Act (1984), to reclassify pulled head hairs and buccal scrapes (mouth swabs) as non-intimate samples, and allowed police officers to take such samples from anyone charged, convicted or reported for a recordable offence under the PACE Section 63a legislation. Furthermore the samples could be taken by force under certain circumstances with the authority of a Police Superintendent (Home Office, 2005)².

The NDNAD was launched on 10th April 1995. Crime scene stains and offender DNA profiles have been added to the database since it started. Initially some restrictions were placed on which crime scene stains and offenders could be added, but as technology improved and the value of the database in supporting crime detections was recognised, these have been extended to cover all crime types. Samples are now loaded onto the database from offenders who have been arrested for a recordable offence (not charged) as well as volunteer samples and samples taken from possessions or homes of people who have gone missing, as well as DNA recovered from all crime scenes. The legislative creep and expansion of the database since its inception has necessitated the governance of the NDNAD to develop to ensure juridico-scientific, administrative and civic accountability, which is the responsibility of the Custodian, who currently sits within the Home Office (Williams & Johnson, 2008).

Profiles from crime scene stains remain on the database until a match is made to a named person. Often a series of matching crime scenes will be generated prior to a match being made to person, in which case the person, once arrested, can be questioned for all offences. Offender DNA profiles and crime scene DNA profiles are compared against each other every day including all historical profiles on the database. This ensures all new crime scenes are checked against all offenders, and all new offenders are checked against old crime stains.

8

DNA profiles that are incomplete may not be good enough to be permanently loaded onto the database but can still be suitable for a one-off speculative search; however, the less detailed the information used to search the more matches that are likely to occur.

1.4 Overview of DNA

The adult human body is composed of approximately 100 000 billion cells and at the centre of most types of cell is a structure called the nucleus. This nucleus contains 46 chromosomes, 23 from the mother and 23 from the father (Hartwell, 2001). These hold our basic genetic information known as DNA (Fig. 1.1).

It is believed to be unique in every individual except monozygotic twins (identical) who inherit the same information from both parents, although sibling nuclear DNA are likely to be similar (Farfan, *et al.*, 2004).

It is often thought that the science surrounding DNA originates in the twentieth century somewhere around the mid fifties; however, its discovery predates this by nearly 100 years. In 1869, a Swiss researcher Friedrich Miescher originally discovered nuclein, later known as DNA, however, the significance of this substance was not realised until the mid 20th century (Dahm, 2005).

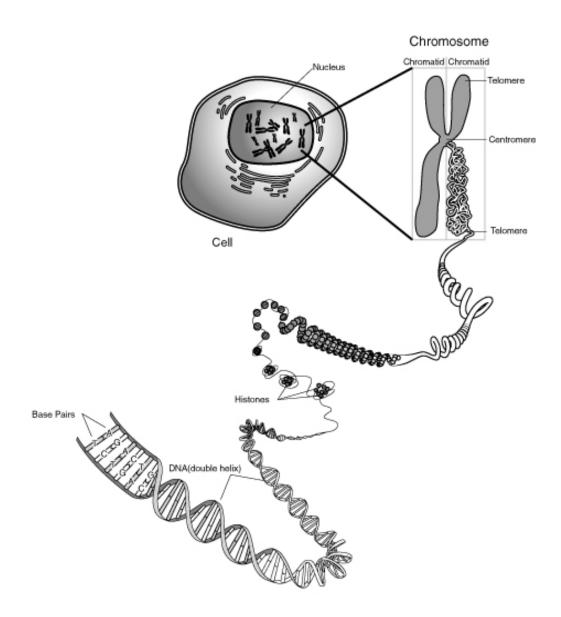


Figure 1.1. Basic cell structure showing the nucleus, chromosome and DNA structure. Source: National Human Genome Research Institute, by artist Darryl Leja at www.accessexcellence.org

In addition to nuclear DNA, mitochondrial DNA (mtDNA) is found in large quantities within the cytoplasm of a cell outside of the nucleus (Fig. 1.2). This mtDNA is inherited from the mother and as there is no contribution from a father it remains the same within the female line of a family, therefore is not unique, although mutation is not uncommon. There is less variability in mtDNA than nuclear and it is not compatible with the National DNA database (Carracedo, *et al.*, 2000).

All further references to DNA, in the text, refer to nuclear DNA unless otherwise stated.

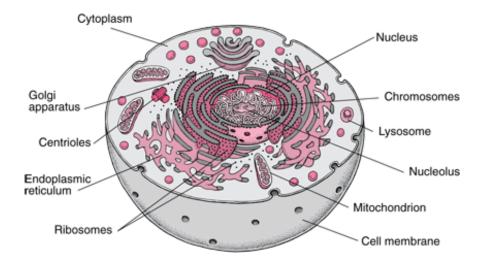


Figure 1.2. Basic cell structure showing the mitochondria outside of the nucleus. Adapted from Source: <u>http://www.merck.com</u>

DNA is a double stranded molecule twisted into a helix. The molecule is built from four nucleotides, which interlink as base pairs (Fig. 1.3). The base pairs are always the same, adenine and thymine, cytosine and guanine. However, the sequence of the pairs creates individuality (Butler, 2005).

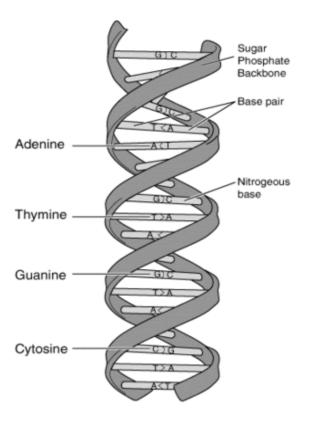


Figure 1.3. DNA Interlinking Base Pairs, adenine & thymine, cytosine & guanine. Source: <u>www.en.wikipedia.org</u>

It was the leap forward in 1953 by Watson & Crick in understanding the structure that laid the foundations for Professor Alec Jeffreys, a research fellow at the Lister Institute at Leicester University 1984, to make one of the breakthroughs that made the National DNA Database possible (Watson & Crick, 1953; Crick, 1993) Jeffreys played a key role in identifying the hyper-variable regions of the DNA and establishing that these were stable and repeatable within individuals and different cell types (Jeffreys, *et al.*, 1985¹). Gill noted that the DNA profiles obtained were individually specific even between family members, which was a significant move away from the blood group testing used at the time to identify offenders (Gill, *et al.*, 1985). Jeffreys recognised the potential of these advances with regard to forensic biology specifically the effect it could have on identifying offenders of rape as sperm cells could be extracted from victim samples with mixed vaginal and sperm cells (Jeffreys, *et al.*, 1985²).

Polymerase chain reaction (PCR) developed by Kary Mullis around 1985 became available for DNA profiling in 1991. This technique allows small sections of DNA to be replicated, thereby increasing the volume of original material to a workable level, for analysis. This technique splits the double strand of DNA in to separate strands (denature) for which the complementary base pairs can be attached (as these always remain the same) thereby duplicating the original sample. It is likened to photocopying and is often referred to as DNA amplification (Butler, 2005).

However, PCR amplification is not always successful as once a cell leaves the living organism its dies and the DNA starts to degrade. The rate of degradation is dependant on numerous factors and environmental circumstances such as insect and bacteria attacks (Poinar, 2003), UV light (Hori, *et al.*, 2007) and heat (Dobberstein, *et al.*, 2008). These cause the breakdown of the sugar bonds via hydrolysis and oxidation. Other PCR inhibitors include chemical and biological contaminants within the original sample such as detergents and salts. Methods are available to try to overcome inhibition but may not always be successful (Wilson, 1997).

Prior to any analysis the DNA molecules have to be extracted from the cellular material that it is contained within. There are several different extraction methods available the common ones being organic (often referred to as phenol-chloroform), Chelex, silica based and FTA paper. Each has its advantages and disadvantages, of time, complexity and resources.

Bright and Petricevic (2004) found that organic extraction methods gave a higher yield of DNA than Chelex which supports earlier research by Hoff-Olsen, *et al.*, (1999) who compared five different methods of extraction concluding that phenol-chloroform and silica gave the best results. A disadvantage of this technique is the multiple stages in which contamination can occur.

A more recent method of magnetic bead extraction may reduce contamination as it is semi automated but as yet it has not been evaluated for samples with low levels of DNA and problems extracting mixed samples have already been recognised (Haak, *et al.*, 2008).

Regardless of the method of choice, DNA extraction first requires the cellular material and DNA molecules to be separated. The cells form a protective barrier around the DNA and its removal is sometimes referred to as cell digestion.

In phenol-chloroform extraction, equal volumes of phenol-chloroform are added to an aqueous DNA sample, which is then centrifuged to separate out the unwanted material. The DNA is retained in the aqueous layer and can be removed into a clean tube. This process is often repeated without adding more Phenol-Chloroform to remove residual phenol from the sample. Following this the DNA is precipitated, usually in ethanol, to concentrate and purify the sample removing any salts remaining (Powell & Gannon, 2002; Butler, 2005).

Chelex extraction is usually considered a faster and cheaper method of extraction but it has limitations in any subsequent analysis where it is only suitable for PCR techniques as it extracts denatured DNA strands. This makes it more appropriate for degraded samples. In this extraction method the sample is added to the Chelex and boiled to separate out the DNA molecule (Butler, 2005).

Phenol-chloroform and Chelex were the extraction methods of choice at the laboratory used to process samples within this research.

In the application to criminal investigation, initially PCR only copied one area of the DNA, however, further developments allowed several areas to be copied simultaneously. The areas copied are Short Tandem Repeats (STRs), which are hyper-variable areas of short sequences of DNA that are repeated. The number of repeated core sequences is what forms the individuality of the profile. In 1994 when STR was introduced, it analysed 4 areas of DNA and gave a discriminating power of 1:40,000 (Lygo, *et al*, 1994).

The nomenclature for the STR loci is directly related to the gene and chromosome where it is found and given in an alphanumeric format which is usually abbreviated i.e., D3S1358 is D3, HUMVWF31 is vWA (Butler, 2005). When profiling each STR loci is represented by two peaks, which can be seen in the electropherogram at Fig. 1.4, one inherited from each parent, heterozygote, unless the same STR is inherited from both parents, when only one peak will be seen, homozygote.

In 1995 technological advances introduced the Second Generation Multiplex (SGM) which analysed 6 areas of DNA and gave a discriminating power of 1:50 million. This test also included a sex marker (Amelogenin) thereby determining if the DNA is male or female; potentially a useful piece of information if the gender of the source was not known (Sparkes, *et al.*, 1996).

Since 1999 DNA has been analysed using SGMplus[™] (FSS, 2003). This is an extension of SGM and analyses 4 additional loci, making a total of 10 plus the Amelogenin (Fig. 1.4), raising the discriminating power to 1:1 billion (Foreman & Evett, 2001). A further advantage of SGMplus[™] is that two of the additional loci, D3S1358 and D19S433, are more sensitive which increases the ability to profile degraded samples (Cotton, *et al.*, 2000).

The graphical representation of the DNA profile, the eletropherogram, as shown in figure 1.4, is converted into a numerical format to enable the DNA profile to be loaded and searched on the NDNAD (Table 1.1). The two peaks shown on Fig. 1.4 and represented at TH01 in Table 1.1, show one peak of 7 repeats of base pairs, and the other peak shows 9 repeats of base pairs and 3 extra bases (if there had been 4 bases that would have made 10 repeats).

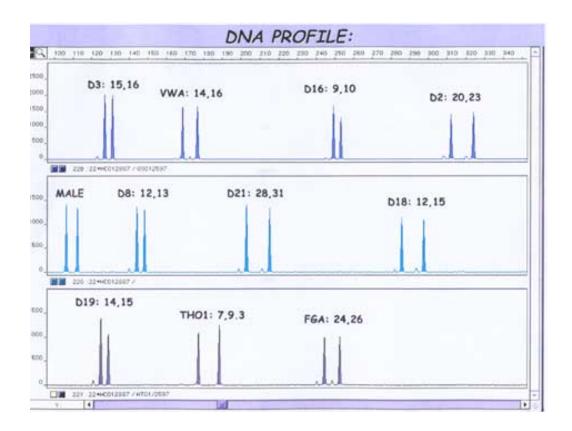


Figure 1.4. Electropherogram showing a full SGMplus DNA profile at 10 STR loci. Each locus having 2 peaks (one from each parent) totalling 20 and the additional sex marker.

www.forensic.gov.uk

| Loci | D3 | vWA | D16 | D2 | D8 |
|------------|------------|-------|-------|-------|-------|
| Alleles | 15,16 | 14,16 | 9,10 | 20,23 | 12,13 |
| Loci | D21 | D18 | D19 | Th01 | FGA |
| Alleles | 28,31 | 12,15 | 14,15 | 7,9.3 | 24,26 |
| Loci | Amelogenin | | | | |
| Sex marker | X,Y | | | | |

Table 1.1 – Example of a full male DNA profile in numerical form, as it would be loaded onto the NDNAD

The Society of Forensic Haemogenetics recommends using allelic ladders. There are an expected number of repeat base pairs at each loci which should fall within set parameters depending on the laboratory techniques used (NIST, 2009). Commercial STR kits include allele ladders that can be run with the same PCR primers to provide a quality assured system and unknown samples can be assigned the right DNA profile (Butler, 2005). An example of allelic ladders detailing the loci and chromosome location can be found in Appendix 1.

1.5 LCN DNA

For criminal investigation purposes the standard SGMplus[™] process goes through 28 PCR cycles and is considered appropriate where there is sufficient nucleated cellular material within a sample. In the majority of cases the DNA bearing material can be seen or visualised using a chemical test, as is the case with blood deposits at a scene or amylase testing on items believed to be contaminated with saliva. However, where the DNA material cannot be seen or is in extremely small amounts, referred to as Low Template DNA, typically less than 100pg, it is more appropriate to increase the PCR cycles or use enhancement methods. The Low Copy Number technique increases the cycles, usually to 34 as this was considered to be the optimum number, dramatically boosting the amount of material that a scientist has available to DNA profile as each cycle doubles the copies of the DNA (Gill, *et al.*, 2000). However, increasing the cycles to identify such small amounts of cellular material also increases the background contamination (Whitaker, *et al.*, 2001).

DNA profiles may not always be complete and it is not unusual to get mixed or partial profiles (See Chapter 5). With such small amounts of material the validity of any results are confirmed by repeating the analysis on the same DNA extract due to the phenomenon of allele drop in (potential contamination), allele drop out (fails to repeat) and stutters (a smaller repeat of the true allele profile peak). Only then is it considered to be a true representation of the DNA present in a sample (Butler, 2005).

17

Experiments carried out by Van Oorschot & Jones (1997), Van Oorschot, *et al.*, (2003) and Wickensheiser (2002), show DNA can be left behind from fingerprint residues by merely touching an item. This requires a different approach as there are very small amounts of cellular material deposited which cannot be seen. LCN DNA analysis using 34 PCR cycles is a method that can be considered.

It is logical to assume that the deposition of DNA from touching equally applies to offenders at crime scenes who may have handled objects, weapons or touched surfaces. This raises the possibility of obtaining an offender's DNA profile from every crime scene as DNA could be left from touch, sneezing, coughing or even talking. The wearing of gloves would prevent the deposition of fingerprints but might still deposit DNA material as they could have been handled on the outside layer, during dressing, which may then be transferred onto objects. The potential ease of transfer also makes it difficult for an offender to prevent DNA deposition at a crime scene and, thereby, it also raises the questions of contamination, transfer and persistence of DNA.

Further research is underway with regard to identifying the origin of the cell type from recoveries of trace DNA, which may be evidentially useful (French, *et al.*, 2006; Home Office, 2004). However, this is likely to be a laboratory based solution and will not assist a CSI in the initial identification of areas that will provide good recovery or profiling rates. Chapter 2

Review of Current Literature and Publications

2.1 LCN DNA Technique

Much of the research and published material available involves proving the technique of acquiring a DNA profile from very small amounts of non-visible cellular material or single cells. In a laboratory setting Findlay, *et al.*, (1997), profiled individual buccal cells, obtaining a DNA profile from 6 STR markers in 50% of the results, and Schulz & Reichert (2000) repeatedly obtained profiles from the residue left behind in fingerprints. The recent research by Kita, *et al.*, (2008) supports the premise that DNA can be obtained from skin cells of the cornified layer, i.e. dead sloughed skin which is constantly being shed. Such papers demonstrate the ability to DNA profile trace material within controlled settings and offer the prospect of being able to utilise such techniques for criminal investigation in circumstances where it may not have been considered before.

There is also a significant amount of literature regarding the interpretation and reporting of results from such small amounts of DNA material, Gill, *et al.*, (2000), Evett, *et al.*, (2000), Curran, *et al.*, (2005), Anjos, *et al.*, (2006), to name a few. These papers identified the phenomenon of allele stutter, allele drop out and failure to repeat the results which demonstrates the complexities of evaluating trace DNA samples and results. Overall they provide a good foundation to understand the difficulties of interpretation but add little or no value to the crime scene investigator in determining which surfaces or what items are likely to be successful.

Although, of course, it is not disputed that there is a need to establish the technique works, establish protocols for the finer points of interpretation and reporting and to ensure the technique is valid to prevent a miscarriage of justice. It remains that there is little being done with regard to the application of LCN DNA within the criminal investigation arena, at its originating point, the crime scene, although it is apparent that this is one of the intended uses of this technology.

Ultimately the success or failure of this technique, in criminal investigation, relies on suitable material being recovered and presented to the laboratory. Only then, are the factors that can affect the reliability of the interpretation of the results relevant.

2.2 The Shedder Factor

As demonstrated by Schulz & Reichert (2000), it is known that a person who touches an object may deposit some of his or her DNA on that item, however it has been established by Lowe, *et al.*, (2002), that there are differences between individuals in the amount of DNA that they leave behind even under controlled circumstances.

This is generally known as the 'shedder factor' with persons being good or poor shedders, when deposited DNA is measured following timed and controlled handling of pre cleaned objects. A good shedder may deposit a full DNA profile immediately after hand washing whereas it may be six hours or more before a poor shedder leaves sufficient material behind to yield a DNA profile. The research suggests the majority of people can deposit a DNA profile 15 minutes after hand washing.

Kobilinsky, *et al.*, (2004), who are in agreement with Lowe, *et al.*, (2002), stated that the reasons for this variable shedding factor are not fully understood. The reasons for the difference could include such things as perspiration, surface area and material, activity and medical conditions. This is not an unfamiliar variable for CSIs as similar factors also affect the deposition of fingerprints. Not finding fingerprints or DNA does not positively exclude a person from having handled or from having been present at a particular place or time, only that the DNA and fingerprints were either not deposited or recovered.

The shedder factor of a person has little value for a CSI, as this is an unknown variable that cannot be measured at the time of recovering a sample. Initial thoughts are that it would be preferred if all offenders were good shedders but

this would bring its own drawbacks as DNA would be everywhere resulting in complex mixtures that could not be separated. More recent research by Farmen, *et al.*, (2008) appears to repeat much of the earlier research in support of the ability of people to shed DNA and transfer it to objects in a secondary manner. However, the research by Phipps & Petricevic (2007) states that good shedders may be significantly rarer than previously estimated; in fact the paper challenges their existence and the validity of this being a genuine variable between people. The shedder factor is probably more relevant at the interpretation stage and to the criminal justice system in understanding any matches that may be generated from scene DNA profiles, to ensure that defence arguments can be fully explored.

2.3 Contamination and Transfer of DNA

With extremely sensitive profiling techniques the possibility of contamination is greatly increased. It is accepted that the background levels of DNA on any given item will remain unknown, however, inadvertent contamination after the event is unacceptable. This can even arise from personnel who legitimately attend crime scenes if precautions are not taken and the crime scene controlled.

Rutty, *et al.*, (2002) performed a series of experiments that demonstrated how easily contamination of crime scenes could occur by the personnel who legitimately attended them. The contamination that was observed occurred through talking, coughing and manipulation of protective clothing such as facemasks. This is a valuable piece of research demonstrating the ease with which DNA can be deposited unintentionally. It also highlights the importance of the Elimination DNA Database and the requirement for Police Officers and staff who attend crime scenes to provide an elimination sample (Appendix 2. Elimination DNA Databases). In essence, as a minimum, all personnel should wear disposable gloves, coveralls and facemasks to minimise DNA deposition. It is also recommended that hoods or hairnets are used. CSIs undergo training to prevent accidental contamination and further guidance is published by the FSS in the Scenes of Crime Handbook (FSS, 2004).

22

It has also been established by research that equipment used during the course of a scene examination can be a source of accidental contamination when taken into a scene and used by investigators. This could include camera equipment, packaging material and even pens. Proff, *et al.*, (2006) clearly demonstrated that a variety of fingerprint powder brushes were heavily contaminated with DNA and that this was transferable between scenes. Although this is a possibility it would be hoped that any LCN DNA sampling should have occurred prior to any fingerprint examination being carried out. As a precaution it is preferable that all equipment taken into a scene should be disposable or pre cleaned with a Chlorhexidine solution or wipe (FSS, 2004).

All kits and swabs used in the recovery of any DNA sample should be from a reputable source that ensures the manufacturing process is free from detectable levels of DNA. Even with these measures, as a basic good practice, control materials should be retained along with any samples taken.

With the variations in a person's shedding ability and the potential for accidental contamination, also comes the possibility of DNA transfer. This can be tertiary transfer (object to person to object) or secondary transfer (person to person to object). The results of the research that tested tertiary and secondary transfer in laboratory settings have varied. Van Oorschot & Jones (1997) suggested that DNA profiles are more likely to be of mixed origin, however, Lowe, *et al.*, (2002) determined that the result was more likely to be dependent on the shedding capacity of the donor, whereas Ladd, *et al.*, (1999), found little evidence of any transfer. A more recent study by Poy and Oorschot (2006) demonstrated that the possibility of contamination and / or transfer of DNA material extends beyond the scene and into the laboratory environment with precautions being considered and required at every stage to prevent its occurrence. These differing results would suggest it is a possibility that should be considered by anyone using LCN DNA in an investigatory context and like the shedder factor should be considered by the judicial system.

There are numerous other published research papers that demonstrate the need for caution due to the potential of contamination and / or transfer issues such as

the research done by Petricevic, *et al.*, (2006) who sought to establish if epidermal skin cells could be recovered from bedding. The results from this paper clearly show cross contamination between participants in the study, either through direct contact or other means. The paper raises more questions than it answers, nevertheless, although an unintended outcome of the research, it demonstrates the ease with which transfer and contamination can occur even in controlled circumstances.

All of the above research provides the CSI with the knowledge that it is possible to obtain DNA profiles from minute sources of cells and that consideration should be given to contamination issues, but it provides little knowledge with regard to crime scene location and recovery and what the probabilities are for achieving a successful outcome. Research based on laboratory simulations and reports on individual case studies may provide slightly more information for CSIs with regard to crime scene examination.

2.4 Laboratory Simulation of Crimes for LCN DNA

A number of studies have been carried out to simulate criminal activity and to test the viability of DNA transfer that would be useful to criminal investigation under certain circumstances. Rutty (2002) carried out tests simulating manual strangulation between two work colleagues. Partial DNA profiles were recovered from the role play victim and the offender for up to 10 days after the simulation occurred. However, Rutty cast doubts on the validity of his own research citing possible secondary or tertiary transfer between the parties and a recurring third party DNA profile of unknown origin. Also a review carried out by Lowe (2002) challenges the design of the experiments citing several fundamental errors that would affect the results. Both Rutty's and Lowe's doubts devalue the results of the research although it may demonstrate the possibilities of obtaining a DNA profile in such circumstances.

Further laboratory simulation is detailed by Lowe (2002), with experiments to determine the effect that the presence of illicit drugs may have on profiling rates

of drug wraps and packaging of varying types, including magazine paper wraps, snap seal bags and knotted bags. The results varied between the different types of wrap but DNA profiles were obtained in all cases; the snap seal bags in these cases being more successful than the knotted type. This was attributed to the difficulties in handling and undoing the knot in order to recover any DNA material. In all cases the quantity of DNA recovered diminished as consecutive simulated drugs packages were wrapped. The effect of drugs on the packaging was not addressed only the ability to DNA profile the resultant wrap. Again this is a useful piece of research in that it demonstrates the possibility of obtaining a useful DNA profile but it lacks a realistic context with only small numbers of wraps being analysed and different numbers for each wrap type. No direct comparison is done between the different wraps, neither is it specified if the same four individuals simulated each wrap type, which, considering it was Lowe who reported the differences in shedding ability seems to show a lack of consistency in research methods. A more rigorously designed project could have given some direction to investigators on which type of wrap is more likely to produce a useful DNA profile.

In the same paper, Lowe (2002) also reviews a piece of laboratory research, which considered the ability to recover an assailants DNA profile from a t-shirt and pair of knickers that the assailant had touched but not worn. The laboratory simulations required the t-shirts to be grabbed on the shoulder area for a period of 30 seconds, and the knickers to be rapidly pulled down from a standing 'simulated' victim; thus target areas for sampling being well defined and identifiable. Full DNA profiles were obtained from the t-shirt and a very limited DNA profile from the knickers. In reality 30 seconds is an extended period of contact and would be more likely found in trying to remove knickers than the grabbing of clothing in one place during an attack. A detailed understanding of the crimes any research is attempting to simulate is required to ensure any results are valid.

2.5 LCN DNA Used Within Criminal Investigations

There are very few published studies available on the application of LCN DNA to actual criminal offences and those that have been published are often detailing a specific case study and item that was analysed. The knowledge gained in reading these works, although interesting, does not allow the information to be readily transferred in a meaningful way to a wider crime scene application.

One of the few wider studies that has been published is from Switzerland, where Castella, *et al.*, (2004) analysed 563 standard DNA and LCN DNA casework samples categorised into blood, semen, saliva, hairs, epidermal on clothes and epidermal swabs. The parameters for LCN DNA were slightly higher than in the UK with DNA concentrations of less than 200 pg being subjected to LCN techniques (100 pg in UK). Of the 563 samples 337 fell into the <200 pg range, of these 119 DNA profiled (35%) but no figures are given for each of the sample categories so this data cannot be compared with this research and provides no information as to what samples may or may not be successful.

A fact sheet available through the Forensic Science Service (FSS), which is one of the largest supplies of forensic services to Police Forces in England and Wales, gives some brief details on a number of cases where success has been achieved with LCN DNA profiling from old microscopy slides, a knife handle and a case with a very low sperm count. Most of these cases are historic and predate LCN DNA technology, the samples being recovered from exhibits that had been retained in unsolved cases, or from countries that had not developed DNA technology as extensively as the UK (FSS, 2005). With the exception of the knife handle, it gives little indication on where DNA profiles may best be obtained from, nor the likely success rates.

In Italy, Pizzamiglio, *et al.*, (2004¹) provides details of two linked robberies where a pillowcase and pair of glasses were successfully DNA profiled using LCN DNA techniques. Both items had been taken to the scene by the offender and abandoned after the offence. In this case it should be noted that the

pillowcase tested positive for saliva and therefore, is likely to have been suitable for standard SGMplus[™] profiling, however, both items were subjected to LCN DNA testing. These cases also highlighted the value of a searchable DNA database in linking the two crimes together, even before a suspect was identified.

A further case described by Pizzamiglio, *et al.*, (2004²) is of a murder that involves DNA recovered from a steering wheel, handbrake and gear lever. Successful DNA profiles were gained from the steering wheel and gear lever although no results are given for the hand brake so it is presumed that no DNA profile was obtained from this area. In this case it was indicated from witness testimony and CCTV that the offender drove the victim's car for a short period. It is unfortunate that wider areas of the vehicle weren't sampled for comparison with results from this research. Overall, Pizzamiglio, *et al.*, place significant importance on the immediate availability and preservation of the vehicle for examination and a strategy for dealing with LCN DNA within an investigation.

Also in Italy, during an attempted strangulation, a steel cable was placed around a victim's neck and although the contact was limited, Saravo, *et al.*, (2003) suggested useful results were obtained. The cable in this case was recovered from the offenders home and not left in the victim location. Little detail is provided on how the offender was identified enabling the recovery of the cable, or the victim–offender relationship. This crime prompted further experimentation to prove that DNA transfer was possible with a limited contact of 30 seconds for this material type. The Saravo, *et al.*, paper falls more into a laboratory simulation category and simply confirms what is already known; that small quantities of DNA can be transferred onto surfaces from touch.

An additional case is later reported by Staiti, *et al.*, (2008) on the results from a nylon rope ligature tied around a murder victim's arms and legs. In this case a male DNA profile was obtained from the knotted portions of the rope that ultimately assisted with the successful prosecution of an offender. Care was taken during the sampling of the rope to avoid areas that had come into direct contact with the victim.

Another case that occurred in Italy is detailed by Barbaro, *et al.*, (2006) where DNA profiles were successfully gained from marker pens and a comb. The detail is scant but it would appear that these were known to be personal possessions of the 'suspect'. The extracted DNA was less than 100 pg and the number of cycles was increased to 35, one more than LCN DNA profiling within the UK. Mixed and partial DNA profiles were found on the material from the pens and 'cells' on the comb. It does not specify whether the DNA profile on the comb was full, partial or mixed, only that it matched the scene stain. It is also not stated to what degree it matched the scene stain. However, it does further demonstrate the ability to acquire a useful DNA profile from a touched item. An explanation is not given as to why LCN DNA profiling was used on the suspects' personal possessions as opposed to obtaining a routine SGMplusTM DNA sample from him and compared directly with the scene stain.

More detail is provided in a case from Sweden, which was solved using LCN DNA recovered from a victim's shirt following a robbery. The offender had grabbed the victim on the shoulder and proceeded to push her roughly through a room. Immediately after the attack the victim removed her shirt, secured it in a locker from which it was recovered by the police officer attending the scene and sealed in a bag (Schold, et al., 2006). In this case adhesive tape lifts were used to recover the DNA and initially the standard 28 cycles were carried out. This only generated a weak DNA profile so the cycles were then increased to 31, which resulted in a mixed DNA profile (see Chapter 5 for explanation of mixed profiles). The minor element of the profile belonged to the victim and the major element was sufficient to search on the Swedish National Database. The case has several significant elements; the victim was handled in a rough manner for an extended period of time, a specific target area on the shirt was identified by the victim and the item was immediately preserved for examination. The emphasis on the immediate availability and preservation of the item for examination reinforces the similar findings in the case reported by Pizzamiglio, et al,. (2004) ²; it also supports the results found in the laboratory simulations that recovered DNA from T-shirts, Lowe (2002).

More useful information, in that it covers a larger number of cases and could be transferable to other cases, is available on success rates for LCN DNA profiling, from the FSS with regard to investigations involving firearms (Wells & Taylor, 2002). The Wells and Taylor (2002) report follows a joint firearms project between Greater Manchester Police and the FSS, where the LCN DNA results from 31 firearms related crime cases were analysed. The results show a large variation in the success rates of obtaining profiles from the different areas sampled on firearms and ammunition. Although the research only covered a small number of cases it did demonstrate the ability to obtain a DNA profile from fired cartridge cases and indicated that samples from magazines and triggers could be more successful than other areas of a weapon. This type of research is particularly valuable to investigators as it allows targeting of specific areas for sampling and gave some indication of the likelihood of obtaining a DNA profile. Unfortunately, this work has not been published within the public domain and remains with the FSS and Greater Manchester Police who received a copy of the report.

The ability of DNA to survive the firing event of a weapon where high temperatures are achieved is also replicated in the research detailed by Lowe (2002) around explosive devices. Post blast survivability of DNA was achieved in five devices that were tested although each of these was a different type. The research indicated that devices with a small explosive charge were more successful than those with a larger charge. No indication was given on the amount of DNA recovered or whether it would be compatible with searching on the NDNAD. The overall conclusion of the research being that DNA recovery from devices 'post blast' was 'limited'. Due to the serious nature of any such criminal offence, consideration should still be given to analysing any recovered components for LCN DNA techniques, however, the term 'limited' should be born in mind as it gives little indication as to the results that were achieved or could be expected in the future.

Both the Wells & Taylor (2002) and Lowe (2002) reports support the idea that there are several factors which influence the success rates of obtaining a LCN DNA profile and that some areas will have a much higher chance of success than

others. In effect the profiling success rates are not random but are affected by numerous factors. However, both of these documents remain outside of the public domain and have very limited circulation.

A potentially useful piece of Home Office funded research, known as the Pathfinder Project, was undertaken as a joint endeavour between Lancashire Constabulary, Greater Manchester Police (GMP) and the FSS. The research was complex and crossed multiple agencies, including Police, Forensic Service providers and the Crown Prosecution Service (CPS). The Home Office commissioned Morgan Harris and Burrows consultants to evaluate the research. One element of the research detailed the success rates of LCN DNA when the technique was applied to samples recovered from burglary and vehicle crime. Overall 15% of the swabs taken generated a LCN DNA profile, and 9% resulted in a match. Some items were particularly successful, when swabbed, in generating a LCN DNA profile; these included bottles at 64%, keys at 27% and screwdrivers 23%. Items less successful included ignition cowlings 8%, car radios 0% and torches 10%. No information was provided on how many of these went on to generate a match or how many were legitimately eliminated. A final evaluation report was produced for the Home Office and the parties who participated in the project, but the document did not get a wider publication (Morgan Harris Burrows, 2002). The value and results of the LCN DNA research is lost within a complex and multifaceted piece of work that has not reached the discipline where it could add intrinsic value. Like previously detailed research it indicates there are differences in profiling rates but fails to put it into a context that CSIs or investigators can use.

2.6 Literature and Research Gaps

The dearth of information available to the Police Service and other agencies means that investigators often rely on media sensationalist publications (Dixon, 2000; Fogg,1999) and anecdotal stories. Police Officers also have access to marketing material, one of which is a bulletin produced by the FSS which gives some detail on the application of LCN DNA to volume crime and makes some

suggestions on where CSIs should target their recoveries (FSS, 2006). The circulation of this bulletin varies between Police Forces and agencies depending on who their forensic supplier is. The bulletin gives impressive success rates for profiling and subsequent match rates on a small number of items. However, further research into these statistics reveal a significantly less rigorous approach to the data than that applied to this research, as detailed in Chapter 5, and is misleading from an investigators perspective, it should therefore be treated with the utmost caution.

As discussed in this chapter there are multiple studies within laboratory or preplanned settings that have clearly demonstrated the transfer of DNA in very small quantities from a person to an object; these small quantities being sufficient to generate a LCN DNA profile. Criminal investigations do not have the luxury of pre-prepared surfaces to examine therefore background material could significantly interfere with the value of applying the science in real situations. What is less clear from the current research is the number of failures and whether the DNA profiles obtained would be useful to an investigation.

