University of Technology, Sydney

A Criminalistic Approach to Biological Evidence:

Trace DNA and Volume Crime Offences

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Certificate of authorship and originality

I certify that the work in this thesis has not previously been submitted for a degree nor has it been submitted as part of the requirements for a degree except as fully acknowledged within the text.

I also certify that the thesis has been written by me. Any help that I have received in my research work and the preparation of the thesis itself has been acknowledged. In addition, I certify that all the information sources and literature used are indicated in the thesis.

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Abbreviations

ACT	Australian Capital Territory
AFP	Australian Federal Police
ANOVA	Analysis of Variance
ANZPAA	Australian and New Zealand Policing Advisory Agency
BNs	Bayesian Networks
BSAG	Biology Specialist Advisory Group
CCTV	Closed circuit television
CODIS	Combined DNA Index System
COPS	Computerised Operational Policing System
DAB	Diaminobenzidine
DAL	The Division of Analytical Laboratories
DFO	1,8-diaza-9-fluorenone
DNA	Deoxyribonucleic acid
dsDNA	Double-stranded DNA
EDTA	Ethylenediaminetetraacetic acid
FBI	Federal Bureau of Investigation
FPs	Fingerprints
FSG	Forensic Services Group
FSS	Forensic Science Service (UK)
IT	Information Technology
LCN	Low copy number
LCV	Leucocrystal Violet
NAFIS	National Automated Fingerprint Identification System
NAS	National Academy of Sciences
NCIDD	National Criminal Investigation DNA Database

NIFS	National Institute of Forensic Science
NSW	New South Wales
NT	Northern Territory
NZ	New Zealand
PCR	Polymerase chain reaction
POE	Point of entry
QLD	Queensland
RFU	Relative Fluorescence Units
SA	South Australia
SMANZFL	Senior Managers of Australian and New Zealand Forensic Laboratories
SOCO	Scenes of Crime Officer
STR	Short tandem repeat
SNP	Single nucleotide polymorphism
TAS	Tasmania
TE	Tris-EDTA buffer
UK	United Kingdom
USA	United States of America
UV	Ultraviolet
VIC	Victoria
WA	Western Australia

List of Papers

This thesis is based in part on the following publications and conference presentations.

Published Articles

- **Trace DNA: An underutilised resource or Pandora's Box? A discussion of the use of trace DNA analysis in the investigation of volume crime.**
  Raymond, J.J., Walsh, S.J., van Oorschot, R.A.H., Gunn, P.R., Roux, C. *Journal of Forensic Identification,* 54 (6), 2004, 668-686.
- **Trace DNA analysis: Do you know what your neighbour is doing? A multi-jurisdictional survey.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Roux, C. *Forensic Science International: Genetics,* 2(1), 2008, 19-28.
- **Assessing trace DNA evidence from a residential burglary: Abundance, transfer and persistence.**
  Raymond, J.J., Walsh, S.J., van Oorschot, R.A.H., Gunn, P.R., Evans, L., Roux, C. *Forensic Science International: Genetics Supplement Series,* 1(1), 2008, 442-443.
- **Trace Evidence Characteristics of DNA: A Preliminary Investigation of the Persistence of DNA at Crime Scenes.**
  Raymond, J.J., van Oorschot, R.A.H., Gunn, P.R., Walsh, S.J., Roux, C. *Forensic Science International: Genetics,* 4(1), 2009, 26-33.
- **Trace DNA success rates relating to volume crime offences.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Gunn, P.R., Roux, C. *Forensic Science International: Genetics Supplement Series,* 2(1), 2009, 136-137.
- **Trace DNA and street robbery: a criminalistic approach to DNA evidence.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Gunn, P.R., Roux, C. *Forensic Science International: Genetics Supplement Series,* 2(1), 2009, 544-546.

Conference Presentations

- **DNA: Just any other trace evidence?**
  Raymond, J.J., Walsh, S.J., Gunn, P. R., Van Oorschot, R.A., Roux, C., In: the 17th International Symposium of the Australian and New Zealand Forensic Science Society (ANZFSS), 2004, Wellington, New Zealand
- **Trace Evidence Characteristics of DNA: Abundance and Persistence studies.** Raymond, J.J., Gunn, P., Walsh, S.J., Van Oorschot, R.A., Roux, C. In: International Association of Forensic Sciences (IAFS), 2005, Hong Kong, China.
- **Trace DNA Analysis: Australian and New Zealand methods survey.**
  Raymond, J.J, Van Oorschot, R.A., Walsh, S.J., Roux, C. In: the 18th International Symposium of the ANZFSS, 2006, Fremantle, Western Australia.
- **Assessing trace DNA evidence from a residential burglary: Abundance, transfer and persistence.**
  Raymond, J.J., Walsh, S.J., Van Oorschot, R.A., Gunn, P.R., Evans, L., Roux, C. In: the 22nd Congress of the International Society for Forensic Genetics (ISFG), 2007, Copenhagen, Denmark.
- **Trace evidence characteristics of DNA: background levels and transfer of trace DNA in volume crime.**
  Raymond, J.J., van Oorschot, R.A., Walsh, S.J., Roux, C., Gunn, P.R. In: the 19th International Symposium of the ANZFSS, 2008, Melbourne, Victoria.
- **Trace evidence characteristics of DNA: the persistence of DNA in volume crime scenes.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Roux, C., Gunn, P.R. In: the 19th International Symposium of the ANZFSS, 2008, Melbourne, Victoria.
- **A criminalistic approach to biological evidence: trace DNA and volume crime.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Gunn, P.R., Roux, C. In: the 5th meeting of the European Academy of Forensic Science, 2009, Glasgow, United Kingdom.

- **Trace DNA success rates relating to volume crime offences.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Gunn, P.R., Roux, C. In: the 23rd congress of the International Society for Forensic Genetics, 2009, Buenos Aires, Argentina.
- **Trace DNA and street robbery: a criminalistic approach to DNA evidence.**
  Raymond, J.J., van Oorschot, R.A.H., Walsh, S.J., Gunn, P.R., Roux, C. In: the 23rd congress of the International Society for Forensic Genetics, 2009, Buenos Aires, Argentina.

Abstract

Volume crimes such as burglary and street robbery present an enormous cost to the Australian community each year. These ubiquitous crimes traditionally have a low resolution rate, but the use of information gathered through DNA databases provides another avenue of investigation. The forensic response to these crimes could be increased with the use of trace DNA; however the lack of awareness of forensic science as a holistic discipline focusing on the study of traces, often leads to a lack of knowledge into the trace evidence characteristics of DNA. This problem is compounded by practical and interpretive difficulties. The main hypothesis tested through this study is that, with an increased understanding into the criminalistic properties of trace DNA, it may prove to be more useful and effective evidence in the investigation of volume crime than is currently the case.

The project encompassed three parts. The first component was a detailed survey sent to every jurisdiction in Australia and New Zealand to benchmark methods and protocols, education and training of personnel, and opinions and uses of trace DNA. The second involved the analysis of the results of 250 trace DNA swabs collected from New South Wales crime scenes, in order to provide a comparison point to the experimental work. The final section comprised preliminary experimental work to investigate the abundance, transfer and persistence of trace DNA within the context of residential burglary and street robbery offences.

The methods survey helped to identify methods to be used in the experimental component of the project, but also highlighted issues in the field including a lack of training and proficiency testing. The absence of data collation across the jurisdictions was also a point for concern, and prevented the identification of factors that may affect trace DNA success rates. The pervading outcome of the survey was the need for effective data management systems and strong communication lines to facilitate best practice. From the analysis of the casework data a success rate[1] in the order of 15-20% was identified for New South Wales trace DNA swabs, with an average of 1.7ng of DNA recovered. Subsets of the data were used to directly compare to the experimental results in terms of transfer and persistence.

[1] Defined here as swabs resulting in a profile with 12 or more alleles, and therefore suitable for inclusion on the state DNA database.

The experimental work gave an insight into the behaviour of trace DNA in crime scene scenarios. The level of background DNA on surfaces encountered in forensic investigations was varied; for example residential doors were found to hold more background DNA than windows. Whilst the level of DNA on personal items such as bags and wallets was found to be relatively high, DNA from the offenders of simulated robberies could still be detected in usable quantities on these items. DNA was found to persist in sheltered locations for at least six weeks, but declined more rapidly in outdoor environments, with profiles not recovered after two weeks. This information may help to assist the interpretation and presentation of trace DNA evidence when the judicial question is one of activity, rather than source. The data also may be used in the education of crime scene examiners to assist them to target the most probative evidential samples. With further work in this field, trace DNA will be more easily applied to investigations.

Trace DNA may be a useful tool in volume crime investigations, but individual jurisdictions should assess their capacity to manage the evidence to ensure results can be disseminated and actioned in a timely manner, otherwise the investment may prove to be fruitless. Effective and ongoing training programs and functional data management systems should be implemented to maximise both the investigative and intelligence value of trace DNA evidence. A holistic approach to the implementation of forensic evidence, encompassing the groundwork of theoretical analysis, review of capabilities and logistical and technical improvements, would greatly increase its value in policing and the criminal justice system.

Chapter 1:

Introduction

Chapter 1: Introduction

"Wherever he steps, whatever he touches, whatever he leaves, even unconsciously, will serve as a silent witness against him. Not only his fingerprints or his footprints, but his hair, the fibres from his clothes, the glass he breaks, the tool mark he leaves, the paint he scratches, the blood or semen he deposits or collects. All of these and more bear mute witness against him. This is evidence that does not forget. It is not confused by the excitement of the moment. It is not absent because human witnesses are. It is factual evidence. Physical evidence cannot be wrong, it cannot perjure itself, it cannot be wholly absent. Only human failure to find it, study and understand it can diminish its value. "

—Paul Kirk, 1974 [1]

The often (simplistically) quoted forensic axiom, 'every contact leaves a trace', was described by criminalist Edmond Locard [2] close to a century ago. It was first applied to dust and dirt traces, and then more widely to other trace evidence types such as glass, fibres and paint. The theory postulates that whenever there is a contact between objects, some form of matter will be transferred. It is of particular relevance to forensic science and crime scene investigation, where the primary aim is to determine Quintilian's who, what, where, when and how from the physical evidence left behind. What limits this theory in practice is our ability to detect the transferred matter.

In the early days of forensic DNA analysis, the technology's sensitivity was limited to biological stains such as blood and semen, and issues relating to the transfer of such biological substances were not a major concern. However with technological developments it is possible to detect and analyse DNA from handled objects, or trace DNA[2], and therefore the principles of criminalistics are more relevant and can now be applied to such evidence. As

[2] The author concedes that an internationally recognised standard definition of 'trace DNA' is yet to be developed. For the purpose of this thesis, 'trace DNA' is defined as DNA that does not originate from a discrete biological stain or from a large discrete biological source. It refers primarily to material resulting from skin contact that is not visible to the eye. This term is commonly used in the Australian region for such evidence. The author also acknowledges that the ambiguity between the scientist's definition of a 'trace' as a small quantity, and the fundamental forensic definition as a remnant of an activity, continues to cause conceptual issues.

DNA dips into the realm of trace evidence, the interpretation becomes much less straightforward. The contested issue in legal argument over DNA evidence is now less often regarding the identification of the profile, but rather trace evidence issues such as transfer and persistence and exactly how that profile came to be present at the crime scene. The focus of this thesis is the trace evidence characteristics of DNA, with the aim of increasing our understanding into the 'behaviour' of trace DNA.

This chapter will outline the background information and relevant literature supporting the dissertation. A basic overview of forensic DNA technology past and present, a look at future technologies and challenges, and a detailed review of research into trace DNA are provided. The concepts of trace evidence and criminalistics are also introduced. Volume crime offences are described and defined, leading into a discussion of the use of DNA in combating these crimes, in particular through DNA databases. The many issues compounding the application of trace DNA evidence, including its trace evidence properties, the 'randomness' of its recovery, and interpretation, are discussed including several legal challenges to trace DNA evidence in Australia. The gaps in current research are highlighted, providing a basis for this thesis, which is outlined.

It should be noted that the research is based primarily in the Australian context, given the location of the author; however the results are compared to literature from international jurisdictions to provide conclusions with wider applicability.

1.1 DNA technology and its use in the criminal justice system

DNA technology is a relative newcomer to the field of forensic science, unlike the more established disciplines of fingerprints and other physical evidence. DNA analysis was first applied to forensic cases in the United Kingdom in the mid 1980s, such as the Pitchfork murders[3] [4].

[3] Whilst the first use of DNA in a criminal trial was the Pitchfork murders, its first use in any forensic sense was the paternity case of Andrew Sarbah, who had been born in the United Kingdom but lived in

The breakthrough in the forensic application of DNA technology came with the realisation that repeated sequences in certain sections of DNA varied between individuals in terms of the number of repeats. The length variation of these repeated regions, called 'minisatellites' or restriction fragment length polymorphisms (RFLP), was analysed through the use of a restriction enzyme which cut up the DNA into fragments at sites surrounding the region. This technique was termed 'DNA fingerprinting', now referred to as DNA profiling.

At first, the technology was such that only relatively fresh samples present in large quantities, such as blood and semen, could be tested successfully. As forensic samples are often minute or degraded this limited the use of DNA analysis to crime scene investigation. This constraint was eased in the early 1990s with the adoption of the polymerase chain reaction (PCR) in forensic DNA analysis. The reaction was first described in the mid 1980s, and it enables small sections of DNA to be replicated numerous times, effectively amplifying the template material up to a workable level [5, 6]. Using the temperature sensitivity of DNA, the molecule is denatured, and then cooled to allow primers to bind to the now single-stranded DNA. The primers are short sequences synthesised to target the relevant section of DNA that is being analysed. Once the primers have surrounded the region of interest, a DNA polymerase extends the section between the primers and the length of the alternate primer to produce a copy of the strand. This process is repeated a selected number of times, and during each cycle the number of DNA molecules theoretically doubles. Following the introduction of the PCR, usable DNA profiles were able to be obtained from crime scene samples such as cigarette butts [7] and hairs [8].

The next significant advance in forensic DNA analyses came with the use of short tandem repeats (STRs)[9], which are small, repeated units of DNA. STRs used by forensic scientists are typically only 3, 4 or 5 base pairs long and have significant length variability within human populations. The small size of these segments gave them higher stability than sections previously targeted, and meant STR profiles were able to be obtained from older, more degraded material [10, 11]. The number of STR loci present in the human genome has been estimated at over a million, making up 3% of the entire human genome [12]. Most STR loci are di-nucleotide repeats (two repeat units), however tetra- or pentanucleotide repeats are

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Ghana. On return to the UK, he was refused entry on suspicion of falsified documents, however later DNA analysis of the family proved his rightful UK citizenship [3].

preferred for forensic analysis, as the longer repeat units are less likely to suffer artefacts during the amplification process, and are more robust to survive environmental conditions.

DNA typing from a forensic perspective refers to the generation of DNA profiles made up of genotypes from a number of highly variable sites in the DNA molecule. The greater the number of variable sites genotyped, the higher the resulting discrimination potential will be. Originally, separate aliquots of template DNA were required for PCR amplification of different markers. The validation of multiplex systems that can simultaneously amplify several different regions on the same stretch of DNA prior to analysis has increased the ability to generate highly discriminating profiles from smaller amounts of crime scene sample.

In order to allow for comparison of profiles within and between jurisdictions, the same set of loci needs to be analysed. The international forensic community has identified, and recommended the use of, a small set of core STRs [13, 14]. The core loci were chosen for their high degree of polymorphism (allowing for greater discrimination) low mutation rates, robustness and reproducibility, and smaller allelic length. The Australian forensic community utilise a kit (AmpFlSTR® Profiler Plus™, Applied Biosystems) that includes nine of these core STRs, that together have a discrimination power sufficient to distinguish every Australian bar identical twins [15]. Other kits that have been validated for forensic use include AmpFlSTR® SGM Plus™, an 11 loci kit used in the United Kingdom and New Zealand, and AmpFlSTR® Identifiler and PowerPlex® 16 (Promega Corporation), which are both 16 loci kits, allowing for greater discrimination between individuals. These kits all contain nine core STRs, which therefore ensures their applicability for use in current databases and for cross-jurisdictional comparison.

1.1.1 DNA Technology: New innovations and challenges

The technology of forensic DNA analyses has progressed in the two decades since its inception. Samples encountered in forensic science are rarely pristine, and are often exposed to the environment, subjected to lengthy time delays as in cold case investigations, or are present in such minute quantities making detection and analysis extremely difficult. The forensic community have adapted standard methods in an attempt to generate profiles from smaller amounts of template DNA. An example of such research is the development of miniSTRs, where the primers for the CODIS loci have been redesigned to sit closer to the relevant STR. Thereby shorter amplicons of around 100 base pairs are generated, when

compared with the 400 base pairs or greater amplicons resulting from traditional STR primers. These primers are more efficient than standard primers with degraded samples, and can reduce stochastic effects yet still be used for databasing purposes. Many forensic laboratories have or are in the process of validating a commercial miniSTR kit, MiniFiler™, for use in casework [16]. Other novel PCR methods have recently been investigated to determine their applicability to forensic samples. Whole Genome Amplification (WGA), whereby large portions of the DNA are amplified prior to forensic STR amplification, and the inclusion of locked nucleic acids (LNAs) in primer design to increase their binding strength and specificity, have both shown promising signs in preliminary research [17, 18].

A further advance in forensic DNA analysis has been the use of single nucleotide polymorphisms or SNPs. These polymorphisms are single base variations at a specific location, and are the most common human sequence variation [19]. Since 2001 when the draft human genome was published, over 5 million SNPs have been identified. Though less discriminating than STRs, SNPs are particularly effective for forensic analyses as they have low mutation rates, and are suitable for more degraded samples and high throughput analyses. Low mutation rates are required for parentage testing, and are useful in the inference of biogeographic ancestry, as particular mutations become 'locked' in a population. This use is being explored as intelligence for the investigation of crimes, where the inference of a suspect's ancestry and appearance may assist in the production of new lines of enquiry [20]. There has been some debate as to whether SNPs may replace STRs as the method of choice for forensic analyses, however with such large numbers of STR profiles currently existing on national DNA databases it is difficult to see this occurring in the near future.

One of the biggest issues currently affecting forensic DNA analysis is the lengthy delay in analysis times caused by backlogs, as evidence submission rates has increased exponentially in recent years [21, 22]. Automated and robotic platforms have been designed and implemented to assist with the high throughput of samples with minimal need for human interaction [23-26]. The capacity of laboratories has vastly increased with these developments and it is hoped that backlogs will be alleviated by these advances.

Another development which may help to reduce backlogs is the miniaturisation of analysis instruments, or 'lab on a chip' technology. Instruments have been developed where the capillary electrophoresis has been reduced from a 30cm long tube to a microchannel of only a centimetre, allowing the processing of samples in around 30 minutes [27, 28], and

researchers have also merged the extraction and amplification into a single device [29, 30]. The instruments are relatively small and portable, enabling their deployment at scenes. The use of alternative enzymes to the standard Taq polymerase also reduces the extraction and amplification stages to two hours in total. These developments have great potential for use as a quick screening tool to rapidly eliminate suspects and prioritise evidence, thereby reducing the overall number of samples needing to be processed. They also have obvious potential applications in the context of Disaster Victim Identification.

Still a relatively new tool in forensic science, DNA profiling has faced more challenges in its short life than traditional forensic analyses. Only four years after the first use of DNA in forensic casework, questions were arising into the quality assurance of the technology. In the 1989 American case *People v Castro* [31], the admissibility and reliability of DNA evidence was challenged for the first time. The case found that the science of DNA profiling was inherently sound and reliable, but due to faults in the testing procedure employed in the case the DNA evidence was not admitted. This resulted in a much-increased focus on accreditation and quality in the field of forensic DNA typing. In 1992 the National Research Council of the United States issued a report on *DNA Technology in forensic science* [32] and a secondary report was conducted in 1996 [33]. The recommendations of the reports involved all aspects of forensic DNA profiling, including interpretation statistics, quality standards, proficiency testing and databanks. The reports recommended that rather than to establish an error rate for DNA testing, which was found to be prohibitively expensive and time consuming, laboratory standards should instead be raised. In response in 1998 the Federal Bureau of Investigation (FBI) issued a document detailing the quality assurance standards for forensic DNA laboratories [14]. Forensic laboratories must comply with these standards in order to submit profiles to the US national DNA database. Currently the Scientific Working Group for DNA Analysis Methods (SWGDAM), facilitated by the FBI, oversees the national standards and proposes revisions as they arise. Other countries have followed the lead of the United States in establishing quality and validation standards, and in Australasia this function is provided by the Biology Specialist Advisory Group (BSAG) to the Senior Managers of Australian and New Zealand Forensic Laboratories (SMANZFL). The intense scrutiny on DNA analyses and the subsequent response by the forensic community has proven to be of immense benefit to the field. A recent report by the US National Academy of Sciences (NAS) [34], tasked with assessing the present state of forensic science in the US, found that though '*barely 20 years old, DNA typing is now universally recognised as the standard against which many other forensic individualisation techniques are judged*'.