In the individual case studies, only positive results have been published, no detail is provided of other LCN DNA submissions that may have failed to profile, neither can it be assumed that success is likely in the future. It is also noted that in the majority of cases published, the offender is already known or suspected from other intelligence. It should also be noted that the case studies reported all originate from outside of the UK. The UK's contribution appears to concentrate more on laboratory analysis and reporting, or the literature remains outside of the public domain.

Overall the focus is around the laboratory and laboratory processes which fail to address the issues of initially locating and recovering LCN DNA from crime scenes. The current situation leaves investigators with maximum possibilities but limited knowledge of probabilities. Best guesses are made where to take samples from and which to submit for analysis. These guesses are subjective or based on a limited previous experience and not on any supporting scientific research.

Chapter 3

Filling the Knowledge Gap

3.1 Why the research is needed

Following a thematic inspection by Her Majesty's Inspectorate of Constabulary (HMIC) in 2000, a report called *'Under the Microscope'* was published, and followed up 2 years later with *'Under the Microscope Refocused'*. These reports criticised the Police Service for failing to implement technological advances within the forensic science arena, particularly with regard to achieving detections for volume crime (HMIC, 2000; HMIC, 2002).

In defence of the Police Service it is difficult to take up new technologies such as LCN DNA, when it has been demonstrated there is little research available to show how and when it can be applied to criminal investigation in an efficient and effective way. Raymond, *et al.*, (2004) also recognised a trend for 'underutilization' with regard to trace DNA and attributed this to a lack of knowledge and understanding as to how it could be used.

As previously stated, it is not possible to visualise touch DNA at the scene and therefore, areas that could be considered for sampling would be of a speculative nature. This leaves the CSI with the problem of identifying the most suitable areas to sample with, at this stage, no idea of the likely success rates or the potential value to the investigation. This is particularly relevant due to the high analysis and interpretation costs; along with the time it takes the CSI to carry out the swabbing and recovery processes. Police forces like all public bodies are duty bound to ensure they are efficient and cost effective.

ACPO (2005), states:-

'in view of the complexities and cost implications of using LCN DNA, each submission needs to be considered on a case by case basis and should be discussed with the force Scientific Support Unit'.

A vehicle used as transport in the commission of a crime has many areas that could be sampled for LCN DNA; steering wheel, rear view mirror, handbrake, gear stick, indicator controls, lights, radio, window winders, inside and outside door handles, petrol cap and cover, seat adjusters to name a few. On average there are 30 potential areas that can be swabbed on a standard motorcar. To carry out the LCN DNA swabbing of such a vehicle and the associated documentation required can easily take a full day without any additional forensic recoveries. Associated with this is the cost of submitting all the samples for analysis making it prohibitively expensive for investigators to realistically consider as an option. A vehicle stolen and used for transport in a murder is just as likely to yield (or not) a DNA profile, as one stolen and used for transport in a burglary. However, due to the lack of research available on the likelihood of any samples securing a DNA profile, the technique is not usually applied to volume crime.

If target areas can be defined, along with the probability of successfully profiling a sample, the time and financial burden can be reduced significantly. In effect quality not quantity is required, using recovery and subsequent LCN DNA techniques where they work best and not just speculatively.

Further to this is the additional conflict between whether to attempt LCN DNA sampling of an item or examine it for fingerprints. Best practice would be for the swabbing technique to be carried out prior to any fingerprint examination. A danger of this could be that it would wipe any fingerprint detail off the item. The risk to fingerprints and any other trace evidence should be considered on a case by case basis, where necessary maintaining preservation techniques, having joint examinations for DNA and fingerprints or carrying out the fingerprint examination first which may compromise the DNA.

The potential for carrying out fingerprint examinations prior to LCN DNA swabbing is supported by a number of studies which demonstrate LCN DNA profiles can be obtained from the residue of fingerprints. This has proved successful, in experimental laboratory work, even after chemical treatments such as cyanoacrylate and vacuum metal deposition (Wickenheiser, 2002), and the application of fingerprint powders (Van Hoofstat, *et al.*, 1999; Schulz, *et al.*, 2002). Additional research by Lowe, *et al.*, (2003) stated the results of any DNA

profiling may be affected by the time between the fingerprint mark enhancement and DNA recovery and processing. It should also be noted that some researchers consider that contamination can occur between scenes, as DNA may be carried on fingerprint brushes (Sutherland, *et al.*, 2003; Wickenheiser, 2002; Proff, *et al.*, 2006). This process also limits subsequent DNA sampling to areas where fingerprint residues have been highlighted, as it is the residual ridge detail or smudges that are scraped, which could miss other DNA contaminated locations.

Then again if adequate research was available such difficult decisions and compromises may not have to be made, if it was established that a particular item rarely generated a LCN DNA profile.

Consideration has been given as to whether the results for standard SGMplus[™] DNA profiling give any direction as to the likely success rates or target areas for LCN DNA recovery. Standard SGMplus[™] DNA results are currently categorised by cell type such as blood, saliva, semen, and give no indication of where these are more likely to be deposited, as they require a body fluid spillage. Touch DNA is categorised as cellular material but gives no indication of the location it was found.

This research seeked to establish the best opportunities for maximising the recovery of LCN DNA from a crime scene, allowing a more scientific approach to crime scene investigation and to provide information to CSIs on what, how and where to sample. In addition police investigators need this information to facilitate submission priorities of samples recovered based on success factors, in effect the difference between what is possible and what is a probable outcome.

3.2 Research for Crime Scene Investigation

At present there is a significant knowledge gap for CSIs in knowing what and where to recover samples from for LCN DNA. Successfully DNA profiling any sample is directly related to the quality of the sample obtained at the scene. If the right samples are not taken the DNA profiling will fail regardless of how good the laboratory techniques are.

Therefore, a fundamental aspect of this research is that it was directly applied to the crime scene investigation process to assess the viability of the technique in live situations without predetermined experimental conditions. As such, the target areas had not been pre-cleaned and the length of contact an offender had had with an article was not known.

3.3 Detections

A strategic objective, set by the Home Office for the Police Service, was to increase DNA recovery at crime scenes, which would lead to detections (Home Office, 2003). LCN DNA profiling is a legitimate way of increasing DNA recovery if it can be applied effectively to volume crime scenes.

The research initially looks at the likelihood of obtaining a LCN DNA profile from a variety of recovered samples. Once this is established it then goes on to look at the percentage of those that provide a match to a suspect and those that are legitimately eliminated.

Criminal detections and convictions were not considered during this research as these were dependent on a number of other factors that may not be relevant to the research in question. These included the CPS determining not to proceed with a case, or the police being unable to locate the suspect. Although detections were not being reviewed, research by Burrows and Tarling (2004) clearly showed the significant effect the recovery of DNA has on securing detections and subsequent convictions in court.

Figures quoted by ACPO (2005) and the Home Office (2004), although they vary slightly, show detections in all crime increasing from 24% to 38% when DNA is recovered. This is significantly increased in domestic burglary where detections

rise from 15% to 48% with a DNA recovery; each of these detections preventing a further 7.4 crimes being committed.

3.4 Research Aims

This research aims:-

- a) To identify the differences in LCN DNA profiling success rates and what factors affect the profiling rates.
- b) To provide knowledge suitable to be supplied to crime scene examiners enabling them to determine where and how to collect material suitable for LCN DNA profiling.

Furthermore to ensure there is clarity in the results, for the purposes of this research, what is meant by a 'useful DNA profile' and 'match' will clearly be defined with regard to criminal investigation.

3.5 Research Stages

The research is split into two distinct stages.

<u>Phase 1</u>

The initial research:-

- Defines what a 'useful DNA profile' and 'match' is, in the context of a criminal investigation.
- Derives a mechanism for classifying samples that can be applied to crime scenes by crime scene investigators.
- Established differences in LCN DNA profiling rates from different sampling categories.

• Analysed the DNA profiling success rates, with specific regard to assisting CSIs in scene examination and investigators in prioritising submissions.

Phase 2

Having established there were significant differences in profiling success rates from the DNA material recovered and utilising the mechanism for classifying samples; the second stage of the research explored:-

- Why there were differences in the LCN DNA profiling success rates.
- The common factors that corresponded to the differences in DNA profiling rates.
- Those factors that were more influential than others.

Chapter 4

Process and Methodology

4.1 Processes and Methodology

Prior to the research commencing and throughout the research process, techniques were reviewed and reinforced that may have a bearing on the results. It was particularly important to ensure new staff were aware of the processes and these formed part of the staff induction process.

4.2 Reinforced Anti Contamination Measures.

The recovery of LCN DNA was carried out by CSIs using appropriate anti contamination measures. Full protective clothing was used during recovery of LCN DNA swabs or items for consideration of LCN profiling. This included a protective disposable body suit, hairnet or hood, facemask and two pairs of gloves (Fig. 4.1).



Figure 4.1 - Full protective suit with hood, face mask, overshoes and gloves taped at wrists.

Advice was given with regard to minimum personnel accessing any scene. The introduction of equipment into a scene was kept to a minimum and cleaned prior to entry; this included writing materials as well as scene examination equipment. Where possible, disposable equipment was used and talking kept to a minimum when recovering items. These measures are supported by the research carried out by Rutty, *et al.*, (2002), which confirmed the possibility of accidental contamination by CSI personnel although it is accepted that accidental contamination cannot be totally eliminated. In addition all staff that had not previously provided their DNA for purposes of elimination were now required to do so.

4.3 Standardisation of Swabbing Technique

In certain cases it is not possible to remove and submit the item that is believed to have been touched, to the laboratory for analysis and the only alternative is to take samples in situ. This could include items such as a window frame which is fixed within the building structure, a human body, items of value, or other large cumbersome objects. It also applied to items that needed to undergo other forensic testing, in which case swabbing for LCN DNA allowed this to continue without delay.

Standard DNA traces such as blood or saliva are routinely recovered using a single swab, wetted if the sample was dry, lifting all the visible material present. Little research was available at the introduction of LCN DNA technology as to the best method for recovery of material. Some research by Wiegand & Kleiber (1997) utilised a wet and dry swabbing technique to recovery touch DNA from manual strangulation cases, a technique later supported by Rutty (2002). Sweet, *et al.*, (1997) used similar methods in recovering saliva from skin. This technique required little additional training of staff and no additional equipment and was therefore adopted by GMP and used throughout the period of this research.

The technique involves using a moistened cotton wool swab with a fine tip, followed by a dry swab to mop up any moisture and cellular residues left behind. Sterile water was used for the process and control samples were taken from the swabs and the water. The wet and dry swabs are combined at the analysis phase to maximise their DNA potential. The LCN DNA swabbing process is detailed in Appendix 3.

Recent research by Pang and Cheung (2007) also provides support for this technique as they found it increased the DNA yield recovered from the crime scene when compared to the single swabbing method.

4.4 Examination Protocols

Body swabbing and ligature recovery at the scene

In cases where a body required examination, where possible, all swabs for LCN DNA were taken at the scene and ligatures removed. This was to reduce the potential for contamination from the mortuary environment as detailed by Rutty (2000) and Rutty, *et al.*, (2000). It also prevents contamination by body fluid spillage due to movement of the cadaver (Ackerley, 2002). This considerably delayed the time to remove a body from a scene which had to be managed with good communication between the CSI manager, Senior Investigation Officer, Home Office Pathologist, the Coroner and often the victim's families. Documentation was also provided to ensure the location of sites on the body of any swabs taken were clearly identifiable.

Firearms recovery

The retrieval of firearms and ammunition from crime scenes followed a detailed procedure to maximise the recovery of LCN DNA and still maintain the safety of officers dealing with such weapons. All firearm weapons and ammunition have to be made safe by a firearms specialist prior to removal from their location into police custody. Training was provided to the Armed Response (firearms) Officers and Detectives regarding the preservation of DNA and fingerprints and the use of personal protective equipment (PPE), such as nitrile/latex gloves and facemasks. In the majority of cases, firearm weapon recoveries were made jointly with a firearms officer and CSI at the scene. This was supported by a Chief Constables Order giving instruction to staff of the adopted procedures (Chief Constable Order, 2000; Chief Constable Order, 2002). Swabbing of weapons and ammunition for LCN DNA was carried out prior to any ballistic or fingerprint examination as part of a joint examination in a controlled laboratory environment.

Joint examinations

Portable items that could be subject to examination for fingerprint or other trace forensic material in addition to the LCN DNA recovery were subject to a joint examination between specialists such as laboratory staff, fingerprint experts and CSIs. This enabled specialist light sources to be utilised to identify fingerprint ridge detail and to maximise all forensic recoveries prior to any swabs being taken. A dedicated laboratory was set up within GMP to carry out such examinations.

Swab and pend

Due to the inability to return to crime scenes and the difficulties in preserving items for LCN DNA whilst they underwent other processes, a policy of 'swab and pend' was applied to items that were considered suitable for LCN DNA but where other forensic evidence types may prove faster and more economical. This applied to vast amounts of swabs taken at major crime scenes which were pended during the initial investigation phase. Swabs were taken for LCN DNA using all the preservation methods and then frozen for storage. This ensured that if other evidence types failed to generate a result, i.e. fingerprints, or the investigation was not progressing, the swabs could then be considered at a later date for submission.

4.5 Submissions Policy

All LCN DNA submissions were routed through the researcher. In 2001 the submissions policy for LCN DNA was published on Chief Constables Orders as instruction to police officers and staff and reiterated throughout the research period (Appendix 4 – LCN DNA submissions policy). The policy required full details of the case, recovery and contamination issues and control of the crime scene to be detailed. This ensured the researcher was aware of all LCN DNA cases within the GMP area and provided the initial information required (Chief Constable Order, 2001; Chief Constable Order, 2004).

Full details of all the cases submitted were entered onto a database prior to any laboratory analysis. Initial checks were made to ensure they met with the predefined sample frame and where cases failed to meet the strict criteria they were rejected from the research. The data set had to be complete and meet the sample frame for any case to be considered within the research findings.

The researcher ensured that details of all samples taken for LCN DNA were included on each submission and determined which samples were subjected to analysis. This ensured consistency in submissions and an ability to compare data.

In many cases submission for LCN DNA analysis was refused when the details of the case were explored, as there were clear multiple contamination issues or standard SGMplusTM was more appropriate. A common occurrence being items recovered by members of the public such as a firearm, handled by their friends and family, and then passed to an enquiry desk assistant before being preserved by an investigator and then presented for LCN DNA consideration.

However, to take account of the investigators needs which sometimes followed a different agenda to that of the researcher an appeal process could be instigated if submission for analysis was refused. Refusal to submit was usually due to contamination issues. Appeals were considered by the Director of Scientific

Services within GMP for technical issues, and by the Detective Chief Superintendent for major crime on investigative grounds. Any submission that was agreed through the appeal process was excluded from the research findings although the researcher did track these cases and all of them failed to produce a result of any value.

Often a substantial number of items and swabs were taken relating to a single case. These were prioritised into those samples taken from areas most likely or known to have been directly handled by the offender and submitted in smaller batches to take account of financial constraints. In other cases some samples could be excluded when the case details were reviewed, such as multiple cartridge cases in a shooting. These were reviewed using the photographic records to establish whether the area around the recovery was contaminated with litter, excrement, blood, or which cartridge cases were squashed as they had been driven over or which had landed in mud or puddles (Fig. 4.2).



Figure 4.2 – Cartridge Case in Wet Muddy Area.

The results of the analysis and subsequent matches were added to the database as they became available and cases were actively tracked.

4.6 Laboratory Processes

Samples were submitted to the FSS for analysis. Quantification of the sample was not carried out as a routine procedure, and therefore it is accepted that there may be an unknown number of samples that would have succeeded using standard SGM PlusTM analysis. However, where there was no known bodily fluid contamination and the item had merely been touched, or if the scientist indicated that standard procedures were likely to fail, i.e. very small amounts of sperm heads, LCN DNA analysis was considered appropriate.

The DNA was extracted from the sample using either Chelex or Phenolchloroform as previously described. The samples then underwent 34 PCR amplification cycles with the Applied Biosystems AMP*FI*STR[®]SGM PlusTM kit, as decribed by Cotton, *et al.*, (2000), but with the additional cycles described by Gill, *et al.*, (2000). An automated DNA sequencer from Applied Biosystems was used for the allele designations. Results were duplicated to gain a consensus profile that met with the interpretation guidelines described by Gill, *et al.*, (2000).

4.7 Methodology

Access to data

The research required access to criminal cases that were subject of LCN DNA submissions, the associated case histories, documentation, exhibits and staff. Greater Manchester Police (GMP) was a high user of this technique in many different criminal investigations and granted permission for access to all LCN DNA cases throughout the period of research.

Minimal caveats were placed on the data and information that had no effect on the results. These were: -

- Individuals or specific crime cases would not be identified in any published work.
- The data would only be used for the purposes of the research.

Sample Frame

All cases submitted by GMP for LCN DNA analysis between 2000 and 2005 were utilised. By covering all submissions over a period of 6 years it was hoped to gain a representative sample across a broad range of categories. In all 3 552 samples were used in the research.

Some cases were excluded from the research for the following reasons:-

- Items that were recovered without using LCN DNA recovery and preservation techniques or that were known to be contaminated from any source.
- Where information regarding the recovery of the sample was incomplete.
- If the scientist didn't produce a report or statement of the results.
- When work was stopped prior to completion of the analysis by the investigator.
- Where new information changed the parameters of the investigation in relation to the LCN DNA sample.
- Samples submitted to prove a negative (to show the absence of DNA).
- Submissions from cold case reviews predating LCN DNA technology.
- Control and environmental samples.

The numbers of cases that were excluded from the research were not counted.

Data Collection Methods

A variety of methods were used to collect the data, all of which came from genuine crime scenes or police incidents. Data were collected using case histories, crime reports and scene examination reports. Forensic submissions data, computerised work management systems and criminal justice statements supplemented this as did the scientists reports.

In addition photographic evidence, item examination and attendance at crime scenes were used to complete the information required. Finally interviews with investigators were used to answer specific queries on individual cases and exhibits to clarify data.

Reducing variables

ACPO (2005) showed that there is a difference in profiling rates between different forces for standard SGMplus[™] DNA submissions. Although most of this could be attributed to the submissions policy for each force, to reduce this variable only samples submitted through GMP were included and samples were submitted for analysis to the same forensic provider throughout the course of the research.

4.8 Statistical Significance

Statistical evaluation usually uses the phrase 'sample' to indicate a set of related measurements. However, throughout this research the word sample has been used to indicate a field sample taken for analysis. To ensure clarity the phrase 'data set' has been used with regard to related measurements.

The classification system used to evaluate the results placed the samples into categories and sub groups. However, it was recognised that the actual numbers of samples for each category varied significantly. Therefore it had to be considered if this difference, in actual numbers of samples analysed, truly reflected statistical significance between the groups.

The chi-square test is a statistical technique which evaluates the differences between the proportions in comparable data sets, to test the probability of them occurring by chance or being statistically significant. The test compares what is actually observed with what would be expected under a null hypothesis between the data sets. The test result is compared to Chi-square distribution tables, which confirm whether the results are consistent with chance thereby supporting a null hypothesis or are significantly different from what would be expected (McKillup, 2005). Therefore, in this research a null hypothesis demonstrated no systematic differences between the sample recovery situations whereas the alternative supported some sample recovery situations were more successful than others.

Chi-square testing examines the relationship between two variables (Hinton, 2004), therefore, the results for the categories and sub-groups were considered in terms of giving value to an investigation or not. Those samples that DNA profiled were considered to have added value and those that were either anticipated eliminations or failed to produce a useful profile (see Chapter 5) were considered not to have contributed to the investigation. Whether a match was generated was irrelevant to the consideration of the potential to add value to the investigation. A selection of these data sets were then chi-square tested to ascertain if the results had a statistical significance as opposed to a random distribution, accepting that statistical significance does not necessarily prove a causal link.

The obtained chi-square value was then compared against the distribution table to establish whether the differences occurred by chance i.e. a null hypothesis or if they were statistically significant, known as the probability value or 'p' value. Statistical significance is only usually considered with a probability figure of less than 0.05; in effect there is less than a 95% expectation of the null hypothesis.

A detailed example and summary charts of results are provided in Appendix 5.

Chapter 5

Defining Useful DNA Profiles & Matches and Categorising Samples

5.1 Defining a 'Useful' DNA Profile

Before a 'useful' DNA profile for criminal investigation can be determined it is essential to understand what constitutes a profile. SGMplus[™] DNA profiles are usually categorised depending on the results. They are defined into four categories, full DNA profile, mixed DNA profile, partial DNA profile or no result / insufficient (sometimes referred to as sub-threshold).

With regard to LCN DNA analysis stringent guidelines within the FSS cover issues such as allele drop out, allele drop in, background contamination and stutters. Before DNA profiles are reported alleles must be confirmed by duplicating results, and control negatives confirmed (Gill, *et al.*, 2000).

Full DNA Profile

An example of a complete male SGMplus[™] DNA profile containing 20 alleles and the sex marker from a single person can be seen at Table 5.1. Each locus shows the two alleles, one inherited from the mother and one from the father.

| Loci | D3 | vWA | D16 | D2 | D8 |
|------------|------------|-------|-------|-------|-------|
| Alleles | 16,19 | 14,16 | 10,11 | 20,23 | 11,13 |
| Loci | D21 | D18 | D19 | Th01 | FGA |
| Alleles | 28,30 | 12,16 | 13,14 | 7,9 | 21,26 |
| Loci | Amelogenin | | | | |
| Sex marker | X,Y | | | | |

Table 5.1 – Example of a full male SGMplus[™] DNA profile.

On rare occasions it is possible for more than two alleles to present at certain loci. For example in Down's syndrome 3 alleles may show at D21, other genetic conditions may also affect a profile but this is very rare (Katz-Jaffe, 2004). Triallelic patterns are recorded and listed on the NIST website along with the allelic ladders (NIST, 2009).

Mixed DNA profile

This is where a DNA profile shows more than 2 alleles at any given locus therefore (excluding the rare genetic conditions) must come from more than one person as only one allele can be donated from each parent at any given locus. When seen clearly the mixture may be resolvable into major and minor contributors or may be so complex with many results at multiple loci that it is not possible to place any significance on any result.

| Loci | D3 | vWA | D16 | D2 | D8 |
|------------|------------|-------|----------|-------|-----------|
| Alleles | 14,16,19 | 14,16 | 10,11 | 20,23 | 11,13 |
| Loci | D21 | D18 | D19 | Th01 | FGA |
| Alleles | 28,30 | 12,16 | 12,13,14 | 7,9 | 21,24, 26 |
| Loci | Amelogenin | | | | |
| Sex marker | X,Y | | | | |

Table 5.2 – Example of a mixed DNA profile, showing more than 2 alleles at several loci.

The presence of 3 alleles at any given locus indicates at least 2 persons; 5 would indicate a minimum of 3 and so on. Table 5.2 shows multiple alleles at D3, D19 and FGA loci and therefore the DNA profile must be from a minimum of two people.

Partial DNA profile

In a partial SGMplus[™] DNA profile some of the alleles are missing at any given locus (Table 5.3). This may be due to the limited amount of cellular material available or degradation of the sample. Depending on how many alleles are missing it still may be loadable on the NDNAD or be suitable for a one off speculative search. The quality of the partial profiles that are suitable for loading onto the NDNAD must include a minimum of both alleles in four of the following loci, HUMVWFA31/A (vWA), HUMTH01 (TH01), D8S1179 (D8), HUMFIBRA (FGA), D21S11 (D21), D18S51 (D18), along with the amelogenin (NPIA, 2008²). A partial DNA profile is more likely to match other profiles depending on how many alleles are absent. It is possible for a single allele to be missing at a given locus if the allele is shared by both parents as shown at D3 in Table 5.3. In these cases the electropherogram usually shows a higher peak size where the allele is shared. However, it must be a partial profile if there are no alleles at any given point as shown at D8 and Th01 in Table 5.3.

| Loci | D3 | vWA | D16 | D2 | D8 |
|------------|------------|-------|-------|-------|-------|
| Alleles | 19 | 14,16 | 10,11 | 20,23 | |
| Loci | D21 | D18 | D19 | Th01 | FGA |
| Alleles | 28,30 | 12,16 | 13,14 | | 21,26 |
| Loci | Amelogenin | | | | |
| Sex marker | X,Y | | | | |

Table 5.3 – Example of a partial SGMplus[™] DNA profile, showing missing alleles at several loci.

No result / Insufficient

When no alleles are found at any loci this may be due to no DNA being present, or the results are so few as to have no value or they are not of a reportable level. This can also occur when the sample has degraded or something has inhibited the extraction process such as a chemical or biological contaminant.

Anticipated Eliminated Samples

In a number of circumstances it can be expected that a LCN DNA sample could be legitimately eliminated, and in fact anticipated. For example, it could be expected that swabs taken from a steering wheel of a vehicle would match the legitimate owner even if the vehicle had been stolen and driven by an offender. It could also be expected that samples taken from a person's underwear that had been ripped off may belong to the wearer or that swabs taken from skin on a body would come from the person and not the offender. In these cases elimination samples were sent along with the crime scene sample. Although DNA profiles may have been generated from the item or swab submitted they were not considered useful to the investigation as they did not further the case in any way and the elimination had been anticipated. Therefore, profiles that were legitimately eliminated and anticipated prior to the analysis are reported as a separate element of the results.

The key factor in these being excluded as being useful to the investigation was the ability to anticipate the result.

Definition of a useful DNA profile

A full, partial or mixed DNA profile that can be loaded onto the NDNAD, speculatively searched or compared against an individual, that has not been legitimately eliminated by anticipation.

It excludes mixed profiles that are too complex to separate and partial profiles that are insufficient to the point that a large number of the population would be expected to match it by chance.

5.2 Defining a Match

A similar process had to be determined to qualify what constituted a match. This was predominantly relevant to DNA profiles that were loaded or speculatively searched on the NDNAD as this provided investigators with the name of a suspect(s) who could then be legally arrested for questioning.

DNA profiles from suspects and crime scenes are loaded onto the NDNAD and compared against each other on a daily basis. In simplistic terms the DNA profiles are in numerical form and matches occur when the numbers correspond. A match can be between a 'person to crime scene' or 'crime scene to crime scene' (linked offences). The fewer alleles in a sample that are loaded onto the NDNAD the higher the probability of generating a match. This is mainly relevant for partial DNA profiles. Up until 1999 SGM processes were used that only analysed 6 loci as opposed to the 10 loci used with SGMplus[™]. Samples can easily match these limited DNA profiles but are instantly eliminated once the original sample is upgraded to SGMplus[™] with further analysis. This is particularly true of partial DNA profiles that may have detail contained within the additional SGMplus[™] areas and not the original SGM loci, meaning only a very small number of alleles need to correspond to generate a match.

All matches that included a sample that had only been analysed using the SGM technology were upgraded to SGMplusTM to ensure a true match had been generated.

In addition, on occasion where a separate elimination sample had not been submitted, persons who could be considered an anticipated elimination resulted in a NDNAD match. This usually occurred when a victim, who had previously had a DNA sample taken for an offence loaded onto the NDAND, was in hospital or had not been traced. The submitted crime scene stain then matched the victim which could have been anticipated due to their blood spill at the scene. These 'matches' fell into the anticipated elimination category.

Definition of a match

A match is a corresponding DNA profile between a person and crime scene or crime scene and crime scene where samples have been fully upgraded to SGMplusTM standards (even if they remain partial).

It excludes samples that have not been upgraded where it is possible, those that form part of an anticipated elimination and those profiles that are insufficient to the point that a large number of the population would be expected to match it by chance.

5.3 Changes from Cell Type to Surface Type

The forensic suppliers usually classify success rates under the cell type, saliva, blood, semen, hair or cellular (ACPO, 2005); the cellular classification being the one that suppliers use for LCN DNA. This does not assist investigators in determining where or what to sample and submit, when faced with invisible DNA at an entire crime scene where the cell type is unknown. To interpret the data a different mechanism had to be determined.

Forensic suppliers frequently subdivide the standard SGMplus[™] categories into smaller sub-groups, such as saliva being divided into cigarette ends, chewing gum or drinking vessels (ACPO, 2005). In addition CSIs are familiar with considering surface types during scene examination as fingerprint processes depend on the material under examination. The Fingerprint Development Handbook (Home Office, 2005)³ provides guidance using surface and material headings such as plastic or wood.

An indexing system was therefore devised, following consultation with operational CSIs that would be useful to them to identify areas for the recovery of LCN DNA and provide a system to identify differences in results. Surface material types such as wood or plastic appeared to be limiting as they over generalised and therefore the locations of scenes such as house or car were utilised for easy reference.

The overarching categories were determined and then subdivided into smaller sub-groups and target areas, full details are included in Appendix 6 – Sample Categories and Sub-Groups.

The overarching categories are: -

| Body Fluids | Body Samples | Communications | Firearms |
|-------------|---------------------|----------------|----------|
| Ligatures | Personal Belongings | Premises | Tools |
| Vehicles | Weapons | Worn Items | |

An example of some of the sub-groups within the Firearms Category include:-

Handgun Shotgun

An example of some of the target areas within Handgun sub-group include:-

Trigger Handgrip Magazine

In addition to the above categories, some items overlapped into several groups and could be considered together although they also remained in their individual sub-group and category from where they were originally recovered for example:-

Knots Fasteners Handles Adhesive tape Chapter 6

Phase 1

Results of Categories and Sub-Groups

6.1 Success Rates

Prior to detailing the results of the research it is necessary to explain the figures so that a full understanding can be achieved of what the success rates mean within each category. Using the predetermined definition of a useful DNA profile, what constitutes a 'match' and anticipated eliminations, results are shown in percentage rates against the total number of samples analysed.

For example, if the total number of samples analysed is 150. A useful DNA profile is gained from 40 samples of which 15 generate a match. This is illustrated as 17% (25 useful samples) and 10% (15 matching samples) respectively. A total of 110 samples add no value to an investigation. Anticipated eliminations account for 20 of the samples and 90 are insufficient for comparison or did not DNA profile, which is illustrated as 13% and 60% (Fig. 6.1).

Total samples 150 = 100%Useful to an investigation total profiled = 40 Profiled but remain unmatched 25 = 17%Match 15 = 10%No value to an investigation = 110 Eliminated 20 = 13%Insufficient or did not profile 90 = 60%

All results that are shown in blue are useful to an investigation. All figures are generated from the total number of samples analysed, so it is clear to an investigator on submission of a sample for analysis, what the expectations can be of success. It also gives an indicator on the importance of submitting appropriate elimination samples with cases.

The results provided for matches give figures up to the end of 2006. As offender samples are being added to the NDNAD everyday, the number of matches is

likely to increase over time and therefore should be considered as a minimum expectation.

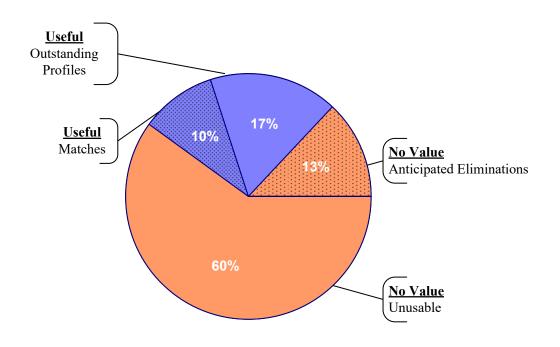


Figure 6.1 -Example of how data will appear in research results.

6.2 Overarching Categories

The initial phase of the research set out to establish if there were significant differences in profiling success rates from different sampling areas.

A total of 3 552 samples were analysed that met with the criteria of the sample frame. These gave the following results when considered as a group. Useful DNA profiles were found in 853 (24%) samples analysed. Of these 391 (11%) went on to generate a match and 462 (13%) remained outstanding. Overall 2 699 samples did not add any value to an investigation of these 710 (20%) were anticipated eliminations (Fig. 6.2). In comparing these results to those found by Morgan Harris Burrows (2002) the final match rate is very similar, their study generating matches in 9% of submissions, although Morgan Harris Burrows

(2002) only achieved a 15% profiling rate, whereas this study achieved a useful DNA profile in 24% of submissions.

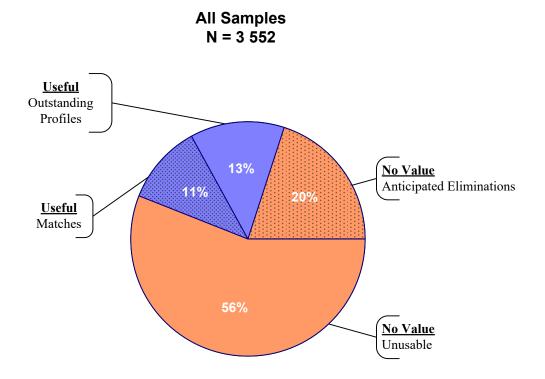


Figure 6.2 - Results of all samples analysed.

If there were no differences in the profiling success rates within different categories a similar pattern of results would be obtained within each overarching category. However, differences were found and the following charts show a variation in the results for samples that generate useful DNA profiles and those that do not add value to an investigation.

When viewing the overarching categories which are set out in Appendix 6, it can clearly be seen that the pattern of results shows variation in the results found: Overall 24% of samples generated a useful DNA profile (11% matches and 13% outstanding). In the individual categories the highest useful profiling rate was 48% and the lowest 9% (Fig. 6.3). Likewise the results for subsequent matches show the variation to be between a highest percentage of 27% and the lowest 3% (Fig. 6.4). With regard to anticipated eliminations, in one category the anticipated eliminations were as high as 44% and the lowest 1% (Fig. 6.5). When

the actual numbers of each category are compared statistically there is a very high probability that this has not occurred by chance (p = 0.001).

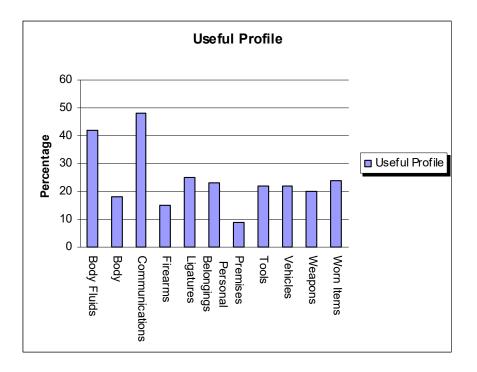


Figure 6.3 – Total percent of samples generating a useful DNA profile within each category. Results include outstanding DNA profiles and those that went on to generate a match.