1.2 DNA from touched objects: Trace DNA

Trace DNA is defined here as DNA transferred via skin contact, and is often referred to as 'contact' or 'touch' DNA. In 1997 with the availability of increased sensitivity in DNA analysis, researchers from Victoria, Australia found that DNA profiles could be recovered from the minute traces left behind from skin contact, or to use their term, DNA 'fingerprints' from fingerprints [35]. This discovery broadened the field of forensic DNA analysis, leading to the current situation where handled items are regularly tested in an attempt to determine the identity of the person who handled them, which in many cases is likely to be the offender. Other studies then expanded on this research. Belgian researchers have recovered profiles from tools, bag grips, clothing and glass with considerable success [36, 37]. Van Renterghem et al. [37] tested separately the outsides and rims of beer glasses used in an assault case, for skin debris and saliva respectively. An interesting discovery was that in one case, the skin debris swab gave a positive profile, whereas the swab for saliva did not.

As new technologies became commonplace in forensic laboratories, the number of casework scenarios applicable to DNA analysis increased, including the recovery of DNA profiles from obscure material such as dandruff [38], lip cosmetics [39], lollypops [40], current conductors [41] and even hotdogs [42].

Other research into trace DNA has been conducted largely in response to casework scenarios, including;

- Wickenheiser and Challoner [43] were able to obtain profiles from the handles of knives left at a crime scene, even after the knives were subjected to the fingerprint enhancement treatments of cyanoacrylate and metal deposition.
- DNA can be recovered from bed sheets after one night of sleeping, and the DNA of the owner of a bed can still be recovered from sheets after being slept in by another person for one night [44].
- The lace and tongue area of a shoe is more likely to produce a single source profile of the owner, however not every shoe will produce a profile [45, 46]. Mixtures from shoes are also common.
- It is also possible to recover full profiles of the manufacturer/handler from exploded pipe bombs, provided the bomb is not highly fragmented [47].
- An attempted strangulation case in Italy prompted research which found that it is possible to recover DNA from steel cables, provided the cable is cut up and

ultrasonically treated to remove contaminants, and preliminary results state that a longer time of contact with the cable may produce stronger profiles [48].

- DNA can also be recovered from touched documents [49], however some paper types (office paper and white card) strongly interfered with the recovery of DNA. In France, a 25 year old murder of a small boy has recently been reopened with the recovery of two DNA profiles from anonymous letters sent at the time of the murder [50].
- In a 2007 Polish study, DNA could not be recovered from fingerprints on surfaces submerged in water, regardless of submersion time (from 1-42 days) [51].
- DNA could be recovered from handled firearms, most successfully from the grips and slide serrations, but is unlikely to be recovered in sufficient quantities from fired cartridge cases, or unfired cartridge cases ejected from the firearm or magazine [52]. Conversely two other studies were able to recover full and partial profiles from fired and ejected cartridge cases and shotgun shells [53, 54].

The recovery of DNA from a vehicle used in an offence can be extremely useful to investigators to provide intelligence into the driver and passengers of the vehicle. Full profiles may be recovered from the steering wheel and gear stick [55], though mixtures are common particularly if the vehicle has been recently stolen. Wickenheiser suggests that the major profile recovered from the steering wheel is likely to be that of the last driver [42]. Lenz et al. found an average success rate (i.e. a profile was recovered) of casework swabs from vehicles to be 22% [56]. Interestingly, the second component to the study involved one officer sampling 14 vehicles, and a success rate of 86% was achieved, suggesting that swabbing technique is significant in affecting recovery. Deployed airbags have also been found to produce DNA profiles [57], however the researchers found that a general swab of the entire airbag was unlikely to produce useful results, instead viable areas should be targeted for sampling using an alternate light source.

From this volume of research the ability to recover DNA from a skin contact has been clearly demonstrated. However unlike discrete sources of DNA such as blood or semen, it has been difficult to precisely determine the source of DNA transferred from skin - which cells are contributing the DNA? Collectively a number of studies have investigated this question, as summarised below.

1.2.1 DNA in skin

The skin is the largest organ in the body, making up 7-15% of the total body weight. Every square centimetre of skin contains approximately 500 000 cells [58], which are constantly being shed and regenerated. The average human sheds around 400 000 skin cells per day [42]. From these figures, it appears obvious that DNA might easily be transferred over a crime scene without the need for biological fluids.

However, the majority of these shed cells are denucleated. The skin is made up of two distinct regions; the outer lying epidermis, containing epithelial cells, and the lower dermis, a tough layer composed of fibrous connective tissue. The epidermis is a proliferative tissue, which renews itself continually through mitotic division [59]. The majority of the epidermis is composed of cells called keratinocytes, which produce the protein keratin to form a protective coating for the underlying tissues of the body. Keratinocytes arise in the deepest part of the epidermis, called the basal layer. As they age, the keratinocytes progress through 3-4 more layers, becoming flattened as their nuclei and organelles begin to disintegrate due to the action of deoxyribonuclease [60]. By the time they reach the surface of the skin, or the corneal layer, they are effectively 'dead', and appear as clear, keratin-filled plasma membranes [61]. This process takes an average of 39 days to complete, although in body areas subjected to higher friction, such as the palms and soles, both cell production and keratin formation are accelerated.

The epidermis also contains other cells; melanocytes, which produce the pigment melanin to protect cell nuclei from ultra-violet radiation, Langerhan's cells, which are a component of the immune system, and Merkel cells, which act as sensory receptors [58]. Passing through the epidermis are the ducts for sweat and sebaceous glands.

Sweat (or sudoriferous) glands are present over the entire skin surface except for the nipple and genital areas. There are two types; eccrine and apocrine glands. Eccrine glands release a filtrate of the blood by exocytosis, composed of 99% water plus salts and metabolic wastes. Apocrine glands are confined to the axillary and anogenital areas of the body. They empty into hair follicles, and have a similar composition to sweat, with the addition of fatty substances and proteins [58].

Sebaceous glands are located all over the body except for the palms and soles. These glands secrete sebum, which is composed of accumulated lipids and cells fragments.

The source of DNA recovered from touched objects was assumed to be from these cell fragments excreted through the skin by sweat and sebaceous glands, however had not been conclusively identified. Surfaces swabbed for trace DNA are generally not subjected to presumptive testing that was previously employed in biological stain analysis, which helped to give an indication of the source of the stain, for example sperm, blood, or saliva. These presumptive tests also helped save time and expense wasted on the analysis of stains that were not of human origin.

Two studies have attempted to investigate the source of DNA in fingerprints by staining and observing fingerprints under a microscope prior to DNA extraction. Balogh et al. [62] found that the majority of epithelial cells present in latent prints are nuclei-free corneocytes, with a minor occurrence of nucleated cells. They determined that the occurrence of nucleated cells was theoretically sufficient for successful DNA typing. Alessandrini et al. [63] observed an average of 5 nucleated cells or stripped nuclei were present in fingerprints applied to glass slides for 30 seconds. The number of cells present generally depended on the size of the print, however some donors were found to leave more nucleated cells regardless of the print size. They suggested that the status of a 'good shedder', or a donor who is likely to leave sufficient DNA in fingerprints to generate a profile, depends on the number of stripped nuclei in the corneal layers, and accelerated turnover of keratinocytes.

In addition to the keratinocytes as the source of nucleated cells for DNA analysis, the hands can act as vectors for transfer of cells from other parts of the body. The sebum secreted from sudoriforous glands present on the forehead, for example, can transport DNA bearing cells to the surface of the face. These could in turn be transferred to the fingertips as the donor wipes their brow. The cells of the eyeball and bulbar epithelium (the underside and edges of the eyelids) are nucleated and regenerated every 6-24 hours. Scratching the eyes may provide more cells for deposition. People who habitually bite nails are also conceivably more likely to have nucleated cells on their hands from saliva.

DNA profiles have also successfully been recovered from dandruff particles [38]. Dandruff consists of epidermal cells at differing degrees of keratinisation, and is caused by a disorder of the normal epidermopoesis. The disorder occurs in approximately 20% of the population,

and accelerates the turnover of keratinocytes. This results in incomplete keratinisation, leaving nucleated cells in the corneal layer. Herber and Herold found an average of 4.7ng of DNA per dandruff particle. Another study [64] found a range of 72.5 – 183.3ng of DNA from 1-1.5mg of dandruff, depending on the extraction method used. Conditions such as psoriasis have also proven to increase the level of nucleated cells present in the outer layers of the epidermis [65]. In a normal epidermis, DNA accounts for approximately 0.1% by weight, compared to 0.55% in psoriatic epidermis.

A recent study by Kita et al. [66] aimed to conclusively determine the source of DNA present in skin transfer, through the use of immunoelectron microscope analysis. They found single-stranded DNA was present in both the corneal layer of skin and in swabs from skin, and suggest that it is conceivable that the DNA from touched objects originate from the corneal layer sloughed from the surface and through sweat. The research indicates that DNA from the skin surface is likely to be already degraded as it leaves the surface, further compounding the difficulty in retrieving such DNA in a forensic sense.

1.3 Trace evidence and criminalistics

Trace evidence is very broadly defined as macro or microscopic physical evidence relevant to a criminal event, and is sometimes referred to as 'transfer evidence' or simply 'traces' [67]. It includes but not limited to glass, paint, soil, fibres and pollen; almost any physical item or mark can become relevant trace evidence in criminal investigations. This field was one of the first disciplines of forensic science, and was exploited at length by Sir Arthur Conan Doyle's fictional detective Sherlock Holmes around the turn of the 20th century [68].

At a conceptual level, there is an emerging view that when considered as remnants of an activity, traces actually define forensic science as a discipline because they constitute the most basic material or physical information on crime [69].

At a practical level, the examination of this evidence involves physical, chemical and microscopic comparison, to determine its characteristics and potential for classification and identification. A primary aim of trace evidence examinations is to 'associate' a trace with its source; for example, paint flakes linked to a specific vehicle with a unique paint layer sequence from numerous repairs. Often, due to the limiting characteristics of the trace, it may only be possible to link to a group of sources; such as a run of vehicles with non-

differentiable paint layers. This identification or association of the trace evidence with a source is an important part of trace evidence examination, but it is just one part. In addition to association, trace evidence can be used to provide investigative leads (such as the colour of paint narrowing down the list of suspect vehicles), or intelligence to reconstruct events and ascertain the activity that led to the deposition of the evidence [70]. It is these additional components that have been somewhat neglected in regards to DNA evidence.

Generally (but not always) trace evidence has less identifying power than DNA or fingerprints, and therefore has been forced to develop a more robust interpretive framework. Once a trace has been associated with a source, scientists must then assess the significance of that association. For example; fibres that were recovered from a victim's body are found to be indistinguishable from fibres in a suspect's jumper, then the odds to find such fibres and the odds for such fibres to be transferred and persist given propositions put forward by the parties are determined. To provide answers or probabilities many studies have assessed such factors in regards to trace evidence [67, 70-80]. The data from these studies may be used in statistical analysis of the evidence, to provide an objective assessment of its value in the investigation. This evidentiary assessment is discussed further in sections 1.5.4 and 8.2.1.

The fundamental concepts of forensic science or criminalistics are most prominent in trace evidence theory; transfer and persistence, identification, source association, and reconstruction. Inman and Rudin [81] propose a paradigm of forensic science, in which characteristics such as transfer are fundamental concepts, and also introduce the principle of divisible matter. DNA evidence has, up to this point, been removed from this philosophy, and instead its interpretation is centred its potentially extraordinary identification power and the associated statistical analysis. The applicability of trace evidence and criminalistic theory to DNA is a central theme of this thesis, and will be discussed and demonstrated throughout.

1.4 Volume Crime and DNA Evidence

The first cases to implement DNA evidence were the most serious kind – homicides and sexual assaults, with apparent and obvious biological residues often encountered due to the violent and intimate nature of these offences. However as generally the case with new technologies, they are first applied to the top of the pyramid and gradually filter down as new uses are identified.

Volume crime is an apt term used to group crimes generally regarded as less serious (mainly as defined by criminal law) but extremely common, including burglary, vehicle theft, vandalism, other theft, and street robbery. In Australia there are an estimated 660 000 residential burglaries and 91 000 personal robberies every year [82]. Burglary is defined as the unlawful entry into a structure with the intent to commit an offence, usually the theft of property, and is also known as break and enter or unlawful entry with intent [83]. Robbery is the unlawful taking of property from the immediate possession of a person, accompanied by the use or threatened use of force or violence. 48% of personal robberies occur in the street or at a public transport terminus, and these are often referred to as 'muggings' [82].

The effect of these volume crimes becomes significantly more serious when one considers their cumulative effect. Studies have been conducted internationally in an attempt to quantitate the cost to society caused by these crimes, and a study by the Australian Institute of Criminology in 2005 attempted to calculate all costs in the Australian context [84]. In addition to the cost of any property lost during the offence, the study estimated values for the medical costs if victims were injured, the loss of output as victims dealt with their event, and intangible costs regarding the stress caused and lowered quality of life. They found that the cost of an average robbery was $2270 per event, and $2700 per burglary. The total cost of crime to Australia in 2005, including the cost of policing, judicial systems and victim support, was estimated at $35.8 billion, or 4.1% of the country's Gross Domestic Product (GDP).

In addition to the considerable cost of volume crime, there is a fear that volume crime offenders may progress to more serious and violent offences. Some, but not all, offenders may escalate from more benign offences such as juvenile vandalism, through to property crime and then violent offences [85, 86]. Cain [87] found that for 40% of juvenile recidivists their last convicted offence was more serious than their first contact with the legal system. Makkai and Payne [88] found similarly; "*for offenders with any history of property offending…, the criminal career began around the age of 13 years with the first incident of vandalism or stealing without break-in (shoplifting).This was followed by the commencement of more serious offences such as break and enter and motor vehicle theft, graduating to offences such as trading in stolen goods".* For other offenders, the escalation comes not in the seriousness of the offence but in a greatly increased number of offences. Drug users in particular were more likely to become 'regular' offenders and increase their number of offences over time [88]. Finally, it is known that some criminals are simultaneously engaged

at different levels of the crime spectrum [85]. All these reasons support the need to provide a strong response to volume crime.

Only 71% of burglaries and 38% of robberies are reported to police, the major reason given for this non-reporting being there was 'nothing the police could do' [82]. This community feeling is evidently fairly accurate, as Australia-wide burglary has the lowest proportion of finalised (offender charged or matter dismissed) cases within 30 days of the offence, at only 12% [83]. Robberies have a superior clearance rate but still three out of four robberies remain unsolved 30 days after their reporting to police. In NSW, just 4.8% of residential burglaries and 16.7% of robberies were cleared within 90 days of the offence [89]. The resolution of so few of these crimes can cause increased fear and dissatisfaction in the community, and the disruption of the criminal careers of recidivist offenders is minimal. Police investigation of these incidents is generally reliant upon witness identification of the offender, CCTV footage or the offender being 'caught in the act'. Prevention methods include the proactive saturation of known high-crime areas with uniformed and plain-clothed officers in the attempt to prevent crimes from occurring. These methods are resource intensive (requiring installation of CCTV cameras, recruitment and training of additional officers and/or overtime costs) and whilst often effective at reducing crime in that area have been shown to merely move criminals onto different offence types [90].

Traditional policing methods are therefore difficult to apply to these offences. With the advent of forensic databases such as the National Automated Fingerprint Identification System (NAFIS) and the National Criminal Investigation DNA Database (NCIDD), forensic science offered another approach to the resolution of these crimes.

1.4.1 DNA Databases

DNA databases generally comprise of two groups of information; DNA profiles of convicted offenders and volunteer donors ('person' samples) and DNA profiles recovered from criminal investigations ('crime scene' samples), stored in electronic format. Comparisons are conducted within and between each group, resulting in either person-to-scene or scene-to-scene matches. The information received can be used for the identification of a suspect, provided that person is included on the database as a result of a prior conviction, or for intelligence purposes to link scenes where an offender may be unknown. It is the first use that has afforded DNA databases such fanfare; the ability to provide a name to investigators

where no leads previously existed. The second use has yet to be fully exploited by many jurisdictions, and is discussed in later chapters.

The potential for national DNA databases was quickly realised, and the first was implemented in the United Kingdom in 1995, less than ten years after DNA's first use in investigation [91]. In 1996 New Zealand followed suit [92], and in 1998 Austria, Germany and the Netherlands introduced national DNA databases [93]. Also in 1998, the Federal Bureau of Investigation (FBI) in the USA implemented the Combined DNA Index System (CODIS) through which law enforcement agencies around their country can compare DNA profiles.

In Australia the development of a national database has been hampered by constrictive legislations in the nine individual jurisdictions (eight states and territories and the federal jurisdiction of the Commonwealth), preventing cross matching [94]. Victoria was the first state to implement a database in 1997, and in 2001 funding for the National Criminal Investigation DNA Database (NCIDD) was provided. However it was not until 2005 that inter-state 'matching' commenced between Queensland and Western Australia, and only as recently as 2007 are all states actively involved in the database. From April 2009 Australia finally had a fully operational national database, as the last missing link in the database was bridged with New South Wales and the Northern Territory being able to compare profiles. Figure 1-1 demonstrates the complexity of the legal compliance of the database. As at the 30th June 2009, there were 479 107 profiles on the national database [95].

Figure 1-1. A representation of the cross-matching between the nine jurisdictions in the National Criminal Investigation DNA Database (NCIDD), serving as a demonstration of the complexity in meshing nine separate legal systems. Courtesy CRIMTRAC.

In the years since their inception the databases have expanded dramatically. The latest available annual report of the UK National DNA Database (2007-2009) stated that they held 4 859 934 person samples, and 350 033 crime scene samples [96]. About 88% of the crime scene samples relate to volume crime offences. For the financial year 2008-2009, 40 687 crime scene samples were matched to individuals on the database, and 4139 scene-to-scene links were established. Over 95% of these links relate to volume crime offences. In 2005 there were 25 000 person samples and 14 000 crime scene samples on the NSW DNA database [21]. From these samples there were 4207 'cold' links, and 2884 (69%) of these links related to burglary offences.

As shown here, most of the database matches result from volume crime. Databasing is thought to be so effective in the investigation of volume crimes because it is believed offenders who commit these crimes are recidivists, and therefore likely to be on the database in the first place. In New South Wales, only 13.5% of offenders convicted of a burglary offence had no prior convictions [97]. This was the lowest rate of any offence type. Even in the Children's court, over two thirds of children convicted of a burglary offence had a prior conviction.

Whilst the statistics provided by DNA database stakeholders appear considerable on paper, they do not give an accurate picture of true effect of DNA on arrest rates and crime levels. As mentioned by Saul [98], DNA Database 'matches' or 'links' do not represent arrests or convictions, but merely that a person *may* have been at a particular scene. More in depth studies, such as that undertaken by Walsh [99] for example, are required to determine any influence the implementation of a DNA database has on crime.

1.4.2 Measuring the effect of DNA on volume crime

Converse to the publicity surrounding DNA databases, and highlighted by Briody and Prenzler [100], the percentage of DNA matches to the total number of crimes is seemingly minimal. Of the estimated 1.8 million volume crime offences that occur in the United Kingdom, 612 000 will be attended by a crime scene officer [101]. Only 18% of these attended scenes will yield DNA evidence, with a smaller percentage actually producing a match on the DNA database. Therefore, of 1.8 million offences, 25 000 matches will result, or around 1%. Given the extensive funding being placed into DNA databasing and technology, one could argue for the need to justify the cost involved in reaching these results.

The UK 'Pathfinder' study was the first to assess the effect of forensic science on volume crime rates [101]. The project ran for one year in 2000-2001 in seven policing divisions and specifically targeted burglary and vehicle theft. In addition to collating data into the number of scenes attended, forensic evidence recovered, and the results of the forensic evidence, 1208 cases were tracked from a forensic match through to finalisation of the case. Studies from the United Kingdom use the term 'detections', inferring the arrest of an offender as a result of evidence. The project did not assess the conviction rate or sentencing details. Whilst concluding that the contribution of forensic science to the detection of volume crime was minimal (at 4%), they found that the detection rate (equivalent to an arrest rate) was low overall (10%), and therefore forensic science contributed a third of this total.

In July 2002, the NSW Police Force implemented Operation Vendas, a seven month project aiming to increase the arrest rate of volume crime offenders in three policing divisions, and therefore assessing any effect on the overall rate of volume crime in these regions [102]. A 100% attendance rate by crime scene officers to burglaries and recovered stolen motor vehicles was attempted, in addition to an improved turnaround time of forensic evidence (DNA and fingerprints), and the prioritisation of investigations of identified suspects from this forensic evidence. Other methods utilised included the interrogation of intelligence data (pawnbroking and modus operandi) and distribution of information to victims. The results of the study found that although a decrease in the number of volume crimes was observed during the study period, it was not statistically significant as the crime rate was found to be already falling prior to the study. Only one policing division showed an increase in offender identifications. The study seems to indicate and is supported by other studies [103, 104] that increased forensic attendance at scenes does not always result in crime reduction.