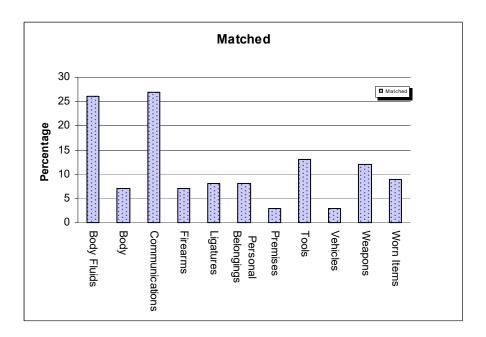


Figure 6.4 – Total percent of samples that went on to generate a match within each category.

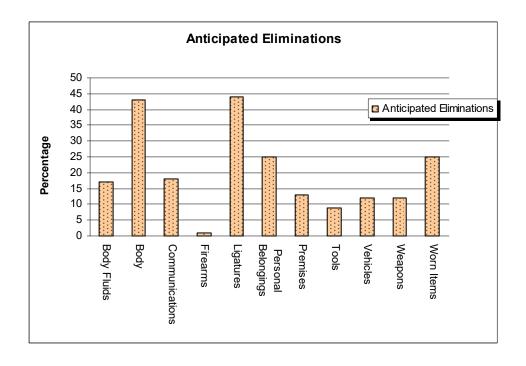


Figure 6.5 – Total percent of samples that resulted in an anticipated elimination result within each category.

A more recent study by Castella & Mangin (2008) analysed the results from 1739 casework samples and had similar findings with regard to the overall number of samples that proved useful, this being 26% and a match rate of 9%. They also split the samples into categories such as car items, personal items, clothes, tools etc., and found great variation in the success rates across the groups, a range of between 7 - 61% of useful profiles being generated which is slightly higher than this research. Unfortunately the categories cannot be compared directly as they contain different items, for instance Castella & Mangins personal items also include mobile phones, which is separated out in this research.

6.3 Individual Category Results

The results for each individual category and the sub-groups within them are detailed in alphabetical order.

6.3.1 Body Fluids

Samples analysed within this group are where known body fluids have been found or can be assumed to be present but in such small quantities that LCN DNA testing was more likely to produce a result.

This included semen with very small sperm counts and tests that had given a weak positive for presumptive blood or saliva testing. It also includes single head hairs where there is very little DNA material to analyse. All DNA material was collected, preserved and packaged according to recognised practices (FSS, 2004¹).

Overall 230 samples were analysed in this category. Higher success rates were expected within this group, as these were known body fluids that should contain cellular material. Overall 97 samples profiled, 60 (26%) generated matches and 37 (16%) remained outstanding. A total of 133 added no value to the investigations of these 39 (17%) were anticipated eliminations (Fig. 6.6).

Even within the sub-groups a wide spread of results can be seen between the different body fluids. Saliva proved to be particularly successful in profiling and subsequent matches. This is similar to the high success rate Findlay, *et al.*, (1997) achieved on single buccal cells.

The anticipated elimination figure for semen of 32% initially appeared high but further enquiries determined that all the crimes involved an allegation of rape and the victim had had sexual intercourse with a known partner within 5 days of the offence. The DNA profiles in these cases had been achieved from high vaginal swabs. Semen can remain within the vagina for up to 14 days and longer within the cervix. The amount diminishes over time and becomes less motile but is still detectable (Green, 2004). Therefore, elimination buccal scrapes were sent from the victim's known partner.

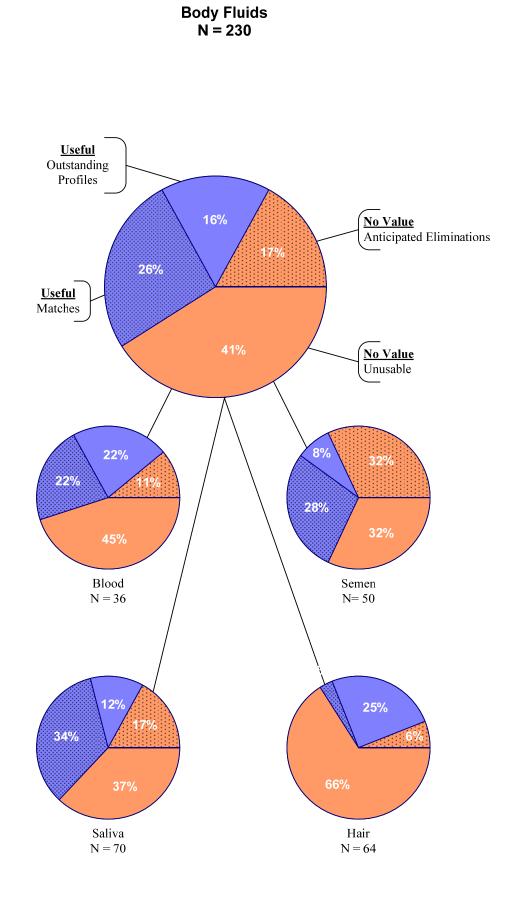


Figure 6.6 – Results of profiling for the category Body fluids and the sub-groups..

6.3.2 Body Samples

Body samples analysed within this category are from samples, usually swabs, taken directly from the skin of a body (living or deceased). They generally refer to body swabs where the witness alleges an offender has punched, kissed or held them in a specific area. However, it also includes speculative swabs from areas of a deceased body where potential body fluids such as blood or semen may have been deposited or loose hairs, including eyelashes, recovered that may belong to an offender.

Where the victim was deceased, the crime scene or position of the victim may have indicated that a body had been carried or manipulated in some way, indicating an area for the crime scene investigator to sample. Or the victim may have died as a result of strangulation thus indicating an area for swabbing.

A total of 306 samples were analysed. As could be expected when directly swabbing skin, 132 (43%) of the samples were anticipated eliminations. Of the remaining samples 55 were useful, of these 22 (7%) went on to generate a match (Fig. 6.7).

Within the body sample sub-groups there continued to be a variation in the results obtained. Swabs from the torso were significantly more successful than other areas of the body as were areas where it was suspected body fluids had been deposited; in particular areas associated with kissing or sucking (p = 0.02). Swabs from exposed extremities were the least valuable in investigative terms, these being hands, arms and legs.

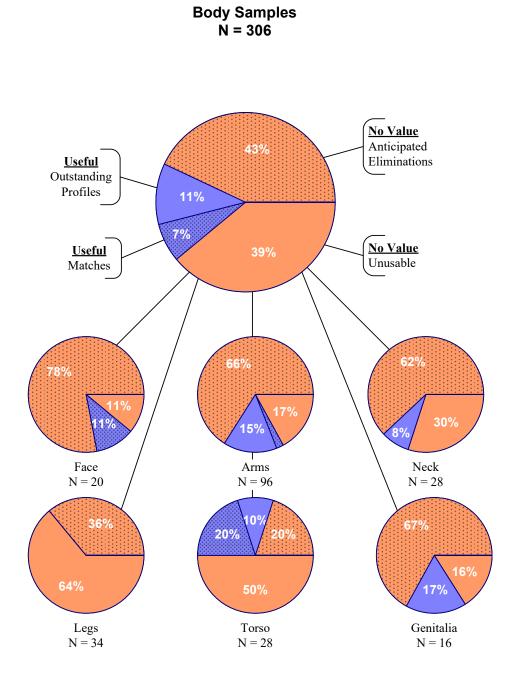


Figure 6.7 - Overall results for Body Samples

Swabs from the torso were significantly more successful than other areas of the body with a profiling rate of 30%, however all the success arose from samples taken from the breast area. Samples from the shoulders or abdomen did not profile or were anticipated eliminations (Fig. 6.8).

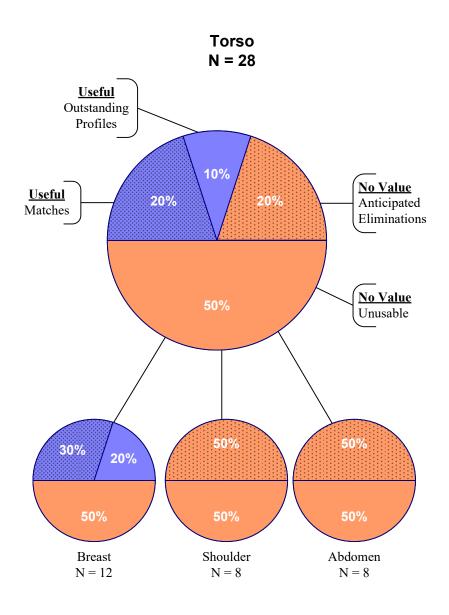
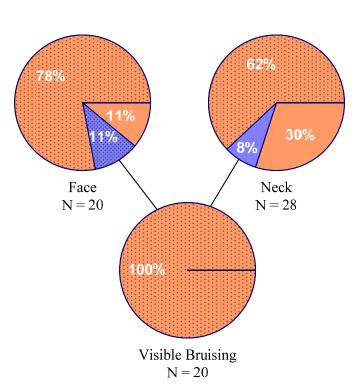


Figure 6.8 - Results of profiling areas of the torso.

Within the 48 results from the face and neck samples, 20 were taken from areas where visible bruising had occurred on the victim either from strangulation or a punch. In all these cases, the DNA profiles generated were eliminated as belonging to the victim (Fig. 6.9).



Face and Neck Samples N = 48

Figure 6.9 - Results of profiling areas with visible bruising

In direct contrast, 24 of the samples taken were analysed following a report of kissing or licking on the face or breast, 18 (75%) resulted in a DNA profile and of these 16 (65%) a match. None of the samples were anticipated eliminations (fig. 6.10).

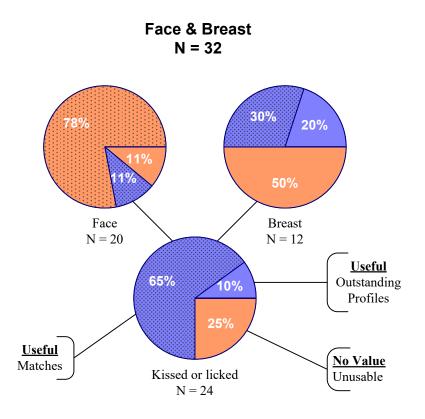


Figure 6.10 - Results of profiling areas associated with kissing and licking

CSIs reported frequent requests to swab a person's arms or hands to detect another's DNA, therefore, this area was considered as a separate sub-group. This usually occurred when someone had been punched and the DNA of the victim was sought on the offenders' hand. It was also requested when a victim had been dragged around by the wrist or arm during the commission of the offence. Results from arms were therefore subdivided further (Fig. 6.11). The subdivision clearly showed the high anticipated elimination rate for this area of the body at 66%; with only 2% generating a match result.

However, a significant variation was noted in the results where it was believed the fingernails had been used as a weapon or in defence, and were subsequently sampled. Although a higher percentage of fingernail samples gave a useful DNA profile (50%), no matches were generated and none were eliminated. While elimination samples were taken from the victims none were submitted from partners which may have an effect on the outstanding profiles. A study by Malsom, *et al.*, (2008) considered DNA transfer under fingernails between cohabiting couples and found that transfer occurred and increased with the more amount of time spent together. Foreign alleles were also found in this study although no crime had been committed and these were attributed to different lifestyles.

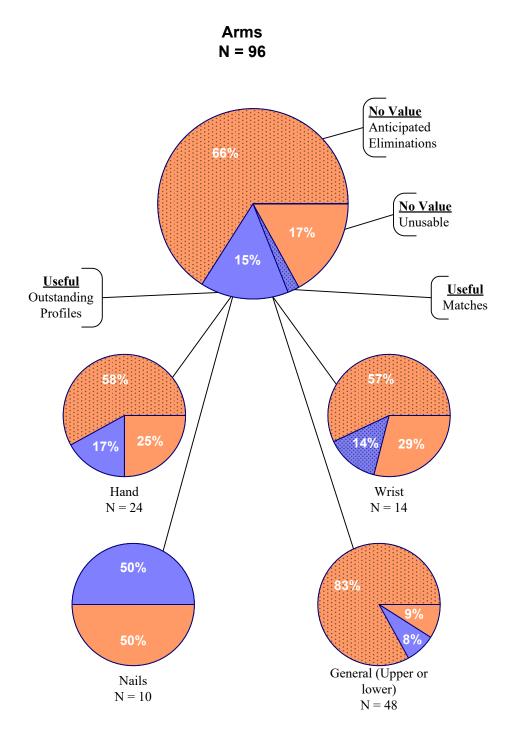


Figure 6.11 – Results of profiling for different areas of the arm.

A small number of samples were taken from genitalia (17) from males and females. Samples were taken to attempt to locate female victim's cells on a suspects penis, others were taken to find a suspects cells on the outside of a vagina when the victim indicated the offender had 'rubbed' his penis or other body part on her. Although only 17 samples were submitted for LCN analysis, all the successful DNA profiles came from female victims of crime however, none generated a match (Fig. 6.12).

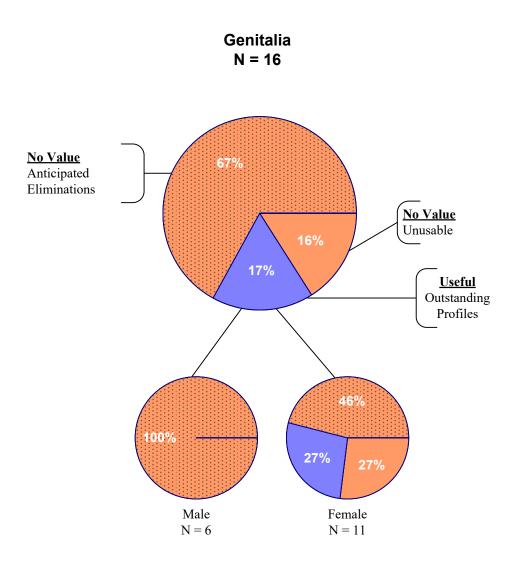


Figure 6.12 – Results of profiling from genitalia.

6.3.3 Communication Items

This group of samples primarily comprised of mobile and other telephones, as well as a small number of scanners and radios.

Within this group 112 samples were analysed, 92 from mobile phones and 20 from scanners and radio equipment. Of these 54 (48%) generated a useful profile, the highest success rate of all the overarching categories. This resulted in 30 (27%) subsequent matches which was the highest percentage match rate of all the groups. Anticipated eliminations arose in 20 (18%) samples analysed (Fig. 6.13).

Mobile phones are a common item targeted in street robbery and are also used in the organisation of crime by offenders and are sometimes left at crime scenes inadvertently. In some cases data held on the phone such as text messages, images or phone numbers could be considered incriminating and it was necessary to identify the owner. Identification of owners and users through service providers such as Orange or Vodaphone, proved difficult with unregistered "pay as you go" mobiles and additional forensic and investigative techniques were required.

Mobile phones offer a multitude of areas that can be sampled for DNA; these include the keypad, edges, buttons, battery, SIM card, mouthpiece and other prominent areas depending on the design of the phone. Some areas are also highly suitable for fingerprinting techniques such as the screen and battery (depending on design). In the case of batteries, if it was suitable for fingerprinting only the edges were swabbed for DNA to retain any fingerprint detail without damage, which may explain the poor results for this area.

Statistically the keypads proved to be the most effective area (p = 0.005). These were often combined with mouthpiece and swabbed as one area as they were so close together. This successful combination produced 24 (60%) profiles and 20 (50%) matches. SIM cards profiled slightly better with 16 (80%) useful profiles, however, they did not generate as many matches with 8 (40%) (Fig. 6.13).

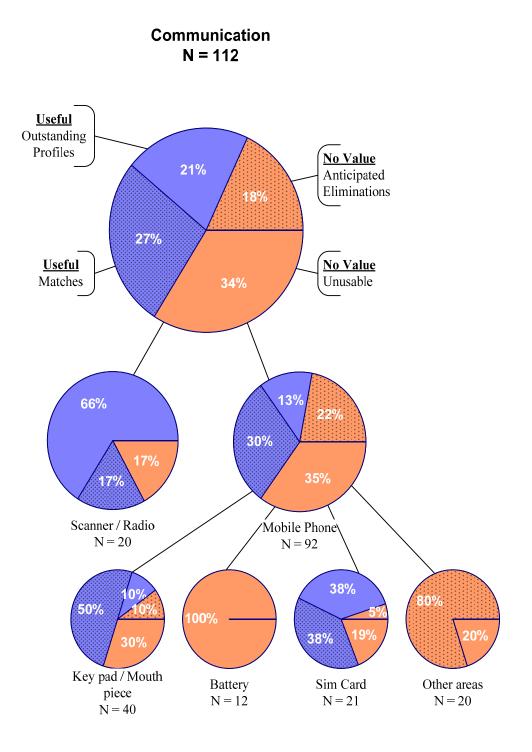


Figure 6.13 – Overall results for Communication items, mobile phones and mobile phone subgroups.

6.3.4 Firearms

Initially it was found that a range of different terminology was used by personnel verbally and on documentation regarding firearms, firearm components and ammunition, not all of which were correct. For example a complete cartridge could be called a bullet, cartridge, shell, ammunition or bulleted cartridge. Standard terminology was established to ensure consistency in results and analysis (Appendix 7 – Firearms terminology).

Within this category 1278 samples were analysed of which only 192 (15%) generated a useful DNA profile resulting in 89 (7%) of these producing a match, however, this is heavily influenced by a large number of cartridge cases which were less successful than the weapons themselves. Only 13 (1%) of the samples were anticipated eliminations (Fig. 6.14).

The small elimination figure was due to the fact that the majority of weapons were illegally held, and therefore had no legitimate owner or handler. Anticipated eliminations only occurred when a victim had contaminated the weapon or ammunition in some way, either by a struggle or body fluid spill, such as blood or saliva.

Firearms were divided into two main categories, shotgun and handgun, this being determined by the way the weapon was held: A hand gun requiring a single hand, and a shotgun requiring support under the front barrel or fore end. Ammunition was also split into handgun and shotgun types each comprising of complete cartridges, cartridge cases, and, in the case of handguns, bullets (Appendix 8 – Firearm Images).

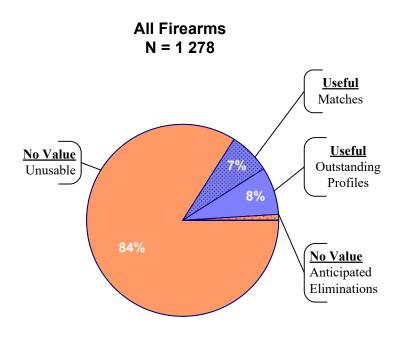


Figure 6.14 – Overall results for firearms and ammunition.

The handgun sub-group clearly indicated areas that were more likely to produce a useful DNA profile and subsequent match. Like the Wells and Taylor (2002) research the magazine, handgrip and trigger were more successful than other areas (Fig. 6.15).

It was expected that bullets would prove unsuccessful with regard to generating a useful profile for the investigation, as items submitted for analysis had had either no contact with any person (protected by the cartridge case prior to missile expulsion) or had injured the victim, resulting in an anticipated elimination. The results clearly demonstrate this to be true with 17% eliminated and no useful profiles generated.

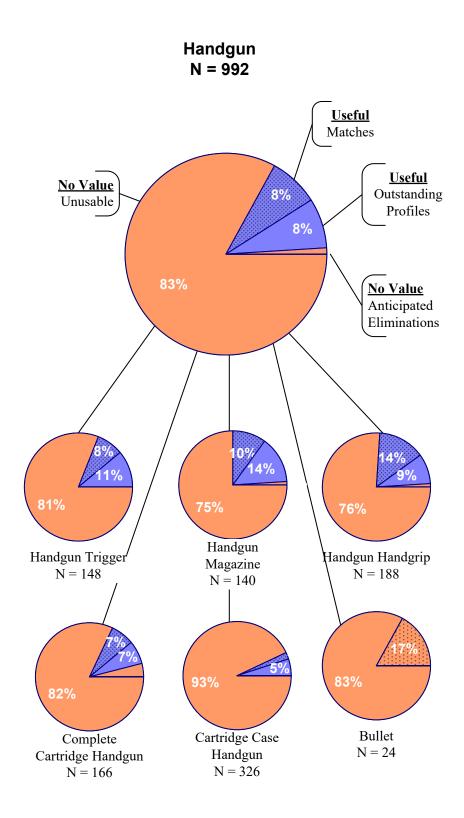


Figure 6.15 – Results for Handgun sub-group.

Statistically the results within the shotgun category showed a variation between the trigger and stock, the stock being significantly more productive than the trigger (p = 0.025). However, there is no statistical difference between a trigger on a handgun and one on a shotgun (p = 0.5). Complete shotgun cartridge cases proved to be the most successful item sampled across all of the firearms and ammunition categories although the small number of submissions within this group is acknowledged (Fig. 6.16).

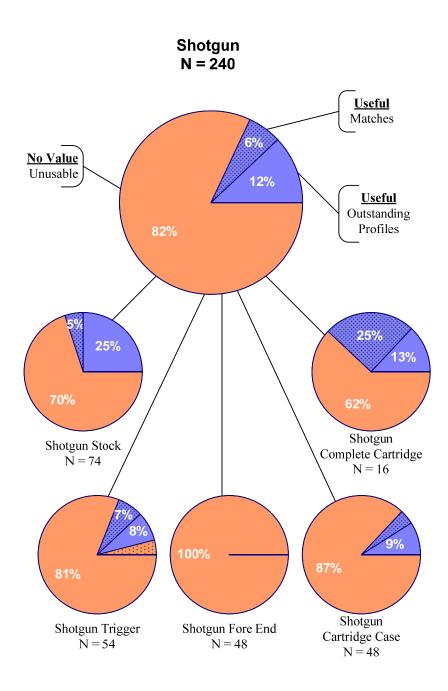


Figure 6.16 – Results for shotgun sub-group.

Complete cartridges were found in varying situations, some having been expelled by the weapon, and some remaining inside the firearm. No difference was found in the results between those expelled and those inside a weapon in either the shotgun or handgun categories. However, a significant different was found in both handgun (p = 0.01) and shotgun (p = 0.025) categories between complete cartridges and casings. Complete cartridges proving to be much better at generating a useful profile. Likewise complete shotgun cartridges proved to be significantly better than handgun ammunition (p = 0.01).

Small numbers of samples were submitted for some common areas on shotguns and handguns and therefore the results were combined together (Fig. 6.17). All the submissions for analysis of samples taken from barrels were following specific information, and in one case CCTV footage of a shotgun being swung around by its barrel.

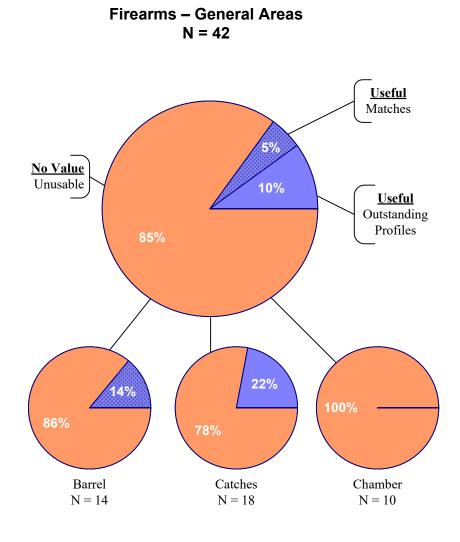


Figure 6.17 – Results for general areas of firearms.

6.3.5 Ligatures

A ligature associated with crime relates to a binding used to secure a persons limbs or a mechanism to attempt strangulation. Many different materials are used to form ligatures, a frequent one encountered, particularly in the commission of robbery, is plastic cable ties. The common theme is that the offender secures the ligature, usually around wrists, ankles or the neck, and it is in direct contact with the victim's skin. It was therefore expected that a high number of samples would be anticipated eliminations. The final result of the 124 samples in this group was 31 (25%) generated useful profiles of which 10 (8%) went on to match and 21 (17%) remain outstanding. Anticipated eliminations accounted for 55 (44%) of the samples. (Fig. 6.18).

The main sub-groups within the ligature category fell into three types; adhesive tape, rope and as mentioned previously, plastic cable ties. In all of the cases the offender introduced the ligature to the crime scene. The sticky side of adhesive tape is mainly protected from touch until used and is of single use. Likewise with cable ties these ligature types are of a single use nature; whereas all the rope in these cases appeared to be well used or handled, none of it looked new. All of the rope was of an abrasive type without a covering sheath.

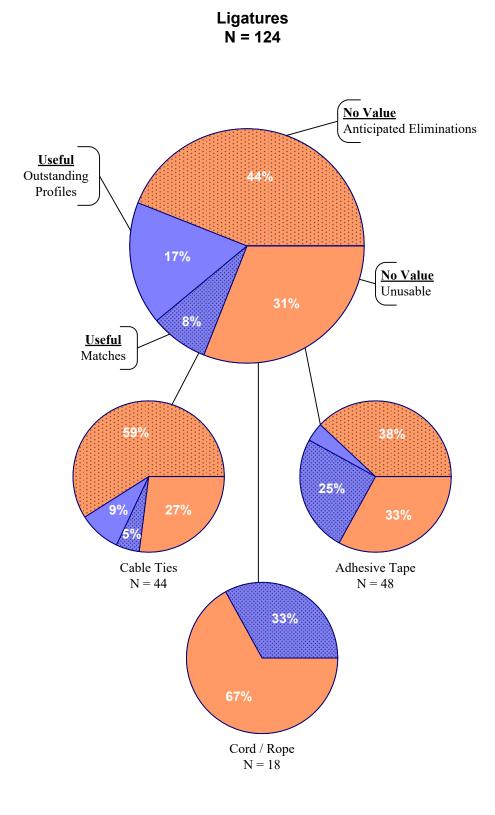


Figure 6.18 – Results for ligatures.

Only used cable ties were submitted for LCN DNA profiling. The sampling of the tie concentrated around the fixing mechanism and the plastic end that required pulling through the hole (Fig. 6.19).



Figure 6.19 - Wrists bound with cable tie showing target area



Figure 6.20 – Ankles bound with adhesive tape showing target area

With the adhesive tape, again the ends that had been torn or cut were targeted for analysis (Fig. 6.20), avoiding the area that had been in direct contact with the victim. The area for sampling ropes was less defined and depended on the victims' statement, unless there was a knot which could be targeted, or it had been left on the victim indicating where or how the offender had tightened it.

At 59%, the cable ties gave a significantly higher number of anticipated eliminations than the other ligature types. Victims in these cases often had areas of abraded skin through the plastic ligature cutting in and they had also experienced difficulty in removing the ligatures. This is likely to account for the high anticipated elimination rate. Despite the variation in the useful profiling rates for adhesive tape and cable ties the resultant matches were very similar with both generating 4-5%.

A smaller number of samples were analysed for rope ligatures. Out of the 18 samples, 6 (33%) generated a useful DNA profile and all of these resulted in a match. None were anticipated eliminations to the victims. The rest failed to produce any useful results for the investigation.

Statistically there was no difference between rope and adhesive tape ligatures in generating useful profiles (p = 0.75), however both of these were more productive than cable ties.

6.3.6 Personal Belongings

This category covers items that can usually be directly associated with an individual and considered personal property such as handbags or purses. In a large proportion of the 182 samples analysed, the owner of the property was known and in many cases was also the victim of the crime. Due to this it was expected that the anticipation elimination rate would have been higher than is demonstrated by the 46 (25%) obtained in these results. This is only marginally higher than the total number of useful profiles of 42. Matches were obtained in 15 (8%) samples and 27 (15%) were useful but remained outstanding (Fig. 6.21).

The main sub-groups within this category were handbags, purses/wallets, lighters/matches and keys, like the other sub-groups within categories these demonstrated a variation in the results obtained.

The 38 handbags and 14 purses proved unsuccessful with no matches being generated, although 2 (14%) useful profiles were obtained from the purses. A significant number, 16 (42%), of handbags generated DNA profiles that belonged to the owner and were anticipated eliminations. The majority of these items originated from street robbery offences and were submitted to establish if LCN DNA techniques could aid the criminal investigation. Details of this initiative are given in Appendix 9 – Street Robbery Initiative.

Greater success was achieved within the 'other bag' category, which included 30 shopping bags and rucksacks. In this category 6 (20%) useful profiles were obtained, resulting in 3 (10%) matches. It was noted that these were all from rucksacks.

Keys had the highest anticipated elimination rate at 58%, contrasting significantly with the 3% from lighters. The 38 keys originated from a variety of sources, some having been stolen to access vehicles, others being house keys taken in street robbery and several being keys used to open safes or strong boxes during armed robberies. All the keys had known owners or users allowing appropriate elimination samples to be submitted. On 30 mechanical lighters, the mechanism to create the 'strike' was targeted for sampling. This was sometimes a wheel or a push button. All of the mechanical lighter samples had been items left by the offender or the origin of the lighter was unknown and believed to be the offender's. As no owners were identified no elimination samples were submitted for comparison resulting in 0% anticipated elimination rate. The mechanical lighters produced 8 (28%) useful profiles with 4 (13%) generating a match and 4 remained outstanding. Although there were small numbers, statistically lighters were more productive than keys (p = 0.005), although striking matches proved even better (p = 0.01).

Samples from 32 striking matches contained used (burnt) and unused samples: A portion of the wooden match had to remain un-burnt for the sample to be taken. All of the striking matches were believed to belong to, or have been used by the offender. Most samples submitted for analysis were from serious arson cases where life was endangered or lost. All striking match samples had been removed from the box and recovered from the floor at the scene of the crime. Where it was possible elimination samples were submitted from the legitimate owners of the premises or victims at the crime scene: This resulted in 2 (6%) anticipated eliminations. A significant 18 (56%) striking matches produced a useful profile; there was no difference in the profiling rates for burnt and un-burnt samples. Of these 18 useful profiles 4 (13%) resulted in a match and 14 (43%) remained outstanding.

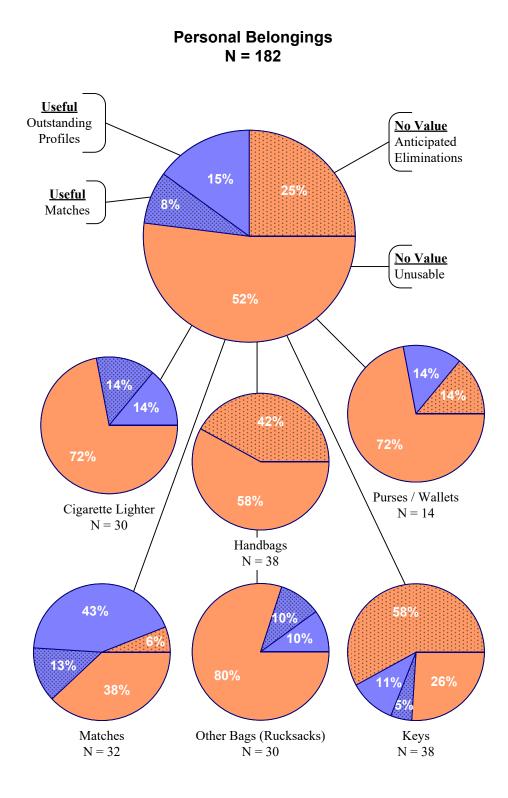


Figure 6.21 – Overall Results for Personal Belongings

Within the 68 samples analysed from handbags and other bags, 24 were taken from the fastening mechanism. These were a variety of zips, clasps and plastic rucksack clips. The fasteners generated 4 (18%) useful profiles of which 2 (9%) went on to match with 2 remaining outstanding. Anticipated eliminations accounted for 6 (25%) of the samples. It was noted that the rucksack clips generated the results whereas the zips or clasps failed to generate any DNA profiles (Fig. 6.22).

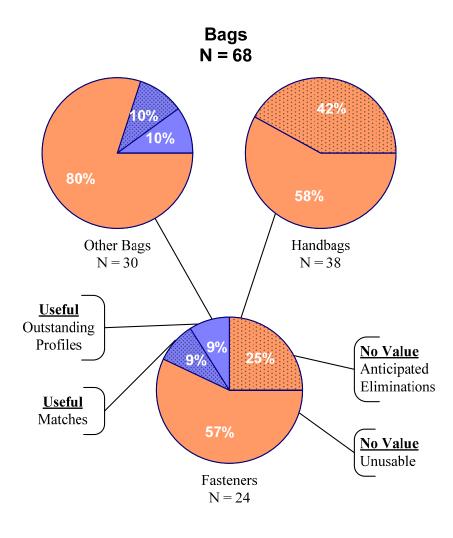


Figure 6.22 – Results for fasteners on bags

6.3.7 Premises

This category covered buildings and fixtures. All the buildings included in the results are from dwelling houses and not commercial premises. Overall very limited results were obtained from the 144 samples within this category and although the occupiers of the premises were known, and appropriate samples submitted, fewer than may have been expected went on to be anticipated eliminations, the final figure being 19 (13%). The number of useful profiles obtained was even less at 12 (8%) and in total only 3 (2%) samples produced a match.

The majority of samples were of a very speculative nature being taken from sites where an offender may have touched or handled an item, such as a door handle or when a cable had been pulled from a wall.

Samples taken from handles were from doors and windows, neither of which produced any useful profiles and as could be expected, provided one of the higher elimination rates. Cable and wire samples related to telephone cables and alarms or electrical equipment that had been pulled from fixings and walls. As with the handles, these also didn't produce any useful profiles. The samples from windows, which included swabs taken from the glass or the frame, fared slightly better with 3 (8%) producing a useful profile but none of these resulted in a match. Swabs from walls and banisters failed to produce any results.

Doors were further subdivided into two areas, the letterbox and handle used for opening or closing. The letterboxes in 32 of the 38 samples analysed were swabbed following a series of linked, high value crimes where prestige vehicles were being stolen using a particular modus operandi (see Appendix 10 – Hook & Cane Burglaries).

Over all, door handles did not produce any useful results. Letterboxes had only a minimal success rate of generating useful profiles in 4 (10%) cases, half of which went on to produce a match giving an overall match rate of 5% (Fig. 6.23).

90

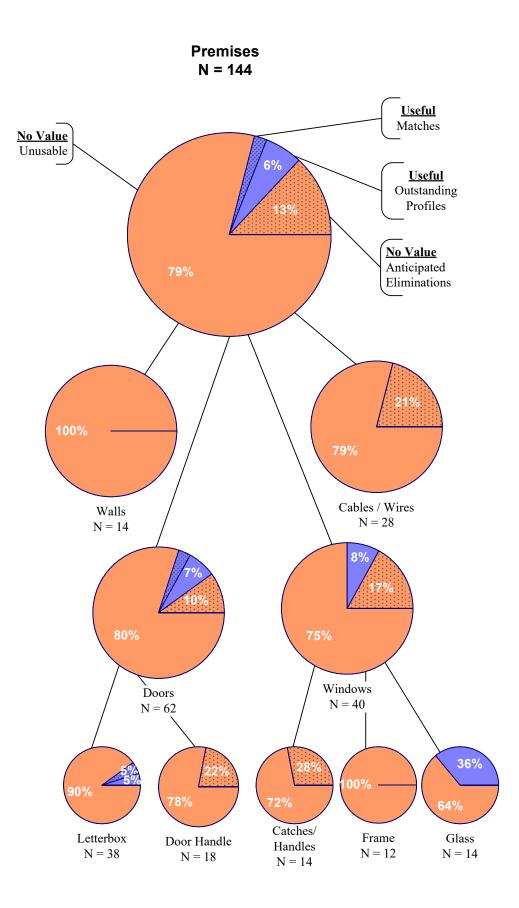


Figure 6.23 – Overall Results for Premises

6.3.8 Tools

The 72 samples from tools within this category have been used as a tool, and not as a weapon, even if not for the purpose they were designed: For instance a large number of the screwdrivers were used as leverage tools to force windows or car doors and not to remove / insert screws. With the exception of screwdrivers, where a small number had been taken out of the owners shed, they were all brought to the scene and left behind by the offender. Tools have clearly defined areas that are held during use and these areas were targeted for sampling.

Despite having a specific handling area to target on each tool, only 16 (22%) of samples generated a useful profile, generating 9 (13%) matches, 7 (9%) remained outstanding. Only 6 (8%) were anticipated eliminations, however, very few elimination samples were submitted for comparison, as the legitimate owners of the tools were not known in the majority of cases.

Further division of this category showed that torches were clearly the most successful item analysed (p = 0.005), with 11 (67%) generating a useful profile and 5 (33%) a subsequent match. Screwdrivers were also fairly successful, in comparison with other categories, with 8 (27%) samples giving a useful profile and 2 (20%) matching. A further 2 (20%) were anticipated eliminations.

Spanners and sledgehammers were sampled in very small numbers and although 2 of the spanners DNA profiled neither generated any matches and the small number limited the value of results (Fig. 6.24).

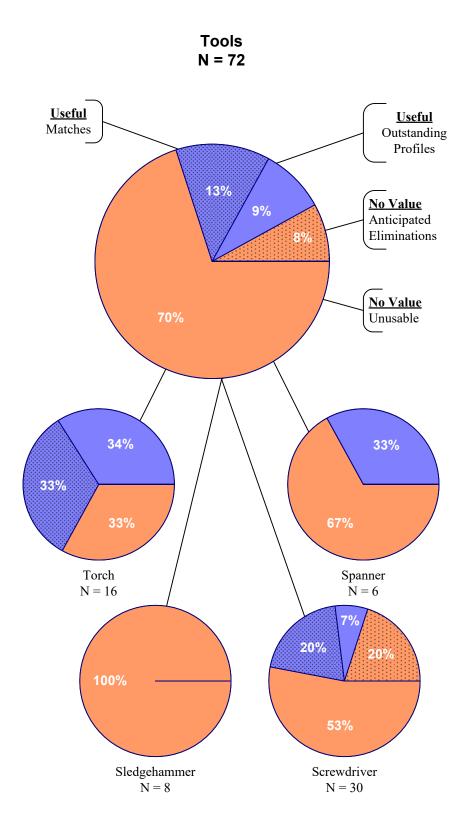


Figure 6.24 – Results for tools.

6.3.9 Vehicles

Cars, motorbikes and bicycles are not only the target of theft but are often used in the perpetration of a crime. They can be used as modes of transport for offenders, as a specific get away vehicle later to be abandoned, or as a method of entry into premises when committing a ram raid type offence (where a vehicle is driven forcibly at premises to break through a barrier such as a door, window or security shutter). In extreme cases they can also be used as a weapon if deliberately driven at another vehicle or person, or become the crime scene when an offence happens in or around the vehicle.

In total 582 samples were analysed from a variety of vehicle types, mainly standard motorcars of varying models. When all the samples were taken together 24% produced a useful profile resulting in 4% matches. The match rate was surprisingly low considering some of the defined target areas for sampling, such as the steering wheel. Where possible, elimination samples were taken from the main driver of each vehicle, which resulted in 12%, anticipated eliminations, all of which came from around the driver's cockpit area. A number of vehicles were not registered and were believed to be 'owned' by criminal gangs; in these cases no elimination samples were available.

The anticipated elimination figures are likely to be under represented. This is due to only the main drivers providing elimination samples for vehicles, when in some cases they were shared within households or had regular passengers (Fig. 6.25).

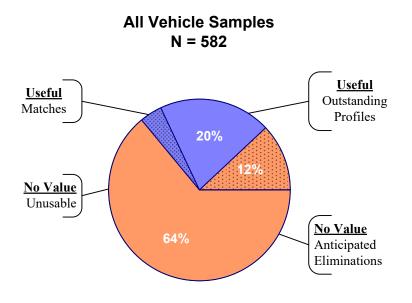


Figure 6.25 – Overall results for vehicle samples

Vehicles had the largest number of sub-groups which covered the interior and exterior of the vehicles. The sub-groups sampled varied significantly in the results produced; the highest useful profiling rate being 67% from windscreens, however, only 6 samples were analysed and none of these went on to produce a match. These were samples where it was believed the offender had made contact with the windscreen, usually following a collision of the vehicle, and a mark or screen damage was clearly visible.

The area within a motor vehicle that produced the most matches, 8%, was from the steering wheel, which supports the Pizzamiglio, *et al.*, (2003) case study that also got a result from a steering wheel. However, statistically the rear view mirror provided the most useful profiles (p = 0.001). In addition the handgrips of bikes (bicycle and motorbike), consistently resulted in useful profiles, with a rate of 30% and resulting in 10% matches. Statistically there was no difference (p =0.2) between the handbrake, gear stick and steering wheel (Fig. 6.26).

Vehicle Sub Groups

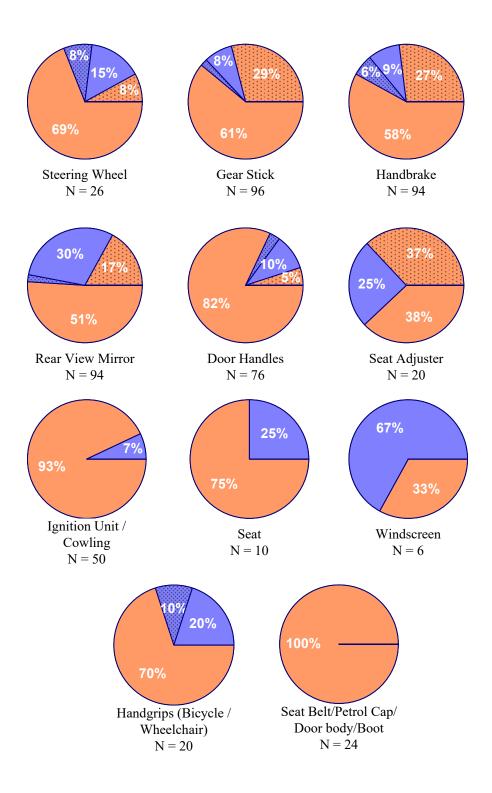


Figure 6.26 – Results for vehicle sub-groups

Stolen motor vehicles and vehicles used in crime are often subject to having the number plates changed so the vehicle will be less easy to detect (Bossier, 2006). This involves handling the actual front and rear number plates and the mechanism to secure it, which is often screws.

The false and changed number plates were sampled around the edges, preserving the smooth surfaces for fingerprinting, but it was noted that the plates were often contaminated with greasy road grime. The fixing screws were recovered as an item; the assumption being that the screw area was protected from being inside the number plate or body of the vehicle.

Although the edges of the number plates gave useful profiles in 10% of cases they did not produce any matches, whereas the screws had useful profiles in 14% of cases and resulted in 7% matches (Fig. 6.27).

It has been suggested by CSIs and vehicle mechanics that not only had the plate or body of the vehicle protected the screws but also they may have been held in between the lips or in the mouth during the fixing process that could have deposited small amounts of saliva and cellular material on the thread.

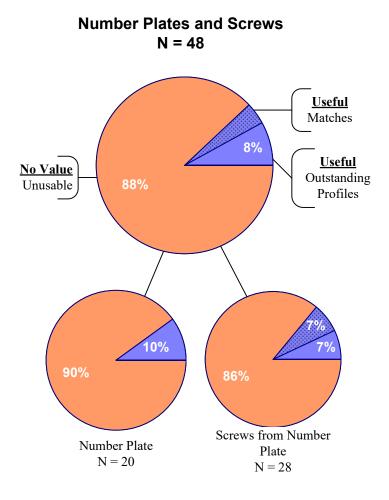


Figure 6.27 – Results for number plates and screws.

6.3.10 Weapons

Within this category any item that had been used deliberately against a person to cause pain or injury was considered a weapon with the exception of firearms which has its own section. This included objects that are familiar as weapons such as knives but also included coshes, metal bars, baseball bats, wooden batons, bricks, stones and hammers.

Of 190 samples analysed 38 (20%) gave useful profiles resulting in 23 (12%) matches and the remainder outstanding. A further 23 (12%) were anticipated eliminations, in the majority of cases due to the victim's blood contaminating the item.

Differences were again shown in the sub-groups but despite these differences in the useful profiling rates there is little variation in the final match rate between knives, metal bars and wooden bats, the range being 12-16%. The anticipated elimination rate also appeared fairly stable at 12-14%, with a slightly lower rate for knives at 7%.

The 16 stones and bricks were the least successful with no DNA profiles of use being generated. In the majority of cases the area that an offender was likely to have handled a weapon was clearly defined. This was less so with bricks and stones, and these also tended to have more debris associated with the item such as soil or moss.

The 88 samples taken from knives were further divided into specific areas that were then targeted to locate an offender's DNA profile. In a small number of cases, where knives had been abandoned, it was necessary not only to try to put an offender's DNA profile onto the knife but also the victims. Knife handles produced useful profiles in 20 (29%) cases (including a small proportion 7% that had been recovered from water or where some attempt had been made to wash the knife).

Knife handles went on to produce 12 (18%) matches with only 4 (6%) being anticipated eliminations from victim contamination. Blades proved to be less successful with no useful profiles being generated.

Although a very small number of knife sheaths were sampled, 6 in total, these showed a significantly higher success rate (p = 0.001). Useful profiles were found in 4 (67%) cases and resulted in 2 (33%) matches. None of the sheaths appeared to have been washed or cleaned in any way. One sheath produced the DNA profile of an offender by standard SGMplusTM DNA profiling and the victims profile by LCN DNA from the interior of the sheath, the transfer of cellular material probably occurring when the knife was re-sheathed. In this particular case the knife was not recovered (Fig. 6.28). Statistically overall, knives were the best weapon to obtain a useful profile from (p = 0.01).

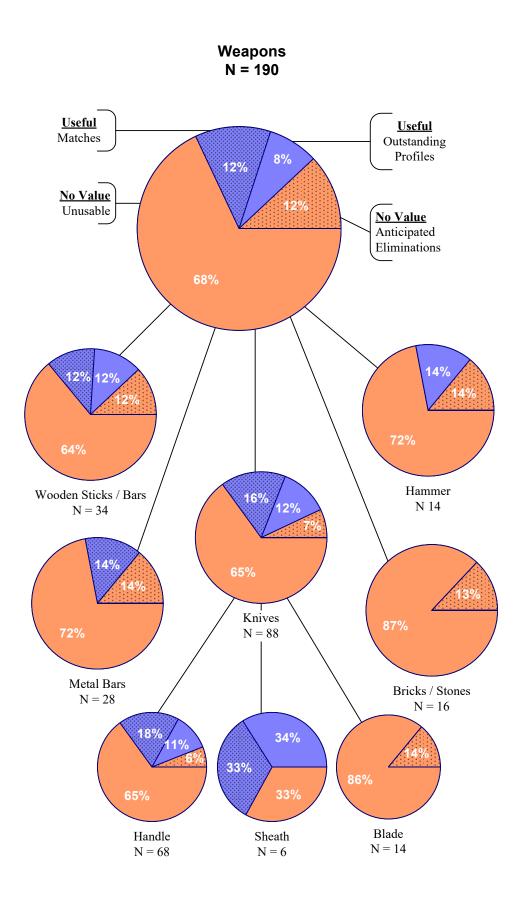


Figure 6.28 – Results for Weapons

6.3.11 Worn Items

In this category the majority of worn items were clothing but it also included jewellery and hair adornments. Overall 336 samples produced 81 (24 %) useful profiles, 50 (15%) of which remained outstanding and 31 (9%) produced matches. As the majority items in this category were directly associated with an innocent individual a high elimination rate was anticipated but when all the samples were taken together only 84 (25%) were anticipated eliminations. However, this is distorted somewhat by the items that had been discarded by offenders at scene, where the aim had been to acquire the wearers DNA profile and no elimination was submitted. Therefore, the anticipated elimination figures should be considered by looking at the sub-groups and nature of submission. Similarly the overall figures in this category which show useful profiles in 24% of cases and 9% of matches belie the extremely variable figures within the sub-groups (Fig. 6.29).

The sub-groups show distinct differences with the useful profiling, match and anticipation elimination rates. Gloves and headwear, in all cases analysed, were believed to have been left by the offender, whereas in the other clothing groups items had been worn by the victim, therefore it is not surprising to find that statistically gloves were more successful than underwear (p = 0.025).

As could be expected samples taken from a victim's clothing had a higher anticipated elimination rate ranging from 27-64%. The useful profiling range being 7-33% and subsequent matches 0-7%, varied significantly depending on the sample submitted.

Other items believed left by the offender profiled slightly better than the victim items and had a higher match rate, with the useful profiling range being 32-42% and match rate 8-18%. However, the sub-groups benefit from further division.

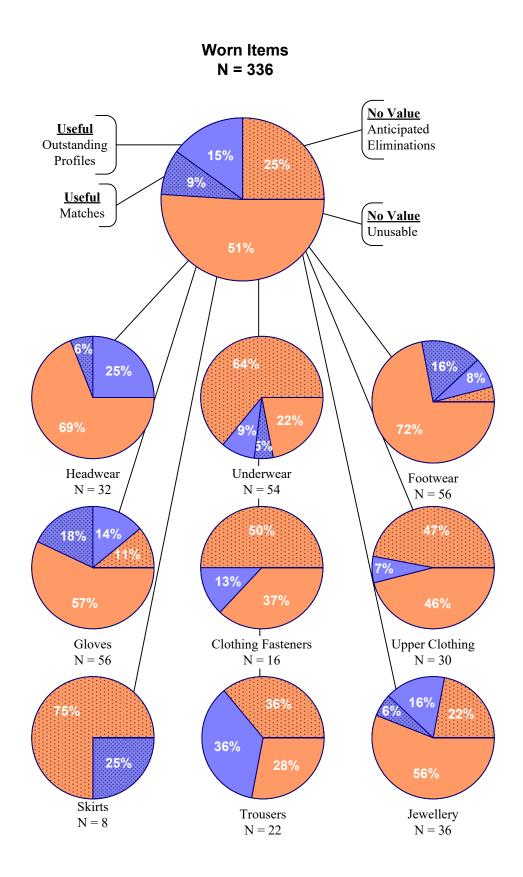
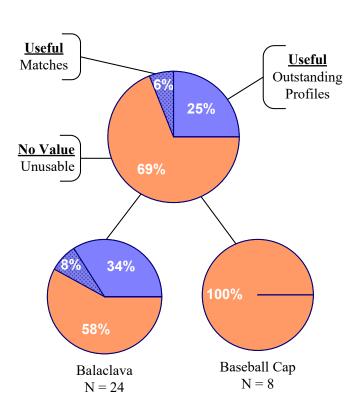


Figure 6.29 – Results for worn items.

Lower clothing produced poor results with the majority of samples being anticipated eliminations. A limited number of samples were submitted from skirts and of these a small number, 2 of the 8 samples (25%), resulted in a match to an offender: The crimes in both of these cases being a sexual offence. Despite the poor results lower clothing was statistically more useful than upper clothing (p = 0.005).

Headwear was split into baseball caps and balaclavas. All the baseball cap submissions had initially undergone standard SGMplus[™] DNA testing (the usual testing procedure for a baseball cap) and had failed to produce a useful profile. Due to the serious nature of the offences these had been recovered from they were submitted for the more sensitive LCN DNA analysis. In these cases LCN DNA analysis did not improve the results and no DNA profiles were generated (Fig. 6.30).



Headwear N = 32

Figure 6.30 – Results for headwear.

Footwear covered an assortment of types such as trainers and shoes, but also included socks. Overall shoes proved to be better than trainers in producing results with 6 (30%) giving a useful profile, 2 (10%) remained outstanding and 4 (20%) generated a match. Trainers gave useful profiles in 2 (12%) cases but failed to generate any subsequent matches. When a useful profile was generated from a sock this went on to produce a match in 2 (17%) of the cases (Fig. 6.31).

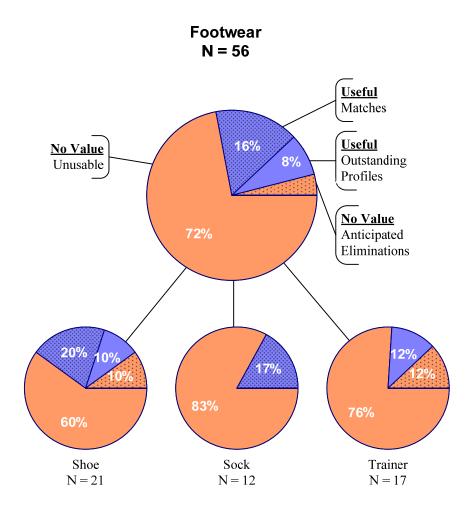


Figure 6.31 – Results for footwear- Shoe type

In addition DNA testing was done for a variety of different reasons. In some cases the wearer of the shoe needed to be determined, in others an offender had taken the shoes off the victim, therefore the handler was required. A final category was also identified where it was required to establish if the footwear had come into contact with a victim, as in the case of a kicking. The details of the crime and recovery of the footwear determined what area was sampled. Samples submitted to establish the wearer of an item of footwear achieved a useful profile in 4 (16%) cases resulting in 2 (9%) matches and 2 outstanding DNA profiles. This is significantly lower than the results achieved in the research carried out by Bright and Petricevic (2004), which achieved a 45% profiling rate from footwear of known donors. However, in Bright and Petricevics' research it would appear that only 2 people contributed footwear for analysis, which diminishes the value of their results.

Trying to identify the handler of footwear proved even less successful with no useful profiles being generated; however successful profiling was achieved in 8 (57%) victim contact submissions resulting in 6 (43%) matches (Fig. 6.32).

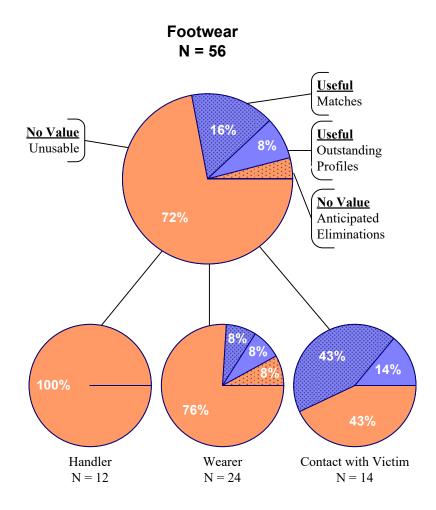


Figure 6.32 – Results for footwear- Aim of profiling

All of the samples in the underwear sub-group were from items that had been pulled, torn or handled by the offender. As could be expected with underwear, a large number of samples were anticipated eliminations from the wearer or victim. All submissions of tights were anticipated eliminations, as were 7 (63%) bras and 18 (50%) pairs of knickers. LCN DNA profiles were obtained from bras and knickers in the range of 11-13% however, only LCN DNA profiles from knickers went on to subsequently match from 2 (5.5%) of the samples (Fig. 6.33).

One of the LCN DNA profiles from the bra samples produced an unknown female profile that was not eliminated but remained outstanding despite the fact the assailant was known to be male. The provenance of the bra could not be determined in this case as the victim was deceased.

Underwear N = 57

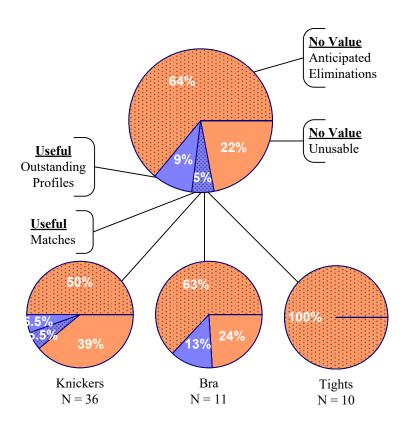
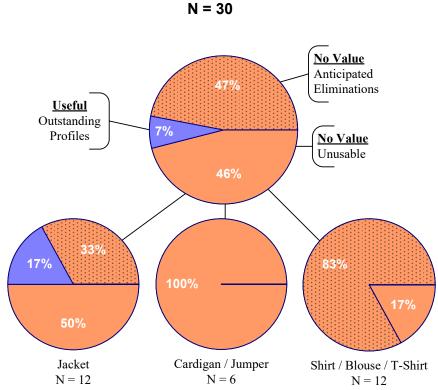


Figure 6.33 – Results for sub-group underwear.

Like the underwear sub-group all of the items in the upper clothing group had been pulled, torn or significantly handled by the offender. In the majority of cases a specific area of the clothing had been identified due to either a stress mark in the fabric or victim / witness testimony. Very few results were obtained from the upper clothing sub-group, the majority of samples producing results of no value to the investigation. T-shirts and blouses / shirts produced no useful profiles and 10 (83%) resulted in an anticipated elimination. Samples taken from jackets did generate 2 (17%) useful profiles however, none went on to produce a match and a further 4 (33%) were anticipated eliminations. Cardigans did not generate any DNA profiles at all, although it is recognised the numbers of submissions was small (Fig. 6.34).



Upper Clothing

Figure 6.34 – Results for upper clothing

The results for the knickers and the t-shirts are in direct contrast with laboratory simulations reviewed by Lowe (2002), which were detailed previously, the knickers in real cases being more productive and the t-shirts less so. This may be due to the unrealistic contact times used in the laboratory simulation research.

Jewellery, like footwear was sampled for a number of reasons, sometimes to establish the wearer or a person it had come into contact with. This could either be a person struck with jewellery, for example punched by someone wearing a ring or sometimes if the jewellery had been forcibly removed from a victim, for example a chain pulled from someone's neck.

Four areas had very small numbers submitted for analysis but they are worthy of note due to the differences in results obtained. The aim in the 4 ring samples was to establish contact with the victim after they had allegedly been punched, which produced 100% useful profiles but no matches. In contrast the hair adornments produced no DNA profiles of any value to an investigation in the 6 cases analysed. Likewise the 6 pairs of glasses failed to generate any profiles. The 3 samples taken from make up that had transferred onto clothing all LCN DNA profiled and went on to generate a match. However, due to the small numbers this may not be indicative of any future results

Overall the results are mixed with only the bracelet / watch sub-group producing any matches (Fig. 6.35).

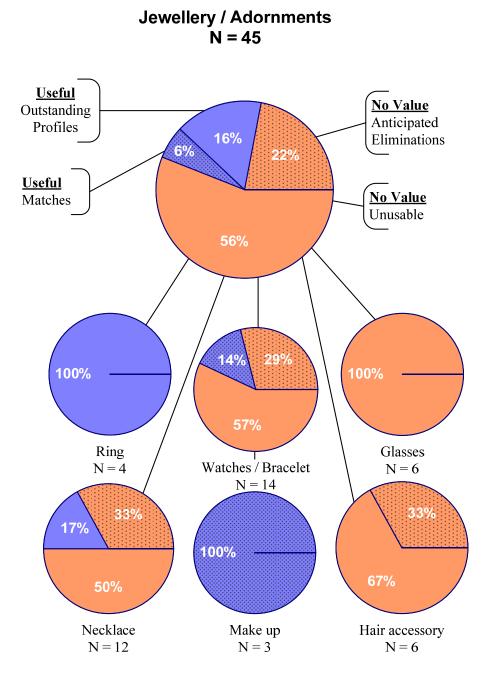


Figure 6.35 – Results for jewellery

6.3.12 Groups

Some items overlapped into several different categories or did not fit into a specific category but could be placed into a general group. Where relevant the results for the item are shown in the individual categories or sub-group, but additionally they have been included in a group of specific types of items. The groups include knots, adhesive tape, fasteners, handles and cables / flexes.

Knots were found on many evidential items including clothing ties, ligatures and drugs bags. The majority were of a simple overhand nature and the material used to form the knot varied in type including rope, plastic and fabric. Overall 4 (22%) of the 18 knots LCN DNA profiled and resulted in 2 (11%) matches and 2 remained outstanding. None of the samples were anticipated eliminations. There was little variation in the results between plastic or rope/fabric knots, however, all the matches came from the rope/fabric group.

Adhesive tape was encountered and considered a potential source of DNA when it had been used as a ligature, on weapon handles, adhered to glass at crime scenes, and on the reverse of number plates as a fixing mechanism. Of the 60 samples analysed, adhesive tape generated 14 (23%) useful profiles with 2 (3%) resulting in subsequent matches and 12 (20%) remained outstanding. A total of 18 (30%) were anticipated eliminations.

The combined results for all 40 fasteners which included zips, buttons, clasps, clips and Velcro from clothing and personal belongings gave 8 (22%) useful profiles, 2 (6%) matches, 6 (16%) profiles remained outstanding and 9 (22%) were anticipated eliminations. The most successful area for profiling and subsequent matches, as mentioned previously, was found to be plastic rucksack clip fasteners. In addition, although only a small number of samples were from zips, 75% of these were anticipated eliminations.

Handles were usually found in premises or on vehicles. This group refers to door or drawer / cupboard handles and excludes handles on bags. Of the 108 samples analysed only 10 (9%) produced a LCN DNA profile and 2 (2%) subsequently a

match. Anticipated eliminations accounted for 12 (11%) of the samples, all of which were from interior door handles. The majority did not LCN DNA profile at all which was a surprising result for an area that was known to be touched on a regular basis. A further surprise was that exterior handles appeared to generate a higher percentage of useful profiles.

The final group was cables and flexes that were mainly found in premises, vehicles or left behind by an offender. The majority were telephone or electric wires with plastic sheaths surrounding a central core of wire. Useful profiles were obtained in 6 (13%) samples and 2 (4%) went on to match. A further 6 (13%) were anticipated eliminations (Fig. 6.36).

<u>Groups</u>

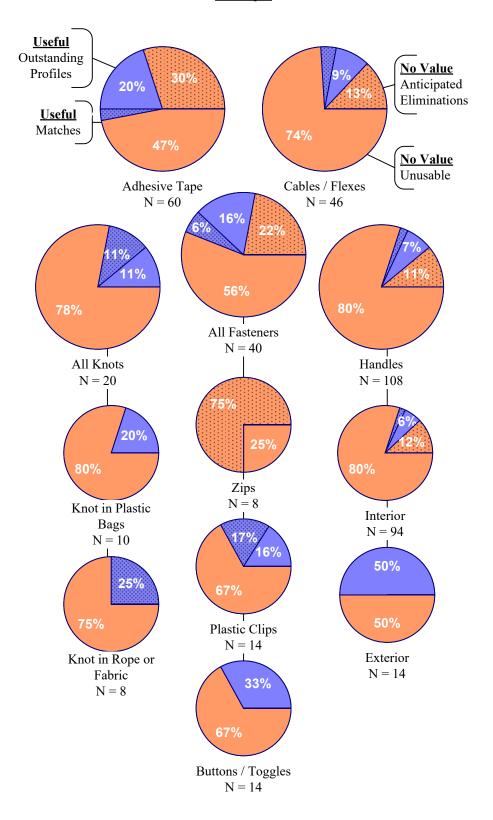


Figure 6.36 – Results for Groups

Chapter 7

Discussion of Phase 1 Results

7.1 Comparison of Sub-Groups

When the results for all samples analysed were viewed together, an overall useful LCN DNA profiling rate of 24% was obtained, 11% of samples went on to generate a match and 20% were anticipated eliminations. However, this belies the significant variations within the overarching categories (p = 0.001), which showed a range of 9% – 48% for obtaining a useful profile, a 3% - 27% range in matches obtained and a 1% - 44% range in anticipated eliminations. These differences were extended even further when the sub-groups within the categories were examined.

The categories could have been compiled differently and sub-groups of items placed together in groups by the way or amount they are handled, for instance screwdrivers and knives could have formed a group as they are handled in a similar manner utilising the palm of the hand. In addition the texture and type of surface material on these items is often of a comparable hard plastic nature. When looking at the results obtained for these items, the samples that were considered useful to an investigation and those that added no value are similar (Fig. 7.1). Useful profiles were generated on 27% of screwdrivers and 29% of knife handles; samples that added no value to an investigation being 63% and 61% respectively.

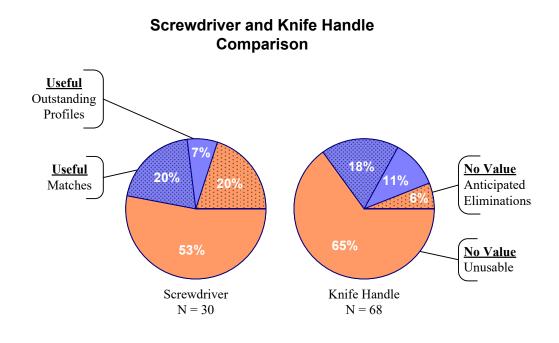


Figure 7.1 - Screwdriver and Knife Handle Comparison

Other items that may be handled in a similar way could be mobile phones and the grip of a handgun. Both are handled in a comparable way but the surface textures are different; a handgun often having a heavily textured grip (Fig. 7.2).



Figure 7.2 – Handgrip of handgun showing textured grip

The comparison between the mobile phone and handgun grip show that these do not have similar results (Fig. 7.3). Mobile phones generated 43% useful profiles and handgun grips only 23%. Samples adding no value being 57% and 77% respectively.

Mobile phone and Handgun grip

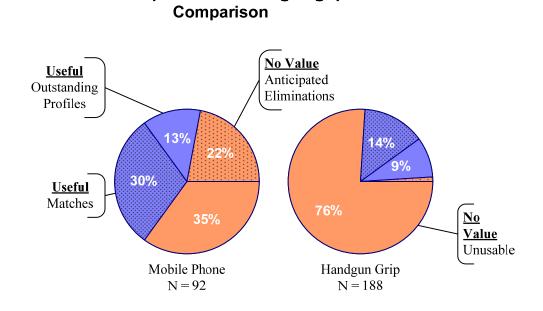


Figure 7.3 - Mobile Phone and Handgun Grip Comparison

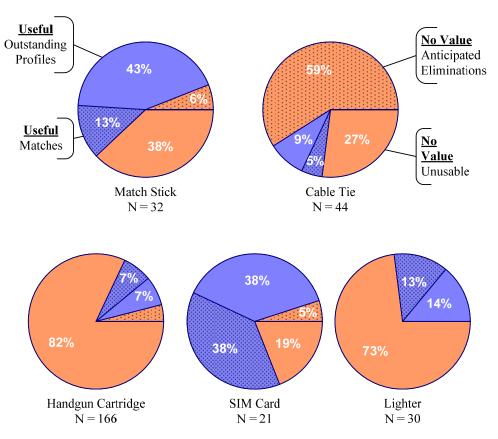
Although mobile phones and handguns may be handled in a similar way, a mobile phone is used in close proximity to a person's mouth (Fig. 7.4). Samples taken from surfaces that may have been in contact with saliva do appear to have a higher success rate than those items merely handled.



Figure 7.4 - Mobile Phone in Use Showing Close Proximity to Persons Mouth

Items that were small, fiddly to manipulate and unlikely to have come into contact with a body fluid were also compared. All the items compared in this group had very specific areas of contact with the fingers for manipulation and not the main area of the hand. These areas were targeted for sampling.

The results between the items in this sub-group were not similar and potentially supported that the method of handling an item was less of a factor in obtaining a useful profile. In the items compared it was noted that the surface material (plastic, wood, metal, mixed) and textures (rough, smooth) were all varied which may support that the surface material and texture have more of an effect on successful LCN DNA recovery (Fig. 7.5).



Comparison of small items

Figure 7.5 – Comparison of small items which require fiddly finger manipulation

If the argument that texture and surface material was valid then items with comparable surfaces should produce similar results. Therefore, a gear stick, handbrake and interior door handle from vehicles were compared as these had been made from the same types of materials and the textures were alike.

When comparing these items the results for the hand brake, gear stick and door handles are statistically similar (p = 0.2), all producing useful profiles in the range of 10-15% (Fig. 7.6).

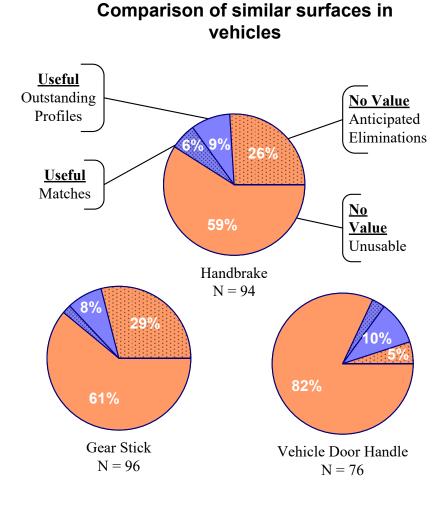


Figure 7.6 – Comparison of similar surfaces in vehicles

7.2 Discussion of Results and Early Findings

One of the aims of Phase 1 was to analyse the profiling success rates with specific regard to assisting CSIs in targeting scene examinations and to help investigators in prioritising forensic submission for analysis, particularly when there are a high number of samples taken from a crime scene. Until this point scene examiners and investigators only had personal and anecdotal experience to rely on when making decisions. This experience was often of a very limited nature as large volumes of LCN DNA submissions had not been made and these were spread across the whole of the GMP area.

Analysis of the categories and sub-groups gave an early indication of some target areas that could be considered more successful than others and also highlighted the importance of submitting elimination samples when at all possible.

In overall terms any sample from an item that was likely to have come into contact with saliva or had been near a person's mouth could be given a greater degree of consideration for sampling and submission for analysis by the examiners and investigators, as these generally provided the highest useful profiling rates.

Within the mobile phone sub-group, two areas were identified which gave a better chance of obtaining a useful profile and subsequent match; these were the keypad area and the SIM card. The batteries from mobile phones proved less useful and therefore fingerprinting was given precedence, due to the large smooth surface that was available.