Recognising the need for research into the effect of DNA on court outcomes in volume offences, Briody [105] assessed 200 completed cases of volume crimes in Queensland, Australia, from 1994 to 2001. 100 of these offences included DNA evidence in the prosecution case, and 100 did not. The statistical research indicated that DNA evidence had a significant effect on the case reaching court, and the offender pleading guilty (82% without DNA evidence, 95% with). DNA evidence was also shown to have a significant association with custodial sentences, however the author could not determine if this implied causation. Whilst these results seem positive, the author noted that DNA evidence was only relevant in a small percentage of the total property offences, and that the majority of property offences result in a guilty plea, with or without DNA evidence.

An interesting UK study on volume crime in 2007 [106] assessed the influence of the following predictors on whether DNA evidence will result in the arrest of an offender :

- The source of DNA (whether blood, cigarette butts, saliva, chewing gum, or trace DNA)
- The number of items recovered from the scene resulting in 'matches'
- Whether the DNA was found inside or outside the scene
- The experience of the crime scene examiner
- The experience of the investigating detective.

Finding blood at a crime scene was found to be more statistically significant at producing an arrest than all the other evidence types, however finding more than one 'match' at a scene of the other sources (cigarette butts, saliva, chewing gum, or trace) was also found to significantly increase the arrest rate. This indicates that limiting the number of items collected at scenes may potentially lower the arrest rate. Whether the blood was found inside or outside the crime scene did not change the arrest rate, but for the other source types far more arrests were achieved when the evidence was recovered inside the scene. The experience of the crime scene examiner did not affect the arrest rate, but an inexperienced detective was found to significantly lower the rate of arrest. The outcome of the study indicates that policy development should include guidelines on the collection of samples (for example preference given to blood evidence, but if trace DNA or other sample types are collected to consider more than one sample, inside the scene), and extensive forensic training to detectives to maximise the value of forensic evidence in investigations.

DNA is not routinely used in volume crime investigations in the USA, and in 2005-2007 the National Institute of Justice conducted a field experiment to compare 500 burglary investigations where DNA evidence was used to those without [107]. They found that the addition of DNA evidence doubled the rate of arrest in burglary offences (from 8% to 16%) but were unable to assess the rate of conviction or sentence. The author was reluctant to recommend the widespread implementation of DNA evidence in volume crime however, estimating the cost per arrest of US$14 169 (the total cost of all tests conducted, in terms of labour and supplies, divided by the number of arrests for these cases) and offered concerns about the potential increase in backlogs and neglect of more serious offences. The study also found that blood evidence was more effective in solving crimes than other evidence. However it was noted that officers collecting an item whole was more effective than

swabbing, indicating that there may be an issue with the swabbing methods used by crime scene and patrol officers.

Despite the publicity accompanying the introduction of DNA databases, their effect on crime has been somewhat muted. However this does not mean forensic evidence databases should be abandoned. As commented by Briody and Prenzler [100], the retribution of offenders for their crimes is still a primary aim of the criminal justice system, and society should use every method available to apprehend criminals. It appears that it is more effective to target the use of DNA intelligently, rather than applying a blanket approach such as the attendance of forensic officers at every volume crime scene [102]. Studies have shown that timeliness of results is a significant factor in the usefulness of DNA evidence [108], and the massive backlogs occurring in many jurisdictions following the implementation of widespread DNA collection greatly impacted on the resolution of offences [21, 22]. The delay of DNA results, which may be disseminated to investigators a year or more after the offence, may render them irrelevant. When it is considered that offenders may commit over 100 burglaries per year [109], how many offences could be prevented with more timely DNA results? To maximise the benefit of DNA evidence, strict measures should be in place such as training of crime scene examiners, policies to target items of best value, training and adequate staffing of laboratories and investigators to follow through with DNA identifications.

What can the forensic community do to maximise the usefulness of DNA evidence? A major point highlighted by critical reviews of DNA databases is the small percentage of volume crime scenes where DNA is recovered (estimated at 3-5% [92, 105, 110]). Is it possible to increase this percentage within a reasonable cost? Whilst the proportion of scenes where blood or saliva will be recovered is believed to be capped, the potential for trace DNA evidence is yet to be fully realised.

1.4.3 The use of trace DNA in Australia

Since the development of the Scenes of Crime Officer program and the DNA Database, DNA evidence has become more widespread in the investigation of volume crime in NSW. In 2008, Sydney SOCOs assessed 96% and physically attended 83% of all burglaries reported to police in that year, a total of 28 600 scenes [111]. Fingerprints were recovered from 19% of examined scenes, and DNA from 4%. Therefore at least 1100 DNA samples (likely to be more,

given that more than one sample can be collected per scene) were collected in NSW in 2008, specifically from volume crime scenes.

'Cold' links from the DNA database, that is, the linking of a scene to an offender by their profile on the database, have increased dramatically over the last few years. However, the majority of the crime scene samples submitted are blood and not trace swabs.

Due to expense and time constraints, trace DNA is generally not tested unless the crime is more 'serious'. For example, a stolen motor vehicle's steering wheel, gear stick or handbrake may be swabbed for trace material if it has been used in other offences such as armed robberies. These swabs often result in mixed or partial profiles, which may not be entered onto the database, and used only if a suspect profile is available for comparison. These types of profiles may still contain exploitable information that is currently not being utilised. Mixtures of two profiles are still very informative but mixtures of four or more profiles are difficult to interpret. Availability of reference swabs can facilitate interpretation of mixtures. For example a swab of a steering wheel of a stolen vehicle may provide a mixture of profiles, one from the regular user and another from the offender. The profiling of a separate swab volunteered by the owner of the vehicle can assist the interpretation of the profile mixture and increase its value. While this system is gradually being employed in NSW with stolen motor vehicles involved in other offences, the use of trace DNA analysis in 'everyday' burglaries has not yet been employed or investigated.

In casework in NSW, as with many other localities, there is a division in the forensic response to volume and major crime scenes. At volume crime scenes, trace evidence is generally not considered and only DNA and fingerprint evidence are collected. It is only at the more serious crimes that the less discriminating trace evidence, for example glass or fibres, is utilised, and even then to a minor extent. By following the approach where only highly identifying evidence is considered for volume crime, a vast amount of valuable information may be neglected. Applying trace DNA analysis would reopen the world of criminalistics to volume crime investigations, with the increased potential to identify suspects and to build an intelligence framework to link crimes. However it is apparent that trace DNA is far less effective than DNA from sources such as blood and saliva at producing arrests [112]. There are likely to be many factors influencing this effect, which must be considered before widespread recovery of trace DNA at volume crimes become policy.

1.5 Trace DNA – Issues and Challenges

DNA analysis can be employed in conjunction with other areas of forensic science, or sometimes give information where fields such as fingerprint evidence may not. For example, it is a common occurrence to develop smudged fingermarks that do not contain sufficient detail for fingerprint comparison. Also, surfaces that are unlikely to be suitable for fingermark development (such as rough or porous materials) have a greater chance of removing and retaining skin cells for DNA analysis. Under these circumstances, it could be feasible to attempt to obtain a DNA profile from these marks to provide investigators with information that would otherwise be lost.

Another advantage is described by Wickenheiser [42],who said; "*The best evidence is that which is recognised by law enforcement officials, yet not by individuals perpetrating the crime."* With the popularisation of forensic science and the numerous television programs expounding the latest developments (whether real or fictitious), criminals are becoming savvy to the techniques employed to detect their involvement in a crime. Whilst it is a simple procedure to avoid leaving fingerprints by wearing gloves, it is more difficult to avoid leaving DNA from discrete forms of skin contact such as ear, arm and sweat marks. By its own nature, trace DNA transfer is difficult to avoid or manage from a criminal viewpoint.

However, as noted in the criminological research on the effectiveness of trace DNA as evidence [100, 105, 106], it brings with it difficulties often not considered by investigators.

1.5.1 Determining the source of the DNA

When the scene sample is a visible stain, for example blood or semen, a direct contact is the most probable conclusion, and association between the suspect source of the sample and the scene can usually be readily implied. However, using shed skin cells as the source of DNA leads us to a problem - because the cells are generally not visible to the naked eye, it cannot conclusively be determined where the DNA has come from. This is a problem for both detection and interpretation.

Current crime scene examination methods do not include any preliminary test to determine where the cells are, or of what type. The collection of trace DNA for analysis from a crime scene or from an item of evidence is commonly performed by a 'blind swab' in the area of

assumed contact. In the days of serology, before DNA analysis became ubiquitous, a reactive chemical was often employed to denote the location of the relevant cells prior to any confirmatory testing, such as spot tests for acid phosphatase in semen [113]. The use of fingerprint enhancement reagents to make latent marks visible could increase the certainty as to the source of the profile resulting from trace DNA swabbing, as a sort of presumptive test. This then leads to the question of whether these reagents would inhibit subsequent DNA analysis.

1.5.1.1 The effect of fingerprint enhancement on DNA analysis

Latent fingerprint enhancement is based on the principle of applying a reagent to render the fingerprint ridges visible against the substrate and maximising the contrast between the ridges and the substrate, either by optical, physical or chemical methods. The enhancement reagent is selected based primarily on the substrate type, whether porous (such as paper) or non-porous (plastics, metal), and also the substrate colour. There are numerous methods available to account for any possibility encountered during a crime scene examination, and a sequence of methods is often applied to maximise fingerprint recovery.

Many studies have tested the effects of enhancement reagents on the recovery of DNA from blood and other biological stains [114-123]. Most of these methods, with the exception of shortwave UV light, DAB, and physical developer, were found to not prohibit further DNA testing of the stains, which were either blood or saliva. As technologies have advanced, the effects of enhancement reagents on latent fingermarks are beginning to be investigated.

Zamir et al. [124] tested the effects of alternate light sources, cyanoacrylate fuming and crystal violet or basic yellow 40 stains on fingerprints placed on adhesive tape. They found DNA typing was successful before and after treatment for three out of four fingerprint donors. In a second study by Zamir and colleagues [125], DNA profiles were generated from envelopes and stamps after they had been treated with DFO (1,8-diaza-9-fluorenone). The DNA typing was also successful in casework, however most profiles were found to be mixtures.

A small study by Raymond et al. [126] tested a range of enhancement reagents on fingerprints on five different substrates; paper, glass, aluminium foil, plastic and adhesive tape. They were able to achieve profiles from prints on glass, plastic and adhesive tape which

had been treated with white and longwave UV light, cyanoacrylate and rhodamine 6G stain or vacuum metal deposition (plastic substrate), white and black fingerprint powders (glass), and sticky-side powder (adhesive tape). Profiles were not obtained from any prints on the paper and foil substrates, even untreated positive controls, suggesting that the surface type may be a more significant influence on recovery than fingerprint enhancement.

Other studies have tested the effects of ninhydrin, iodine, DFO, indanedione, and cyanoacrylate with basic yellow staining on DNA recovery from fingerprints [127-132]. The studies found that while the DNA recovery may be lower after fingerprint enhancement, profiles can still be achieved. Given the negligible effect it has on the recovery of DNA, ninhydrin has even been tested as a screening tool to determine if swabs of skin cell traces contain sufficient DNA for a profile [133]. Whilst 120 of the 158 swabs that gave a reaction to ninhydrin also produced a DNA profile, several false negative results led to the conclusion that this method may be useful in volume crime investigations, but not for serious offences.

Powdering also appears not to prevent DNA analysis of treated fingermarks. Van Hoofstat et al. [134], Schulz et al. [135] and Pesaresi et al. [136] produced profiles from fingerprints treated with white, black or magnetic powders. Schulz et al. were also able to recover profiles from prints that had been lifted with adhesive tape and archived on cards. Van Hoofstat et al. found that some of the DNA was removed during the powdering process, as profiles could be obtained from the swabs used to powder the prints. This is of concern to crime scene officers, as transfer of DNA could occur from scene to scene, carried by the powder brushes. This phenomenon has been demonstrated in research [137-139], but would seem less likely to occur in casework given that the proportion of contaminant DNA 'added' to a biological trace would be small and difficult to detect. However, the possibility exists and should be considered at every crime scene.

In summary, with a few exceptions, fingerprint reagents will not prevent the subsequent DNA profiling of the treated substrate. The exceptions include shortwave UV light, physical developer and DAB. Although, the examiner must be aware that the quantity of DNA recovered will be lower after any treatment, potentially because of physical actions during the fingerprint treatment such as washing steps. Fuming with cyanoacrylate may protect DNA-containing skin cells with a layer of polymer and therefore lower the chance of loss; however this may also make the cells difficult to remove during sampling. Care should also be taken by staff performing the DNA extraction to ensure that all traces of the fingerprint

reagent have been removed before amplification, and extra clean-up methods may be required. Just 5ug of fingerprint powder in the amplification mix can inhibit the PCR reaction [140].

Recognising the need for a screening method for trace DNA, a limited study was conducted as an adjunct to this project with the assistance of an Honours student. Reagents were reviewed and assessed to determine if any could be effective as a screening tool either in the laboratory or at a crime scene [141, 142]. The reagents selected after an extensive literature review were two amino acid stains (ninhydrin and fluorescamine), a DNA quantitation probe (SYBR Green), a histological stain (4',6-diamidino-2-phenylindole, or DAPI), fingerprint enhancement methods (black and aluminium powders), and light sources (Crime-lite® and Polilight® alternate light systems and a 532nm 8W laser). The study found the reagents generally fell into two groups; those of high sensitivity but low specificity to DNA traces (light sources, powdering and ninhydrin), and those with high specificity but low sensitivity (fluorescamine and DAPI). The recommendations were that fingerprint enhancement reagents in common use, whilst not specific, were still the most effective at screening for potential areas of trace DNA.

These studies demonstrate the potential to utilise trace DNA analysis as a step in the examination process. If initial testing such as microscopic or fingerprint examinations are unsuccessful, DNA analysis could be considered to increase the chance of gaining useful information from the evidence. The ability to make latent fingermarks visible prior to DNA swabbing would also appear to increase the chance of obtaining a DNA profile from a single source, as the swabbing process could be centred on the marks rather than swabbing randomly over an area. An additional advantage is that background controls could also be taken from a site adjacent to the prints. Negative controls are an important component of scientific process, and have been somewhat neglected in the collection of material from crime scenes. Performing this step might then lead to more straightforward interpretation, and evidence of more meaningful value. Being able to combine two forms of examination, which individually may only give circumstantial information, increases the overall strength of the evidence and demonstrates the benefits of a holistic approach in forensic science.

1.5.2 Background DNA

Ironically, in Australia it was the combination of fingerprint and DNA evidence from an armed robbery crime scene that highlighted the issue of background DNA [143]. Early in the morning on the 21st December 2004, the victim opened his newsagency business in western Sydney. Two males armed with a knife entered the store and demanded money from the cash register and safe, and one of the offenders searched through cupboards below the counter. The offenders did not touch the victim during the offence. When the scene was examined by crime scene personnel, fingerprints were developed on this cupboard, which were also swabbed for DNA as the victim stated the cupboard was not in use and therefore not regularly handled by staff. The fingerprints were identified to a recidivist armed robbery offender, however the strong single DNA profile recovered did not match this person. A comparison profile was recovered from the victim, and was found to match the profile obtained from the offender's fingerprints. The presence of background levels of the victim's DNA completely overwhelmed any DNA transferred by the offender, which may have led to the dismissal of the evidence had the victim's profile been unavailable. In this event, control swabs taken from adjacent surfaces to the fingerprints may have provided an explanation for the discrepancy between the DNA and the fingerprint results.

Few studies have investigated the presence of background DNA or its impact on casework. Toothman et al. [144] tested areas of dust from 24 locations in a university, and found that human DNA was detected in 97% of occasions, however the amount was low averaging 0.2-1.1pg/cm^2. There was no significant trend between the level of human traffic in the area and the quantity recovered. Around two-thirds of the samples had sufficient DNA for Profiler Plus amplification, but when they were amplified degradation profiles were evident, with larger alleles consistently absent. They concluded that background levels of DNA can be a significant 'contamination source' in forensic samples.

Background levels of foreign DNA on human skin was investigated by Graham and Rutty [145] in a simulation of strangulation offences. Non-self DNA was found to be present on the neck surface of 14 of 24 volunteers. The number of foreign alleles ranged from 1 to 14, and whilst not statistically significant, more foreign alleles were found on the necks of married or defacto volunteers than single volunteers. In a similar vein, Malson et al. [146] found two- and three-person mixtures under the fingernails of 17% of donors. Most of the foreign alleles could be attributed to the cohabiting partner of the donor. Therefore if non-self alleles are

found on the victim's person, it cannot be assumed they are of the attacker. Collecting elimination swabs of cohabitants of the victim may aid the interpretation of results.

Poy and van Oorschot examined the levels of background DNA present inside a DNA laboratory [147]. 195 sites in the laboratory and office areas were sampled and categorised according to the risk of their potential to cause contamination in casework. 52 (27%) of the areas were found to have alleles present. Of 32 interpretable profiles, 28 matched staff profiles, understandably the majority being in the office area where no protective garments are required. Of the four unknown profiles, two matched profiles on the criminal DNA database. One of these profiles, recovered from a magnification lamp, was believed to result from a heavily stained and bulky casework sample examined three months prior to the study. The authors cautioned the need for rigid contamination prevention procedures inside forensic laboratories.

1.5.3 DNA Primary and Secondary Transfer

The advance in DNA analysis to the point where we now have the ability to produce profiles from a single cell [148] has introduced propositions which, if not addressed, could hinder the application of trace DNA evidence to investigations and the court trial. The technology is so sensitive that we are examining material not visible to the human eye, and as such it is difficult to ascertain the source of the material, how the material came to be present at the scene, and for how long it has been there. How are we to estimate the chances of one cell arriving at a particular crime scene by some other means than direct contact?

There has been some debate over the likelihood of secondary transfer of DNA from skin cells. Van Oorschot and Jones [35] found that plastic tubes held consecutively by different users for a fixed length of time produced profiles of the most recent holder, and also some evidence of DNA from the previous holder(s). The authors cautioned practitioners to be aware of the potential for secondary transfer and contamination of samples. Conversely, Ladd et al. [149] found little evidence of secondary transfer in their experiments with coffee mugs and handshakes, and concluded that the phenomenon would not compromise the interpretation of case samples.

The discrepancies observed in these results highlighted the need for further work in this area, to ensure the applicability of trace DNA to investigations. Murray et al. [150], Lowe et al.

[151] and Allen et al. [53] considered the possibility of the variation between individuals in terms of their ability to deposit or 'shed' DNA onto a surface. Murray et al. tested a group of 29 individuals, and found that a typical 'good shedder' (their definition) left a complete profile on the surface of a plastic tube after contact of 10 seconds. A 'poor shedder' left only a few alleles. After testing 22 subjects, Lowe et al. observed the greatest difference between shedder types occurred at a time interval of 15 minutes after hand washing. They used this time interval to define a classification of shedder type: good shedders gave a full profile 15 minutes post washing, whilst poor shedders gave a partial profile. Allen et al. tested single fingerprints from the unwashed hands of 129 individuals deposited onto glass slides, and found that 82% of the individuals were either 'heavy' (depositing over 300pg of DNA) or 'intermediate' (depositing between 50-300pg of DNA) shedders, with the minority depositing less than 50pg of DNA. The study also found significant differences between the hands of individuals, with more DNA resulting from the non-dominant hand of volunteers. Differences were also noted between the sexes, with males more likely to be classed as heavy shedders, but this difference was not statistically significant.

However a New Zealand study found that shedders were less easy to classify [152]. Five individuals were tested over five days using a similar method to Lowe et al., both with and without prior hand washing. The variation within and between volunteers was found to be similar, with no donor providing consistently strong profiles. It was noted that unwashed hands produced stronger profiles than washed hands, but there was no clear correlation with the length of time since washing. In a study of 60 volunteers, no 'good' shedders were identified. This study demonstrates that many other factors are involved in the deposition of trace DNA other than the shedding ability of the individual, such as hand dominance and environmental effects. In another study, Dominick et al. found no link between a donor's DNA shedding ability and the quality of the fingerprints they deposited [153].

In other avenues of research, two research groups have swabbed 'victims' of a simulated manual strangulation [154, 155]. Whilst the profiles were mixed, a full 'offender' profile was obtained up to 6 hours after the initial contact. In Rutty's study, swabs from the offenders' unwashed fingers produced partial profiles from the victims up to 24 hours after the contact.

Murray et al. [150] and Lowe at al. [151] also conducted experiments to test secondary transfer with pairs comprised of a good and poor shedder. A good shedder shook hands with a poor shedder, who then held an object. Both studies found that often the good shedder's

profile was observed, with only a partial profile or a complete negative result from the poor shedder. Van Oorschot and Jones also found transfer of DNA between the hands of individuals after one-minute handshakes [35]. Studies from the NSW DNA laboratory (Division of Analytical Laboratories - DAL) have found similar results; Walton [156] found secondary transfer onto a screwdriver after a handshake of two volunteers for one minute. The 'handshaker' who had never touched the screwdriver was found to be a major component in the recovered profile in four of ten trials, and in one case, a single source profile of that person was found on the screwdriver *and* the swabbed hand of the intermediate volunteer. However the study found that handshakes of 'normal' length (less than 10 seconds) are unlikely to produce secondary transfer. Another study found DNA from a good shedder recovered from a cap they had never worn, and that the major component of a DNA profile recovered from a cap cannot be assumed to be the last wearer [157]. This study however noted that a time delay between the cap wearing may reduce the likelihood of secondary transfer.

A third DAL study [158] was conducted in answer to two NSW court cases, where allegations had arisen that police officers may have inadvertently transferred suspects' DNA to drug balloons and firearms during a searching process. It was suggested that by handling items belonging to the suspect (handbag, clothing or other personal items) then handling the items in question wearing the same gloves, the transfer may have occurred. The study found that secondary transfer was possible to drug balloons immediately after a search of a bag belonging to a volunteer, but if other objects were handled between, this transfer did not occur. Secondary transfer did not occur with the firearms. The study recommended that police change gloves frequently during search warrants, echoed by Poy and van Oorschot who found that gloves can accumulate DNA and potentially transfer it to other sources in their survey of laboratory-based contamination [147].

The studies are in the majority modelled on 'best-case' scenarios in pairs of good and poor shedders – they demonstrate that secondary transfer is possible under ideal conditions. However the question that seems now more pertinent is how *likely* is it to happen? In how many cases would this actually occur? Whilst outside the capacity and means of this project, larger population studies of secondary DNA transfer may be useful to provide statistical analysis of this phenomenon. If it is suggested that secondary transfer is the cause of a suspect's profile being at a crime scene, it would be more informative to state that this is possible but unlikely given research *X*, or to give the probability of it occurring. In addition,

this kind of data is required if a Bayesian model is used to interpret trace DNA similarly to that used to interpret glass (see 1.5.4 below).

1.5.4 Interpreting Trace DNA Evidence

In addition to crime scene considerations, the other greatest challenges in forensic science reside in the presentation of evidence in court. As the theories involved are often quite complex, it is a difficult task for the scientist to explain their results in a manner that avoids misinterpretation but remains scientifically accurate. A field of thought is that forensic evidence should not be presented as pure analytical results, but rather interpreted within the context of the case. If the value of the evidence is inadequately described it could be unintentionally manipulated by legal professionals or the jury. In order to alleviate these difficulties, statistical approaches have been developed in many fields of forensic science to provide a more definitive estimate of the weight of the evidence, or at least to place the evidence in its proper context [79, 159-164]. Bayes' Theorem requires the forensic scientist to determine a 'likelihood ratio' for the evidence, that is, the likelihood of the evidence assuming the prosecution hypothesis, divided by the likelihood of the evidence assuming the defence hypothesis. If accurate databases and interpretation models are used to construct the ratio, it can give a numerical value to the evidence, thereby avoiding terms such as 'is not consistent with', or 'appears to be similar'. These phrases are less accurate and informative than what can be provided by Bayesian interpretation. Even if numerical data is unavailable, this Bayesian approach can still be applied theoretically to ensure objectivity, as the considered propositions (that is, the numerator and denominator in the equation) can be used to assess the opposing views of prosecution and defence.

A classical approach to presenting DNA analysis in court has been to consider whether two profiles match, according to specific guidelines, then to estimate the frequency of the match. The frequency, or the chance that a random, unrelated person other than the subject has the same DNA profile, can be given in numerical terms. With the current technology this estimate can be as low as 1 in 10^{17}[165]. This method, whilst encountering legal challenges, has been largely accepted by the courts. However, interpreting profiles from trace DNA analysis opens up an additional Pandora's box, as unlike the analysis of visible biological stains such as blood or semen, the source of the DNA profile is unclear. In addition to this, given the minute quantity of DNA which is being analysed, the resulting profiles are often complex and difficult to interpret [166].

1.5.4.1 Low Copy Number (or Low Template) Analysis

Low Copy Number (LCN) analysis has been defined as the typing of samples with less than 100pg of DNA present, or the analysis of any results below the stochastic threshold for normal interpretation [166]. Recent articles suggest a shift away from a set definition for these samples, and offer the term 'low-template DNA' to describe samples that fall below a peak-height level determined by the laboratory [167, 168]. Various methods have been employed to analyse such samples, including nested PCR, which involves two rounds of PCR and has been found to reduce artefacts in degraded samples [169], and post-PCR purification using silica columns [170]. The most prevalent method of analysing LCN samples is to increase the standard number of PCR cycles from 28 to 34 or higher [171, 172]. Several countries including the UK [171], New Zealand [6], USA [173], Italy [174] and Portugal [175] have implemented LCN analysis in their laboratories and currently use it in casework.

Deviating from standard methods can lead to unexpected and unreliable results, and caution should be exercised during interpretation. The amplification kits commonly employed in forensic laboratories usually recommend a sensitivity threshold of 250pg of template DNA, and the kits are not validated for samples with DNA quantities below this level. This limit to sensitivity is beneficial as it minimises the propensity for minute contaminants to corrupt the evidential profile. With LCN analysis, the template DNA level can be so low that the effects resulting from stochastic variation are problematic. There is a chance that an extraneous fragment of DNA could be amplified during the first rounds of PCR, and then preferentially amplified during subsequent cycles, leading to artefact peaks in the profile. Alternatively, alleles may be unequally amplified causing one to 'dropout', giving the appearance of a homozygote [176]. Stutter peaks, which are caused by a slippage in the enzyme used to amplify the DNA, also become a greater problem. The end result is that profiles derived from LCN analysis are often complex and difficult to interpret, leading to complications in presenting the evidence to court. However, researchers in the United Kingdom have attempted to give guidelines to facilitate the interpretation of LCN profiles [177, 178]. The guidelines recommend that all amplifications should be duplicated, where possible, and that alleles should be present in both profiles before they can be designated. Other guidelines have been formulated regarding the designation of stutter and artefact peaks, and for the interpretation of allele dropout and peak imbalance [179]. Gill et al. [177] suggests a clause be inserted in expert statements cautioning the court on the lack of interpretative information such as transfer and persistence studies on which to determine the value of the

LCN evidence. Researchers from the United States recommend conducting a minimum of three amplifications, and only designating alleles present in at least two of the three amplifications [173]. Despite these guidelines, LCN analysis is not currently used in any Australian laboratory, although samples from Australian jurisdictions have been sent to the UK for LCN analysis [180].

LCN analysis came under scrutiny in 2007 after the Omagh Bombing trial of Sean Hoey in the United Kingdom [181]. The bombing had occurred in 1998 and 29 people were killed as a result. The prosecution stated they had recovered Hoey's DNA on bomb timers collected during the crime scene examination. The crux of the issue was that in 1998 LCN analysis did not exist and crime scene examiners did not follow the necessary stringent anti-contamination procedures, therefore the samples could be contaminated. In addition, two experts expressed doubt as to the rigour of LCN analysis and its reliability. The deciding judge found the evidence was therefore not of sufficient standard, and the defendant was found not guilty of the charges. As a result of the trial, the UK Home Office ordered an investigation into LCN analysis, during which LCN casework was suspended. The investigation found that the scientific basis for LCN was sound and that so long as laboratories adhered to the standard operating procedures in place the evidence has value in criminal trials [182].

Despite the favourable outcome of the review, a number of legal challenges to LCN analysis arose following the Omagh bombing trial, and in 2009 the appeal of *R v David Reed; R v Terence Reed; R v Garmson* [183] again attacked the validity of the method. The trial of the Reed brothers involved the murder of Peter Hoe, who was found stabbed to death in his house in 2006. The DNA profiles of the Reed brothers was recovered from two plastic knife handles found at the scene, and the primary challenge was that the LCN technique used to achieve these profiles was invalid, and secondly that the evidence the forensic biologist supplied as to the evaluation of primary and secondary transfer was inadmissible. The challenge to LCN fell by the wayside when the samples were retested with standard cycle techniques and found to be accurate, and the court went so far as to suggest that future attacks on DNA evidence will only be allowed in very narrow circumstances. In addition, the court held that it is essential for an expert witness to give some evaluation of the suggested circumstances of transfer, however stated that the biologist may have slightly overstepped the mark in this case when she expressed an opinion that the appellants were handling the knives when they broke. Nevertheless, the appeal was dismissed. It remains to be seen the

extent of the effect that this hearing will have on future challenges to LCN and trace DNA evidence.

It is still an aim of forensic science to gain the maximum amount of information from each item of evidence. With the developments in LCN analysis it is becoming feasible to obtain profiles from samples that had previously been unsuccessful using conventional methods. Although, it may be that these profiles prove to have more value to provide leads during the investigative process rather than as evidence in court. Whilst DNA is so often viewed as a tool purely for absolute identification, there is also value in utilising partial profiles in existing intelligence databases. The information may not be as heavily relied upon in court, but could be used by police to build up profiles of offenders, or to create a new line of inquiry from which other, more conclusive evidence could evolve. With the increase of organised terrorism attacks, intelligence databases are becoming more prevalent and an integral part of policing, whether on a local or global scale.

In addition to these problems, the complex nature of forensic examination and the vast number of possible situations that can occur in casework have made the production of an interpretative framework a difficult task in relation to trace DNA samples. There has been a tendency for trace DNA research to focus on the testing of all possible surfaces for DNA profiles, without subsequent consideration as to what value, if any, that evidence will have. This 'research for research's sake' approach in forensic sciences may be beneficial to the advance of the technology. However, the purpose and end use of any forensic research is to aid in the investigative process, and the court presentation of evidence. Whilst it has been necessary up to the present to centre experiments on the determination of the power of the technology, it may now be more advantageous to focus research on quantifying relevant background information. This information can then be used to assist scientists to interpret the profiles and place the DNA evidence in the appropriate context. For example, providing data to estimate the likelihood that a suspect's DNA will transfer and persist on a window at a break and enter may be more constructive than the mere determination that it is possible to retrieve DNA from windowsills.

1.5.4.2 Placing the evidence in context

Given the difficulties of trace DNA interpretation it is vital that, as with any forensic evidence, the interpretation must be conducted with the circumstances of the case in mind. Finding a

suspect's DNA at a crime scene may be irrelevant if the suspect had regular access to that location.

Communication between investigators and laboratory scientists is often poor. Scientists may receive items of evidence with no background information about the case, and therefore the most appropriate tests may not be applied. Conversely, scientists also need to communicate with and educate investigators regarding the types of testing which can be performed, what the tests are capable of and an interpretation of the results of the testing in context of the case. Results are commonly conveyed to the police in the form of a dry, clinical report that may mean little to non-scientists.

Some degree of separation between police and laboratory forensic scientists is seen by many to have some benefit. However, as stated by Inman and Rudin [184], physical evidence does not exist in a vacuum. Without open lines of communication between the police, prosecutors, and forensic arms of the investigation, the true value of evidence may be misinterpreted and/or not fully exploited.

One of the biggest problems with an expansive separation of police, the legal system and scientists is that it can lead to the scientist producing evidence irrelevant to the issue at hand, and failing to provide answers to the relevant questions. This is particularly evident for trace DNA evidence, as the question is now less often one of identity and more of activity. This problem can be avoided with the provision of relevant background information to the scientist to enable them to form the appropriate opposing propositions to investigate.

The 'hierarchy of propositions' put forward by Cook et al. and Evett et al. [185, 186] is an eloquent description of the fundamental elements of the presentation of evidence in a legal setting. In order to present the evidence in a balanced manner, the scientist must always consider the evidence in regards to the propositions alleged by both sides in the case. The three broad classes of propositions relate to the *offence*, *activity,* and *source* levels of the case. The offence level propositions are those considered by the jury; Mr X committed the burglary, or someone other than Mr X committed the burglary. The source level propositions are those in the realm of the scientist; the DNA from the burglary scene came from Mr X, or the DNA from the burglary scene came from someone other than Mr X.

It is the activity level propositions that are often the most difficult to assess. There is some debate as to whether they are for the jury or the scientist to consider, or whether they fall

somewhere in between these groups. Example activity propositions are as follows; Mr X forced the window, or Mr X was not present when the window was forced. It may not be relevant in a particular case that Mr X's DNA was present on the window, as the defence alleges he had legitimate access to the location some time prior to the offence or that secondary transfer resulted in his DNA being present. The relevant question then becomes one of activity; how likely is it for Mr X's profile to be present given the opposing suggestions from prosecution and defence? The scientist may be able to give relative probabilities to these propositions if they are known prior to the court proceedings, otherwise the production of a report merely stating that Mr X's DNA was on the window may give no assistance to the court. The following Australian criminal cases further demonstrate this problem.

1.5.5 Court Challenges of trace DNA

The interpretive difficulties described in the previous sections have been acknowledged by the legal community, and combined with a knowledge of the apparent random nature of trace DNA analysis have led to an increase in the questioning of trace DNA evidence at trial. In addition to the UK trials of R v Hoey and R v Reed and Reed discussed previously, the following Australian cases are examples of cases where the validity and evidentiary value of trace DNA evidence was questioned, to varying success.

1.5.5.1 Hillier v R

The victim was found dead in her house on the 2nd October 2002, several days after winning a protracted child custody battle with her ex-partner, the appellant. She had not been seen since the 30th September, and her concerned parents gained access to her house and found her body lying on the floor in the bedroom, which was damaged by fire. A pathologist found the cause of death to be neck compression, which had occurred prior to the fire.

The disharmonious relationship between the victim and the appellant comprised a considerable portion of the prosecution's case. In addition to the evidence of motive and witness statements, DNA evidence was produced. Several tapelifts had been taken of the deceased's pyjama top, which she was wearing when she had died, and a mixed profile was recovered from the lifts. The mixture was assessed to be 93 million times more likely to have come from the appellant and the victim, than from another random male and the victim.

The appellant was found guilty of the murder at trial, however appealed on various grounds including the validity of the DNA evidence [187]. The defence suggested that the DNA on the victim's top may have resulted from secondary transfer – that is, the act of the appellant kissing his children goodbye may have resulted in the transfer of his DNA to the victim when she hugged the children. Two of the three judges determined that the verdict was unsafe and upheld the appeal. However an appeal by the prosecution to the High Court of Australia resulted in the appeal being overturned. A second appeal to the Supreme Court of Australia [188] upheld the appeal but denied the appellant an acquittal. A new trial was ordered and the case continues.

1.5.5.2 R v Joyce

This was a case of indecent assault of a child in the accused's home. DNA was recovered from the child's shorts and underpants compatible with that of the accused. The defence alleged that the accused's DNA might have transferred to the victim's clothing from the floor and furniture of the accused's home. No evidence was produced to determine the level of background DNA present in areas of the home, (and indeed no such research is believed to exist in the literature), and whether this allegation is a likely occurrence. The judge stated that "*the Crown has not lead expert evidence to counter this hypothesis, nor laid any scientific basis for preferring one hypothesis over another"*, and found that the DNA evidence was of no probative value and was therefore inadmissible. However with the weight of other evidence the accused was convicted of the crime [189].

1.5.5.3 R v Chahine

On the 4th June 2001, two males robbed a bank in south-western Sydney of $16 585, and left in a vehicle. The vehicle was found shortly after by police outside a block of units in a nearby suburb. The accused attempted to run from police allegedly throwing money away as he ran. A blue baseball cap and bank property was recovered from a unit in the block the accused had been seen leaving before his arrest. One of the bank robbers was described by witnesses as wearing a similar baseball cap. A mixed DNA profile was recovered of which the accused could not be excluded as a contributor, and that 1 in 1,200 people could be a contributor. With this and other evidence the accused was convicted of the offence, however appealed the decision on the ground of the DNA evidence and other factors [12]. On appeal the defence suggested that his DNA came to be on the hat by secondary transfer, that he might

have worn the cap at some stage but not during the robbery. The prosecution countered that this was possible but not likely, which the judge accepted and dismissed the appeal.

1.5.5.4 Howson v R

In this drugs case, the accused was detained at Perth airport after customs officials became suspicious of his behaviour, and observed a lump around his waistband. The accused was taken to an interview room for a strip search, where he was left alone for short time. Nothing was found during the search but as the accused was being released a package was found on the floor near where he had being sitting, which customs officials stated had not been present earlier. On examination, nearly 200 grams of cocaine was found inside, a street value of $136 000. Trace levels of DNA was found on package, resulting in a partial profile of two alleles at a reportable level, which were also found in the profile of the accused, given an evidentiary value of 1 in 112. On appeal the defence alleged that this level of DNA may be a result of secondary transfer, and that the accused had not come into primary contact with the package. The expert witness stated that it could not be conclusively stated whether this level of DNA is resulting from primary or secondary transfer, that each are possible. On consideration the judge allowed the DNA evidence on the basis the strength of the evidence was correctly stated and it had probative value. The appeal was dismissed [190].

DNA evidence comprised only a small fraction of the brief of evidence in these trials, as indeed forensic evidence is rarely the primary focus of any trial. Yet given the public's opinion of DNA as infallible evidence, any doubt regarding its validity can seem catastrophic for the prosecution case. It is now common to find that the issue in conflict regarding DNA evidence is not one of identity, but of timing or action. The defendant does not deny that it is their DNA, but rather as to when and if they were present at the scene, or contests the mechanism that caused their DNA to be present. In other words, in the hierarchy of propositions context, most of the challenging questions relevant to trace DNA reside at the activity level as opposed to the source level. Ironically, the advent of trace DNA made possible by technological progress now requires a retrospective attitude from forensic biologists to think about DNA as another type of trace.

1.5.6 Getting Back to Basics

Recently, the scope of forensic DNA research has had a strong technological focus. Perhaps because the science is now so advanced, it appears that we may benefit from going back to the basic principles of trace evidence in order to allow the interpretative background work to catch up with the technological developments. DNA evidence can truly be treated as any trace evidence. The fundamental questions of 'how was the sample deposited?', 'how long will it persist there?', 'will it be transferred?', and 'how can it be detected/recovered/contaminated?' have been somewhat neglected in light of DNA's exceptional discriminative power.

With the sensitive methods of detection currently available, it seems that proving physical contact between the scene and the suspect, or the deposition of the sample, is becoming as important as proving the sample belongs to the suspect. In trace evidence fields such as glass analysis, much research and data has been collected to quantify the various types of glass, and the trace evidence properties of a glass particle [77, 78]. Interpretation of glass evidence involves firstly determining whether the scene and the suspect samples could have come from the same source, or if they can be discriminated. Then, equally importantly, the probabilities that the glass would have transferred and persisted, or that a random, innocent person would be found with that particular glass are also considered. The same should be asked of trace DNA evidence – was there actually contact between suspect and scene, and what is the chance of the profile being present in 'background' DNA levels on a surface? To answer these questions, data providing information into how likely it is for DNA to be transferred, how long it can persist in certain conditions and locations, and what background levels of DNA are likely to be encountered needs to be gathered.

It is interesting that these basic 'forensic' concepts were first conceived in the late 19th century and early 20th century by generalists such as Gross [191] and Locard [2], long before the DNA molecule was described. Their validity is affirmed as the extraordinary power of DNA evidence has created a need for reconsideration of these issues.

As discussed by Rudin and Inman [192], there is a need for forensic DNA scientists to return to the basic properties of trace evidence, such as transfer, persistence and abundance. The considerable discriminative power of DNA evidence has led to the neglect of these important aspects of forensic evaluation of evidence.

1.5.7 Developing an interpretive framework for trace DNA

Having data to give estimates on the properties of DNA as physical evidence will enable investigators and scientists to assess its value as evidence in a particular case. Combining the particular case circumstances with experimental data on these properties will provide a more grounded, Bayesian-type interpretation of a trace DNA profile. The apparent 'randomness' of trace DNA analysis is known anecdotally, leaving an opportunity for defence lawyers to claim any number of innocent scenarios leading to the recovery of their client's profile from the crime scene, as shown in the cases discussed previously.

The factors affecting trace DNA evidence recovery are many, existing before, during and after the crime event. Figure 1-2 details some of these factors.

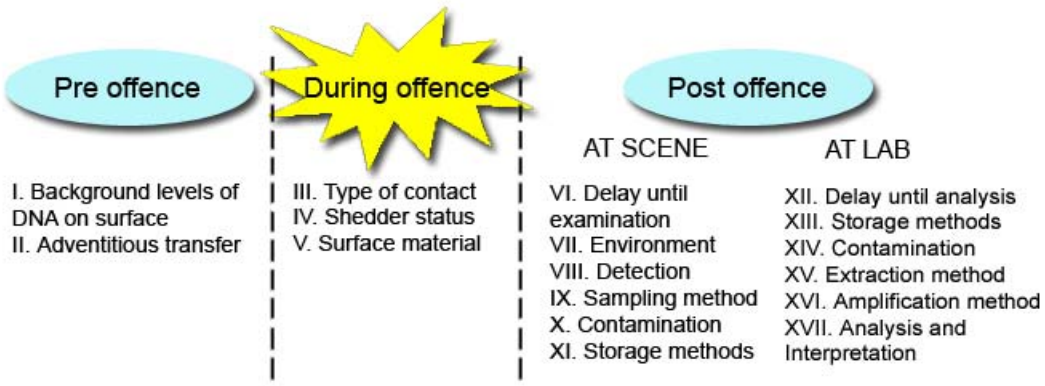

Figure 1-2. Factors affecting trace DNA recovery.