The firearms category also indicated clear areas that could be prioritised when submitting samples for analysis and interestingly these differed between shotguns and handguns. Within the shotgun sub-group complete ammunition provided the best results whereas in the handgun category the handgrip proved most useful. Magazines and triggers where successful for both types of weapon. Examination of vehicles used in crime generated a large number of samples taken by CSIs, with around 50 different areas being targeted on a standard car. Early analysis of the 582 samples submitted for DNA profiling showed that the rear view mirror and steering wheel were the most likely to produce a result that added value to an investigation. In addition, where number plates had been changed the screws proved successful. Although, it was noted that overall the positive results from vehicles were lower than some of the other categories and sub-groups.

Anecdotal information about cable ties being highly successful and comments that handbags 'must' be good because it was known where the offender had handled them, were clearly disproved. In contrast, items such as striking matches from arson scenes and old rope became worthy of consideration at an earlier stage in the investigation.

The early results also allowed for a more informed discussion to take place with regard to compiling forensic strategies particularly when potential evidence types could conflict, for example, fingerprinting and DNA swabbing. Where an item had shown a propensity for very low or had had no success rate in LCN DNA profiling, but was suitable for fingerprinting, this option could be given precedence.

Regardless of the likely success rate, each submission was considered on its own merit and in the context of the crime committed. However, it did allow for the expectations of SIOs to be managed as to what results were likely to be achieved and where negative results occurred these were seen more as a closed line of enquiry rather than a disappointment or failure of new forensic techniques.

Phase one of the research clearly established that there were significant differences in the useful profiling success rates for LCN DNA submissions from different items. The results demonstrate that the recovery of LCN DNA is complex and variable depending on the item sampled. A greater understanding of the reasons for the differences and what common factors influence the success rates formed the second phase of the research. Chapter 8

Phase 2 - Results

8.1 Phase 2 - Areas for Consideration

Phase 2 of the research set out to consider why there were differences in the LCN DNA profiling success rates and to identify common factors that corresponded to these differences.

To retain continuity and consistency of information all of the original 3 552 samples analysed were included in phase 2 of the research and no new samples were added. Individual samples were excluded from results only if the information about the variable specifically being considered was ambiguous or complex. For instance when considering surface materials, some items had mixed components, such as a knife sheath that was made of leather, fabric braid, metal, and glass beads and there was insufficient information as to which area had been sampled.

The results in phase 1 clearly established the differences in the profiling rates across a large variety of sample types. When these results were considered further in Chapter 7, indicators as to why there were differences and what the common factors could be that affect LCN DNA success rates were identified for further investigation.

One indicator was that the type of surface material such as metal, wood, plastic or fabric and the characteristics such as porosity and texture, might have had a bearing on the results, therefore, this was considered in more detail in Phase 2.

The way an item had been handled appeared to have less of a bearing on the results but further consideration was given to the identification of target areas to sample on an item.

In addition to the surface characteristics and material, phase two of the research also analysed the results with regard to factors that surrounded the recovery and sampling of the item such as the month of recovery, whether the item was inside or outside and wet or dry. Further analysis was also undertaken on whether the original item or swabs from the items surface were submitted for analysis, and the length of time taken in submitting samples for analysis.

8.2 Surface Materials

Surface materials were broadly split into 9 areas, plastics, rope, rubber, stone (bricks, rocks, and cement surfaces), wood, glass, metal, paper and textiles. The surface material was determined by the examining staff and not by any technological means in order to retain the ethos of the research in that the findings should be easily translated into an operational environment.

Like the earlier phase 1 results, a large variation was seen in the profiling rates. Paper proved to be the most successful in gaining a useful profile, however none of the LCN DNA profiles went on to secure a match. The paper was not divided into types, unlike the study by Sewell, *et al.*, (2008), where differences were observed between different types, office paper and white card proving less successful than newspaper, magazines and filter papers. It was concluded that the bleaching agents used in white papers inhibited the extraction of DNA.

Overall surface materials made from glass gave consistently good profiling and match rates. Items that were sampled from rubber and stone surfaces proved the least successful for LCN DNA techniques. The samples in the stone group were primarily from assaults and rough ground and could have been contaminated with biological material from the victim or soil. Victim contamination supported the higher anticipated elimination figure and biological material can be a DNA extraction inhibitor, which may explain the lack of results in this area (Fig. 8.1).

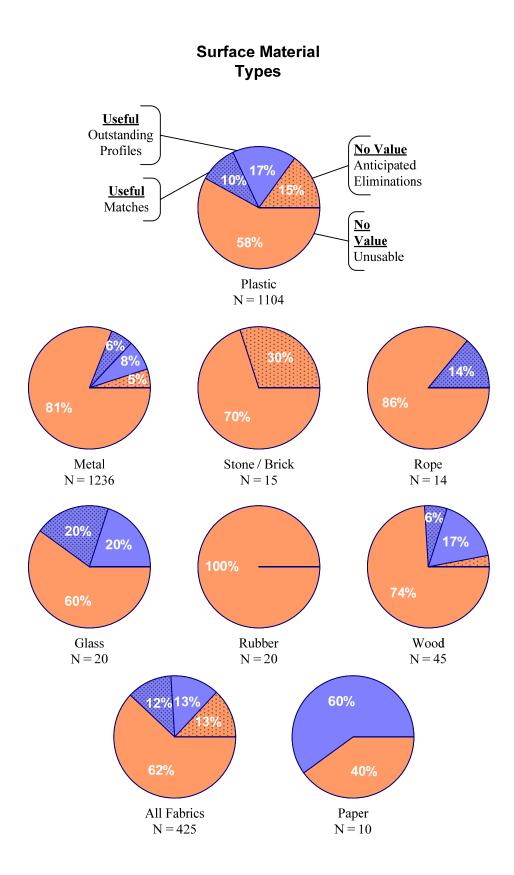


Figure 8.1 – Results of Surface Materials

8.2.1 Plastics

Due to the wide variety of types and grades of plastic it was considered that this may have an impact on any results. Predominantly they could be categorised into two groups, hard or rigid plastics (e.g. credit cards, interiors of vehicles) and soft plastics (e.g. plastic bags, handbags, food wrapping).

In reality the result showed that there was no statistical difference between the two different groups of plastic with regard to gaining a useful profile, however a larger number of soft plastics were anticipated eliminations (Fig. 8.2). On further analysis of the samples submitted for each group, the soft plastics had a larger number of items that were handled extensively by the victim of the crime and where an elimination sample could be submitted. For example, a plastic handbag pulled off a shoulder during a robbery. In contrast, the hard plastics group had a larger number of samples from items such as screwdriver handles, gun grips and the interior of ignition cowlings, where a victim or owner would not have handled the target area; subsequently fewer elimination samples were submitted.

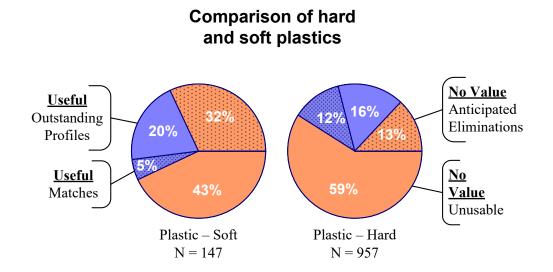


Figure 8.2 – Results of Hard and Soft Plastics

8.2.2 Textiles

Like plastics, the textile category was further divided into smaller groups. During some previous research Seah, *et al.*, (2004) noted a variation in the profiling success rates between different types of fabrics during standard SGMplusTM testing. Seah, *et al.*, found that cotton and nylon were more successful than polyester; wool was in the mid to lower range. Determining the type of textile proved difficult for staff that carried out the examinations, as a large number of fabrics were mixtures or unlabeled. This reduced the groups down to four basic categories of leather, nylon, knitted and general fabric. Therefore, it was not possible to see if the research results of Seah, *et al.*, were replicated within the LCN DNA results. However, a comparison could be made with the research by Bright & Petricevic (2004) where it was suggested DNA recovery was more viable on synthetic materials than leather, which may contain a PCR inhibitor.

The actual results during this research showed leather to have a slightly higher percentage success rate than nylon, however this proved to be statistically insignificant (p = 0.75) and overall there was little variation between the textile groups as to success rates (Fig. 8.3).

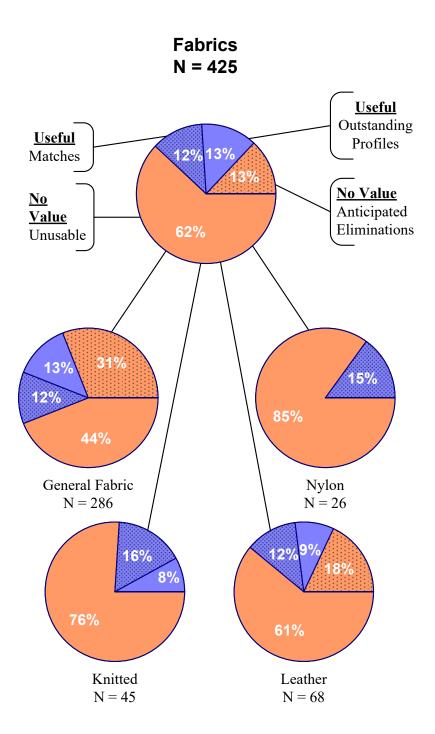


Figure 8.3 – Results of Textile Types

The absence of anticipated eliminations within the knitted and nylon group was notable within the textile categories. Further analysis of the samples submitted showed that these samples were predominately from items of clothing left behind by offenders, i.e. gloves, and therefore no elimination sample was submitted.

8.3 Surface Characteristics

The surface characteristics, like the material type was determined by the staff examining the item and not by any technical means. Items that proved to be ambiguous were omitted from the results. Only two variables were considered, these being porosity and texture.

8.3.1 Porosity

Samples were categorised as either porous or non porous depending on what the sample was taken from. Previous research by Wickenheiser (2002), found that the amount of DNA transferred to an item was independent of the handling time and more greatly related to the porosity of the surface. Wickenheiser found that DNA material more readily adhered to porous surfaces than non porous.

In live crime scene situations it is unusual to know the handling time of any item, unless the victim has been present throughout the handling and can verify the contact or the incident is captured on CCTV providing a recording of the event.

Like Wickenheiser (2002), the results from this research showed porous surfaces to be more successful than non porous surfaces (p = 0.001) in gaining a useful profile and captured more DNA material including that of persons who could be legitimately eliminated (Fig. 8.4).

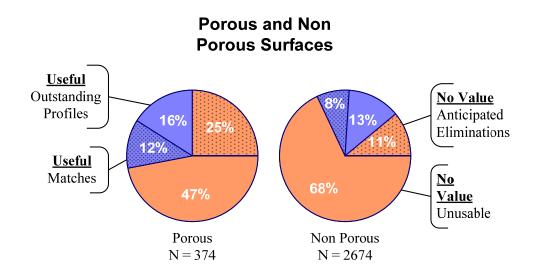


Figure 8.4 – Results of Porous v Non Porous Surfaces

8.3.2 Surface Texture

Determining the texture of an item was subjective. The only guide given was if the area being sampled had a clear edge or ridges or if it could be considered abrasive or rough. As with all the other categories items that proved to be ambiguous or difficult to categorise were omitted from the results.

It was anticipated that rough surfaces would be more successful in producing a useful profile as the abrasive nature of the surface could slough skin cells and the rough texture would provide a surface that the cells could adhere to. However, prior to the results of this research it wasn't known if these cells were deposited and whether they would be recovered during the sampling process.

The results clearly show that rough surfaces were significantly more productive than smooth surfaces (p = 0.001) and as with the porous surfaces, rough surfaces showed a greater propensity for DNA deposition including that from anticipated elimination sources (Fig. 8.5).

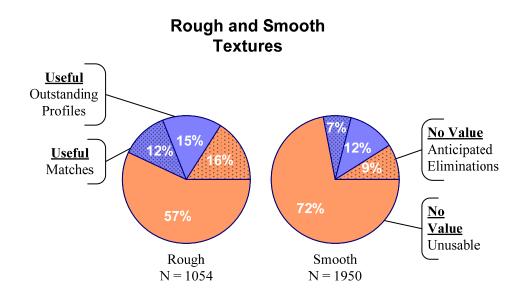


Figure 8.5 – Results of Rough v Smooth Textures

8.4 Recovery Factors

During phase 2 of the research additional areas were considered that had less to do with the actual item being sampled and were around the environmental factors and sample recovery decisions. This included, the time of year, whether the item was seized or a swab was taken and the time taken to submit samples after recovery, to the laboratory for analysis.

8.4.1 Environmental Factors

During crime scene examinations CSIs experience seasonal variations in the occurrence of different evidence types which are attributed to the weather, such as fewer fingerprints being found in the winter and more footwear marks being recovered. Lack of fingerprints is often attributed to the wearing of gloves in cold weather and reduced sweat deposition, again due to the cold. The increase in footwear marks may be caused by the increase in mud and wet debris on soles of shoes that is then more easily transferred to other surfaces. Although no research or statistical information could be found on seasonal effects on DNA recovery, this was considered during the research. In addition, the environmental

factors of a sample being inside or outside and whether it was wet or dry were analysed for any differences.

Seasonal Variation

Initially the sample results were broken down by the month of recovery (Fig. 8.6). A large variation was noted between the months but did not appear to cluster in any particular month or season. Similar variations between the months were also seen when each year of the research was mapped individually (not shown) however, it was noted that the months of variation did not correspond.

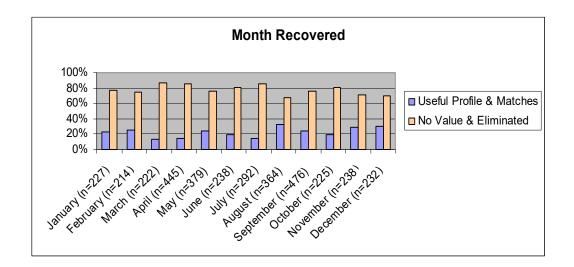


Figure 8.6 – Sample Results by Month Recovered (All Years/Samples)

The results were then grouped into two main seasonal periods of six months each to establish if there was any overall seasonal variation (Fig. 8.7). Statistically the month of recovery proved to be insignificant (p = 0.75) and therefore no seasonal variation was established.

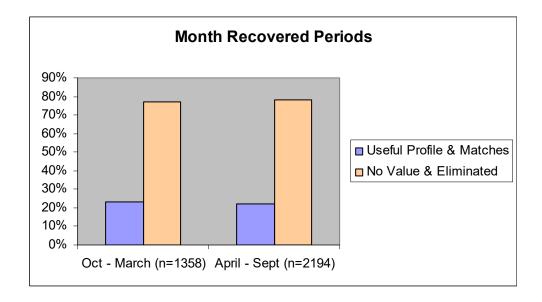
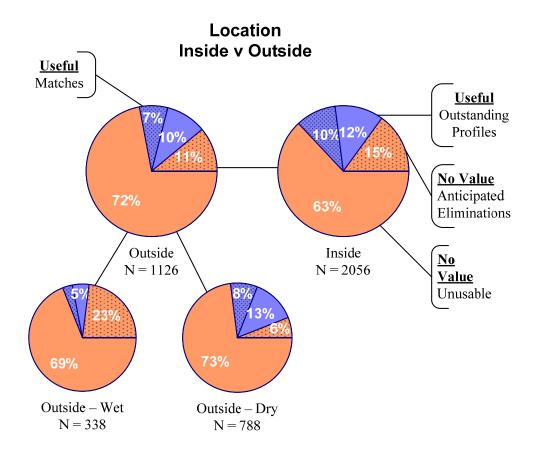


Figure 8.7 – Sample Results by Seasonal Periods (All Years/Samples)

Location

A further environmental factor was considered with regard to the location the sample was recovered from and whether it was inside or outside. A few samples were omitted from the results if the item had been moved between the time of the crime and the recovery of the sample by the CSI. This had happened when the first police officer attending the scene had moved items inside to preserve the forensic potential, for instance pieces of broken glass outside a point of entry window being brought inside to protect the item from rain. This also brought about the variable that samples could be taken from wet items that had been subject to rain, dew or tap water.

A much larger number of samples were taken from the inside of premises and these generally had a statistically (p = 0.001) higher success rate than those taken from outside. A significantly higher success rate (p = 0.001) is also shown for samples taken from dry items or surfaces (Fig. 8.8).



for location, Inside v Outside

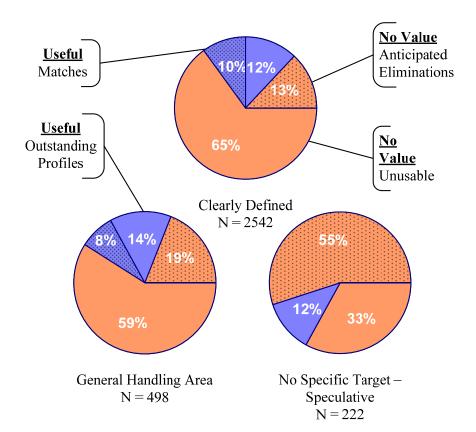
8.4.2 Recovery Decisions

CSIs made decisions on where to take the sample from on any particular item and also whether it was necessary to seize the entire item or take swabs as samples. Wickenheiser (2002) research showed that the time spent handling items had little influence on the ability to recover a DNA profile, and the results of Phase 1 of the research showed that the method of handling also had little influence, however, time and method of handling may be less relevant if the target area could be clearly defined, so this was considered as a separate variable.

<u>Target Areas</u>

Sample target areas were divided into three groups, clearly defined such as a button, switch, trigger, indicated by CCTV footage etc., a known general handling area such as baseball bat handle, steering wheel etc., or where there was no specific target area and speculative swabbing was carried out. This is where there is not a defined handling area and the CSI is 'guessing' based on the presentation of the crime scene.

Statistically there was no difference (p = 0.2) in whether a DNA profile was gained between the different target areas however, a significant difference was noted in anticipated eliminations and matches. Areas that were speculatively swabbed proving to be less successful overall (Fig. 8.9).



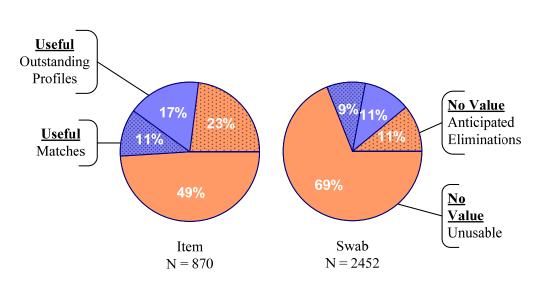
Target Area

Figure 8.9 – Sample Target Areas

Item v Swab

Once the CSI had determined a potential item for LCN DNA deposits, and a suitable area to be targeted, a decision had to be made as to the best method of recovery and whether swabs should be taken or the whole item seized. In some instances it was not possible to seize the whole item, such as parts of buildings or items that were very large or heavy. Also in some cases the value of the item to the owner meant that it was inappropriate to remove it. In such cases swabs were the only alternative. Due to the cost of LCN DNA analysis it was common practice to carry out fingerprint examinations, where possible, prior to LCN DNA submission, however, the DNA samples had to be taken in order that the DNA trace material was not lost during any such procedures. In addition, particularly in the case of firearms, it was desirable for other forensic examinations to run concurrently. In these cases swabs were taken as the preferred method of recovery.

In some cases though, it was possible to seize the item and submit it for LCN DNA analysis without compromising any other forensic trace evidence and this did prove to be statistically more successful (p = 0.001) than swabs that had been submitted (Fig. 8.10).



Item V Swab

Figure 8.10 - Item v Swab Results

8.5 Submission Times

The decision to swab or seize an item potentially had an impact on the submission time between the recovery of the sample and analysis processing within the laboratory. The 'swab and pend', i.e. take the swabs and hold them pending other forensic results or investigative leads, often meant that samples were held for several months prior to submission. Also, as major investigations progressed and leads became more scarce, where the cases remained undetected, decisions to submit LCN DNA were made in an effort to solve serious crime, even if it was considered a 'long shot'. It was expected that the success rates would diminish as time progressed and unsolved cases had the poorer or least viable samples submitted.

This did appear to be the case, with a notable drop off in the ability to profile any DNA, including anticipated eliminations, from samples submitted 5 months after recovery of the sample (Fig. 8.11).

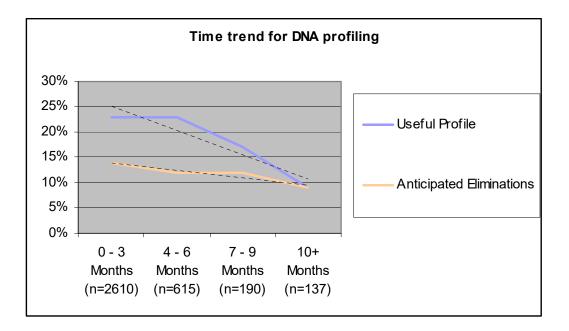


Figure 8.11 – Time trend for DNA profiling.

However, research in 2002 and 2003 also considered the effects of storage on LCN DNA samples. Lowe (2002) carried out research on items (not swabs) stored in controlled dry conditions that had been handled by known good and bad DNA shedders. The items were stored for up to 1 year and DNA was recovered in suitable amounts for profiling. In contrast to Lowe's research, Lund & Dissing (2003) noted a high degradation in blood swabs taken with wet cotton swabs when stored at room temperature for 1 week. This was not replicated with dry stains on filter paper that were stored in humidity conditions and it is noted that Lund & Dissing did not freeze their samples, which is the recommended method of storage (FSS, 2004).

The above research potentially shows that storage may be a key factor and whether items are stored dry or frozen. Phase 2 of this research already supports that there are differences in the results for swabs and dry items. Swabs are stored frozen and items which are predominantly dry, are stored at room temperature. Therefore, the submission time trend was also considered for the two different types of sample, swab or item to take account of the storage.

The ability to obtain a profile from items stored in dry conditions did not deteriorate and remained consistent throughout. In direct contrast the success rates in obtaining a profile from swabs that were stored frozen started to deteriorate at the 5 month period with a significant fall in positive results at 8 months (Fig. 8.12).

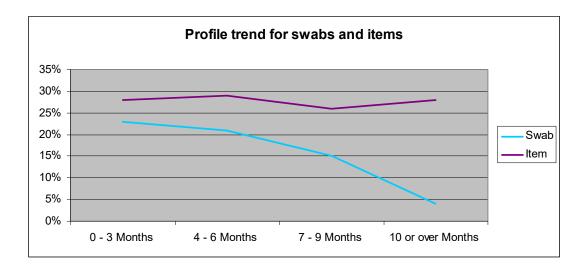


Figure 8.12 – Useful Profile Time Trend for Swabs and Items

Chapter 9

Conclusion & Recommendations for Further Research

9.1 Conclusion

The research was divided into two distinct phases, initially defining what a useful DNA profile was in the context of a criminal investigation, creating a method for CSIs to classify samples and establishing that there were differences in the profiling success rates across the different classifications. Significant differences were found within the phase one results and items were identified that appeared to prove more successful than others. Further analysis of these results also indicated factors that could be explored in more detail during phase 2 with the aim of identifying the common factors that had a positive or negative influence on the success or failure of samples to DNA profile.

Phase 1 of the research clearly highlighted that the ability to obtain a LCN DNA profile from an item did not necessarily add any value to a criminal investigation. The top five items sampled that consistently produced DNA profiles were tights, upper & lower arms, face, scanner/radio and shirt/blouse/t-shirt. However, when these are considered against the top five items sampled that produced a useful profile for criminal investigation, only one corresponds, which is the scanner / radio samples; the remaining 4 areas that fell into the top five for producing a useful profile were SIM cards, kiss / lick, torch and key pad / mouth piece. Conversely, 4 of the top 5 items to produce a profile were in the top five for being anticipated eliminations (Table 9.1). Tights which generated 100% profiles had no profiles which were useful for criminal investigations; all of them were anticipated eliminations. Upper and lower arms which generated 91% profiles only had 8% which fell into the useful profile category.

Therefore, no correlation could be assumed from the ability of a sample to profile and the usefulness to a criminal investigation.

| Item | % Profiled | ltem | % Useful profile | ltem | % Anticipated eliminations |
|---------------------|---------------|-----------------|------------------------|---------------------|----------------------------------|
| Tights | 100 | Scanner / radio | 83 | Tights | 100 |
| Arms upper & | | | | Arms upper & | |
| Lower | 91 | SIM card | 80 | Lower | 83 |
| | | | | Shirt / blouse / t- | |
| Face | 89 | Kiss or licked | 75 | shirt | 83 |
| Scanner / radio | 83 | Torch | 67 | Face | 78 |
| Shirt / blouse / t- | | Key pad / mouth | | | |
| shirt | 83 | piece | 60 | Bra | 63 |

Table 9.1: Top five items for generating a profile, generating a useful profile and anticipated eliminations.

However, when the top 5 items that generated a useful profile are compared against the top 5 that went on to produce a match, these are comparable (Fig. 9.2). This suggests that the useful profiles are not background or innocent profiles of persons that could be legitimately eliminated but are more likely to belong to offenders that have not been identified, provided elimination samples have been submitted for comparison.

| ltem | % Useful profile | Item | N |
|-----------------|---------------------|---------------------|---|
| Scanner / radio | 83 | Kiss or licked | |
| | | Key pad / mouth | |
| SIM card | 80 | piece | |
| | | Footwear for victim | |
| Kiss or licked | 75 | contact | |
| Torch | 67 | SIM card | |
| Key pad / mouth | | | |
| piece | 60 | Saliva | |

Table 9.2: Top five items for generating a useful profile and items to generate a match.

9.2 Key Findings

Phase 2 of the research set out to identify common factors within LCN DNA submissions that corresponded to differences in the LCN DNA profiling success rates. Part of the process was for the examining CSI to classify items as to the surface material and characteristics as well as environmental factors. It is worth repeating that no technological means were used in order to retain the ethos of

the research in that the findings should be easily translated into an operational environment for all CSIs, even though this proved subjective.

The results from phase 1 and 2, do provide supporting evidence to suggest that there are some common factors that are more influential than others in determining whether an item is likely to be successfully sampled and subsequently DNA profiled. Likewise some factors were found to have a negative or neutral impact. No single variable could be taken alone as a determining factor but rather a selection of features that generally proved to be more successful. Table 9.3 summarises the key factors and these are discussed in the following sections.

| KEY FACTORS | | | | | | |
|---------------------------|------------------------|----------------------------|--|--|--|--|
| POSITIVE | NEUTRAL | NEGATIVE | | | | |
| SALIVA | TARGET AREA | HIGH VICTIM | | | | |
| Item that has had contact | The areas targeted for | CONTACT | | | | |
| with or been in close | sampling whether very | Items with high victim | | | | |
| proximity to the mouth. | small and defined or | contact such as underwear | | | | |
| | large and speculative. | and skin swabs, or visibly | | | | |
| | | contaminated with blood. | | | | |
| PHYSICAL ITEM | MONTH | OUTSIDE | | | | |
| Original item submitted | RECOVERED | Items and swabs taken | | | | |
| if it has been stored in | The time of year, | from outside. | | | | |
| dry conditions. | month or recovery and | | | | | |
| | / or submission. | | | | | |
| INSIDE / DRY | SURFACE | WET | | | | |
| Recoveries protected | MATERIAL | Items underwater or wet | | | | |
| from the elements. | All surface material | from rain, dew or tap | | | | |
| | types such as plastic, | water. | | | | |
| POROUS | wood, paper, metal | DELAYED SWAB | | | | |
| Porous and absorbent | showed capacity to | SUBMISSION | | | | |
| materials. | generate a profile. | Swabs that have been | | | | |
| ROUGH TEXTURE | | frozen submitted 5 months | | | | |
| Items with a noticeably | | or longer after recovery. | | | | |
| rough feel or edge. | | | | | | |

Table 9.3: Key findings that can affect LCN DNA analysis results

9.3 Positive Factors

Throughout phase 1 and phase 2, samples that originated from areas that had close contact with a person's mouth, although direct contact was not necessary, consistently provided the highest success rates for profiling. These included areas of the body that had been sucked or kissed (Fig. 6.10) and the key pads from mobile phones (Fig. 6.13).

Another positive factor included samples recovered from the inside of premises and that were dry (Fig. 8.8). Although the majority of samples came from these areas, statistically these still proved significantly better than recoveries from outside and wet areas.

This also appeared to impact on the recovery method and subsequent storage of samples; with physical items stored in dry conditions proving more successful than swabs that had been frozen (Fig. 8.10).

Two other key features that impacted on the success rates in a positive manner were porous surfaces (Fig. 8.4) and rough surfaces (Fig. 8.5). This may be due to the ability of the surfaces in these cases to retain DNA material within the characteristics of the rough texture, whereas DNA may be more easily wiped off a smooth surface.

9.4 Neutral Factors

Three areas were found to have no discernable impact on success or failure rates, these being the area targeted for sampling, seasonal recovery times and surface material.

It did not appear to matter whether the target area being sampled was clearly defined, a general handling area or a speculative swab based on the crime scene assessment. All CSIs did target the areas sampled for various reasons, no totally random swabbing was carried out, although it was notable that more samples were anticipated eliminations, the larger area and more speculative the sampling became (Fig. 8.9).

Seasonal factors affect other forensic recoveries such as fingerprints and footwear marks, as discussed in Section 8.4.1, however no specific research

could be found on the potential effects of season on DNA recovery. The findings from phase 2 suggest that there is no impact or seasonal variation with regard to LCN DNA recovery either negatively or positively (Fig. 8.7). However, this could be looked at further particularly with regard to samples recovered from outside, with more detailed meteorological information and sample information as to exposure to the elements.

With the exception of rubber, all of the different types of surface material showed some capacity to generate a profile. The surface material as a singular factor could not be considered sufficient in itself to determine whether a useful profile would be likely, the detail of which is shown at Fig. 8.1.

9.5 Negative Factors

Importantly phase 2 also identified parameters that were more likely to have a negative impact on profiling success rates. Like the positive features no single cause could be identified that would result in sample failure but rather areas that were more likely to reduce the chance of success. Items that were known to have had high contact with the victim of the crime, either through body fluid spillage (Fig. 6.7) or direct skin contact on clothing (Fig. 6.29), were much less likely to generate a useful profile and significantly increased the anticipated eliminations. This was also borne out with the personal possessions such as handbags (Fig. 6.21) and during the Street Robbery initiative (Appendix 9).

Likewise samples taken from outside and in particular, were, or had been wet, proved to be less successful in producing profiles (Fig. 8.8). Although deterioration is expected in DNA once it has been deposited (See Section 1.4) it would appear that the deterioration is significantly faster in these samples. An additional feature, which was completely under the control of the investigators, was identified as a key factor in determining the potential for profiling a sample. This was the time taken between recovery of a sample, by way of swabbing and subsequent freezing for storage, and the time taken to submit to the laboratory for analysis. The failure rate of swabs was significantly higher if a delay occurred of 5 months or more (Fig. 8.12). Although there is no clear indicator as to why this should be, factors such as degradation must be considered along with the impact of freezing and subsequent defrosting of DNA.

9.6 Profiling and Anticipated Eliminations

Initially it had not been intended to incorporate the results of any anticipated eliminations as a separate feature but to include them within the no value group. However, it was beneficial to know a DNA profile could be gained even if caution then had to be applied regarding higher elimination rates within some categories. It highlights the requirement to submit such samples in certain cases such as the analysis of ligatures and underwear, so that any DNA profiles obtained are not pursued as potentially belonging to an offender. These results also supported the fall off in the ability to gain a profile when a time delay had occurred in submitting the sample for analysis as the trend for reduced results occurred in both the useful and anticipated elimination groups in the same way.

Conversely, during the specific 'Hook and Cane' initiative (Appendix 10) a decision was made not to submit elimination samples. This formed part of the overall forensic strategy for these cases and did not impact on the results, due to the consistent approach and strategy to secure elimination samples following successful profiling. Like Pizzamiglio, *et al.*, (2004^2) great importance was placed on the preservation of the scene for examination, the time lapse between the offence and examination and having a forensic strategy for dealing with LCN DNA.

Although, during this initiative the application of LCN DNA analysis to the crime type of 'Hook and Cane' burglaries did not prove to be successful from an investigators point of view; now the full results of the research are available, the forensic strategy could be adjusted which may affect the results of any future initiative. The original initiative considered 'touch DNA' from fingers, arms or the offenders face and therefore samples were taken from the letterbox. The results of phase 2 of this research suggest that the area the mouth was in closest

contact with would produce the best results. In the case of hook & cane burglaries this would be an area immediately below the letter box (Fig. 9.1). Therefore, it should be more productive to sample the area immediately below the letter box than the letter box itself.



Figure 9.1 – Showing Revised Target Area for Swabbing in Hook and Cane Burglaries.

9.7 Outstanding Profiles

This research covered samples recovered and submitted for analysis from 2000 to 2005, and the results for those samples up to December 2006. It was expected that not all samples would be identified or anticipated eliminations and that some would remain outstanding. This was based on the fact that over 270 000 crime scene stains remained unidentified on the NDNAD as of March 2006 (Home Office, 2006) and had increased to 285 848 at March 2007 (Home Office, 2007).

However, a greater effort could have been made to secure anticipated elimination samples, in all cases, where a DNA profile was achieved even though this would have had a cost implication. It is, therefore, not known how many of the outstanding profiles could be legitimately eliminated. It is also not known how many of the outstanding profiles are due to background levels of DNA.

Graham & Rutty (2008) published a paper on background DNA levels that were found on adult necks. Their research found DNA on 58% of the volunteer's

necks that did not belong to them and without any contact from a potential assailant. In contrast, research by Raymond, *et al.*, (2008)¹ found very low levels of background contamination on burglary points of entry such as doors and windows, however during simulation tests of subjects gaining entry to premises they also found that the levels of DNA deposited were very low. There is little knowledge on background DNA levels and how this affects the ability to gain a useful profile which raises the question of how many useful profiles are crime scene stains and therefore of value to investigation. There remains a need to fill this knowledge gap.

9.8 Recovery of Samples

One issue that arose consistently throughout the period of research was the influence a CSI could have on where, how or even if, a sample was recovered. For example, it was noted that significantly fewer samples were recovered from porous surfaces and on further discussion with CSIs several reasons could contribute to the lack of samples. A number of CSIs did not believe porous surfaces were suitable for LCN DNA sampling and others conceded a lack of knowledge of how to recover such samples from a porous surface in situ. Although the training of CSIs follows a national programme (NPIA¹, 2008), that programme is also heavily based on work experience, which differs from Force to Force. Such information is passed informally between CSIs and their actions are often led by previous limited experience of LCN DNA or any LT DNA recovery.