With experimental data to estimate the extent each factor affects recovery, a holistic assessment of the evidence in terms of the case circumstances can be made. A major criticism of Bayesian-type interpretation of evidence is the lack of numerical data to utilise the likelihood ratio effectively. Other trace evidence disciplines such as glass have constructed databases from which numerical information can be garnered to assist Bayesian interpretation. In fact, with the recent volume of research into trace DNA a considerable amount of this information already exists. However there is some variation in the extent as to each factor has been investigated.

As discussed earlier, the level of background DNA (Factor I) has only begun to be examined [144-147, 154] and the level of influence on the recovery of profiles from scenes is yet to be

realised. Factor II, adventitious transfer, is to be examined in light of the statements of the defendant and/or eyewitnesses. If there is no suggestion that the defendant may have had access to the crime scene some time before the offence, the issue of adventitious transfer is less contentious. Factors III through V relate to the transfer of trace evidence, and have been investigated in a number of studies [35, 42, 52, 62, 149-152, 154]. Several studies came to the conclusion that transfer of trace DNA is instantaneous, with the length of contact being largely irrelevant to the amount transferred. However others suggest that longer or more aggressive contact may result in greater DNA transfer [48, 156]. Several research groups around the world have examined shedding ability, factor IV [53, 150-152], as discussed previously. There have been conflicting results, and a greater population study seems worthy of further research.

The effect of the surface type (factor V) is believed to influence the final recovery, though estimates of the extent of that influence vary amongst the research. Wickenheiser [42] states that the amount of DNA transferred during handling is dependent on the substrate, with cells adhering better to porous surfaces than non-porous. In another study, Pesaresi et al. [136] found that profiles were more successfully recovered from glass than wood or metal, suggesting that increased perspiration occurring as skin contacts glass provides the increased success. Additionally, Alessandrini et al. [63] reports that the substrate characteristics are only a secondary factor to the recovery rate. This study suggests that the amount of DNA present and the suitability of sampling and extraction methods are the primary influences. This view is echoed by Raymond et al. [126], suggesting that factor V is intertwined with factors IX and XV (sampling and extraction), and that methods should be tailored to the type of substrate.

Factors VI and VII together influence the persistence of trace DNA. Little work has been conducted in this area, and given the number of variables in terms of the environment it may be difficult to give a definitive answer as to how long trace DNA will be able to be recovered after a crime. However, case-driven experiments will ultimately provide a collective body of knowledge in this area. For example, a small study by Murray et al. [150] found that full profiles were recovered from objects handled by good shedders after four months, when kept at room temperature. However a notable decrease in the amount of DNA recovered from poor shedders. Factors VIII through XI are dependent on the training and policies of the individual forensic organisation. Various trace DNA sampling methods have been explored; a two-swab (one wet, one dry) method has been shown to be more effective than a single wet

swab [193, 194], and tapelifting is more effective than swabbing for porous surfaces such as material [45, 195, 196]. Studies have assessed which wetting solution is the most effective for swabbing; van Oorschot et al. found water to be the most efficient [197], whereas South Australian research has implemented the use of a popule swab using 91% isopropanol in casework [198]. The prevention of contamination has also been investigated [199, 200], and it is hoped that the standard operating procedures of forensic laboratories would be sufficient to greatly reduce this factor's impact on DNA recovery.

It is the factors occurring at the laboratory stage that have enjoyed the most research attention. Many different extraction, amplification, analysis and interpretation methods have been tested and can be considered to be working effectively given the low level of DNA that it is now possible to recover. Again, the factors of laboratory submission, contamination and storage conditions are dependent on individual protocols and policies, but their effect should be minimal if adequate procedures are in place.

It is seen that these factors have been examined to varying extents in the literature. Factors VIII to XVII are areas to be determined and validated by laboratories and forensic organisations, and are beyond the scope of this research. The persistence of DNA at scenes (Factors VI and VII) has been touched upon [150] but is yet to be comprehensively studied in published journals. Factor I, the effect of background levels of trace DNA on surfaces, is only briefly covered in research. The practical component of this project aimed to provide data to fill gaps in the interpretive framework, in specific respect to two crime types; burglary and robbery.

1.6 Rationale and structure of thesis

From the literature and court cases reviewed it can be seen that forensic DNA research has been largely based on technological improvements and testing the limits of the technology, and there is a gap in knowledge regarding the 'behaviour' of trace DNA. A major criticism of the use of DNA in criminal investigation is that it is only applicable in a small percentage of cases, when compared with the level of time and monetary investment. Given that volume crimes have proven difficult to solve via traditional policing methods, DNA databases do provide an attractive alternative to police if only the percentage of scenes presenting DNA evidence could be increased. Collection of trace DNA evidence would achieve this, however as the previous discussion has shown, a number of problems have recently arisen with

respect to trace DNA, especially its presentation in court. In other words, trace DNA evidence may not be worth the investment. Therefore the rationale for this study is that an increased understanding into the mechanisms of trace DNA may improve its use in the investigation of volume crime. Through this project the benefits of a criminalistic approach to DNA evidence will be explored. It is not an intention of the project to investigate and develop new methods, as this is being competently handled by many other researchers. Instead the author's employment in a police forensic organisation was exploited; experiments were practically based, using current methods and actual case circumstances.

During the initial stages of the project it was realised that little was known about the current state of play in trace DNA evidence within the Australasian region. In order to gain a better understanding, a comprehensive survey was conducted into trace DNA evidence in Australia and New Zealand (see chapter 2). The survey also aimed to be useful for the forensic community to identify training and research needs, direct policy and increase communication lines.

Also noted during the literature review was the difficulty in creating realistic experimental scenarios that would accurately reflect casework. There is no published study of trace DNA casework samples in Australia, including an assessment of factors such as time delays and the sample type on success rates. To complement the experimental work of this thesis, a survey of over 250 trace DNA samples from NSW cases was conducted (see chapter 3). The results of the samples were analysed and used as a comparison to the results obtained experimentally.

As there are so many factors involved in the successful recovery of trace DNA, it was beyond the scope of this project to thoroughly investigate all. The experiment investigation was limited to three trace evidence characteristics that have the least coverage in the literature; the background level or 'abundance', primary transfer, and persistence. To base these experiments, the case types of burglary and street robbery (mugging) were selected as scenarios for the investigation. Chapters 5 through 7 contain the results of the three projects relating to these factors. Methods that were used in all experiments are described in chapter 4, and any variations to these methods are outlined in the relevant experimental chapter. The final chapter, chapter 8, considers the accumulated findings of the experimental work in the context of the interpretive framework, and provides a critical discussion of the value of trace DNA in volume crime investigation.

1.6.1 Aims

- To investigate current methods and practices in trace DNA in the Australasian region and from this identify areas for improvement (chapter 2)

- To investigate casework data regarding trace DNA to gain an understanding of current success rates and factors affecting results in casework (chapter 3)

- Using methods identified from the methods survey, conduct preliminary experiments into trace evidence characteristics of DNA; abundance, transfer and persistence (chapters 5-7)

- Investigate whether the data from experiments and casework can assist with an interpretive framework of trace DNA and aid court presentation (discussion, chapter 8)

- Estimate the value of trace DNA in volume crime investigations in Australia. (discussion, chapter 8)

Chapter 2:

Australasian Survey of Trace DNA Methods

Chapter 2: Australasian Survey of Trace DNA Methods

2.1 Introduction

As discussed the analysis of trace DNA is a much less straightforward task than for other DNA sources. There are numerous factors that affect the rate of recovery of full profiles, such as the ability of the individual to shed cells, the substrate surface, the time of contact and delay until analysis, and the environment [42, 62, 63, 151, 201]. In addition to these external conditions, there are many varying methods used to collect, extract and analyse the samples, each with particular benefits and limitations [140, 178, 202].

There has been little attempt to survey exactly which methods and practices are being employed across the different laboratories in the Australia and New Zealand region. Communication between laboratories is often limited due to the large distances between laboratories. No review exists into the methods and protocols of trace DNA analysis in the Australian forensic laboratories, though a similar study was conducted in regards to forensic education [203]. Indeed it is difficult to find similar surveys around the international forensic community. A survey of US DNA laboratories was conducted in 2001 by the United States National Institute of Justice, assessing empirical data such as staff numbers, caseloads, backlogs, budgets and accreditation status [22]. However the study did not gather in-depth information on methods, training or factors specifically affecting trace DNA.

In recent years reports such as the US National Academy of Science's (NAS) "Strengthening Forensic Science" [34] have put the spotlight on forensic disciplines to justify their practices. Whilst the outcomes of this report have been much debated in the forensic and legal arenas, critical review can be a useful tool to analyse and strengthen any points of weakness in the field. Forensic DNA analysis escaped the most severe criticism of the report, and was in fact referred to as the 'gold standard' in forensic science. However the field should not rest on its laurels, as there are many areas of improvement still to be achieved. The disperse nature of forensics in the United States was noted as an impediment to effective science; *"the fragmentation problem is compounded because operational principles and procedures for many forensic science disciplines are not standardized or embraced, either between or within*

jurisdictions." This problem is echoed in Australia and New Zealand, as the communication lines between jurisdictions can be limited.

This knowledge gap was identified during background research for this thesis, and a survey was developed to collate data into trace DNA analysis and was disseminated to employees of forensic organisations in all jurisdictions in Australia and New Zealand. The survey was constructed to take into account all the non-sample related aspects that may affect the chance of DNA recovery, by investigating every step of the process – sample collection to profile reporting, as well as prior education and directed training. The survey focused solely on trace DNA and the relevant methods involved, and not those for DNA from blood or semen.

The aims of the survey were as follows:

- 'Benchmark' the current methods and practices utilised in trace DNA analysis.
- Compare and share information across borders.
- Identify factors that may contribute to differences in success rates of trace DNA analysis.
- Provide information to identify training needs and the development of training packages.
- Provide information to assist in identifying the direction of research and development, and finally;
- To identify methods in current use for the design of the experimental component of this project.

The survey was divided according to three target groups of forensic practitioners: crime scene officers, DNA laboratory scientists, and managers of these staff. A separate survey was developed according to the types of duties each group might perform. Each survey contained short answer and 'tick a box' type questions calling for information about the methods the individual might use, their opinions on the methods and results, and details about their training and education. Managers were asked to comment on the methods used by their staff, the results their laboratory obtains and the training and education provided to and required of their staff. The surveys are contained in Appendix A.

The surveys were distributed to individuals from the organisations listed in Table 2-1 in September to December 2004.

Table 2-1. Organisations of survey distribution

Jurisdiction	Abbrev.	Organisations
Australian Capital Territory	ACT	Australian Federal Police: Biology and Crime Scene divisions
New South Wales	NSW	NSW Police Forensic Services Group NSW Dept Health – Division of Analytical Laboratories
New Zealand	NZ	New Zealand Police Institute of Environmental Science and Research
Northern Territory	NT	NT Police Fire and Emergency Services – Forensic Services Section
Queensland	QLD	QLD Police Forensic Services QLD Health Scientific Services – Forensic Biology
South Australia	SA	Forensic Science South Australia
Tasmania	TAS	Forensic Science Service Tasmania
Victoria	VIC	Victoria Police Regional Crime Scene Officers Victoria Police Forensic Services – Crime Scene and Biology Divisions
Western Australia	WA	WA Police Service – Forensic Crime Scene Unit WA PathCentre – Forensic Biology

The results of the 2004 survey were collated and analysed (as described in the following sections), and disseminated to the forensic community via presentations at the 18th Australian and New Zealand Forensic Science Symposium and a BSAG meeting in 2006, and published in 2008 [204]. There was also verbal feedback to participants from 2005 onwards.

In order to assess the relevance of these 2004 results and determine if there have been changes in various pertinent aspects in the interim, a follow-up survey was developed in 2009. This study was smaller in scope in terms of the number of participants, and targeted the following aspects which were identified as areas of interest from the first survey; Training and Education, Methods, Protocols and Policies, Communication and Reporting, and Opinions. Instead of constructing separate surveys for each group of respondents, one survey was developed (see Appendix A), and the participants asked to complete only the sections relevant to their duties. The follow-up was distributed to the same organisations as previously.

2.2 Results

2.2.1 2004 Survey

A total of 170 completed surveys were received; 93 Section One (Crime scene), 58 Section Two (Laboratory scientists) and 19 Section Three (Managers). The overall return rate was 54%. Table 2 details the spread of returned surveys according to jurisdiction.

As can be seen from Table 2-2, the return of surveys was not even across jurisdictions. In some cases this can be correlated with the uneven population spread across Australian states and therefore numbers of forensic staff; NSW and Victoria have greater populations than all other jurisdictions and also the highest percentage of return. Appendix B contains detailed tables of responses listed by state of origin, enabling comparison between jurisdictions. Also contained in Appendix B are snapshots of the 'average' crime scene investigator and laboratory scientist, circa 2004.

Table 2-2. Survey return.

State	Crime Scene (Section 1)	Laboratory (Section 2)	Managers (Section 3)	Totals	Total population [205]
ACT	13	2	1	**16**	**351 200**
NSW	19	4	3	**26**	**7 099 700**
NT	4	5	1	**10**	**224 800**
NZ	9	14	4	**27**	**4 076 000**
QLD	8	4	1	**13**	**4 406 800**
SA	7	9	1	**17**	**1 622 700**
TAS	6	1	1	**8**	**502 600**
VIC	26	13	6	**45**	**5 427 700**
WA	1	6	1	**8**	**2 236 900**
TOTAL	***93***	***58***	***19***	***170***	***21 874 900***

2.2.2 Section 1: Crime scene investigators

Crime scene investigators are the most diverse group of the three survey sections. It is evident from the returned surveys that jurisdictions have widely different systems in terms of their personnel response to crime scenes. The investigators varied in terms of their status (police or civilian), duties (either solely fingerprint examiners, physical evidence/photography or both) and types of crime examined (volume/minor crime only or major crime). Of the 93

crime scene investigators who responded, 56 were known to be police and 26 were identified as civilian employees.

2.2.2.1 Crime scene investigators: Training and experience.

The majority (56%) of the responding crime scene investigators did not hold a university degree (Figure 2-1). 77% of respondents had been employed in crime scene for more than two years, 46% for more than five years. For over half (60%) of the respondents it had been two or more years since their original training in trace DNA evidence. Two respondents stated they were not officially provided training on trace DNA evidence.

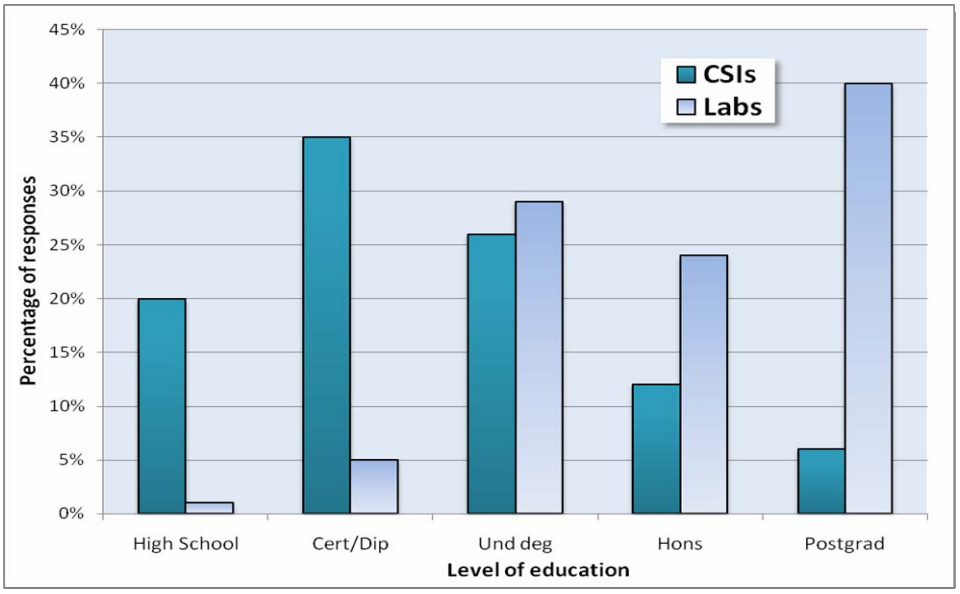

Figure 2-1. Highest education level of respondents, crime scene investigators (CSIs) vs laboratory staff (Labs).

The format of trace DNA training varied both within and between jurisdictions. 16% of crime scene investigators suggested their training was one-on-one, 23% were part of a group tutorial, and 34% had their training as lectures and practical exercises. The remainder had some combination of these methods. It was noted that respondents within the same jurisdiction gave different answers, suggesting either that training methods changed in format over time, or that the training methodology was informal, leading to various interpretations of the format.

The length and method of assessment of the course varied considerably. 41% were provided with 1 to 2 hours of training in trace DNA evidence, followed by 20% with a day-long course.

A half-day course and a weeklong course were the next most common responses, with 16% and 11% of respondents respectively. In terms of assessment, 39% of investigators were given a practical test, and 13% with practical and written tests. 33% were not formally assessed in trace DNA evidence.

Respondents were asked if refresher courses in trace DNA evidence were provided by their organisation. A majority (70%) stated that refresher courses were not provided. 19% were given yearly updates, and for 10% updates were given more than one year apart.

2.2.2.2 Crime scene investigators: Methods

- Fingerprinting

Standard fingerprint powder (black carbon and titanium white) was by far the most common fingerprint development method used at crime scenes (92%), and consequently squirrel fibre brushes were the most common applicator used (84%). These applicators were kept in use by officers generally for six months or longer (95%), and only occasionally cleaned (54%), if at all, with 41% stating they never cleaned applicators.

- DNA Collection

The methods used by crime scene investigators to collect trace DNA are shown in Figure 2-2. 56% of respondents used more than one method for trace DNA collection. The most common solution used during swabbing was sterile water (86%), 7% of investigators used a concentration of ethanol, and 7% water or ethanol. The cotton swab was by far the most popular type of swab (82%), followed by foam and branded swabs (11% and 5% respectively).

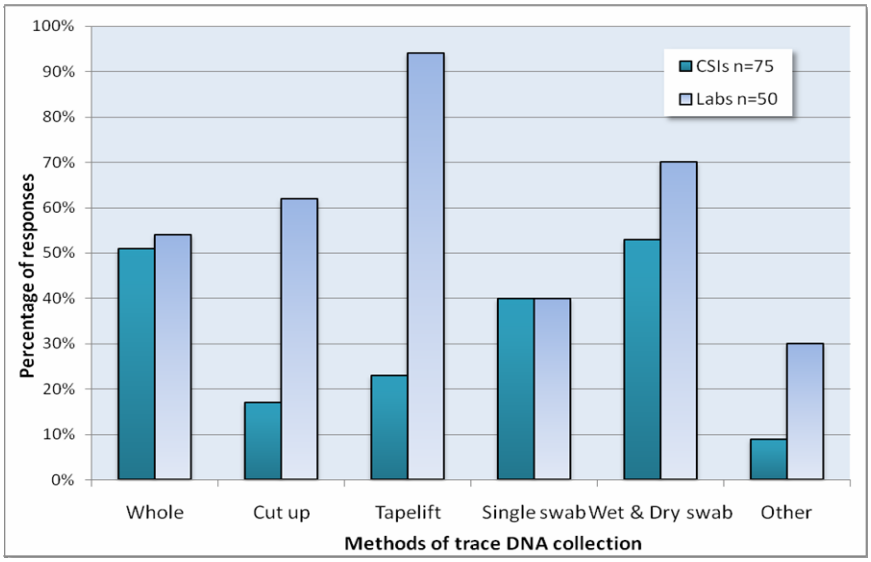

Figure 2-2. DNA collection methods; crime scene investigators (CSIs) vs laboratory staff (Labs).

Crime scene investigators were asked to describe their action when swabbing for trace DNA. Continual rotation of the swab gave the top response (54%), with 31% stating they maintained the swab in fixed orientation so the DNA is concentrated onto one side, and 13% rotating the swab at set times during swabbing. Investigators were also asked approximately how many times they passed the swab over an object when swabbing for trace DNA. 38% stated between 1-5 times and 42% passed the swab 5-10 times over the surface.

24 crime scene investigators provided responses as to their methods used during tapelifting. The most common brand of tape used was 3M or Scotch (38%). 25% of investigators only pressed the tape against the surface once, 50% stated multiple times. 38% submitted their tapelifts to the laboratory on an acetate sheet, 29% put the tape whole in a tube, and 25% in a petri dish.

Most scene investigators store their exhibits at room temperature (72%), with around a third refrigerating samples. 79% of investigators stated they would submit exhibits to a laboratory within a week of their collection, and 13% within one day. 15% take more than two weeks convey their exhibits.

2.2.2.3 Crime scene investigators: Contamination prevention.

Questions regarding the wearing of gloves, facemasks and other body protection during fingerprint and trace DNA collection were asked of investigators.

Reassuringly, the majority of investigators wore gloves during fingerprint examination (90%) and DNA collection (99%). However, the regularity that those gloves were changed varied somewhat. Table 2-3 and Table 2-4 detail the type of gloves used, and how often investigators changed their gloves. Facemasks were not worn as regularly as gloves, with 19% of scene investigators stating they never wear a mask during a DNA examination (Table 2-5). Again, the frequency that facemasks are changed varies considerably, from per exhibit to weekly or monthly.