The method of choice throughout this research was either to seize the whole item or use the double swabbing method and then freeze the swabs. The research results have highlighted the potential for swabs to deteriorate over time. As stated previously it is not known whether this is due to cellular degradation through enzymatic actions or a direct consequence of the freeze and thaw process. The lack of knowledge and different methods available for recovering LCN DNA is reflected in the literature. There are also variations on the double swabbing method from the one used in this research where water was used to moisten the swab. In a study by Franke, *et al.*, (2008) 96% ethanol was used to moisten the swabs. The Franke, *et al.*, (2008) research compared tape lifting and the ethanol swabbing methods on steering wheels, gear sticks and mobile phones and found 3 times as much DNA on the ethanol swabs than the tape lifts. However, this does not address the question about whether it is better to use ethanol or water to moisten swabs.

In several of the case studies detailed in Chapter 2, adhesive tape lifting was the method of choice. Research by Bright & Petricevic (2004) found that adhesive tape lifts gave comparably higher DNA recovery rates than swabbing with a wet swab, which also picked up contaminants (often seen as dirty swab). Adhesive tape lifting is a common procedure in laboratories and the standard method used within Strathclyde Police Forensic Department, and has been found to have additional benefits of concurrently recovering other trace evidence (Hall & Fairley, 2004), but this method is infrequently used at crime scenes in England and Wales.

As an alternative Stouder, *et al.*, (2001) found trace evidence scrapings (brushing) provided more DNA than a friction swab of clothing when t shirts and hosiery were tested. Like the adhesive tape lifting this method also allowed other trace material to be separated out such as fibres and hairs. However, drawbacks can instantly be seen with the potential for material to become airborne and provide a source of contamination.

The Caddy report (2008) mentions the need for standardised processes and recovery techniques in relation to low template DNA as well as enhanced training for practitioners. In essence research needs to be carried out to determine the best methods of recovery from different surface types to maximise the potential of DNA recovery useful to an investigation, and to ensure that 'standardised processes' do not restrict more successful methodologies. Following on from identifying the best recovery methods the next task would be

151

to identify the most appropriate storage for each method that maintains the DNA potential.

The results of any research then need to be disseminated to CSI practitioners. The levels of knowledge that the researcher encountered across CSIs, with regard to DNA, varied greatly and there did not appear to be any specific publication or mechanism for keeping CSIs up to date or aware of current research or technologies once they had completed their training.

9.9 New Technology

Due to the longitudinal nature of this research changes in technology have been made which may improve on the ability to profile successfully very small amounts of DNA. The newer techniques include laboratory processes that occur after the sample recovery stage. Variations in extraction methods were highlighted by Castella, *et al.*, (2006) who found a combination of Chelex and phenol-chloroform improved amounts that could be quantified, likewise Phipps & Pertricevic (2007) comment on the differences between laboratories using different methods of extraction. Studies by Smith & Ballentyne (2007), Ballentyne, *et al.*, (2008) and Forster, *et al.*, (2008) show post PCR purification techniques and locked nuclei acids are now viable alternatives, to the increase in cycles carried out in LCN DNA analysis, for any low template DNA sample and may reduce sample consumption and produce profiles that are easier to interpret. Laboratories are constantly striving to offer more robust and sensitive methods to improve the potential of DNA samples.

Research offers these as alternatives to the LCN DNA technique to obtain profiles from small quantities of DNA material, whether LCN DNA techniques or these alternatives are used, the benefits of this research are that it shows the most likely places for trace amounts of DNA to be deposited and key factors that affect success rates. As any technique is dependent on sufficient material being recovered from the scene for analysis this research should be applicable to the new technologies.

<u>9.10 Summary</u>

Overall this research has highlighted the complexities of recovering trace amounts of invisible DNA nevertheless there are identifiable factors that can assist investigators in making decisions at both the recovery and sample submission stages.

The ability to obtain a profile from a sample, although a valuable piece of information, clearly does not necessarily mean that it would be useful to a criminal investigation. Key factors that affect the success or failure rates of samples have been identified along with areas that are more likely to produce useful profiles. This gives police investigators and CSIs the knowledge they require to be able to target areas to sample and the ability to prioritise samples for analysis, thereby expediting the detection of crime.

A further non quantifiable finding of this research was that in general terms, CSIs lacked knowledge of new DNA techniques and did not have systems in place for ongoing continuous professional development. Likewise, researchers / scientists appeared to have little understanding of crime scene processes or what knowledge was lacking or required out in the field. The deficiencies of a coherent method of identifying knowledge gaps, conducting research and relaying back the acquired knowledge, without the constraints of commercial confidences, were notably absent.

All future research should take account of the complexities that are encountered in the field. Even some of the most recent research that had tried to take account of the multiple facets of crime scene processes failed to deliver any conclusive results or direction. Raymond, *et al.*, $(2008)^2$ considered LCN DNA analysis across the 4 territorial regions of Australia. Although the research covered multiple variables that could affect successful profiling, such as the practitioners preference for a specific recovery method, they failed to provide any results to help choose between the different methods of recovery. Likewise they discussed anti contamination methods but not how this affected profiling and the ultimate criticism of the research is that the results were based on CSIs, laboratory staff and managers guesses and opinions of how useful such trace evidence was!

No amount of technological advances or research will ever override the need to have a comprehensive strategy for the preservation, recovery and management of low template DNA samples, which should include elimination samples, however, this research goes some way to providing a level of knowledge that can now be substantiated as to the likelihood of success and the value such techniques can add to an investigation.

9.11 Recommendations for Further Research

This research has highlighted four areas that would benefit from further research or development.

1. <u>Recovery techniques for trace DNA</u>

Further research needs to examine the best recovery techniques for different surface types that can be used at a crime scene. Double swabbing using either water or ethanol, adhesive tape lifting and brushing all need to be compared against each other on a variety of surfaces. The best recovery techniques for each surface type should be available to CSIs. This could be done on the same basis as the Fingerprint Development Handbook, which gives different flow charts of techniques for surface material types (Home Office, 2005)³.

2. Storage of samples

The best method of storage needs to be determined for each recovery technique, particularly taking into account long-term effects. Freezing or drying of swabs prior to storage needs to be assessed as to the best method to maximise DNA potential but prevent contamination that can occur during the drying processes. This should not only include swabs but also items, such as clothing and the best packaging and conditions such as temperature to preserve any DNA potential.

3. Levels of background DNA.

Very little information is currently available as to the current levels of background DNA contamination and how this affects profiles that could be deposited by an offender. Common surfaces such as door handles, petrol pumps, telephones, vehicles are regularly handled and often by multiple people. Some effort should be made to identify where there are high levels of background DNA, the ease of transfer and how long it can persist for.

4. Database for sample results

Consideration should be given to creating an accessible database that could hold information as to the success and failure rates of different sample types and methodologies used, to take account of new techniques, which has sufficient information to advise Investigators and share the intelligence gained. Some smaller Police Forces rarely utilise any form of LT DNA techniques and have little expertise to call upon; an accessible database could prove invaluable in advising investigators as to sampling and prioritising of sample submissions.

References

ACKERLEY, P. (2002) Project 3.9 – Examination and movement of bodies. Consulted document. *ACPO Homicide Working Group* – Unclassified.

Association of Chief Police Officers. (2005) *DNA Good Practice Manual*. 2nd Edition. ACPO.

ALBERT, A. M., RICANEK, K., PATTERSON, E. (2007) A review of the literature on the ageing adult skull and face: Implications for forensic science research and applications. *Forensic Science International*. Vol 172, Issue 1, p 1-9.

ANJOS, M. J., ANDRADE, L., CARVALHO, M., LOPES, V., SERRA, A., OLIVEIRA, C., BATISTA, L., BALSA, F., BRITO, P., CORTE-REAL, F., VIDE, M. C. (2006) Low Copy Number: Interpretation of evidence results. *International Congress Series*. Vol 1288, p 616-618.

ARONSON, J. D. (2005) DNA fingerprinting on trial: the dramatic early history of a new forensic technique. *Endeavour*. Vol 29, Issue 3, p 126–131.

BALLANTYNE, K.N., van OORSCHOT, R.A.H., MITCHELL, R.J. (2008) Locked nucleic acids: Increased trace DNA amplification success with improved primers. *Forensic Science International: Genetics Supplement Series*. Vol 1, Issue 1, p 4-6.

BARBARO, A., CORMACI, P., BARBARO. A. (2006) LCN DNA typing from touched objects. *International Congress Series*. Vol 1288, p 553-555.

BODZIAK, W. J. (2000) Footwear Impression Evidence: Detection, recovery and examination. CRC Press.

BOSSIER, D. (2006) Examination of vehicle license plates. *Forensic Investigation of stolen-recovered and other crime related vehicles*. Edited by STAUFFER, E., BONFANTI, M. Academic Press.

BRIGHT, J., PETRICEVIC, S. F. (2004) Recovery of trace DNA and its application to DNA profiling of shoe insoles. *Forensic Science International*. Vol 145, Issue 1, p 7-12.

BURROWS, J., TARLING, R. (2004) Measuring the impact of forensic science in detecting burglary and autocrime offences. *Science & Justice*. Volume 44, Issue 4, p 217-222.

BUTLER, J. M. (2005) Forensic DNA typing. Biology, Technology, and Genetics of STR markers. 2nd Edition. Elsevier Academic Press.

CADDY, B. (2008) A Review of the Science of Low Template DNA Analysis. Available at: <u>http://police.homeoffice.gov.uk/publications/operational-</u> <u>policing/Review_of_Low_Template_DNA_1.pdf</u> (Accessed: 14th April 2008)

CARRACEDO, A., BAR, W., LINCOLN, P., MAYR, W., MORLING, N., OLAISEN. B., SCHNEIDER. P., BUDOWLE. B., BRINKMANN. B., GILL. P., HOLLAND. M., TULLY. G., WILSON. M. (2000) DNA Commission of the International Society for Forensic Genetics: guidelines for mitochondrial DNA typing. *Forensic Science International*. Vol 110, Issue 2, p 79-85.

CASTELLA, V., DIMO-SIMONIN, N., BRANDT-CASADEVALL, C., MANGIN, P. (2004) Consensus profiles and databasing of casework samples amplified with 34 PCR cycles: an empirical approach. *International Congress Series*. Vol 1261, p 532-534.

CASTELLA, V., DIMO-SIMONIN, N., BRANDT-CASADEVALL, C., MANGIN, P. (2006) Forensic evaluation of the QIAshredder/QIAamp DNA extraction procedure. *Forensic Science International*. Vol 156, Issue 1, p 70-73.

CASTELLA, V., MANGIN, P. (2008) DNA profiling success and relevance of 1739 contact stains from caseworks. *Forensic Science International: Genetics Supplement Series*. Vol 1, Issue 1, p 405-407.

CHIEF CONSTABLE ORDER. (2000) Recovery and forensic examination of firearms, parts of firearms and ammunition. *Chief Constable Order*, 2000/20, Item 2. Greater Manchester Police.

CHIEF CONSTABLE ORDER. (2001) Low Copy Number (LCN) DNA submissions. *Chief Constable Order*, 2001/30, Item 5. Greater Manchester Police.

CHIEF CONSTABLE ORDER. (2002) Recovery and forensic examination of firearms, parts of firearms and ammunition. *Chief Constable Order*, 2002/27, Item 2. Greater Manchester Police.

CHIEF CONSTABLE ORDER. (2004) Low Copy Number (LCN) DNA submissions. *Chief Constable Order*, 2004/31, Item 6. Greater Manchester Police.

COLE, S. (2001) Suspect Identities: A History of Fingerprinting and Criminal Identification. Harvard University Press.

COTTON, E. A., ALLSOP, R. F., GUEST, J. L., FRAZIER, R. R. E., KOUMI, P., CALLOW, I. P., SEAGER, A., SPARKES, R. L. (2000) Validation of the AMP*FL*STR SGM Plus system for use in forensic casework. *Forensic Science International*. Vol 112, Issue 2-3, p 151-161.

CRICK, F. (1993) Looking Backwards: a birthday card for the double helix. *Gene.* Vol. 135, Issue 1-2, p 15-18.

CURRAN, J. M., GILL, P., BILL, M. R. (2005) Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure. *Forensic Science International*. Vol 148, Issue 1, p 47-53.

DAHM, R. (2005) Friedrich Miescher and the discovery of DNA. *Developmental Biology*. Vol 278, Issue 2, p 274-288.

DAUBER, E. M., DORNER, G., MITTERBAUER, M., WENDER, S., FAE, I., GLOCK, B., MAYR, W. R. (2004) Discrepant results of samples taken from different tissues of a single individual. *International Congress Series*. Vol 1261, p 48-49.

DIXON, C. (2000) Super – DNA test that spots any brush with law. *Sunday Express*. May 14th 2000.

DOBBERSTEIN, R. C., HUPPERTZ, J., WURMB-SCHWARK, N., RITZ-TIMME, S. (2008) Degradation of biomolecules in artificially and naturally aged teeth: Implications for age estimation based on aspartic acid racemization and DNA analysis. *Forensic Science International*. Vol 179, Issue 2-3, p 181-191

European Court of Human Rights. Case of S. and Marper V The United Kingdom. Judgement available on <u>http://www.bailii.org/eu/cases/ECHR/2008/1581.html</u> (last accessed January 2009).

EVETT, I. W., FOREMAN, L. A., JACKSON, G., LAMBERT, J. A. (2000) DNA profiling: A discussion of issue relating to the reporting of very small match probabilities. *Criminal Law Review*. May 2000, p 341-355.

FARFAN, M. J., PRIETO, V., SANZ, P. (2004) Allele sharing in related and unrelated individuals: implications in kinship analysis. *International Congress Series*. Vol 1261, p 449-451.

FARMEN, R.K., JAGHO, R., CORTEZ, P., FROYLAND, E.S. (2008) Assessment of individual shedder status and implication for secondary DNA transfer. *Forensic Science International: Genetics Supplement Series*. Vol 1, Issue 1, p 415-417.

FINDLAY, J., TAYLOR, A., QUIRKE, P., FRAZIER, R., URQUHART, A. (1997) DNA fingerprinting from single cells. *Nature*. Vol. 389, p 555-556.

FOGG, E. (1999) New DNA tests to put unsolved murders under the microscope. *Police Review.* 11th June 1999.

FOREMAN, L. A., EVETT, I.W. (2001) Statistical analysis to support forensic interpretation for a new 10-locus STR profiling system. *International Journal of Legal Medicine*. Vol 114, Issue 1-2, p 147-155.

FORENSIC SCIENCE SERVICE. (2003) DNA – Present & Correct. A guide to DNA profiling. FSS.

FORENSIC SCIENCE SERVICE. (2004) *Scenes of Crime Handbook* (2004 Edition). FSS.

FORENSIC SCIENCE SERVICE. (2005) DNA Low Copy Number. Fact Sheet 6. Available at: <u>http://www.forensic.gov.uk</u> (Accessed: 28th Dec 2007).

FORENSIC SCIENCE SERVICE. (2006) Volume Crime DNA Low Copy Number. *Forensic Bulletin*. Issue 17. FSS.

FORSTER, L., THOMSON, J., KUTRANOV, S. (2008) Direct comparison of post-28-cycle PCR purification and modified capillary electrophoresis methods with the 34-cycle "low copy number" (LCN) method for analysis of trace forensic DNA samples. *Forensic Science International: Genetics*. Vol 2,Issue 4, p 318-328.

FRANKE, N., AUGUSTIN. C., PUSCHEL. K. (2008) Optimization of DNAextraction and typing from contact stains. *Forensic Science International: Genetics Supplement Series*. Vol 1, Issuel, p 423-425.

FRENCH, C.E.V., McGLASHAN, S.R., JENSEN, C.G., VINTINER, S.K. (2006) Validation of a staining technique for distinguishing between skin, buccal and vaginal epithelial cells. *The University of Auckland, New Zealand*. Poster presentation, EAFS Conference, Helsinki.

GILL, P., JEFFREYS, A. J., WERRETT, D. J. (1985) Forensic applications of DNA 'fingerprints'. *Nature*. Vol. 318, p 577-579.

GILL, P., WHITAKER, J. P., FLAXMAN, C., BROWN, N., BUCKLETON, J. (2000) An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. *Forensic Science International*. Vol 112, Issue 1, p 17-40.

GRAHAM, E. A. M., RUTTY, G. N. (2008) Investigation into "Normal" Background DNA on Adult Necks: Implications for DNA Profiling of Manual Strangulation Victims. *Journal of Forensic Sciences*. Vol. 53, Issue 5, p 1074-1082.

GREEN, W. (2004) Clinical Forensic Medicine: Sexual Assault and Semen Persistence. *Encyclopaedia of Forensic Sciences*. Academic Press. P 397-403.

GUILLEN, M., LAREU, M. V., PESTONI, C., SALAS, S., CARRACEDO, A. (2000) Ethical-legal problems of DNA databases in criminal investigation. *Journal of Medical Ethics*. Vol 26, Issue 4, p 266-271.

HAAK, B., PORSCHE, A., VOLLACK, K., ZIMMERMANN, P., PFLUG, W. (2008) Evaluation of a semi-automated, magnetic bead-based DNA extraction method for genetic fingerprinting of forensic casework samples. *Forensic Science International; Genetics Supplement Series*. Vol 1, Issue 1, p 35-36.

HALL, D., FAIRLEY, M. (2004) A single approach to the recovery of DNA and firearm discharge residue evidence. *Science & Justice*. Volume 44, Issue 1, p 15-19.

HARTWELL, H. L., HUNT, R. T., NURSE, P. M. (2001) The Nobel Prize in Physiology or Medicine 2001. Key regulators of the cell cycle. Available at: <u>http://nobelprize.org/nobel_prizes/medicine/laureates/2001/press.html</u> (last accessed February 2009).

HER MAJESTY'S INSPECTORATE OF CONSTABULARY. (2000) Under the *Microscope: Thematic Inspection report on Scientific and Technical Support*. Home Office.

HER MAJESTY'S INSPECTORATE OF CONSTABULARY. (2002) Under the Microscope Refocused: A Revisit to the investigative use of DNA and Fingerprints. Home Office.

HINTON, P. R. (2004) *Statistics Explained: A guide for social science students.* Routledge.

HOFF-OLSEN, P., MEVAG, B., STAALSTROM, E., HOVDE, B., EGELAND, T., OLAISEN, B. (1999) Extraction of DNA from decomposed human tissue: An evaluation of five extraction methods for short tandem repeat typing. *Forensic Science International. Vol* 105, Issue 3, p 171-183.

HOME OFFICE. (1995) The National DNA Database. Circular 16/95.

HOME OFFICE. (2003) *The National Policing Plan 2004-2007*. Home Office Communication Directorate.

HOME OFFICE. (2004) *Police Science & Technology Strategy 2004-2009*. Home Office Science Policy Unit.

HOME OFFICE. $(2005)^1$ Police and Criminal Evidence Act 1984 (s.60(1)(a), s.60A and s.66(1)). The Stationary Office. London.

HOME OFFICE. (2005)² Police and Criminal Evidence Act 1984 Code D. Code of Practice for the identification of persons by Police Officers.

HOME OFFICE. (2005)³ *Fingerprint Development Handbook.* Home Office Scientific Development Branch.

HOME OFFICE. (2006) The National DNA Database Annual Report 2005-06. http://www.homeoffice.gov.uk/science-research/using-science/dna-database/ (Accessed August 2008).

HOME OFFICE. (2007) *The National DNA Database Annual Report 2006-2007*. <u>http://www.npia.police.uk/en/11403.htm</u> (Accessed February 2009). HORI, M., ISHIGURO, C., SUZUKI, T., NAKAGAWA, N., NUNOSHIBA, T., KURAMITSU, S., YAMAMOTO, K., KASAI, H., HARASHIMA, H., KAMIYA, H. (2007) UvrA and UvrB enhance mutations induced by oxidized deoxyribonucleotides. *DNA Repair*. Vol 6, Issue 12, p 1786-1793.

JEFFREYS, A. J., WILSON, V., THEIN, S. L. (1985¹) Hypervariable 'minisatellite' regions in human DNA. *Nature*. Vol. 314, p 67-73.

JEFFREYS, A. J., WILSON, V., THEIN, S. L. (1985²) Individual-specific 'fingerprints' of human DNA. *Nature*. Vol. 316, p 76-79.

JOBLING, M. A., GILL, P. (2004) Encoded Evidence: DNA in Forensic Analysis. *Nature Reviews*. Vol. 5, October, p 739-751.

KATZ-JAFFE, M.G., TROUNSON, A.O., CRAM, D.S. (2004) Mitotic errors in chromosome 21 of human preimplantation embryos are associated with non-viability. *Molecular Human Reproduction*. Vol. 10, Issue 2. p 143-147.

KITA, T., YAMAGUCHI, H., YOKOYAMA, M., TANAKA, T., TANAKA, N. (2008) Morphological study of fragmented DNA on touched objects. *Forensic Science International: Genetics*. Vol 3, Issue 1, p 32-36.

KOBILINSKY, L., LIOTTI, T. F., OWSER-SWEAT, J., WATSON, J. (Foreword), WITKOWSKI, J. (2004) *DNA: Forensic and Legal Applications*. Wiley.

KUCKEN, M. (2007) Models for fingerprint pattern formation. *Forensic Science International*. Vol 171, Issue 2-3, p 85-96.

LADD, C., ADAMOWICZ, M. S., BOURKE, M. T., SCHERCZINGER, C. A., LEE, H. C. (1999) A systematic Analysis of Secondary DNA transfer. *Journal of Forensic Sciences. Vol* 44, Issue 6, p 1270-1272.

LEJA D. Structure of DNA. Available at: <u>http://www.accessexcellence.org/RC/VL/GG/chromosome.html</u> (Accessed: 19th September 2007).

LOWE, A. (2002) FSS report TN 863 Review of LCN research projects 070 and 129. FSS – CONFIDENTIAL (Crown Copyright).

LOWE, A., MURRAY, C., WHITAKER, J., TULLY, G., GILL, P. (2002) The propensity of individuals to deposit DNA and secondary transfer of low level DNA from individuals to inert surfaces. *Forensic Science International*. Vol 129, Issue 1, p 25-34.

LOWE, A., MURRAY, C., RICHARDSON, P., WIVELL, R., GILL, P., TULLY, G., WHITAKER, J. (2003) Use of low copy number DNA in forensic inference. *International Congress Series*. Vol 1239, p 799-801. LUND, S., DISSING, J. (2004) Surprising stability of DNA in stains at extreme humidity and temperature. *International Congress Series*. Vol 1261, p 616-618.

LYGO, J. E., JOHNSON, P. E., HOLDAWAY, D. J., WOODROFFE, S., WHITTAKER, J. P., CLAYTON, T. M., KIMPTON, C. P., GILL, P. (1994) The validation of short tandem repeat (STR) loci for use in forensic casework. *International Journal Legal Medicine*. Vol 107, Issue 1, p 77-89.

MALSOM, S., FLANAGAN, N., MCALISTER, C., DIXON, L. (2009) The prevalence of mixed DNA profiles in fingernail samples taken from couples who co-habit using autosomal and Y-STRs. *Forensic Science International: Genetics*. Volume 3, Issue 2. p 57-62.

McKILLUP, S. (2005) *Statistics Explained: An introductory guide for life scientists.* Cambridge University Press.

MERCK. Basic cell structure. Adapted from <u>http://www.merck.com</u> (Accessed: January 2009).

MORGAN HARRIS BURROWS. (2002) *The evaluation of increased forensic activity in GMP and Lancashire. Final evaluation report.* Morgan Harris Burrows. April 2002.

NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY. (2009) Allelic Ladders and Tri-allelic patterns. Available from <u>http://www.cstl.nist.gov</u> (Accessed: February 2009)

NPIA (National Policing Improvement Agency)¹. Crime Scene Training Programme. <u>http://www.npia.police.uk/en/5235.htm</u> (Accessed: December 2008)

NPIA. (2008)² Standards of performance and monitoring of suppliers of profiles to the National DNA Database. Custp-GP-004. Issued 29th April 2008. Published NPIA.

NUFFIELD COUNCIL ON BIOETHICS. (2007) *The forensic use of bioinformation: ethical issues*. Cambridge Publishers.

PANG, B. C. M., CHEUNG, B. K. K. (2007) Double swab technique for collecting touched evidence. *Legal Medicine*. Vol 9, Issue 4, p 181-184.

PEPPER, I. K. (2004) *Crime Scene Investigation Methods and Procedures*. Open University Press.

PETRICEVIC, S. F., BRIGHT, J., COCKERTON, S. L. (2006) DNA profiling of trace DNA recovered from bedding. *Forensic Science International*. Vol 159, Issue 1, p 21-26.

PHIPPS, M., PETRICEVIC, S. (2007) The tendency of individuals to transfer DNA to handled items. *Forensic Science International*. Vol 168, Issue 2-3, p 162-168.

PIZZAMIGLIO, M., MAMELI, A., MAUGERI, G., GAROFANO, L. (2004)¹ Identifying the culprit from LCN DNA obtained from saliva and sweat traces linked to two different robberies and use of a database. *International Congress Series*. Vol 1261, p 443-445.

PIZZAMIGLIO, M., MAMELI, A., MY, D., GAROFANO, L. (2004)² Forensic identification of a murderer by LCN DNA collected from the inside of the victims car. *International Congress Series*. Vol 1261, p 437-439.

POINAR, H. N. (2003) The top 10 list: criteria of authenticity for DNA from ancient and forensic samples. *International congress Series*. Vol 1239, p 575-579.

POWELL, R., GANNON, F. (2002) *Purification of DNA by phenol extraction and ethanol precipitation*. Oxford Practical Approach Series. Oxford University Press.

POY, A., VAN OORSCHOT, R. A. H. (2006) Beware; gloves and equipment used during the examination of exhibits are potential vectors for transfer of DNA containing material. *International Congress Series*. Vol 1288, p 556-558.

PROFF, C., SCHMITT, C., SCHNEIDER, P. M., FOERSTER, G., ROTHSCHILD, M. A. (2006). Experiments on the DNA contamination risk via latent fingerprint brushes. *International Congress Series*. Vol 1288, p 601-603.

RAYMOND, J. J., WALSH, S. J., van OORSCHOT, R. A., GUNN, P. R., EVANS. L., ROUX, C. (2008)¹. Assessing trace DNA evidence from a residential burglary: Abundance, transfer and persistence. *Forensic Science International: Genetics Supplement Series*. Vol 1, Issue 1, p 442-443.

RAYMOND, J. J., van OORSCHOT, R. A. H., WALSH, S. J., ROUX, C. (2008)². Trace DNA analysis: Do you know what your neighbour is doing? A multi-jurisdictional survey. *Forensic Science International: Genetics*. Vol 2, Issue 1, p 19-28.

RAYMOND, J. J., WALSH, S. J., van OORSCHOT, R. A., GUNN, P. R., ROUX, C. (2004) Trace DNA: An underutilized Resource or Pandora's Box? A review of the use of Trace DNA Analysis in the investigation of volume crime. *Journal of Forensic Identification*. Vol 54, Issue 6, p 668-686.

RENNISON, A. (2008) Response to Professor Brian Caddy's Review of the Science of Low Template DNA Analysis. *The Forensic Science Regulator*. 7th May 2008.

RUTTY, G. N. (2000) Human DNA contamination of mortuaries: does it matter? *Journal of Pathology*. Vol 190, Issue 4, p 410-411.

RUTTY, G. N (2002) An investigation into the transference and survivability of human DNA following simulated manual strangulation with consideration of the problem of third party contamination. *International Journal Legal Medicine*. Vol 116, Issue 3, p 170-173.

RUTTY, G.N., HOPWOOD, A., TUCKER, V. (2002) FSS report RR 826. The effectiveness of protective clothing in the reduction of potential DNA contamination of the scene of crime. FSS.

RUTTY, G.N., WATSON, S., DAVISON, J. (2000) DNA contamination of mortuary instruments and work surfaces: a significant problem in forensic practice? *International Journal Legal Medicine*. Vol 114, Issue 1-2, p 56-60.

SARAVO, L., SPITALERI, S., PISCITELLO, D., TRAVALI, S. (2004) DNA typing from steel cable. *International Congress Series*. Vol 1261, p 473-475.

SCHOLD, M., DUFVA, C., FORSSLUND, S., JANGBLAD, A. (2006) The hand on the shoulder. A case report where low copy number DNA analysis was the vital for solving a robbery. *Swedish National Laboratory of Forensic Science*. Poster presentation EAFS conference, Helsinki.

SCHULZ, M. M., REICHERT, W. (2000) A strategy for STR-analysis of cryptic epithelial cells on several textiles in practical casework. *Progress in Forensic Genetics 8*, GF sensabaugh, LINCOLN, P. J., OLAISEN B (Editors). 2000 Elsevier Science.

SCHULZ, M. M., REICHERT, W. (2002) Archived or directly swabbed latent fingerprints as a DNA source for STR typing. *Forensic Science International*. Vol 127, Issues 1-2, p 128-130.

SEAH, L. H., OTHMAN, M. I., JAVA, P., JEEVAN, H. (2004) DNA profiling on fabrics: and in-situ method. *International Congress Series*. Vol 1261, p 565-567.

SEWELL, J., QUINONES, I., AMES, C., MULTANEY, B., CURTIS, S., SEEBORUTH, H., MOORE, S., DANIEL, B. (2008) Recovery of DNA and fingerprints from touched documents. *Forensic Science Intenational: Genetics*. Vol 2, Issue 4, p 281-285.

SHETTY, B. S. K., RAO, P. P. J., SAMEER, K. S. M., SALIAN, P., SHETTY, M. (2009) Forensic evaluation of occupational marks in establishing identity – A case report. *Forensic Science International*. Vol 183, Issues 1-3, p 17-20.

SMITH, P. J., BALLANTYNE, J. (2007) Simplified Low-Copy-Number DNA Analysis by Post-PCR Purification. *Journal of Forensic Science*. Vol.52, Issue 4. p 820-829. SPARKES, R., KIMPTON, C., GILBARD, S., CARNE, P., ANDERSEN, J., OLDROYD, N., THOMAS, D., URQUHART, A., GILL, P. (1996) The validation of a 7 locus multiplex STR test for use in forensic casework (ll). *International Journal Legal Medicine*. Vol 109, Issue 4, p 195-204.

STAITI, N., ROMANO, C., TRAPANI, C., GINESTRA, E., LEO, B., SCHIAVONE, S. (2008) Analysis of LCN DNA from synthetic ropes: A practical approach used in real homicide investigation. *Forensic Science International: Genetics Supplement Series.* Vol 1, Issue 1, p 446-447.

STOUDER, S. L., REUBUSH, K. J., HOBSON, D. L., SMITH, J. L. (2001) Trace evidence scrapings: A valuable source of DNA? *Forensic Science Communications*, Vol. 3, No. 4. Available at: <u>http://www.fbi.gov/hq/lab/fsc/backissu/oct2001/stouder.htm</u> (Accessed: 14th Sept. 07)

SWEET, D., LORENTE, J. A., VALENZUELA, A., VILLANEUVA, E. (1997) An improved method to recover saliva from human skin: the double swab technique. *Journal of Forensic Sciences*. Vol 42, Issue 2, p 320-322.

SUTHERLAND, B., CORDINER, S., BRIGHT, J., WALSH, S. J. (2003) Commentary. *Journal of Forensic Sciences*. Vol 48, Issue 2.

TOWNLEY, L., EDE, R. (2004) *Forensic Practice in Criminal Cases*. The Law Society.

VAN HOOFSTAT, D. E. O., DEFORCE, D. L. D., DE PAUW, I., VAN DEN EECKHOUT, E. G. (1999) DNA typing of fingerprints using capillary electrophoresis: Effect of Dactyloscopic powders. *Electrophoresis*. Vol 20, Issue 14, p 2870-2876.

VAN OORSCHOT, R. A., JONES, M. (1997) DNA fingerprints from fingerprints. *Nature*. Vol 387, p 767.

VAN OORSCHOT, R. A. H., PHELAN, D. G., FURLONG, S., SCARFO, G. M., HOLDING, N. L., CUMMINS, M. J. (2003) Are you collecting all the available DNA from touched objects? *International Congress Series*. Vol 1239, p 803-807.

WATSON, J., CRICK, F. (1953) A structure for deoxyribose nucleic acid. *Nature*. Vol 171, p 7737-738.

WEIR, J. (2007). Neutral Citation No [2007] NICC 49. Available at: <u>http://www.courtsni.gov.uk/en-</u> <u>GB/Judicial+Decisions/Judgments/j_j_wei7021final.htm (</u>Accessed: 4th January 2008)

WELLS, M., TAYLOR, L. (2002) *Firearms Projects – casework analysis*. Forensic Science Service and Greater Manchester Police. WERRETT, D. J. (1997) The National DNA Database. *Forensic Science International*. Vol 88, Issue 1, p 33-42.

WHITAKER, J. P., COTTON, E. A., GILL, P. (2001) A comparison of the characteristics of profiles produced with the AMPF1STR® SGM PlusTM multiplex system for both standard and low copy number (LCN) STR DNA analysis. *Forensic Science International*. Vol 123, Issues 2-3, p 215-223.

WICKENHEISER, R. A. (2002) Trace DNA: A review. Discussion of theory and amplification of the transfer of trace quantities of DNA through skin contact. *Journal of Forensic Science*. Vol 47, Issue 3, p 442-450.

WIEGAND, P., KLEIBER, M. (1997) DNA typing of epithelial cells after strangulation. *International Journal Legal Medicine*, 110, p 181-183.

WIKIPEDIA. DNA Base Pair. Available at: <u>http://en.wikipedia.org/?title=basepair</u> (Accessed: 29th July 2007)

WILLIAMS, R., JOHNSON, P. (2008) *Genetic Policing. The use of DNA in criminal investigations.* Willan Publishing.

WILSON, I. G. (1997) Inhibition and Facilitation of Nucleic Acid Amplification. *Applied and Environmental Microbiology*. Vol 63, Issue 10, p 3741-3751.

YATES, F. (1934) Contingency table involving small numbers and the X^2 test. *Journal of the Royal Statistical Society*. Supplement 1. p 217-235.

Further Reading

FORENSIC SCIENCE SERVICE. (2006) The National DNA Database (NDNAD). Fact Sheet 3. Available at: <u>http://www.forensic.gov.uk</u> (Accessed: 28th Dec 2007).

GOODWIN, W., LINACRE, A., HADI, S. (2007) An introduction to Forensic Genetics. Wiley.

TOWNLEY, L., EDE, R. (2004) Forensic Practice in Criminal Cases. Law Society.