Table 2-3. Crime scene investigators: Contamination prevention during fingerprint examinations

Gloves changed during FP exam	**%**	**Facemask worn during FP exam**	**%**
>Once/scene	40	Never	30
Once per scene	**41**	**Sometimes**	**49**
Daily	4	Always	21
Weekly	9		
>Weekly	6		

Table 2-4. Glove use during DNA sampling: Laboratory staff (Labs) vs crime scene investigators (CSIs)

Type of gloves worn				**How often gloves changed**			
Labs	**%**	**CSIs**	**%**	**Labs**	**%**	**CSIs**	**%**
Latex	**92**	**Latex**	**54**	**>Once per exhibit**	**60**	>Once per exhibit	12
2prs latex	8	2prs latex	24	Per exhibit	38	**Per exhibit**	**72**
		Nitrile	11	Per case	2	Per scene	16
		Cotton	1				
		Other	9				

Table 2-5. Facemask use during sampling: Laboratory staff (Labs) vs crime scene investigators (CSIs)

Facemask worn				**How often facemask changed**			
Labs	**%**	**CSIs**	**%**	**Labs**	**%**	**CSIs**	**%**
Never	0	Never	19	Per exhibit	28	>Once per scene	17
Sometimes	20	Sometimes	20	Per case	10	Per scene	13
Always	**80**	**Always**	**61**	**Daily**	**48**	Daily	3
				Weekly	8	**Weekly**	**22**
				Monthly	4	Monthly	0
				>Monthly	2	>Monthly	7

43% of investigators said they wear no other body covering other than their standard work wear. 31% stated they wore overalls, and 6% another type of full body covering. Only 4% professed to wear hairnets.

2.2.2.4 Crime scene investigators: General practices

Majorities of investigators stated they would collect trace DNA when a fingerprint (92%) or other DNA evidence such as blood, semen or saliva (84%) was available at a scene. 88% of investigators would collect trace DNA from volume crime offences, however a third stated only for more serious volume crime offences. 73% of investigators collect five or fewer trace DNA samples per week, however, 5% collect more than 20 trace DNA samples every week. The most common items submitted for trace DNA analysis were food and drink related, vehicle swabs, and clothing (data not shown).

2.2.3 Section 2: Laboratory staff.

Staff employed in forensic DNA laboratories in Australia and New Zealand are generally divided into two broad categories: 'Biologists', who examine the sample after its receipt, determine what methods are to be employed, and interpret the results, and 'Technicians', who perform the extraction, amplification and analysis steps, without any interpretation. In the main, biologists have more experience than technicians. There are slight variations in the roles of these two categories between jurisdictions, or duties may be merged in some areas.

All respondents to this section of the survey were civilians. Forensic laboratories in this region are most commonly government run. Four jurisdictions (Victoria, Tasmania, the Northern Territory, and the Australian Capital Territory) have the DNA laboratory as a division of the police service, employing civilian scientists. In the remaining five jurisdictions the laboratories are separate organisations to the police. Of these, four are run by the state health or Attorney General's department (New South Wales, Western Australia, South Australia and Queensland), and the fifth (New Zealand) is a semi-private entity.

2.2.3.1 Laboratory staff: Training and experience.

As evident in Figure 2-1, page 49, a large percentage of laboratory staff had an education level of an undergraduate degree or higher (93%). 40% of laboratory scientists had post-graduate qualifications. The type of degree laboratory scientists hold varies, with the most common type found to be a degree majoring in molecular biology and genetics (47%).

22% of laboratory staff had been employed for more than five years, 60% between one and five years, leaving 18% of staff with under one year experience.

Figure 2-3 shows the comparison between the level of experience in crime scene investigators and laboratory staff. Crime scene investigators were found to have more experience than laboratory staff, with 78% of DNA laboratory staff having less than five years experience. This is to be expected given the considerable increase in the workload of DNA laboratories in recent years, and the subsequent large recruitment of staff.

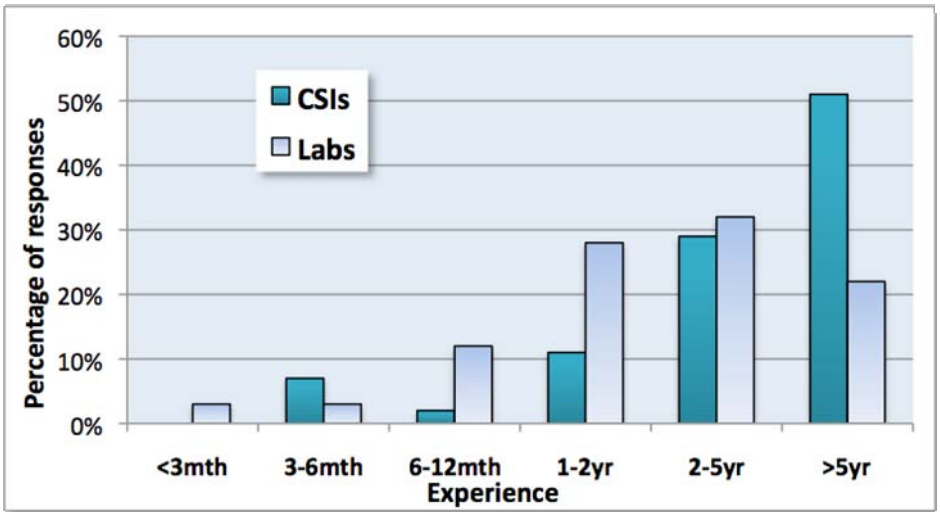

Figure 2-3. Comparison in experience of crime scene investigators (CSIs) and DNA laboratory staff (Labs)

59% of respondents stated it had been more than two years since their initial training in trace DNA analysis. The length of this training was stated to be greater than a week in the majority of cases (43%), the next most common a half-day course or shorter (32%). The most common format of the training was one-on-one (56%), followed by practical demonstration (32%). 42% of respondents were not assessed in trace DNA analysis, 41% stated they undertook a practical test. 92% of laboratory staff have never received a refresher course in trace DNA analysis.

2.2.3.2 Laboratory staff: Methods

- Sampling

The various types of sampling methods employed by laboratory staff are listed in Figure 2-2, page 51. Tapelifting and wet and dry swabbing were the two most common sampling

methods used. All respondents use more than one method of sampling. Cotton swabs were by far the most common type used (67%), and 13% of laboratory staff use a combination of cotton, foam or branded swabs. The majority (70%) use sterile water as a swabbing solution.

60% of respondents continually rotate the swab whilst swabbing, only 14% maintain the swab in a fixed orientation. 40% pass the swab 1-5 times over the target surface and 58% between 5 and 20 times. The most common brand of tape used in tapelifting was again 3M/Scotch (43%). 38% of laboratory staff press the tape 2-3 times on the target surface when tapelifting, and 26% between 5 and 20 times. 15% stated they only press the tape once against the target surface.

- *Extraction*

Standard chelex and organic extraction methods were equally the most common extraction methods used (33% each). 18% of respondents stated they use both chelex and organic methods, and 13% use a 20% chelex method. 37% of laboratory staff stated they would always use a clean-up method during extraction. 63% stated some type of variation is permitted in their standard extraction procedures, generally adding an additional step or varying the volumes to suit the sample.

- *Quantitation*

Quantiblot was by far the most common quantification method used, with 70% of responses. 37% of laboratory staff reported quantitation estimates as equal to one of the standards, the remainder reported a specific amount or concentration. 75% repeated all negative samples if the lowest standard was not detectable. 65% of respondents who used the Quantiblot methods always amplified samples with a negative result, 3% never did.

A majority of 80% of respondents stated they were not entirely happy with their quantitation method. Various comments included; '*Quantiblot result is frequently unreliable, particularly with tapelift samples*', '*not happy, insensitive and unable to tell if inhibitory agents present in samples*', and '*very subjective, insensitive and has a very limited upper range*'.

- PCR

Profiler Plus™ was the most common PCR kit used in forensic laboratories in this region, and 92% of respondents use 28 PCR cycles for amplification. Only one jurisdiction (New Zealand) used SGM Plus®, and a minority of respondents (12%) stated they use Profiler Plus™ and Cofiler®, or Identifiler®. 88% of responding lab staff stated they are not permitted any variation in their standard PCR methods. The four positive responses were allowed to vary cycle number (two responses, stating this would occur vary rarely), reaction volume, or the addition of bovine serum albumin (BSA). 74% of lab staff used a Perkin-Elmer 9700 thermocycler for their PCR.

A minority of laboratory staff had tried low-copy number (LCN) analysis (28%), however most are aware of LCN analysis (86%). It was unspecified whether those who had experience with LCN work had used it in casework or purely for research purposes.

2.2.3.3 Laboratory staff: Contamination prevention

In addition to specific methods used, participants were asked what contamination prevention measures they take during sampling and extraction. As would be expected, all of the respondents stated they wore gloves during sampling and extraction, most commonly one pair of latex gloves (Table 2-4 and Table 2-6). During sampling, these gloves were changed at least once per exhibit (98%). The number of times gloves were changed during extraction varied from a time period of 15 to 30 minutes, or after touching something outside the extraction, or other variables.

Facemasks were worn less often than gloves, during both sampling (80% of respondents) and extraction (48%), as shown in Table 2-4 and Table 2-6. Some of the respondents stated they wore facemasks for specific conditions only, such as odorous samples. Facemasks were most often changed daily for both sampling (48%) and extraction (46%).

Hairnets were not often worn, according to the responses (figures not shown). 33% wore hairnets during sampling, and none stated they wore hairnets during extraction procedures.

Table 2-6. Laboratory staff: Glove and facemask use during DNA extraction

DNA Extraction							
Type Gloves	%	Changed	%	Facemask	%	Changed	%
Latex	**95**	15mins	10	**Always worn**	**48**	Per batch	35
2 pairs latex	5	30mins	7	Spec cond only	14	When exit lab	4
		When exit lab	2	Never worn	36	**Daily**	**46**
		Per batch	2			Weekly	8
		After touching	17			Other/Varies	8
		Other/Varies	**62**				

2.2.3.4 Laboratory staff: Analysis

68% of respondents were using ABI 3100 instruments for their analysis. There was wide variation between the responses for volume of amplified product used (1 – 10uL), the total injection volume (4.5 – 28uL), injection time (5 – 22 seconds), and the run time (20 – 45 minutes).

Peak height was the major criteria for calling alleles (52%), with 21% also considering the morphology of the peak. The minimum heights limit for calling heterozygote alleles varied between 50rfu (54%), 100rfu (22%), and 150rfu (3%). The remaining respondents stated their limits varied depending on the circumstances. For homozygote alleles, the calling limit ranged amongst 200rfu (38%), 250rfu (30%), 300rfu (20%) and 400rfu (3%).

2.2.3.5 Laboratory staff: Time and storage

The average time periods taken between each step of sample analysis, from the time a sample is booked in to the laboratory through to the typing of the sample, are shown in Figure 2-4. Respondents commented that these times were average only, and that cases are expedited when requested.

Laboratory staff were also asked at what temperature samples were kept at each stage of analysis. Exhibits were mainly kept at room temperature on receipt at the lab (47%), however an equal percentage stated that this varied depending on the needs of the sample. The majority stated pre- and post-amplification extracts were stored in the refrigerator (87% and 82% respectively). 63% of respondents indicated the amplified products were stored in a –15˚C freezer (or cooler), along with 75% of products after typing.

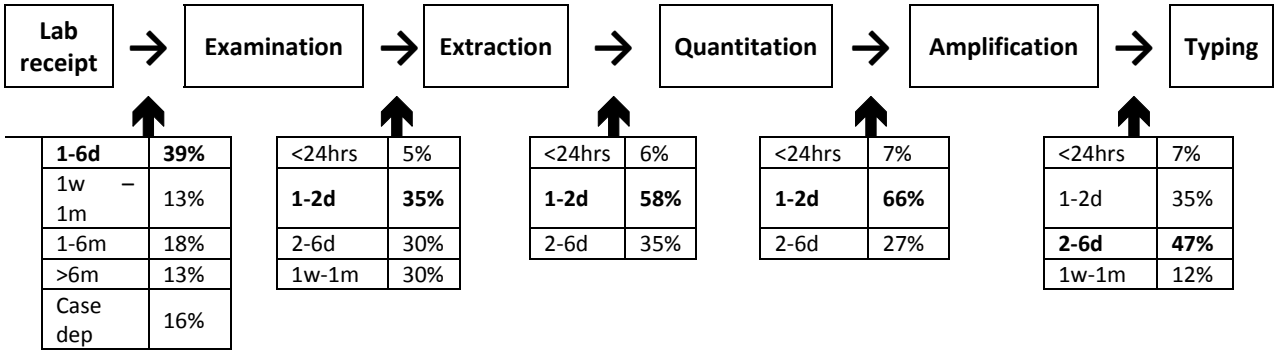

Figure 2-4. Laboratory staff: Time between analysis steps.

2.2.3.6 Laboratory staff: Results

The majority (69%) of laboratory staff indicated that they personally processed fewer than 20 trace DNA samples per week, and 7% would process in excess of 50 samples. Laboratory staff were asked to estimate the proportion of the trace samples processed which provide a result suitable for entry onto their DNA database, or that is of use to investigators through intelligence links. Over half (52%) estimated the overall success rate of trace samples to be between 25 and 50%. 45% of respondents were more conservative with an estimate of between 10 and 25%. Laboratory staff also estimated success rates for different trace DNA sample types, with rough estimates suggesting trace swabs of food and drink items, clothing items and personal effects produced more useful profiles (Figure 2-5). Whilst the survey asked participants to consider only the trace aspects of food and drink items (for example the handled area rather than the mouth of a drink container), it is possible that respondents may have taken into account saliva samples in their estimates.

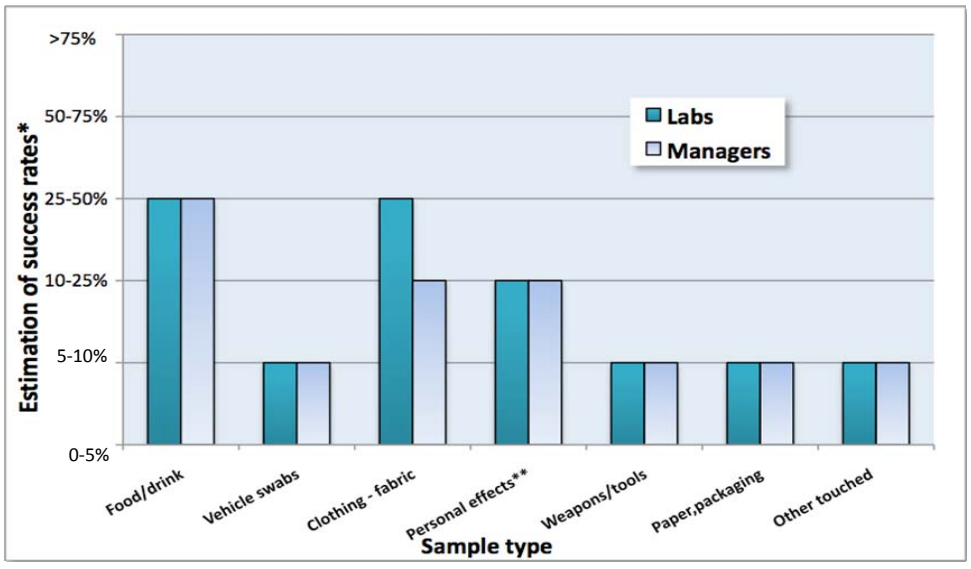

Figure 2-5. Estimates of success rates* of different sample types: Laboratory staff (Labs) vs Managers.
****Percentage of samples deemed to provide a result that is suitable for use in the particular case or for inclusion on the DNA database. ** Personal effects= watches, jewellery, reading and sunglasses, shoes, belts***

2.2.4 Section 3: Managers

Of the 19 surveys received from managers, six were from managers of crime scene sections, two from fingerprint sections, and 11 from DNA laboratories. The number of staff supervised by each manager was fairly evenly spread from less than ten staff to more than 40 (Table 2-7). The numbers of staff under the manager who were trained to collect trace DNA ranged similarly. The number of staff trained to analyse or interpret trace DNA was lower however, with 53% having no staff trained in these procedures.

Table 2-7. Managers: Staff numbers and duties

No. of staff		% of staff trained to collect trace DNA		% of staff trained to analyse/interpret trace DNA	
	%		%		%
<10	21	0	5	**0**	**53**
10-20	**26**	1-39	10	1-39	21
21-40	21	40-59	10	40-59	21
>40	**26**	60-79	20	60-79	5
nil	5	80-99	10	80-99	0
		100	**42**	100	0

2.2.4.1 Managers: Training and assessment

The minimum level of education required for staff at these organisations was most commonly an undergraduate degree (50%). However 39% of managers stated a university degree is not a pre-requisite for employment in their organisation.

Managers were asked as to the type of training in trace DNA analysis or collection their organisation provided to staff. The majority (64%) gave 'on the job' training only, with the remainder providing a course, lectures or tutorials. Refresher courses in trace DNA analysis were only occasionally conducted (32%), or in a response to specific needs (53%). 16% of managers stated their organisation never conducted refresher courses in trace DNA.

Proficiency testing in trace DNA was also rarely conducted. 84% (n= 19) of the organisations never undertook proficiency testing specifically including trace DNA analysis, according to the responding managers.

2.2.4.2 Managers: Methods and research

The questions for this section of the survey were relevant for managers of DNA laboratories only, and were not answered by fingerprint or crime scene section managers.

Managers were asked if their staff were permitted to vary any methods used in trace DNA analysis. Four responded yes, four only on rare occasions or limited circumstances, and four were not permitted any variation.

The survey found that not all laboratories were conducting research into alternative procedures or methods in each step of trace DNA analysis. Of the 11 responding managers of DNA laboratories, the most common research topics were extraction and typing or interpretation methods (five and four responses respectively), followed by sampling methods and Low Copy Number techniques (each with three responses).

2.2.4.3 Managers: Results

Managers were asked if they kept statistical records at the various stages of trace DNA analysis. 35% collected statistics on the type and number of samples that had been submitted to the laboratory, and nearly half collected statistics on the number of samples submitted for extraction. Only two respondents stated they kept a record of the number of samples able to be amplified. 35% kept records of the amount of samples that resulted in full or partial profiles.

The number of trace samples analysed per week by the managers' sections ranged from none (four responses) to more than 50 (four responses). The percentage of all items tested that were trace DNA samples was most commonly between 10-50% (eight responses). These trace samples were more likely to come from volume crime scenes as opposed to major offences, with seven responses greater than 50%. Figure 2-5, page 58, shows the estimated success rates managers attributed to different sample types.

2.2.4.4 Opinions of trace DNA evidence

A final question in the survey was to ask all respondents whether they thought trace DNA was highly significant, of average significance, or insignificant as evidence in criminal cases (Figure

2-6). The responses were relatively evenly divided between the average and highly significant categories, however a number of laboratory and manager respondents provided their own 'depends' category. There were no statistically significant differences observed between the responses of the different groups.

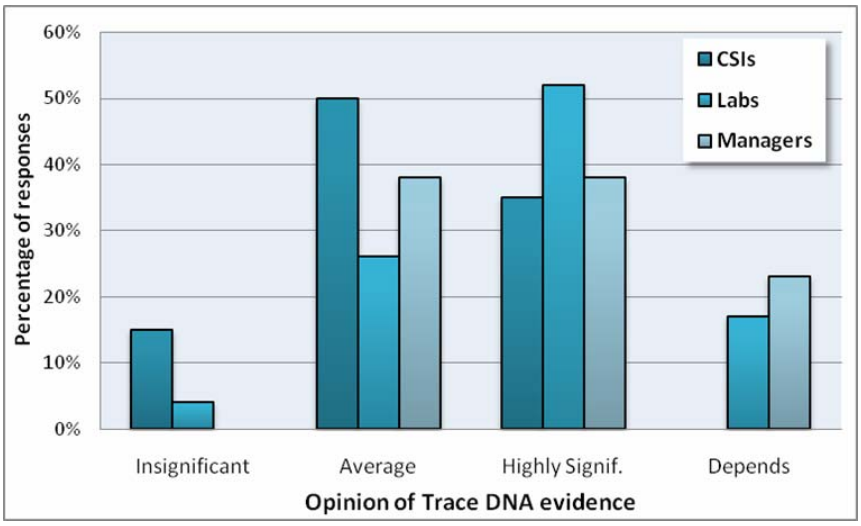

Figure 2-6. Opinions of trace DNA evidence from the three survey groups

2.2.5 2009 follow-up survey

A total of 77 surveys were completed, giving a return rate of approximately 67%. As before, the return from the various jurisdictions was not even. Table 2-8 shows the rate of return by jurisdiction. The percentage level of return from the managers was much higher than for the other groups, however it was noted that the majority of these managers were middle-level managers who still undertook casework.

As there was an uneven distribution across the jurisdictions, the results were analysed both from the total responses and the average of responses per jurisdiction, as described in the following section. Intra-variability in the responses from individuals from the same jurisdiction was noted for several questions, and in this case the average response from that jurisdiction was taken.

Table 2-8. 2009 Survey return.

State	Crime Scene	Laboratory	Managers	Totals
ACT	3	10	1	**14**
NSW	7	1	1	**9**
NT	1	0	1	**2**
NZ	2	2	7	**11**
QLD	0	0	0	**0**
SA	2	1	2	**5**
TAS	5	2	2	**9**
VIC	8	6	7	**21**
WA	4	1	1	**6**
TOTAL	***32***	***23***	***22***	***77***

2.2.5.1 Training and Education

The participants in the 2009 survey were, on average, first trained in trace DNA collection and/or analysis in 2002. 73% of respondents stated that the level of education in the entry requirements of their position had not changed since 2004, however 14% stated there had been an increase in these requirements. Large majorities of participants had not seen a change in the level of refresher training regarding trace DNA collection or analysis. 85% had not undertaken a proficiency test specifically involving trace DNA since their original training. 8% stated they received such proficiency tests annually. Table 2-9 and Table 2-10 detail the responses to the levels of internal training and research activities involving trace DNA. Equal percentages of respondents stated they did not spend time on research activities relating to trace DNA, or spent limited time but would like more. The primary reason for this was a lack of time.

Table 2-9. 2009 survey; levels and frequency of internal training.

Has the level of internal training changed in your organisation since 2004?		
	Regarding trace DNA collection (%)	Regarding trace DNA analysis (%)
Yes increased	34	31
Yes decreased	0	0
No, stayed the same	**51**	**50**
Unsure	15	19
Has the frequency of refresher training changed in your organisation since 2004?		
	Regarding trace DNA collection (%)	Regarding trace DNA analysis (%)
Yes increased	9	11
Yes decreased	0	0
No, stayed the same	**81**	**74**
Unsure	9	22

Table 2-10. 2009 survey; time spent on research activities.

Do you spend time researching or reading literature regarding trace DNA? (%)		*Reason for not spending time on these activities (%)*	
Yes, considerable time	5	**Lack time**	**58**
Limited time but happy with amount	19	Lack facilities/resources	14
Limited time but want more	**38**	Lack interest	3
No	**38**	Not encouraged to	8
		Happy with knowledge level	12
		Other	6

2.2.5.2 Methods, Protocols and Policies

Participants were asked if any methods used to collect or analyse trace DNA had changed in the past five years. Figure 2-7 demonstrates that the majority of organisations have changed various analysis steps. The changes implemented include the use of robotics (and consequent changes in extraction technologies such as the use of Invitrogen ChargeSwitch® or Promega DNA IQ™), real-time PCR for quantitation, the use of larger multiplexes such as PowerPlex®16 or Identifiler™, changing to high throughput analysis instruments, using GeneMapper™ software for analysis, and increased contamination prevention measures. Several jurisdictions also changed their sampling/collection methods, by using foam popule swabs instead of cotton, and switching to 'minitapes' made in-house for tapelifting. One jurisdiction (New Zealand) had implemented LCN analysis and was currently using it in casework.

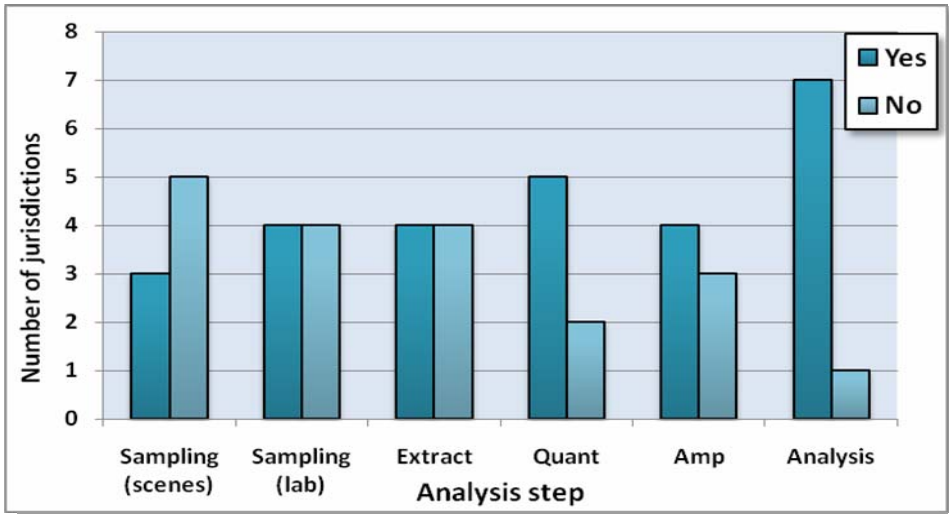

Figure 2-7. 2009 survey; Have trace DNA collection and analysis methods changed since 2004?

Of the eight responding jurisdictions, four are currently using or are in the process of implementing robotics for extraction, quantitation, amplification and analysis set up, one uses robotics for extraction set up only, and three had not yet implemented robotics for any process.

The follow-up survey also questioned whether there were any changes in the submission policies regarding trace DNA in the interim five year period. Majorities (46% and 40%) of respondents stated that the numbers of trace DNA samples permitted to be collected or submitted had not changed, nor the types of items or offences where trace DNA samples could be collected from (Table 2-11). 18% stated that the number had increased for volume crimes, and conversely, 15% suggested that numbers had decreased for volume crimes. In those jurisdictions where a change was noted, 24% of respondents stated that this policy change was due to in-house research and validation, and 19% because of a need to reduce backlogs.

Table 2-11. 2009 survey; changes in trace DNA submission policies.

Has the number of trace DNA samples permitted to be collected or submitted changed? (%)	
Increased for volume crime	18
Increased for major crime	14
Decreased for volume crime	15
Decreased for major crime	1
No	**46**
Unsure	5
Has there been a change in the type of items from which trace DNA samples can be collected? (%)	
Yes additional offence types	4
Yes additional object types	14
Yes fewer offence types	12
Yes fewer object types	19
No	**40**
Unsure	11
Reason for any change in trace DNA submission policies (%)	
Internal research & validation	**24**
External research & validation	10
Cost savings	14
Backlog reduction	19
Change in methods	11
Change in lab staff numbers	6
Change in CSI numbers	10
Change in crime rates	6

2.2.5.3 Communication and Reporting

Participants were asked if their jurisdiction had implemented or improved an electronic data management system, as it was noted that in 2004 data collation was limited, and when done was primarily conducted manually. Whilst 23% of respondents stated they still had the same system as in 2004, nearly half (47%) said their system had improved, either 'somewhat' or considerably, and 9% had an electronic system implemented where they previously did not have one (Table 2-12).

Table 2-12. 2009 survey; electronic data management systems.

Has your organisation implemented or improved an electronic data management system? (%)	
Yes, system considerably improved	21
Yes, system somewhat improved	**26**
Did not have one, have since implemented	9
No, still same system	23
Unsure/other	21

Figure 2-8 shows whether the respondents' data management systems enabled them to collate data in ten different areas that may be relevant to trace DNA analysis, from the number of trace DNA samples submitted, through to the number proving to be useful in the investigation. Majorities of respondents were unsure whether this was possible or stated that it was not possible. The managers did not respond significantly differently to the other respondents in these questions (p= 0.2, *t*-test for equal variance). Categories that were most able to be collated where the number of trace DNA samples submitted and the region where the samples were collected.

Table 2-13 details how often this data was collated, and again most commonly the respondents did not know. Only small percentages of respondents stated it was collated on a regular basis.

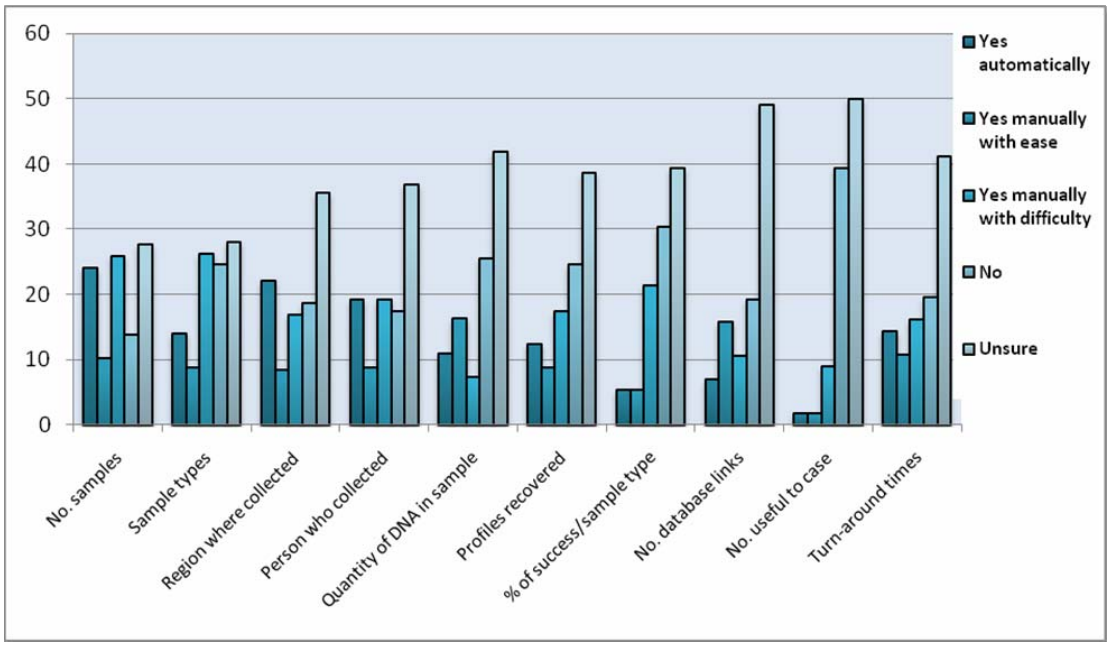

Figure 2-8. Does your electronic data management system allow the collection of statistics in the following areas?

Table 2-13. Is this data collated, and if so, how often? Responses are in percentages.

	No. samples	*Sample types*	*Region where collected*	*Person who collected*	*DNA quant in sample*	*Profiles recovered*	*% success /sample type*	*No. DB links*	*No. useful to case*	*Turn-around times*
Yes <weekly	2	2	4	3	2	1	2	1	0	3
Yes, monthly	10	0	1	3	1	3	1	4	0	5
Yes, every 6-12mths	3	4	3	2	1	2	1	2	0	0
Sporadically	13	15	9	6	12	13	17	13	7	12
No	7	13	17	19	14	13	11	11	23	12
Unsure	**24**	**24**	**23**	**25**	**26**	**26**	**25**	**27**	**26**	**25**

Table 2-14 details the dissemination of trace DNA results to crime scene examiners, sample collectors whether internal or external to the laboratory, and police investigators. Whilst a third of crime scene investigators stated they did not receive results of the samples they had submitted, 77% of laboratory staff stated this was performed, at least on an irregular basis. 70% of laboratory staff stated that the results were disseminated to police investigators on a regular basis.

Table 2-14. Dissemination of trace DNA results.

	Crime scene respondents	***DNA Lab respondents – are results disseminated to;***		
	Are you informed of the results of trace DNA samples?	***The collector of the sample if external to the lab?***	***The collector of the sample if internal to the lab?***	***Police investigators?***
Yes regularly	21	**30**	28	**70**
Yes in response to request	19	27	20	15
Yes irregularly	28	20	**44**	4
No	**32**	23	8	11

As a summary question, all participants were asked if they had easy access to all the data that they would like (Figure 2-9). Over half stated they did not, and a further 25% only partly. There was no significant difference between the responses of managers and their subordinates to this question (p= 0.9, *t*-test for equal variance).

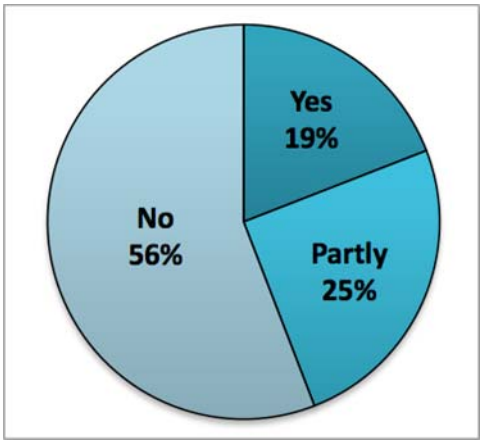

Figure 2-9. Are you easily able to access all the data that you would like?

2.2.5.4 Opinions

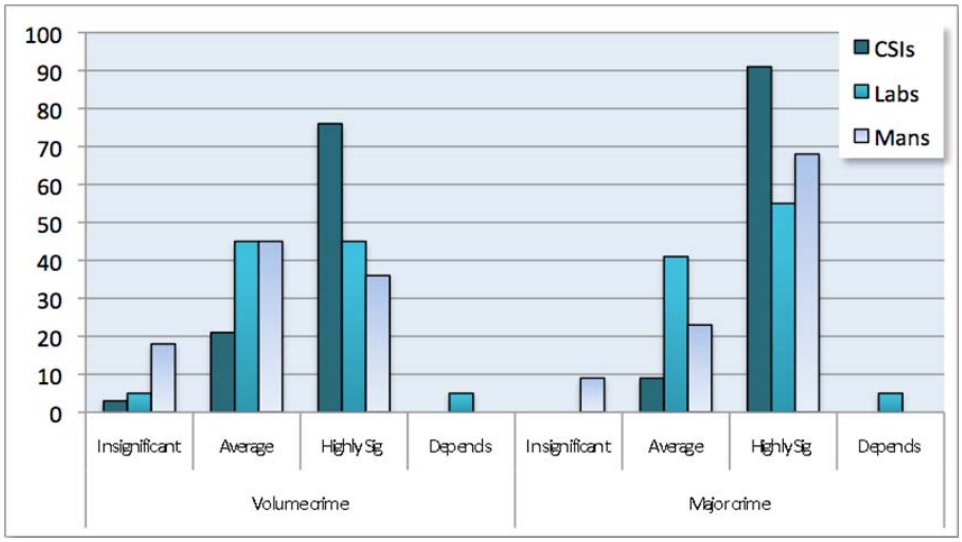

Figure 2-10. 2009 survey; opinions of trace DNA as evidence in volume and major crime.

The 2009 survey again asked the question; 'in your opinion, how significant are trace DNA samples as items of evidence?' However in this survey the question was asked separately of volume and major crimes. A greater percentage of all three respondent groups thought that trace DNA evidence was highly significant in major crime, however the differences between the two crime categories was not statistically significant (Figure 2-10).

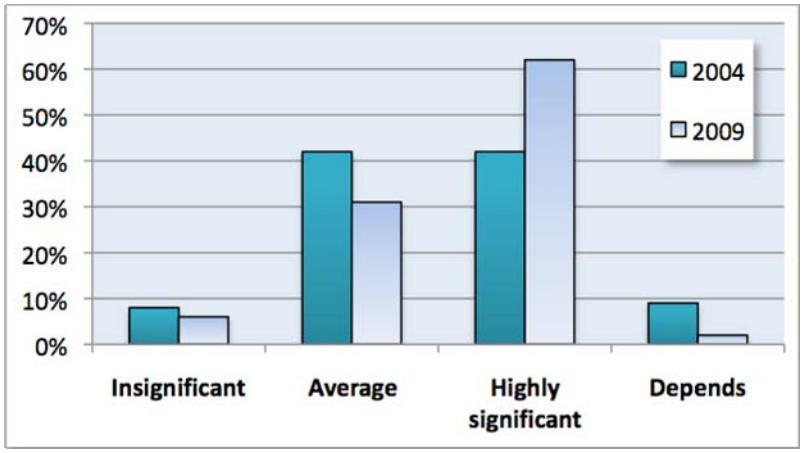

Figure 2-11. Opinions of trace DNA as evidence; comparison between 2004 and 2009.

There was no statistically significant change in the opinion of trace DNA evidence between 2004 and 2009 (Figure 2-11), however the percentage of respondents who valued trace DNA as highly significant evidence rose from 42% to 62%.

2.3 Discussion

The following discussion is divided into four sections, with the bulk concentrating on the primary 2004 survey. The first three sections detail areas of interest noted from the 2004 survey results; Training and Research, Methods and Processes, and Results and Opinions. The fourth section discussed and compares the results of the 2009 follow-up with the original survey.

2.3.1 Training and Research

The recent US National Academy of Sciences (NAS) report on forensic science emphasised the importance of a strong foundation of knowledge in increasing the professionalism of forensic organisations [34]. Training and research form a vital component of building knowledge and retaining staff and hence a major purpose of this survey was to investigate the state of this area in the Australasian region.

The finding that laboratory staff had higher background levels of education than crime scene investigators was expected (Figure 2-1) given the tradition of on-the-job training of police officers into forensic sciences and scene examination roles. Currently, several jurisdictions in the region are recruiting crime scene investigators with science degrees, whilst in others the reverse is occurring, with scene investigators being recruited from police ranks with little to no emphasis on scientific background. It may be of interest to track the effect (if any) of these differing recruitment policies on the quality of evidence and results.

30-40% of scene investigators and laboratory staff had not been formally assessed in trace DNA collection or analysis. Evaluation of some kind is an important component of training courses to ensure correct concepts and techniques have been absorbed by participants. Given the large percentages of junior staff in DNA laboratories, effective training and assessment would seem to be crucial. However, an alternative point of view is that the newer staff would have a good theoretical grounding in the latest techniques, given the fast progression of the molecular biology field. This could lead in turn to the 'more experienced' staff lacking a formal education in DNA methodology.

Equally concerning as the lack of formal initial training courses was the absence of regular refresher training and proficiency testing. Refresher courses were in the majority only

conducted in specific circumstances, and proficiency testing was generally not conducted specifically towards trace DNA. Unfortunately this was not found to have improved in the 2009 survey. DNA analysis is a constantly changing field and it would seem that keeping staff abreast of the latest developments would be of benefit to employers. In addition, the move towards analysing lower levels of DNA demands that the analysts are accurate and precise in trace DNA analysis. Ongoing training and education also provides for a much higher job satisfaction and employee loyalty, in an age where technology has allowed analyses to be robotic and repetitive.

A difference in perception of training between the managers and their staff was noted, for both crime scene and laboratory scientists. 85% of managers suggested that refresher courses in trace DNA were conducted occasionally or in a response to specific need, however 92% of laboratory staff stated they had never received a refresher course. From the responses of managers it appears that the approach to refresher courses is reactive, occurring only when a problem arises rather than as a preventative measure. Employees and employers are equally responsible for ensuring self-learning progress; managers should ensure there are sufficient literary resources and time available, even with obvious time and monetary constraints, whilst the employee must take ownership of his or her professionalism.

In response to the absence of proficiency testing, national bodies could develop and facilitate testing incorporating trace DNA analysis, rather than each laboratory developing separate standards and criteria. Given the random nature of trace DNA analysis, proficiency testing may be difficult to oversee, however the benefits of having some mechanism to ensure that labs are analysing and interpreting in an acceptable manner warrants further investigation of this area. In the past proficiency testing has often been focussed on laboratory staff rather than scene investigators. It would be feasible to test investigators in their swabbing ability to ensure appropriate methodology is used and that the best possible results are achieved. Investigators who regularly give poor results from their casework swabs could be targeted for proficiency testing if laboratories were able to provide accurate statistics for each examiner. This level of results reporting is generally not possible at this stage, however would be an extremely useful review tool.

Several managers stated that their laboratories were conducting research into various areas of DNA analysis, with extraction and typing/interpretation receiving the most attention. Few

laboratories in the region are known to have specific research and development sections or personnel. It was interesting and encouraging to note that laboratories were able to conduct research despite many comments of overwork and lack of time. The benefits of operational laboratories conducting or collaborating in research are to ensure quality and efficiency of methods and results, to ensure that research is relevant and appropriate, and to provide staff with stimulating working conditions that encourage professional development. With the cost of staffing, reagents and instruments being so considerable, research and development is seen as a luxury rather than a necessity and consequently funding can be lean and sporadic. Currently when research is conducted it is disseminated in an ad hoc fashion, often by word of mouth between staff.

2.3.2 Methods and Processes

2.3.2.1 Sampling

Similarities were observed between scene investigators and laboratory staff in terms of their sampling methods. Majorities of both groups stated they rotated swabs continually during swabbing, however a third of scene investigators maintain swabs in a fixed position whilst swabbing, concentrating DNA onto one side. This method of swabbing is useful and effective for bloodstains, but is likely to be less so for invisible trace samples [193]. Laboratory staff were slightly more likely to swab for a longer time than scene investigators, with 27% passing the swab more than ten times over the substrate as opposed to 21% of scene investigators. Brief swabbing of a surface may reduce the chance of successful profiling. Many crime scene investigators also suggested they use a single swab to collect trace DNA, even though it is known that a 'wet and dry' or multiple swabbing method will tend to retrieve more DNA [140, 193, 194, 197]. These results lend support to the need for more and/or better training, and for proficiency testing to identify investigators with poor technique. Lenz et al. demonstrated the importance of efficient sampling methods [56]. They found that in a controlled experiment of vehicle steering wheels with one volunteer sampler the success rate was 86%, whereas a survey of casework steering wheel samples from a range of crime scene staff found an average success rate of 22%.