<u>Appendix 1</u>

Allelic Ladders

Allelic Ladders

The Society of Forensic Haemogenetics recommends using allelic ladders. There are an expected number of repeat base pairs at each loci which should fall within set parameters depending on the laboratory techniques used (NIST, 2009). Allelic ladders detailing the loci and chromosome location can be found on the http://www.cstl.nist.gov/website.

The following allelic ladders give an example of what can be accessed on the website and are not replicated in their entirety.

<u>D3S1358</u>

| Other Names | Chromosomal Location | GenBank Accession |
|----------------|---|----------------------------|
| UniSTS: 148226 | 3p21.31 Chr 3; 45.557 Mb (May 2004, NCBI build 35) | AC099539 has 16 repeats |

Repeat: [AGAT], [TCTA]= bottom strand

| Reported Primers | Ref. | PCR Primer Sequences |
|---------------------|----------|---|
| Set 1 | 148, 502 | 5'-ACT GCA GTC CAA TCT GGG T-3' (AGAT strand) 5'-ATG AAA TCA ACA GAG GCT TG-3' (TCTA strand) |
| Set 2 | ABI | Profiler Plus, COfiler, SGM Plus, Identifiler |
| Set 3 | Promega | PowerPlex 2.1, PowerPlex 16 (FL labeled) primer sequences 5'-ACTGCAGTCCAATCTGGGT-3' 5'-[FL]-ATGAAATCAACAGAGGCTTGC-3' |

PCR Product Sizes of Observed Alleles

| Allele (Repeat #) | Set 1,3 | Set 2 | Repeat Structure | Ref. |
|----------------------|------------|-----------|------------------|-------------------|
| 8 | 99 bp | 97 bp | | variant allele |
| 8.3 | 102 bp | 100 bp | | variant allele |
| 9 | 103 bp | 101 bp | | variant allele |
| 10 | 107 bp | 105 bp | | variant allele |
| 11 | 111 | 109 | | variant |

| | bp | bp | | allele |
|------|-----------|-----------|---------------------|-------------------|
| 12 | 115 bp | 113 bp | | SGM Plus |
| 13 | 119 bp | 117 bp | TCTA[TCTG]2[TCTA]10 | 729 |
| 14 | 123 bp | 121 bp | TCTA[TCTG]2[TCTA]11 | 668 |
| 14.3 | 126 bp | 124 bp | | variant allele |
| 15 | 127 bp | 125 bp | TCTA[TCTG]₃[TCTA]11 | 668 |
| 15' | 127 bp | 125 bp | TCTA[TCTG]2[TCTA]12 | 668 |
| 15.1 | 128 bp | 126 bp | | variant allele |
| 15.2 | 129 bp | 127 bp | | variant allele |
| 15.3 | 130 bp | 128 bp | | variant allele |
| 16 | 131 bp | 129 bp | TCTA[TCTG]3[TCTA]12 | 668 |
| 16' | 131 bp | 129 bp | TCTA[TCTG]2[TCTA]13 | 729 |
| 16.2 | 133 bp | 131 bp | | 642 |

Allelic Ladders: Commercially available from Promega and Applied Biosystems

Common Multiplexes: PowerPlex 2.1, PowerPlex 16, Profiler Plus, COfiler, SGM Plus, Identifiler

Mutation Rate: 0.12%

<u>VWA</u>

| Other Names | Chromosomal Location | GenBank Accession |
|----------------------------------|--|--------------------------------|
| vWF, VWA31A UniSTS: 240640 | 12p13.31 ; von Willebrand Factor, 40 th intron Chr 12; 5.963 Mb (May 2004, NCBI build 35) | M25858; has 18 repeat units |

Repeat: [AGAT] = bottom strand (commonly used); [TCTA] with [TCTG] and [TCCA] inserts = GenBank top strand

| Reported Primers | Ref. | PCR Primer Sequences |
|---------------------|---------|---|
| Set 1 | 113 | 5'-CCCTAGTGGATAAGAATAATC-3' 5'-GGACAGATGATAAATACATAGGATGGATGG-3' |
| Set 1' | 7 | 5'-CCCTAGTGGATGATAAGAATAATCAGTATG-3' 5'-GGACAGATGATAAATACATAGGATGGATGG-3' |
| Set 2 | Promega | PowerPlex 1.1, PowerPlex 2.1, PowerPlex 16 (TMR labeled) primer sequences 5'- GCCCTAGTGGATGATAAGAATAATCAGTATGTG- 3' 5'-[TMR]- GGACAGATGATAAATACATAGGATGGATGG-3' |
| Set 3 | ABI | Profiler Plus (5-FAM labeled), SGM Plus (5-FAM labeled), Identifiler (NED labeled) |

PCR Product Sizes of Observed Alleles

| Allele (Repea t #) | Set 1, 1' | Set 2 | Set 3 | Repeat Structure | Ref. |
|--------------------------|-----------------|---------------|---------------|---|------|
| 10 | 12 2 bp | 12 3 bp | 15 2 bp | TCTA TCTG TCTA [TCTG]₄[TCTA]₃ | 716 |
| 11 (13')* | 12 6 bp | 12 7 bp | 15 6 bp | TCTA[TCTG]₃[TCTA]7 | 76 |
| 12 | 13 0 bp | 13 1 bp | 16 0 bp | TCTA[TCTG]₄[TCTA]7 | 7 |
| 13 | 13 4 bp | 13 5 bp | 16 4 bp | [TCTA]₂[TCTG]₄[TCTA]₃TCCA[T CTA]₃ | 716 |
| 13 (15) | 13 4 bp | 13 5 bp | 16 4 bp | TCTA[TCTG]₄[TCTA]₀TCCA TCTA | 76 |
| 13 (15") | 13 4 bp | 13 5 bp | 16 4 bp | TCTA[TCTG]4[TCTA]10 | 76 |
| 14 (16") | 13 8 bp | 13 9 bp | 16 8 bp | TCTA[TCTG]4[TCTA]11 | 76 |
| 14' (16''') | 13 8 bp | 13 9 bp | 16 8 bp | TCTA TCTG [TCTA]₁[TCTG]₄[TCTA]₃TCCA [TCTA]₃ | 76 |
| 14" | 13 8 bp | 13 9 bp | 16 8 bp | TCTA [TCTG]₅[TCTA]₃TCCA [TCTA]₃ | 721 |
| 15 (17) | 14 2 bp | 14 3 bp | 17 2 bp | TCTA[TCTG]₄[TCTA]10TCCA TCTA | 76 |

| 15 (17') | 14 2 bp | 14 3 bp | 17 2 bp | TCTA[TCTG]₃[TCTA]11TCCA TCTA | 76 |
|----------|---------------|---------------|---------------|---|---------------------------|
| 15.2 | 14 4 bp | 14 5 bp | 17 4 bp | | 7 |
| 16 (18) | 14 6 bp | 14 7 bp | 17 6 bp | TCTA[TCTG]₄[TCTA]11TCCA TCTA | 76 |
| 16 (18') | 14 6 bp | 14 7 bp | 17 6 bp | TCTA[TCTG] ₃ [TCTA] ₁₂ TCCA TCTA | 76 |
| 16.1 | 14 7 bp | 14 8 bp | 17 7 bp | | vari ant allel e |
| 17 (19) | 15 0 bp | 15 1 bp | 18 0 bp | TCTA[TCTG]₄[TCTA]12TCCA TCTA | 76 |

Mutation Rate: 0.17%

<u>D8S1179</u>

| Other Names | Chromosomal Location | GenBank Accession |
|-------------------------|--|--|
| D6S502 UniSTS: 83408 | 8q24.13 Chr 8; 125.976 Mb (May 2004, NCBI build 35) | GO8710; has 12 repeat units AF216671; has 13 repeat units |

Repeat: [TATC] = GenBank top strand (called [TCTA] by FSS {375})

| Reported Primers | Ref. | PCR Primer Sequences |
|---------------------|---------|--|
| Set 1 | 369 | 5' - TTTTTGTATTTCATGTGTACATTCG - 3' 5' - CGTAGCTATAATTAGTTCATTTTCA - 3' |
| Set 2 | PE ABI | Profiler Plus (JOE labeled), SGM Plus (JOE labeled), Identifiler (6-FAM labeled) |
| Set 3 | Promega | PowerPlex 2.1 (TMR labeled), PowerPlex 16 (TMR labeled) primer sequences 5'- ATTGCAACTTATATGTATTTTGTATTTCATG- 3' 5'-[TMR]- ACCAAATTGTGTTCATGAGTATAGTTTC-3' |

PCR Product Sizes of Observed Alleles

| Allele (Repeat #) | Set 1 | Set 2 | Set 3 | Repeat Structure | Ref. |
|-------------------------|-----------|-----------|-----------|---------------------|------|
| 7 | 157 bp | 123 bp | 203 bp | [TCTA] ₇ | 716 |
| 8 | 161 bp | 127 bp | 207 bp | [TCTA] ₈ | 369 |
| 9 | 165 bp | 131 bp | 211 bp | [TCTA] ₉ | 369 |

| | | 1 | | | |
|------|-----------|-----------|-----------|--|-------------------|
| 10 | 169 bp | 135 bp | 215 bp | [TCTA] ₁₀ | 369 |
| 10.2 | 171 bp | 137 bp | 217 bp | | variant allele |
| 11 | 173 bp | 139 bp | 219 bp | [TCTA] ₁₁ | 369 |
| 12 | 177 bp | 143 bp | 223 bp | [TCTA] ₁₂ | 369 |
| 12.3 | 180 bp | 146 bp | 226 bp | | variant allele |
| 13 | 181 bp | 147 bp | 227 bp | [TCTA]1[TCTG]1[TCTA]11 | 369 |
| 14 | 185 bp | 151 bp | 231 bp | [TCTA] ₁ [TCTG] ₁ [TCTA] ₁₂ | 369 |
| 15 | 189 bp | 155 bp | 235 bp | [TCTA] ₁ [TCTG] ₁ [TCTA] ₁₃ | 369 |
| 15.3 | 192 bp | 158 bp | 238 bp | | variant allele |
| 16 | 193 bp | 159 bp | 239 bp | [TCTA] ₂ [TCTG] ₁ [TCTA] ₁₃ | 369 |
| 17 | 197 bp | 163 bp | 243 bp | [TCTA] ₂ [TCTG] ₂ [TCTA] ₁₃ | 369 |
| 17.1 | 198 bp | 164 bp | 244 bp | | variant allele |
| 18 | 201 bp | 167 bp | 247 bp | [TCTA] ₂ [TCTG] ₁ [TCTA] ₁₅ | 369 |

Allelic Ladders: Commercially available from Promega and Applied Biosystems

Common Multiplexes: PowerPlex 2.1, PowerPlex 16, Profiler Plus, SGM Plus, Identifiler

Mutation Rate: 0.14%

FGA

| Other Names | Chromosomal Location | GenBank Accession |
|----------------------------|--|---------------------------|
| FIBRA UniSTS: 240635 | 4 q28; located in the third intron of the human alpha fibrinogen gene Chr 4; 155.866 Mb (May 2004, NCBI build 35) | M64982; has 21 repeats |

 Repeat:
 complex
 tetranucleotide
 repeat;

 [TTTC]₃TTTTTTCT[CTTT]_nCTCC[TTCC]₂ = GenBank top strand

| Reported Primers | Ref. | PCR Primer Sequences |
|---------------------|---------|--|
| Set 1 | 7 | 5'-GCCCCATAGGTTTTGAACTCA-3' (CTTT strand) 5'-TGATTTGTCTGTAATTGCCAGC-3' (GAAA strand) |
| Set 2 | 363 | AmpFISTR Profiler Plus (5-FAM labeled), SGM Plus (NED labeled), Identifiler (PET labeled) |
| Set 3 | Promega | PowerPlex 16 (TMR labeled) primer sequences 5'-[TMR]-GGCTGCAGGGCATAACATTA-3' 5' -A TTCTATGACTTTGCGCTTCAGGA-3' |

PCR Product Sizes of Observed Alleles

| Allele (Repeat #) | Set 1 | Set 2 | Set 3 | Repeat Structure | Ref. |
|-------------------------|-----------|-----------|-----------|------------------|-----------------------|
| 12.2 | 158 bp | 196 bp | 308 bp | | varia nt allele |
| 13 | 160 bp | 198 bp | 310 bp | | varia nt allele |
| 13.2 | 162 bp | 200 bp | 312 bp | | varia nt allele |

| 14 | 164 bp | 202 bp | 314 bp | | varia nt allele |
|------|-----------|-----------|-----------|--|-----------------------|
| 14.3 | 167 bp | 205 bp | 317 bp | | varia nt allele |
| 15 | 168 bp | 206 bp | 318 bp | [TTTC]₃TTTT TTCT[CTTT]7CTCC[TTCC]2 | 142 |
| 15.3 | 171 bp | 209 bp | 321 bp | | varia nt allele |
| 16 | 172 bp | 210 bp | 322 bp | [TTTC]₃TTTTTTCT[CTTT] ₈ C TCC[TTCC]₂ | 363 |
| 16.1 | 173 bp | 211 bp | 323 bp | [TTTC]₃TTTTTTCT[CTTT]₅T [CTTT]₃CTCC[TTCC]2 | 716 |
| 16.2 | 174 bp | 212 bp | 324 bp | [TTTC]₃TTTT TT [CTTT]₀CTCC[TTCC]2 | 363 |
| 17 | 176 bp | 214 bp | 326 bp | [TTTC]₃TTTT TTCT[CTTT]₀CTCC[TTCC]2 | 142 |
| 17.1 | 177 bp | 215 bp | 327 bp | | varia nt allele |
| 17.2 | 178 bp | 216 bp | 328 bp | | varia nt allele |
| 18 | 180 bp | 218 bp | 330 bp | [TTTC]₃TTTT TTCT[CTTT]10CTCC[TTCC] 2 | 142 |
| 18.1 | 181 bp | 219 bp | 331 bp | | varia nt allele |
| 18.2 | 182 bp | 220 bp | 332 bp | [TTTC]₃TTTT TT [CTTT]11CTCC[TTCC]2 | 142 |

Allelic Ladders: Commercially available from Promega and Applied Biosystems

Common Multiplexes: Profiler Plus, SGM Plus, Identifiler, PowerPlex 2.1, PowerPlex 16

Mutation Rate: 0.28%

<u>Appendix 2</u>

Elimination DNA Databases

Elimination DNA Databases

The increased sensitivity of DNA analysis and the ability to profile non-visible cellular material means that it is not only offenders who may have difficulty in preventing DNA being left at a crime scene but also those who attend scenes post event may deposit minute biological traces. This equally applies to exhibits that are examined in laboratory settings. Accidental contamination can occur even if no specific activity of recovery and packaging of an exhibit has taken place by an officer, but through talking, coughing or by the introduction of equipment to a scene such as pens or cameras.

Police elimination DNA databases hold profiles of persons who may legitimately attend crime scenes, for investigative purposes, on a regular basis and prevents the need for repeated samples for elimination to be taken. The personnel include police officers, CSIs and Home Office pathologists. Samples can also be added to the database on a voluntary basis from other experts such as entomologists or anthropologists who may regularly work for the police service.

Buccal scrapes, a scrape taken from the inside cheek, usually provides sufficient DNA material, which is analysed and added to the database. Although the DNA profiles are compatible with the NDNAD the police elimination database (PED) is held separately.

The PED started in 2000, initially on a voluntary basis however, Police Regulations were amended and have required police officers to provide their DNA and fingerprints since 1st August 2002 as a condition of employment (Police Regulations, 2002). Elimination samples are destroyed once an employee leaves the service.

As the elimination database is held separately a formal process is adopted when any Police Officer or police staff's DNA profile is requested to be checked against a crime scene sample. Elimination samples are not speculatively searched; they are only compared directly with a specific case. Authority for the comparison is either from the SIO or SSM. Officers are informed of the result of any checks (ACPO, 2005).

Forensic supplier laboratories and manufacturers also hold databases of their staff to provide elimination samples in the case any contamination is identified during handling or analysis of exhibits or in the manufacturing process.

Appendix 3

DNA Swabbing Process

PROCEDURES FOR DNA SWABBING (APRIL 2002) SGM+ LCN

| | <u>LCN</u> |
|---|--|
| This procedure to be undertaken for each individual stain. | This procedure to be undertaken for all targeted areas: |
| 1. Minimum 3 swabs required. | 1. 3 swabs required. Use small tipped swabs where possible. |
| 2. Moisten first swab with sterile water - label as batch and water control. | 2. Moisten first swab with sterile water - label as batch and water control. |
| | |
| 3. Moisten second swab with sterile water and take background control. Sample an area adjacent to the staining. | 3. No background swab required. |
| | |
| 4. Moisten third swab with sterile water and swab stain - concentrating onto tip. Use as many swabs as are required to complete the sample. | 4. Moisten second swab with sterile water and swab target area, concentrating onto tip. Label as MOIST. |
| | |
| 5. Package all swabs together in a Tamper Evident bag under one exhibit reference. | 5. Swab the same target area with a DRY swab. This recovers moisture left by first swab which may contain DNA. Label as DRY. |
| | |
| | 6. Package all three swabs together in a Tamper Evident bag under the same exhibit reference. |

Appendix 4

Submissions Policy for LCN DNA

The Chief Constable's Order



Issue: 2001/30

24th July

Item 5

'Low Copy Number' (LCN) DNA submissions

'Low Copy Number' is a particularly sensitive technique for retrieving DNA.

In view of the increasing demand for this service, we have reviewed the procedure for LCN submissions. This procedure comes into force immediately.

Serious crime and murder or attempted murder

LCN DNA will only be considered in the most serious crime cases.

Cases of murder or attempted murder will be financed from the part of the forensic science budget allocated to such cases. Other serious cases will be financed from the divisional allocation of the forensic science budget for the division where the crime occurred. The average cost is £1,500 per item.

Officer in the case

You should submit a report to your detective chief inspector containing:

details of the case and any linked cases;

details of any other forensic and fingerprint evidence recovered;

consideration of how any LCN intelligence will be used;

consideration of contamination and transfer issues; and

how the items submitted link to the offence being charged.

Detective chief inspector

You should:

consider the report before endorsing and signing it; and

consider the suitability of the exhibit for LCN with regard to:

the type of offence;

the likely cost of analysis;

control of the crime scene and therefore the integrity of exhibits; and

the way in which any intelligence will be used.

If the subdivisional or unit detective chief inspector is not available, another detective chief inspector must sponsor the submission.

Officer in the case

Each case will be assessed on its own merits and therefore depends on your report being sufficiently detailed.

When your report has been endorsed by the detective chief inspector, you should fax it to the Forensic Submissions Unit (Fax 66609), together with a completed Forensic Submissions Form (form MG/FSS). If the request for LCN examinations has been received from the CPS or Counsel, it must be supported by a written report from them.

Forensic Submissions Unit staff

When you receive the request, you should cost the submission and advise the Scientific Services Manager or nominated deputy, who may refer the matter to the Head of Investigative Support [V] for final authorisation.

We will review this procedure as more results and research become available.

[Crime Policy Unit [V] : Constable D. Shuttleworth, Tel. 62721]

The Chief Constable's Order



Issue: 2004/31

3rd August

Item 5 Forensic submission procedure

This item replaces all previous guidance in Chief Constable's Orders.

Every submission to any forensic supplier should be made on a form MGFSS, previously known as a 'holab'. The current version of the form is available on the Force Forms site on the intranet. Only the current form will be accepted.

Investigating officer

You should:

complete three copies of form MG FSS, using the guidelines;

get your crime manager's signature for urgent and critical submissions;

fax one copy of the completed form to the Forensic Submissions Unit [V], on fax number 66609;

take the recommendation form, when you receive it, with a copy of your MGFSS form, to the crime manager.

When your crime manager makes a decision on your submission, you should:

fax a copy of urgent or critical MG FSS forms to the forensic laboratory;

fax the recommendation form back to the Forensic Submissions Unit [V]; once it has been signed by the crime manager; and

arrange delivery of the authorised exhibits to the laboratory with the remaining copies of the form MG FSS and the recommendation form.

Forensic Submissions Unit staff

You should:

enter the submission details onto the work management system, generating a unique case reference for a new case, or further submission on a previous case;

assess the submission request and make a decision with respect to examination options and priorities;

prepare the recommendation form, with any necessary explanation, and the estimated cost, and forward it to the Officer in the Case.

Divisional crime manager

You should:

sign the relevant section for urgent or critical jobs on the MG FSS, before submitting it to the Forensic Submission Unit;

sign the recommendation form and return it to the investigating officer.

When you are given the MGFSS form and the recommendation form, you may opt to authorise it as it stands, or not to authorise some, or any, of the recommendations. You may not authorise work which has not been recommended by the Forensic Submissions Unit.

Changes of circumstances

Should the circumstances of the case change or the forensic evidence is no longer required, you should inform the Forensic Science Service, and the Forensic Submissions Unit.

Vehicles for examination by the Forensic Science Service

If you require a vehicle to be examined at the laboratory, you should complete a 'request for vehicle examination' (form 295H) and follow the forensic submissions procedure. You can get copies of the form from the Forensic Submissions Unit.

The laboratory will not accept any vehicle without:

prior arrangement, as there is limited space for vehicles at the laboratory;

previous submission of a form MG FSS referring to the vehicle; and

a completed form 295H.

Levels of service - urgent, critical, standard

Examples of urgent, critical and standard cases can be found below. These levels of service categories ensure that cases are put in order of priority to comply with custody and statutory time limits. In complex cases, work may be prioritised so the most relevant examinations are completed first.

Urgent and Critical Cases

Officer in the case

You should identify these cases and progress them without delay. The 'critical case key dates' page should be completed within the MG FSS, and you should have urgent and critical submissions signed and authorised in the appropriate section of the form, before submission the Forensic Submission Unit. If the submission is urgent, you will need to endorse the form with your specific requirements.

Forensic Submissions Unit staff will add the status of the case onto the recommendation form for submission to the forensic service provider.

Forensic Submissions Unit [V]

You should:

prioritise any critical submissions;

inform the officer in the case if an urgent or critical case has not been properly identified.

Urgent cases

Examples of urgent cases are:

PACE requirements where the detention of people without charge is an issue;

jobs within a case where the results of the examination are essential to the direction of the investigation, and the speed of response is imperative, such as:

drugs test purchases;

DNA samples, for example from rape victims or offender blood stains on clothing; or

fatal fail-to-stop road traffic accidents with unknown suspects.

When Premium DNA services have been authorised

Any case, which has had Premium DNA services authorised, must be submitted to the FSS laboratory within the guidelines shown below.

Premium 1 (2 day service) - submit within 24 hours

Premium 2 (5 day service) – submit within 2 working days

Failure to submit the case within the times shown could result in the authorisation for the premium service being revoked.

Critical cases

Cases with certain Home Office stipulated criteria are deemed 'critical', and will be given a guaranteed delivery date of results.

Definition of 'critical' case

You should categorize cases as 'critical' if they involve:

a youth offender (any offender under the age of 18);

a persistent youth offender (PYO);

a persistent offender;

an offender charged with an indictable offence falling under Section 51 of the Crime and Disorder Act 1998 (see Chief Constable's Order 2000/52);

an adult offender remanded in custody;

a child victim or witness (under the age of 16);

others at the request of the CPS; a copy of the CPS memo should accompany the MGFSS form.

Indictable only cases, with charged offenders - Section 51 Crime and Disorder Act 1998

You should forewarn the FSS about submissions for cases falling within this part of the definition (known as 'pre-ordering'), using the critical case key dates form. Complete the MGFSS and fax it to the FSS within two days of the first appearance at Magistrates Court, even if the exhibits are not ready for submission or authorised by the Forensic Submissions Unit [V].

Time limits for critical submissions to reach the FSS

So that cases can proceed as quickly as possible, the following time limits have been set for critical submissions to reach the FSS:

Indictable only offence with adult in custody - two days

Indictable only offence with adult charged on bail - ten days

Persistent Youth Offender - seven days

All other critical cases - ten days

Please note that time limits start at the point of charge, except for PYO cases, which start at the point of arrest.

In all critical cases, the Forensic Science Service will issue a guaranteed delivery date. You should pass this date on to your divisional judicial support unit.

Critical submissions not identified or delivered late to laboratory

Analysis of our performance in this area shows that many cases that should be critical submissions are not identified, and of those which are correctly identified, many are delivered late to the FSS laboratory.

These failings can result in:

suspects being released from remand in custody; or

cases being withdrawn.

Standard cases

All cases, which are neither critical nor urgent, are 'standard'. Delivery time for results will depend on Forensic Science Service response times. These cannot be guaranteed but we will try to provide results on time.

You are not required to 'pre-order' standard cases. However, you should complete Part B of the 'critical case key dates' form to assist in ensuring that essential dates can be met.

Submissions to the FSS in Drugs Driving cases

From this date, such submissions should go directly to the FSS. Authorisation is no longer required from the Forensic Submission Unit.

Officer in the Case and custody office staff

You should:

follow the correct procedures for taking the sample;

ensure that a form MGDDE, available from the Intox machine, is completed;

follow your divisional protocol for the submission of the item to the FSS.

You should not submit any sample for drug testing without the form MGDDE.

[Scientific Services Branch [V] : Jackie Newman, Tel. 66601]

Item 6 'Low Copy Number' (LCN) DNA submissions

This item replaces the policy in Chief Constable's Order 2001/30.

Murder and Major Crime cases

The form 'MGFSS' should be submitted to the Forensic Submissions Unit, along with supporting minutes from the forensic strategy meeting. In the absence of forensic strategy meeting minutes, a report must be submitted as for Serious Crime.

Serious Crime

Officer in the case

You should submit a report to your detective chief inspector, containing:

details of the case and any linked cases;

details of any other forensic and fingerprint evidence recovered;

consideration of how any LCN intelligence will be used;

consideration of contamination and transfer issues; and

how the items submitted link to the offence being charged.

Detective chief inspector

You should:

consider the report before endorsing and signing it; and

consider the suitability of the exhibit for LCN with regard to:

the type of offence;

the likely cost of analysis (average £1,800 per item);

control of the crime scene and therefore the integrity of exhibits; and

the way in which any intelligence will be used.

If the divisional or unit detective chief inspector is not available, another detective chief inspector must sponsor the submission.

Officer in the case

Each case will be assessed on its own merits, therefore your report should be sufficiently detailed.

When your report has been endorsed by the detective chief inspector, you should fax it to the Forensic Submissions Unit, fax number 66609, together with a completed Forensic Submissions Form (form MG/FSS). If the request for LCN examinations has been received from the CPS or counsel, it must be supported by their written report.

Forensic Submissions Unit staff

When you receive the request, you should advise the Director of Scientific Services or nominated deputy, who may authorise the request or refer the matter to the Head of Investigative Support [V].

[Scientific Services Branch [V] : Jackie Newman, Tel. 66601]

<u>Appendix 5</u>

Statistical Evaluation

Statistical Significance

As stated previously statistical evaluation usually uses the phrase 'sample' to indicate a set of related measurements. However, throughout this research the word sample has been used to indicate a field sample taken for analysis. To ensure clarity the phrase 'data set' has been used with regard to related measurements.

So far the results of this research have been presented in charts showing the percentage of samples that DNA profiled, matched, eliminated or were of no value. However, it was recognised that the actual numbers of samples for each category and sub-group varied significantly. Therefore, it had to be considered if this difference, in actual numbers of samples analysed, truly reflected the percentage values shown. This enabled an informed judgement to be made whether the percentage values demonstrated a statistically significant difference between categories and sub-groups.

The chi-square test was used throughout this research to evaluate the differences between the proportions in comparable data sets.

For example, the observations from saliva and blood within the body fluids category showed actual frequencies occurring for adding value, or not, to an investigation, as follows:-

| | | No Value to | |
|-----------|----------------|----------------|-------|
| | Added value to | Investigation | |
| Actual | Investigation | (Elimination / | |
| Frequency | (Profiled) | No Profile) | TOTAL |
| Saliva | 32 | 38 | 70 |
| Blood | 16 | 20 | 36 |
| TOTAL | 48 | 58 | 106 |

The first stage was calculating the expected value for each cell if all things are treated equally:-

Row total x Column total

Total y for Table

The expected frequency for Saliva that has added value to an investigation is therefore calculated as:-

<u>70 x 48</u>

106

The remaining cells were calculated in a similar manner.

| | | No Value to |
|-----------|----------------|----------------|
| | Added value to | Investigation |
| Expected | Investigation | (Elimination / |
| Frequency | (Profiled) | No Profile) |
| Saliva | 31.70 | 38.30 |
| Blood | 16.30 | 19.70 |

Chi-square is calculated by finding the difference between the actually observed (Oi) occurrence and the expected (Ei) occurrence. This is then squared and divided by the expected. The values for each cell are then added to calculate the chi-square value: -

$$\chi^{2} = \sum_{i=1}^{k} \frac{(O_{i} - E_{i})^{2}}{E_{i}}$$

| | | No Value to |
|-------------------|----------------|-------------------|
| | Added value to | Investigation |
| | Investigation | (Elimination / No |
| | (Profiled) | Profile) |
| Saliva | 0.002875112 | 0.002379 |
| Blood | 0.005590496 | 0.004627 |
| Chi-square | | |
| Value | | 0.015472 |

The final consideration to enable the chi-square value to be compared against the distribution table is the number of degrees of freedom associated with the sample. Degrees of freedom are directly related to the number of independent sample observations (McKillup, 2005), in this case two, saliva and blood, usually identified as rows in the earlier calculations. Therefore, the degrees of freedom are calculated as follows:-

$$n_{rows}$$
-1 x $n_{columns}$ -1 = $d.o.f.$

The obtained chi-square value is then compared against the distribution table to establish whether the differences occurred by chance i.e. a null hypothesis or if they are statistically significant, known as the probability value or 'p' value (Table A5.1).

| | Nu | ll Hypothe | esis | Statis | tically Sign | ificant |
|-----------------|-------|------------|-------|--------|--------------|---------|
| $d.o.f. \mid p$ | 0.95 | 0.9 | 0.10 | 0.050 | 0.025 | 0.010 |
| 1 | 0.004 | 0.016 | 2.706 | 3.841 | 5.024 | 6.635 |
| 2 | 0.103 | 0.211 | 4.605 | 5.991 | 7.378 | 9.210 |

Table A5.1 – Sample of the Probability points of the Chi-Square Distribution Table

The comparison between saliva and blood gave a chi-square value of 0.015472, which sits between 0.016 and 0.004 corresponding with a probability value (p value) of between 0.9 and 0.95. This means that assuming the null hypothesis is true, there is a greater that 90% chance of seeing the observed results, therefore the null hypothesis cannot be rejected. Statistical significance is only usually considered with a probability figure of less than 0.05; in effect there is less than a 95% expectation of the null hypothesis.

This corresponds to the similar percentage rates previously reported in Chapter 6, section 6.3.1, for these sub-groups. Blood profiled at 44% and saliva at 46%, and a statistically significant difference was not expected. A more extensive Chi-square distribution table can be found at the end of this appendix in table A5.3.

Yates Correction

In some of the data sets subjected to chi-square testing, the numbers of samples were very small. The results of chi-square testing are considered invalid if one or more of the calculated expected values is less than 5 (Yates, 1934). When this occurred the Yates correction was applied for 2 x 2 tables: -

$$\chi^{2} = \sum_{i=1}^{k} \frac{\left(|O_{i} - E_{i}| - 0.5 \right)^{2}}{E_{i}}$$

However, this did not cause any noteworthy change to the results and the outcomes remained the same with regard to accepting or rejecting the null hypothesis for the data sets compared.

Summary of Phase 1 and Phase 2 Chi-square Results

The statistical analysis validated the research figures and also confirmed that the results shown in percentage form were a suitable method of illustration. This proved useful, as the majority of people that would be the likely end users of such research, such as police officers and crime scene investigators, could be expected to understand graphs, charts and percentage rates. A summary of the results can be seen in table A5.2.

| Category | Sub-Group Comparison | Previously Stated % Useful Profiling Rate | Chi- Square | P Value |
|------------------------|-------------------------|--|----------------|--------------|
| | | | | |
| | Body Fluids | 42% | | |
| | Body Fluids | 18% | | |
| | Communication | 48% | | |
| | Firearms | 15% | | |
| | Ligatures | 25% | | |
| All Categories | Personal | | 158.02 | < 0.001 |
| (d.o.f 10) | Belongings | 23% | 138.02 | <0.001 |
| | Premises | 9% | | |
| | Tools | 22% | | |
| | Vehicles | 22% | | |
| | Weapons | 20% | | |
| | Worn Items | 24% | | |
| | | | | |
| D 1 | Torso | 30% | 7 1 1 | 0.025 - |
| Body | Face / Neck | 8% | 5.11 | 0.02 |
| | | | | |
| Communication | Keypad / Mouth | | | |
| | area | 60% | | 0.01 - |
| | All other mobile | 0070 | 7.86 | 0.005 |
| | phone areas | 31% | | |
| | | 5170 | | |
| | Shotgun Stock | 30% | | 0.05 - |
| Firearms | Shotgun Trigger | 15% | 3.87 | 0.025 |
| | | 1070 | | 01020 |
| | Shotgun Cartridge | | | |
| Firearms | (complete) | 38% | 4.92 | 0.05 - |
| | Shotgun Casing | 13% | , _ | 0.025 |
| | | 1070 | | |
| | Handgun Cartridge | | | |
| Firearms | (complete) | 14% | 6 | 0.02 - |
| | Handgun Casing | 7% | Ũ | 0.01 |
| | Thundgun Cubing | ,,,, | | |
| | Shotgun Cartridge | 38% | | 0.02 - |
| Firearms | Handgun Cartridge | 14% | 6.09 | 0.01 |
| | Tunugun Curtifuge | 11/0 | | 0.01 |
| | Shotgun Trigger | 15% | | 0.5 – |
| Firearms | Handgun Trigger | 19% | 0.46 | 0.25 |
| | | 1770 | | 0.25 |
| | Rope | 33% | | 0.75 – |
| Ligatures | Adhesive tape | 29% | 0.16 | 0.73 - 0.5 |
| | Autosive tape | 27/0 | | 0.5 |
| | | | | |
| Dersonal | Lighters | 200/_ | | 0.01 |
| Personal Belongings | Lighters Keys | 28% 16% | 7.4 | 0.01 - 0.005 |

| Category | Sub-Group Comparison | Previously Stated % Useful Profiling Rate | Chi- Square | P Value |
|------------------|-------------------------|--|----------------|------------|
| | | | | |
| Personal | Lighters | 28% | 5.57 | 0.02 - |
| Belongings | Matches | 56% | | 0.01 |
| | Screwdriver | 27% | | 0.01 - |
| Tools | Torch | 67% | 7.62 | 0.005 |
| | Toten | 0770 | | 0.005 |
| | Handbrake | 15% | | |
| Vehicle | Gear Stick | 10% | 15.8 | < 0.001 |
| (d.o.f. 2) | Rear View Mirror | 32% | 1010 | 0.001 |
| | | | | |
| Vehicle (similar | Handbrake | 15% | | |
| surfaces) | Gear Stick | 10% | 3.4 | 0.2 - 0.1 |
| (d.o.f. 2) | Steering Wheel | 23% | | |
| | | | | |
| Weapon | Knife Handle | 29% | | |
| $(d.o.f.^{1}2)$ | Knife Blade | 0% | 19.62 | < 0.001 |
| | Knife Sheath | 67% | | |
| | | | | |
| Waanan | Knife (all) | 28% | 5.84 | 0.02 - |
| Weapon | Brick | 0% | 5.84 | 0.01 |
| | | | | |
| Worn Items | Upper Clothing | 7% | 6.67 | 0.01 - |
| | Lower Clothing | 33% | 0.07 | 0.005 |
| | | | | |
| Worn Items | Underwear | 14% | 4.57 | 0.05 - |
| | Gloves | 32% | 1.0 / | 0.025 |
| | | | | T |
| Fabrics | Leather | 21% | 0.33 | 0.75 - 0.5 |
| | Nylon | 15% | 0.000 | 0.72 0.2 |
| | . | | | |
| Location | Inside | 22% | 13.53 | < 0.001 |
| | Outside | 17% | | |
| | | 00/ | | |
| Wet v Dry | Outside Wet | 8% | 28.05 | < 0.001 |
| | Outside Dry | 21% | | |
| | Demonstr | 200/ | | 0.002 |
| Porous | Porous | 28% | 9.56 | 0.002 - |
| | Non Porous | 21% | | 0.001 |
| | Item | 28% | | |
| Item v Swab | Swab | 28% | 24.25 | < 0.001 |
| | Swau | 2070 | | |
| | | | | |
| | | | | |

| Category | Sub-Group Comparison | Previously Stated % Useful Profiling Rate | Chi- Square | P Value | |
|---------------------------|-------------------------|--|----------------|-----------|--|
| | D 1 | 270/ | | | |
| Surface Texture | Rough | 27% | 25.67 | < 0.001 | |
| | Smooth | 19% | 20107 | 0.001 | |
| | | | | | |
| Target Area (d.o.f. 2) | Clearly Defined | 22% | | | |
| | General Handling | | | | |
| | Area | 22% | 1.94 | 0.2 - 0.1 | |
| | No specific target - | | | | |
| | speculative | 18% | | | |
| | | | | | |
| Month Recovered | Oct - March | 23% | 0.44 | 0.75 – | |
| | April - Sept | 22% | 0.44 | 0.5 | |
| | | | | | |

Table A5.2 – Summary of Phase 1 and Phase 2 Chi-square test results, showing which items within phase 1 and phase 2 sub-groups were compared, the previously reported percentage profiling rate from Chapters 6 and 8 (which relates to whether the sample could be considered useful to an investigation) and the probability value. Probability values in blue are considered statistically significant and the null hypothesis has been rejected. All of these correspond to the visible difference in percentage rates.

| | Null Hypothesis | | | | | | | Statistically Significant | | | | | | |
|-------|-----------------|---------|---------|---------|----------|--------|----------|---------------------------|--------|--------|--------|--------|--------|--------|
| Р | | | | | | | | | | | | | | |
| / | 0.95 | 0.9 | 0.75 | 0.5 | 0.25 | 0.20 | 0.10 | 0.050 | 0.025 | 0.02 | 0.01 | 0.005 | 0.002 | 0.001 |
| d.o.f | | | | | | | | | | | | | | |
| 1 | 0.00393 | 0.01579 | 0.10153 | 0.45494 | 1.32330 | 1.64 | 2.70554 | 3.841 | 5.024 | 5.412 | 6.635 | 7.879 | 9.550 | 10.828 |
| 2 | 0.10259 | 0.21072 | 0.57536 | 1.38629 | 2.77259 | 3.22 | 4.60517 | 5.991 | 7.378 | 7.824 | 9.210 | 10.597 | 12.429 | 13.816 |
| 3 | 0.35185 | 0.58437 | 1.21253 | 2.36597 | 4.10834 | 4.64 | 6.25139 | 7.815 | 9.348 | 9.837 | 11.345 | 12.838 | 14.796 | 16.266 |
| 4 | 0.71072 | 1.06362 | 1.92256 | 3.35669 | 5.38527 | 5.99 | 7.77944 | 9.488 | 11.143 | 11.668 | 13.277 | 14.860 | 16.924 | 18.467 |
| | | | | | | | | | | | | | | |
| 9 | 3.32511 | 4.16816 | 5.89883 | 8.34283 | 11.38875 | 12.242 | 14.68366 | 16.919 | 19.023 | 19.679 | 21.666 | 23.589 | 26.056 | 27.877 |
| 10 | 3.94030 | 4.86518 | 6.73720 | 9.34182 | 12.54886 | 13.442 | 15.98718 | 18.307 | 20.483 | 21.161 | 23.209 | 25.188 | 27.722 | 29.588 |

Table A5.3 – Abridged Sample of the Chi-Square Distribution Table.

<u>Appendix 6</u>

Sample Categories and Sub Groups

Sample Categories and Sub Groups

Charts detailing the overarching categories and sub groups are found on the following pages. The overarching categories are: -

Body Fluids

These are known body fluids that are not suitable for standard DNA testing.

<u>Body</u>

Any samples taken directly from a body (live or dead) such as neck swabs from a strangulation.

Communication

Communication devices such as mobile telephones

<u>Firearms</u>

All categories of firearms and ammunition

Groups

Items that may fall into several groups such as handles, knots.

Ligatures

Items used to bind a person

Personal belongings

Items belonging to a person such as a wallet or handbag.

Premises

Houses and commercial premises or buildings.

Tools

Tools that have not been used as a weapon but in the commission of other crime such as screwdriver.

Vehicles

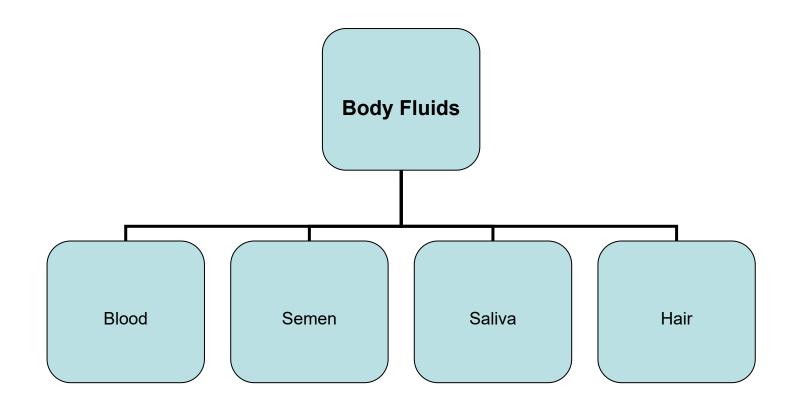
Any means of transport, car, bicycle, wheelchair.

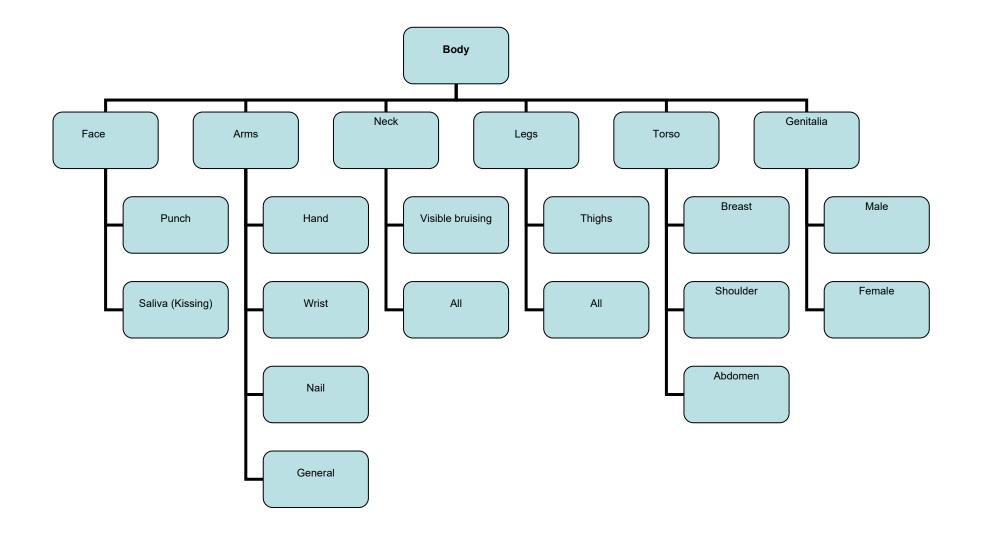
Weapons

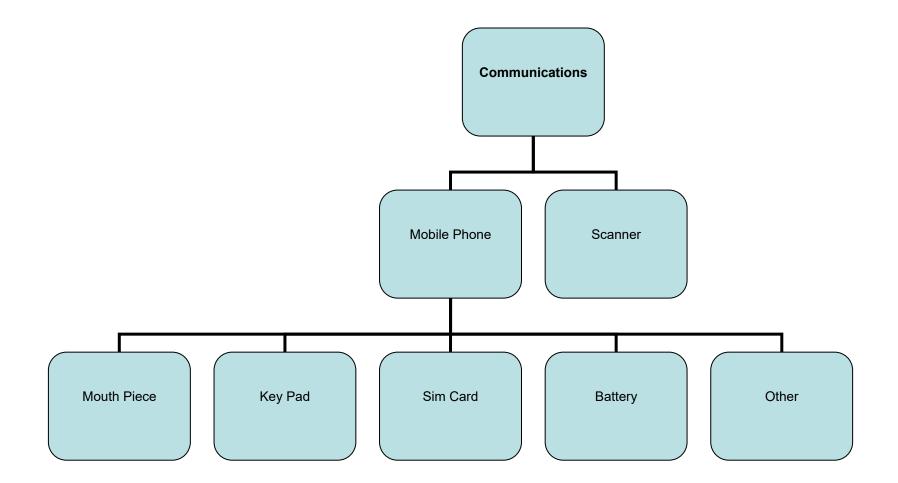
Any items used as a weapon against a person.

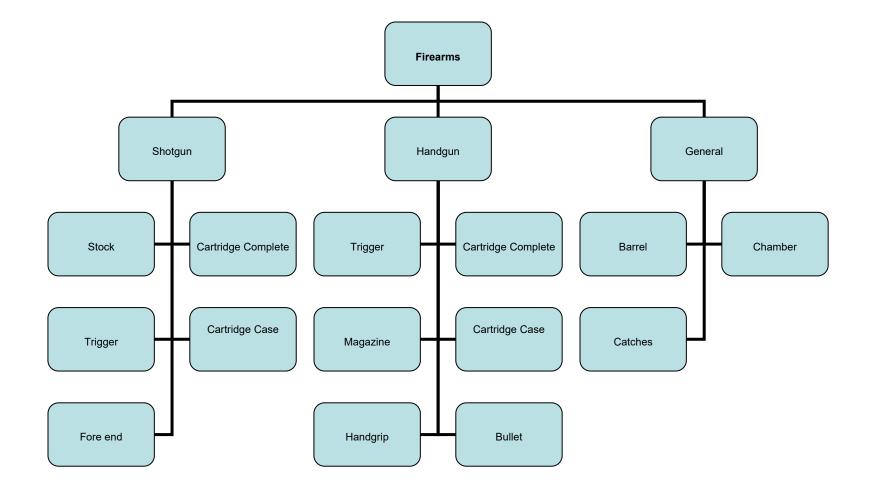
Worn Items

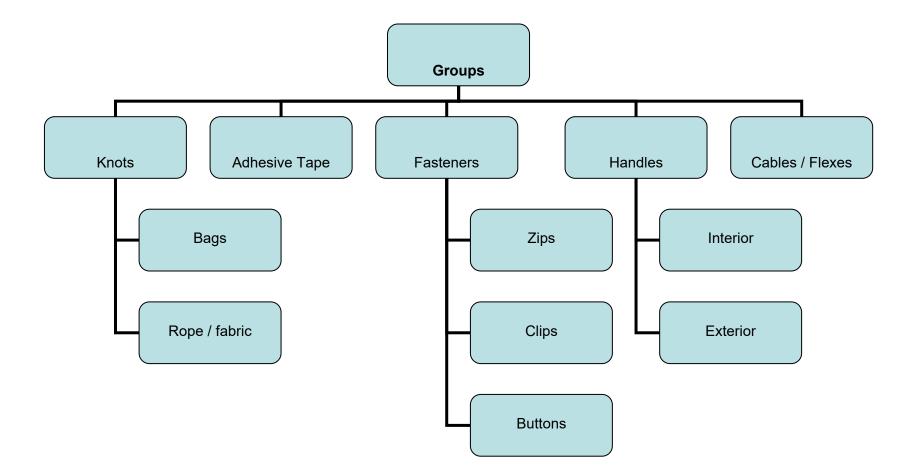
Items that are usually worn by a person such as clothing or jewellery.

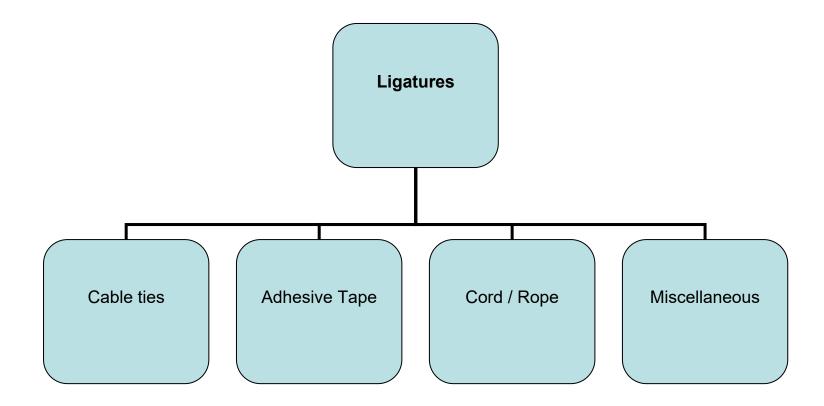


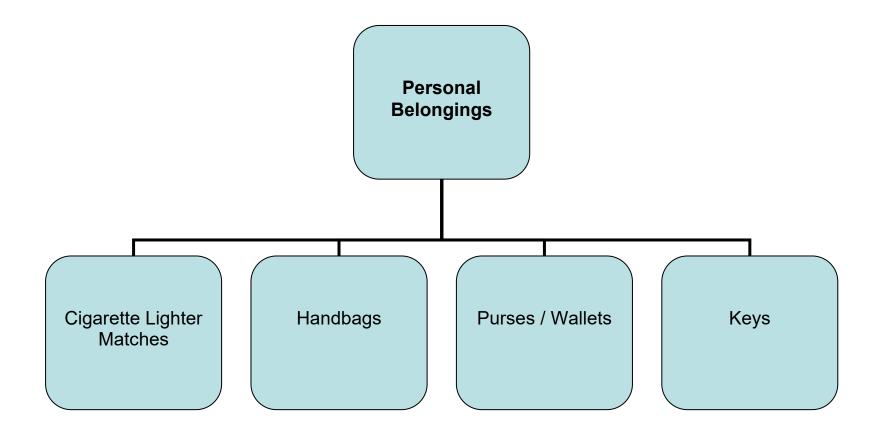


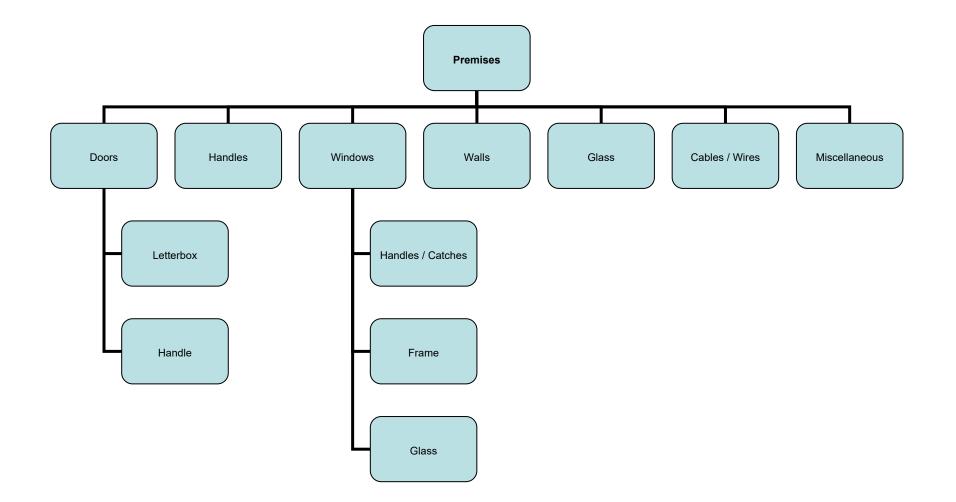


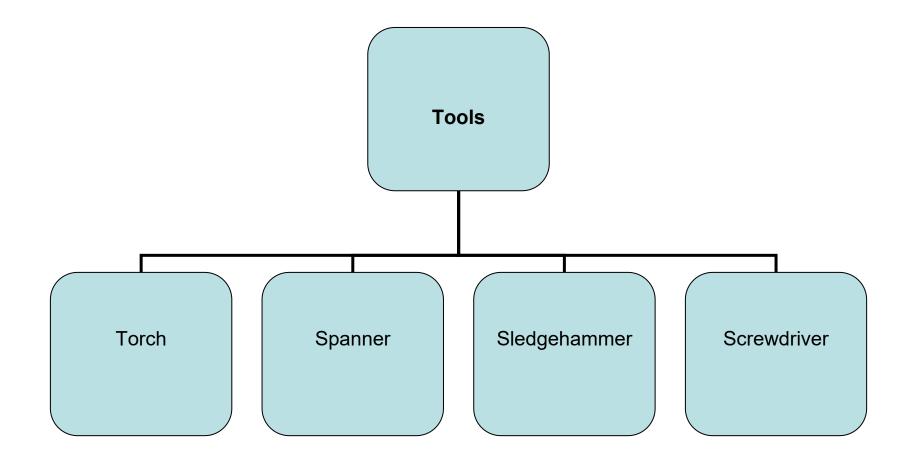


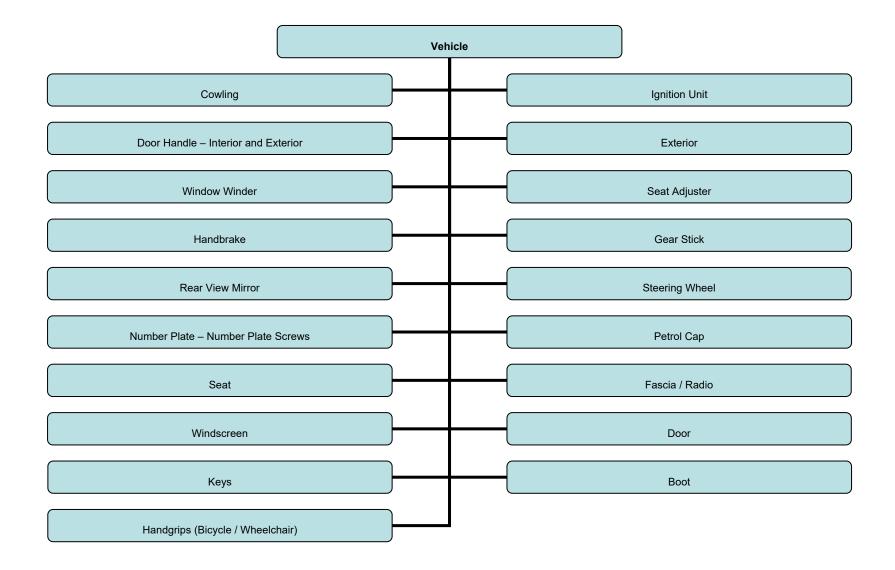


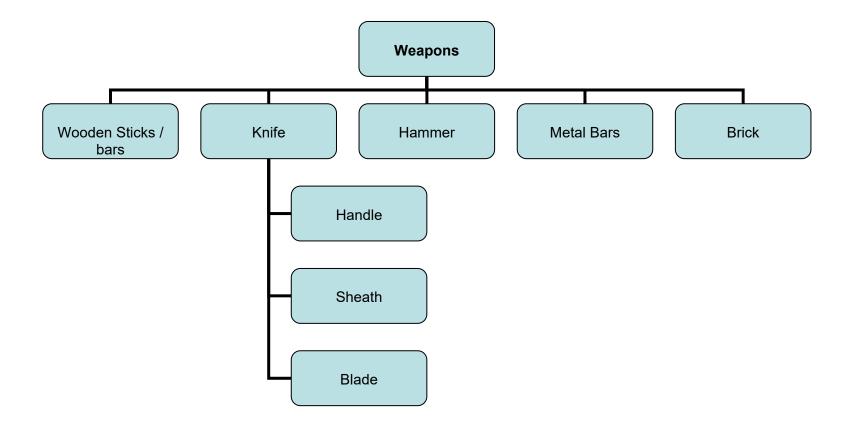


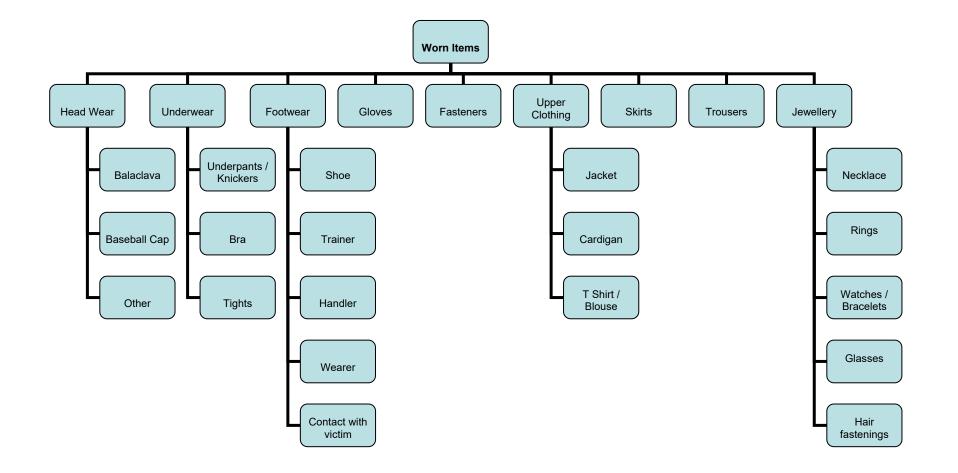






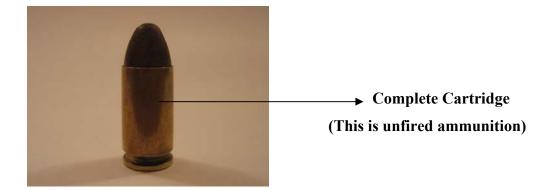






Appendix 7

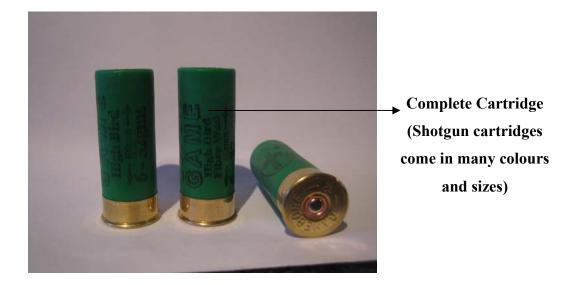
Firearms and Ammunition Terminology



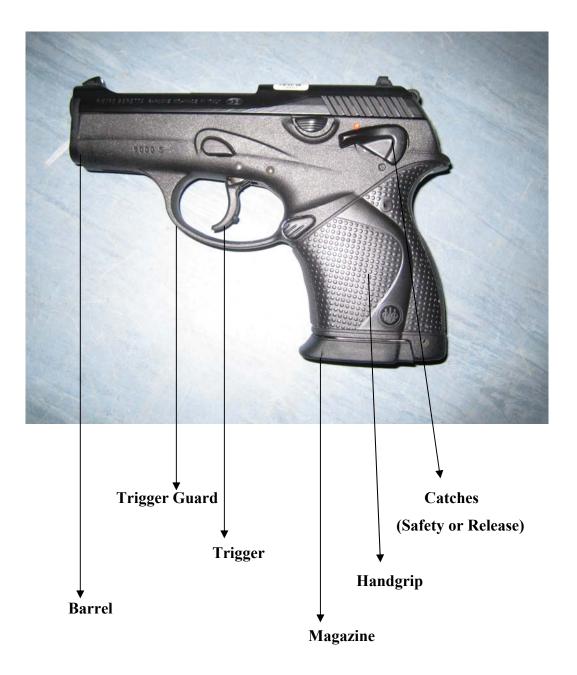


Bullet (This is the projectile that is fired from the cartridge) Cartridge Case

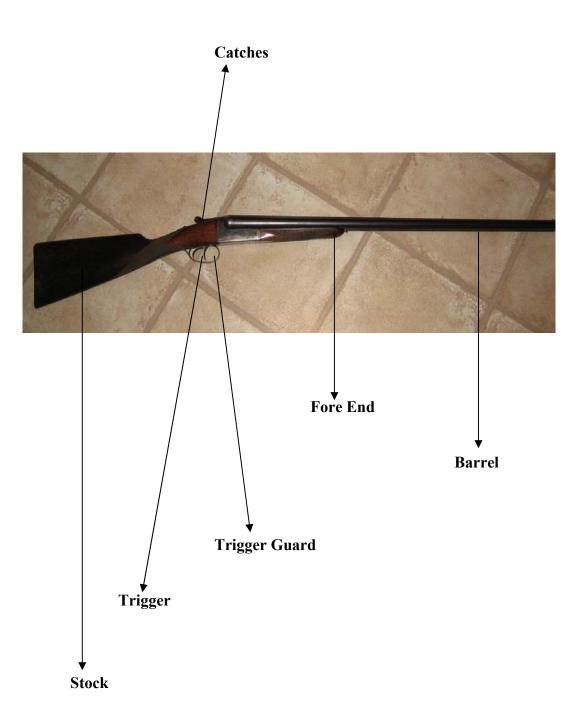
(The ammunition casing that is either expelled from the firearm or remains in the chamber after firing)



<u>Handgun Terminology</u>



Shotgun Terminology



Appendix 8

Firearm Images

Examples of Weapons within Shotgun Categories







Examples of Weapons within Handgun Categories





Appendix 9

Street Robbery Initiative

Crime Issues

Police Forces regularly face specific issues around particular crime trends, which affect the performance of the Force and impact on the local communities and sometimes attract media attention. During the period of this research Greater Manchester Police faced two such issues (also see Appendix 10 – Hook & Cane Burglaries), which presented difficulties in providing investigative leads to detect the crimes.

Meetings were held between Divisional Commanders and the managers of GMP's Scientific Services Branch to see if any new scientific technologies could be utilised to assist with the investigations and, although the research was not complete, the opportunity of utilising Low Template DNA techniques was considered an option.

Strategies were developed for these specific crime types and the results carefully monitored and evaluated.

Street Robbery

Street robbery, often referred to as personal robbery, occurs when a person's property is taken by force in a public area. Mobile phones, handbags, cash and portable MP3 players (Ipods) were and still are frequent targets of such crimes. The offence included bag snatches and can vary from a quick snatch to a violent attack with the victim being seriously assaulted.

In some cases the offender engaged in conversation with the victim and stole the mobile phone after removing and returning the SIM card to the victim.

In the majority of cases the offender leaves little forensic evidence behind of a useful nature. Investigations often rely on poor quality CCTV, victim accounts, and in close contact cases, fibre evidence. For fibre analysis to take place it

normally requires a suspect to have been identified and their clothing seized for comparison.

Items that the offender has taken from the victim and are known to have been handled by them, are frequently discarded. Sometimes these are recovered in the vicinity of the offence. This property often includes handbags and purses, the majority of which are frequently of a material that is unsuitable or very poor for fingerprinting techniques.

Agreement was sought to apply LCN DNA techniques to this type of crime in an effort to aid detection. Handbags, purses and SIM cards, that had been known to have been handled by the offender, were targeted for LCN DNA. Due to their size, handbags were only sampled if a target area could be specified as to where the offender had handled the bag. This often occurred following a struggle where straps had been pulled, torn or ripped during the offence. This information was usually available from the victim but in some cases also from CCTV coverage. Opening areas of purses and relevant fastenings on purses and bags were also sampled. SIM cards were only sampled if the offender had removed it from the mobile and given it back to the victim, or it was recovered with other items of the victims' property. In these cases, as the property under examination was of a personal nature, elimination samples were submitted with each case, but only from the immediate owner.

<u>Results</u>

In all, 57 samples were analysed with very poor profiling results, only 2 (4%) profiled. No matches were generated and 20 (35%) of the samples were anticipated eliminations (Fig. A9.1).

The sub-group of purses was the only group to produce a useful profile in 2 (20%) of the submissions. However, all of these remained outstanding.

It should be noted that SIM cards in the Communications Section 6.3.3, LCN DNA profiled at a much higher rate and proved to be successful. This is likely to

be due to the different nature of the recovery and extent of handling, which in this type of robbery is minimal.

Following the poor results achieved for handbags and purses, subsequent samples were only analysed in the most serious of street robbery cases and investigators were made aware of the probability of failure.

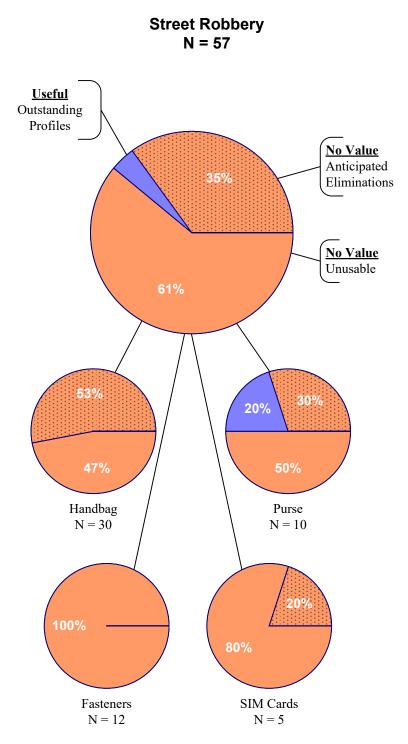


Figure A9.1 – Results for Street Robbery

<u>Appendix 10</u>

Hook & Cane Burglaries

Hook and Cane Burglaries

A crime trend was noted where a specific modus operandi (MO) for stealing high value prestige vehicles was being used. This involved inserting a cane with a hook attached to the end, through a letterbox, in the hope of retrieving car keys that had been left within reach, usually on a hall or porch table. Once the keys had been retrieved the offender could then drive the vehicle away without activating any vehicle alarms or damaging the vehicle in any way. In these cases the vehicles were rarely recovered and there was little, if any, forensic evidence left at the scene. The crime was classed as a burglary as entry had been gained to a person's home, even if it was by remote means.

Fingerprinting the letterboxes and exterior of the doors had proved unsuccessful with no useful fingerprints being recovered; as had fingerprinting the few canes that had been left behind at the scene. The cars had not been recovered and other forensic evidence types, such as footwear and fibres, were absent or there were no suspects to match this type of evidence to. Due to the MO requiring very close proximity of the offender to the letterbox, the offender had to look through the narrow gap to hook the keys on the cane, lifting the flap with their hands and possibly touching it with their face or arm, it was considered a possibility to recover LCN DNA from these surfaces. An additional potential source for DNA were the canes that had been brought to the scene by the offenders and on occasion left behind.

During a long and particularly high value series of these types of offences in the Bolton area of Manchester, LCN DNA recovery was attempted at the scenes of crime that met the following criteria:-

- A hook and cane was believed to be the MO
- A prestige vehicle had been stolen and had not been recovered
- The offence had occurred within 24 hours
- The scene had been preserved for CSI attendance
- No entry had been gained to the premises other than via the letterbox

In these cases the CSIs were instructed to recover LCN DNA swabs from the letterbox and to recover the cane if it had been left behind for LCN DNA analysis.

As part of the forensic strategy for this initiative, a decision was made not to take elimination DNA samples in any of the cases as the victims should not have had contact with the cane and would have had limited, if any, contact with the outside of the letterbox. It was possible that several legitimate persons could have touched the letterbox including the postal worker, paper delivery person and anyone delivering flyers to the area. It was decided not to pursue eliminations from these persons for two reasons, firstly the additional cost of analysis and secondly not to alert the public and possible offenders in the area of the tactics being used to try to detect the offences. The process would be that any DNA profile obtained would first be searched on the NDNAD and if it remained outstanding a decision could then be made whether to obtain elimination samples at that stage. If a match was found due consideration was given to the fact it could be eliminated, if the householder or person who used the letterbox legitimately had previously been placed onto the NDNAD.

Initially, it was agreed that 20 scenes would be examined to 'test' the possibility of gaining a result and establish the probability of obtaining a DNA profile from canes and letterboxes. However, following an early success on one of the letterboxes, in profiling and a subsequent NDNAD match, this was extended to 32 scenes which were examined over a period of 6 months.

<u>Results</u>

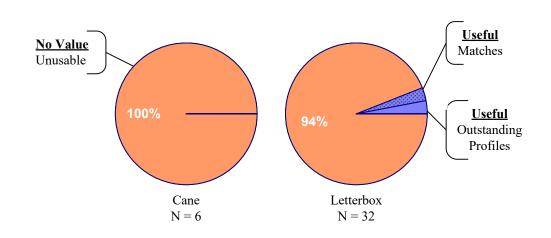
Samples were submitted from 32 letterboxes and 6 canes. None of the samples from the canes produced a useful profile. Of the 32 letterbox swabs, 2 (6%) generated a useful profile resulting in 1 (3%) match, from the NDNAD (Fig. A10.1).

The one match result from the NDNAD provided a useful line of enquiry to the investigators and duly a suspect was arrested. However, the person was

234

subsequently released as he successfully argued legitimate access to the letterbox previously although he didn't fall into any of the anticipated elimination groups (postal worker, leaflet distributor, resident).

In conclusion, of the 32 letterboxes sampled no useful results were obtained and it did not lead to any detection in crime. Further samples from letterboxes and canes were not submitted for this crime type with this specific MO.



Hook & Cane

Figure A10.1 – Results for Hook & Cane Burglaries