Cotton swabs may have been so prevalent for historical and/or financial reasons, however there is limited research into their actual efficiency. Van Oorschot et al. [140] found that a significant proportion of DNA collected by a cotton swab is not retrieved during the

extraction phase. Also, the brittle nature of wooden swab sticks may prevent investigators from swabbing with adequate pressure or for an appropriate length of time. It was noted in the 2009 survey that several jurisdictions have switched to foam popule swabs. Likewise, other solvents such as dilute ethanol have been shown to produce better results than sterile water [197, 198, 206], yet sterile water was still most commonly used. A collective approach to determine the most effective sampling method would seem beneficial.

2.3.2.2 Fingerprint examination

The overwhelming majority of crime scene investigators around the region used squirrel hair brushes and regular black and white powders for fingerprint examinations. It is interesting that these methods have such wide appeal, given that in other countries metallic powders and zephyr or feather brushes are far more popular, and have been shown to have a less abrasive affect on fingerprint ridges [207, 208]. However metallic and magnetic powders have shown to inhibit DNA analysis and quantitation methods [134], so it is conceivable that the widespread use of granular powders may be beneficial to trace DNA analysis. In either case, van Oorschot et al. [140] found that powdered samples gave a 25% decline in the amount of DNA retrieved as compared to un-powdered samples. This could in part be due to the action of powdering which may remove DNA-containing material loosely adhered to the surface. Furthermore, the DNA extraction methodologies employed need to remove all powder, as it is known that its presence in the DNA extract can inhibit DNA amplification [140].

Another implication for trace DNA analysis in a legal context may be the length of time powder brushes were kept in use (over six months in 74% of cases), and how rarely they were cleaned. Whilst the risk is minimal, powder brushes have been shown to carry DNA with the potential for transfer between samples [138, 139]. As testing becomes more sensitive and as LCN analysis is becoming routine in other countries [209], the detection of transfer will increase and any potential for contamination should be considered. There is little research in to the effectiveness or appropriate methodology of brush cleaning (although such projects are in planning). Many of the jurisdictions have a division between the fingerprint and biology groups, which could create a knowledge gap and prevent efficient examinations when the evidence types overlap. A multi-jurisdictional multi-disciplinary discussion group into issues surrounding the combination of DNA and fingerprint evidence would be beneficial, leading to a collective approach to examinations and presentation of such evidence in court. The legal

community is becoming more aware of issues surrounding trace DNA analysis, and many questions put to witnesses in court are difficult to answer without strong empirical research and cohesive organisational policy [189].

2.3.2.3 Contamination prevention

The contamination prevention procedures undertaken appeared to be adequate in the most part. Gloves and masks were changed regularly during examinations. Scene and laboratory investigators generally wore additional protection such as overalls or lab coats. The measures taken by scene investigators during trace DNA sampling were comparable to those employed by laboratory scientists. Latex gloves were mostly worn, however, only 26% of scene investigators and 8% of laboratory staff wore two pairs during examinations. A concerning observation is that 19% of scene investigators 'never' wore face masks during trace DNA sampling. 20% of laboratory staff only wore facemasks in certain situations, generally when a sample is malodorous. Only 4% of scene investigators and 49% of lab staff wore hairnets during examinations. The experiments conducted by Rutty et al. [200] demonstrate the contamination that can occur through the general movement, actions and conversation of an examiner when protective clothing is not worn during an examination.

The level of contamination prevention employed by scene investigators during fingerprint examination was considerably lower than that used during DNA sampling. Gloves worn during fingerprint examination may have been kept in use for up to or beyond a week, and facemasks were only worn for specific situations (additional comments suggested this is usually to prevent inhalation of powder rather than prevent contamination). The survey did not question whether the fingerprint examination was undertaken after DNA sampling, and therefore caution would not be necessary. However there is always a chance that an area or exhibit may be considered for DNA analysis in the future, and perhaps greater consideration is needed from fingerprint investigators.

As for sampling methods, intra-jurisdictional variation was observed in contamination prevention procedures, indicating that organisational policies have not been developed or are not enforced. Either methods were not demonstrated clearly in training, or proficiency testing has not corrected lapsed procedures. Whilst some variation in scene examination is necessary to allow for personal preferences and initiative, contamination prevention is one area where strict protocols are essential.

2.3.2.4 DNA analysis methods: Extraction, Amplification and Analysis.

Specific methods used in these stages of analysis were difficult to ascertain, as protocols were not provided by the laboratories. Often sections were left blank regarding details such as precise volumes and times, or varied intra-laboratory, suggesting perhaps that staff did not know off-hand or did not refer to exact protocols.

'Standard' chelex and organic extraction methods were equally popular. A research article has suggested that simple chelex or buffer extraction methods are more effective than commercial kits, and are suitable for automation unlike organic protocols [210]. Incubation time varied little, with most incubating at 56°C for 30 minutes and all at 100°C for eight minutes. Methods of incubation ranged from heatblocks to waterbaths and shaking waterbaths. Responses to vortex and centrifuge times and locations of these in the protocol were variable and difficult to group. Over a third of respondents stated they always used a clean-up method during or after extractions (section 2.2.3.2). Unnecessary use of clean-up methods may result in a loss of valuable DNA in trace samples, and it may be worth investigating whether standard procedures decree that staff always employ clean-up procedures, or if each sample actually demanded it.

This leads into a discussion of the freedom (or lack of) given to staff in the variation of standard methods. Trace DNA samples are notoriously difficult to recover useable profiles from and it would be conceivable that some variation would be necessary to achieve results from the diverse conditions of the samples. 63% of laboratory staff (and at least one from every jurisdiction) were permitted to vary standard extraction procedures for difficult samples. The staff permitted variation did not hold higher education levels or have more experience than those who were not. Far fewer (12%) were permitted to vary standard amplification methods. Only a small proportion of lab staff were utilising extra cycles or other modifications to enhance their chance of acquiring a useful profile from trace samples. It would be interesting to determine if better results could be achieved when scientists are permitted to apply their knowledge and training to analyses. This may cause friction between scientific judgement and accreditation requirements, however if such freedom were to be allowed thorough training and assessment would of course be essential.

DNA analysis was generally found to be similar amongst laboratories. Discrepancies were found in details such as the injection volumes and run times. Minimum height limits for calling hetero- and homozygotes varied between the jurisdictions, but reassuringly not within each jurisdiction. An additional question could have been to ask why these values are set at such, and the extent of validation undertaken to assess the limits. Setting high minimum levels may unnecessarily reduce the opportunity to generate informative profiles.

2.3.2.5 General Practices.

The delay from collection to laboratory submission varied amongst investigators, likewise the time for each analysis step amongst lab staff. Extensive delays in sample collection and/or extraction could limit recovery of high quality DNA. Many of the crime scene sections and laboratories responded that they do not have set protocols but would prioritise samples according to their seriousness. Taking the most common responses of laboratory scientists, on average the analysis of a sample is completed less than three weeks after its receipt. If the time taken from receipt of a sample to its extraction is discounted, the return time is much quicker again. It appears the analysis process is time efficient but the major delay is actually getting the sample to the analysis stage. This step is where staff use discretion to expedite urgent samples, and conversely delay samples from crime types with a perceived lesser value. The survey did not ask how long the reporting phase would take or the time for the result to actually reach investigators, which is often another limiting step.

2.3.3 Results and Opinions.

There were differences in estimates of success rates for particular sample types amongst jurisdictions. An aim of the survey was to identify possible reasons as to differences in success rates between the jurisdictions, and then to evaluate to what extent these differences are associated with the education and/or training received and the processes or methodologies used. However this could not be measured precisely as laboratories either did not record statistics and results or did so in a manner that restricted the ability to cross-compare. Only one manager stated that their laboratory collected detailed statistics, with the majority collecting only ‘general’ or ‘some’ statistics. Several anecdotal comments suggest that laboratory scientists are left to collate statistics themselves rather than having dedicated administrative employees.

The issue of results collation needs to be rectified, as laboratories should be able to provide detailed results to their clients in order to ensure the efficiency and transparency of their service. As mentioned previously, having detailed statistics available could be used to identify training needs, or to develop policies for different sample types (for example after assessing the value of swabbing steering wheels or fired cartridge cases). Results collation and analysis and the ability to compare across jurisdictions would identify improvement opportunities, aid the direction of research and greatly assist laboratory managers in both their staff management and quality of service.

High work-load was a recurring theme amongst the comments of respondents. It is apparent that such caseloads hinder data collection and process review. This in turn negatively affects customer service and the professional development and motivation of staff. This should be an important consideration for managers as they assess finances and resource requirements.

2.3.3.1 Opinions of trace DNA evidence

The regard in which trace DNA evidence is held as evidence in court cases was evenly divided between 'average' and 'highly significant'. Crime scene investigators were the most cynical of the three groups, with several comments stating that trace DNA evidence was insignificant due to budget constraints that prevent such evidence being fully utilised. Several laboratory scientists and managers provided their own 'depends' category. These responders commented that trace DNA is highly significant in terms of application during the investigative stage, but only mediocre if it is needed to be relied upon as evidence in court. This point of view demonstrates a paradigm shift in the way DNA is used in criminal cases. Because of its identifying power, DNA evidence has often been used as a crutch in investigations. As trace DNA often provides only partial profiles it can sometimes be discounted as usable evidence as it may not identify a specific offender. However partial profiles can provide new lines of inquiry where there may be none, and with further investigation may lead to a successful outcome. It is positive that practitioners and managers are recognising this potentially valuable aspect of trace DNA evidence. As technology and procedures continue to improve, along with advancements in the understanding of the trace evidence characteristics (transfer, persistence) of DNA, this type of evidence will become more valuable to investigations in the future.

2.3.4 2009 update

The follow up survey was constructed in a different manner to the 2004 version, and the areas of interest noted from the primary study were targeted. Participants were asked to self-disclose any changes in methods, processes and systems they perceived, and the results of the previous survey were available prior to this update.

2.3.4.1 Training and Education

Several areas of concern have unfortunately not improved in the five years since 2004. Ongoing training and proficiency tests are still extremely limited, disappointingly as a factor noted in the United States review of the use of DNA in volume crime investigation was that "*training appeared to be most effective when it was ongoing*" [109]. This dearth of refresher training is somewhat unexpected as new methods and procedures have been implemented, several of relevance to trace samples (such as swabs and subsequent collection methods) and one would expect that additional training and assessment would be necessary. Additionally in recent years the number of court challenges to aspects of trace DNA evidence has increased [99], and an in-depth understanding of the latest developments and literature in the field may be necessary to investigate and counter these challenges. These findings are echoed around the world; the 2008 Caddy report into Low Template DNA [211] found disparity in the training around the United Kingdom, as it recommended that '*training both laboratory personnel and those involved in the recovery of DNA samples from crime scenes requires to be standardised'.* One of the stressed points in the US National Academy of Sciences (NAS) report into forensic science was the importance of the knowledge base of forensic organisations, both in terms of the baseline requirements of university education and the need for ongoing training and development of scientists [34]. The report recommended that forensic education move beyond the 'apprenticeships' that occur currently to standardised education programs based on scientific principles. The lack of standard, nationally recognised training programs in trace DNA evidence was noted in this survey.

Unfortunately, participants in the Australasian study also reported they had limited time to spend on self-development and research. Some stated that they were happy with this amount of time (19%), but double this number stated they wanted more time than they currently spent. Under-resourcing of laboratories has seen priority placed on backlog reduction and current casework, rather than on training and development. A 'catch-22'

situation results; there is limited time and money to spend on research, but if conducted, research could result in time and monetary savings in the long term by increasing efficiency, service delivery and success rates. Again, the Caddy report found similarly, "*we have become aware that there is a desperate need for independent research funding in order to advance the discipline of forensic science*" [211].

A small percentage (8%) of respondents stated they received proficiency tests in trace DNA annually. It is uncertain whether this was a misunderstanding of the question, and merely refers to the standard DNA proficiency tests that do not contain an assessment of trace DNA analysis. On the other hand if these organisations are conducting proficiency tests specifically designed for trace DNA analysis it would be of interest to determine how this is being undertaken, and how other jurisdictions may be able to adopt similar proficiency testing procedures. Proficiency testing is an integral part of an effective quality assurance program, by ensuring the validity and quality output of standard procedures [212]. With the spotlight on the validity of forensic sciences as a result of the NAS report [34] and the Caddy report, proficiency testing is an important component of demonstrating and upholding the scientific method. This is particularly important for trace DNA analysis where stochastic results often occur, to ensure any variability in results is not due to the operator.

2.3.4.2 Methods, Protocols and Policies

The greatest change in the past five years was seen in the methods used, particularly in the area of robotics. Sampling and extraction methods have also been altered, primarily in response to internal laboratory research and validation. This is encouraging, in that the field is not stagnating but rather current methods are reviewed and new technologies implemented. Forensic organisations are obviously able to invest heavily in instrumentation and have the time to implement and validate new methods. The use of robotics will no doubt increase the capacities of DNA laboratories to deal with large sample numbers and reduce backlogs, whilst also potentially giving staff members more time to fulfil other functions.

Despite the time saving benefits, these methodological changes may or may not have direct influence on the success of trace DNA samples. It appears the impetus driving the technological developments was to increase the capacity of the laboratories and reduce backlogs. As a result, analysis processes have been selected to be more easily automated and with minimal human input, rather than a primary focus on increasing sensitivity or success

rates. In hindsight a probative question which could have been included in the survey is the motivation for technological change; this may have providing a telling indicator of the current focus of the industry, whether for backlog reduction or improvement of success rates. Despite these points, anecdotal comments from participants stated that they were now achieving more success from low level samples. It is uncertain to which process or processes this success can be attributed to. The changes to sampling methods, such as popule swabs and mini-tapes, more directly affect trace DNA samples and may be contributors. The introduction of real-time PCR for DNA quantitation may also assist by reducing the chance of over-amplified products and indicating potentially inhibited samples. Without directly comparable success rates between organisations it is difficult to assess the impact of the different protocols on the final result. What is unknown from the survey is the extent of the studies and validation conducted in the implementation of new methods in each jurisdiction. Little of this has been published or informally distributed between the jurisdictions, and yet such dissemination could save the reinvention of the proverbial wheel.

Minorities of respondents stated there had been a change in the submission policies of trace DNA samples; roughly equal numbers stated increases or decreases in the number allowed to be submitted from volume crime scenes. It was noted however that there was some discrepancy in the responses from individuals in the same jurisdiction, therefore these responses may be based on the perception of the respondents rather than firm policy changes. However from the comments of participants, two jurisdictions clearly had implemented a reduction in the number of trace DNA samples from volume crimes such as stolen vehicles. Around a third of respondents stated that any change in submission policies had resulted from research and validation, a positive finding provided this was thorough and wide-ranging. Whilst pragmatically understandable, a negative outcome for victims of crime and the criminal justice system is the third of respondents stating that the decision to reduce sample numbers was based on cost savings and backlog reduction.

2.3.4.3 Communication and Reporting

Perhaps the greatest deficiency still noted in 2009 was in communication and reporting. The 2004 survey noted that a lack of statistical reporting prevented the comparison of success rates from different evidence types and between jurisdictions, limiting improvement opportunities. This survey found no development in this area. As stated in the US review of DNA evidence in volume crime investigations, "*using DNA evidence to solve property crimes*

requires a level of collaboration among police, crime laboratories and prosecutors that is not routine in many jurisdictions" [107]. It was encouraging that a majority of respondents stated that their organisation had implemented or improved its electronic data management system, yet statistics must still be collected manually. It also appears that the data management systems are not actively used or understood by majorities of staff, as many did not know how or if data collation is performed. Managers were equally likely to be in the dark as to data collation as their staff, and also responded similarly poorly to their satisfaction at the amount of accessible data.

If staff working within DNA laboratories cannot access sufficient data, it seems unlikely that the external users of this service would be happy with the data they receive. Yet 70% of respondents stated results were regularly disseminated to police investigators, whether this is on an ad hoc basis or through computerised systems is not known. It would be interesting to survey police to determine if a similar number report receiving results on a regular basis, and if they are happy with this dissemination. This lack of computerised data management systems evidently results in gaps in the information flow in other areas of the criminal justice system, and there appears to be greater problems than merely ineffective data systems. The frustration felt by many crime scene investigators due to the lack of information and results forthcoming from the laboratories was obvious in their comments. One officer who worked in a small locality commented that he more often learned of the results of the samples he collected through information from the victims of the crime, rather than from the laboratory. Others stated that very little feedback was given to crime scene investigators regarding results, their sampling effectiveness or new research. The ongoing training of crime scene examiners must be performed effectively as they are a crucial point in the analysis chain; they control the quality of sample that will eventually be analysed by the lab, and if they are sampling inefficiently then even the most advanced analysis systems may not redeem the evidence.

Whilst it may seem that effective data collation and dissemination is secondary to the work of forensic DNA laboratories, the primary purpose of these organisations is to assist criminal investigations. The main output is the reporting of DNA links or exclusions. If this is not performed in an effective, efficient, clear and timely manner, their usefulness to investigations will be greatly reduced. Similarly, a lack of statistical analysis of success rates and turn-around times means the organisation cannot prove that it is providing a good

service to its customers (the police, the government, and the community as a whole), and that value for money is being achieved. An absence of data collation will also mean that submission policy development is extremely limited, and the organisation will be hampered in its ability to educate crime scene officers and investigators as to the samples most or least likely to produce a successful result. Finally, cross-jurisdictional comparison is not possible under the current conditions, which greatly hampers endeavours to identify 'best practise' in trace DNA analysis, training and assessment.

The introduction of data collation and analysis systems is vitally important to the effective use of forensic evidence, however most importantly prior to their development organisations should take a step back to conceptualise the flow of information. If factors such as the individuals or groups who need the information, and how often and in what form the information should be reported are not fully understood, the total intelligence value of the information will not be realised. Forensic science has the potential to play a much greater role in national security than in the conviction of individual offenders for 'one-off' offences. Its use in intelligence-led policing is only beginning to be exploited, and as resources are already stretched to their capacity, forensic intelligence capabilities can be slapped on as an afterthought rather than incorporating a ground-up review of the processes and systems to ensure best value is achieved from the investment.

2.3.4.4 Opinions

Despite considerable changes in methods and protocols, the opinions of participants in terms of the significance of trace DNA as evidence did not significantly increase. As previously indicated, several respondents stated that the quality of the results has improved. However as they are now able to successfully profile samples from lower quantities of DNA, mixtures more often result and there is increased complication in the interpretation of such samples. Whilst not statistically significant, some increase in opinion of trace DNA significance was noted between the two surveys as shown in Figure 2-11, page 68. Whether this is due to improved awareness of these samples, because poor performing samples are no longer tested, or because of an improvement in success rates, is not known. An interesting but perhaps unsurprising factor noted was that participants were more likely to think of trace DNA as highly significant evidence in major crime investigations than for volume crimes. This highlights the current focus of forensic science based on criminal law-led applications, as

outlined by Ribaux et al. [69]. Alternatively, the intelligence-led view recognises the value in the application of trace DNA in the disruption of volume crimes, but this introduces resource challenges that are obviously in the forefront of the minds of the respondents to this survey.

2.4 Summary and Conclusions

2.4.1 Conclusions

The survey results provided a useful benchmark of the state of trace DNA analysis (circa late 2004) in Australia and New Zealand. Similarities were noted between sampling, examination and analysis methods and aspects of education, training and data collection. Several issues that were identified include the lack of uniform training courses and proficiency testing, a lack of data gathering and uniform results reporting, and contamination prevention. The one aim of the survey that could not be met was to identify factors that may contribute to differences in success rates of trace DNA analysis. Because jurisdictions do not collate statistics in a comparable manner (if at all), it was not possible to assess the influence that the varying protocols may have on successful profiling.

A common theme from this exercise is the need for an overseeing body to collate research and determine best practice in all areas of trace DNA analysis. The relatively small forensic community present in the region is in an excellent position to provide a cohesive approach, in that despite the large distances between organisations, members are aware of and have good relationships with their interstate colleagues.

The distribution of the 2004 survey results has already triggered some discussion between jurisdictions into protocols and better methods of results reporting. However the 2009 update found that results collation and dissemination is still severely lacking and that only a minority of participants have access to all the data they would like. It appears as though in the past five years the majority of time and investment has been in implementing new technologies such as robotics and associated extraction methods, but extremely limited in other areas. Perhaps the emphasis and investment in the next five years could be placed on promoting organisational changes to improve the communication and exchange of information between all the relevant actors in law enforcement and the criminal justice system. This would include, but not limited to, improving electronic data management

systems to streamline the process of results reporting and increase the amount of information provided to police organisations in a timely manner. Most importantly and prior to any logistical development, organisations should review the integration of forensic evidence data into policing models to realise the potential of forensic science in intelligence applications to national security, not just the conviction of individual offenders. Additionally, investment in research to identify and implement 'best practise' in relation to trace DNA would greatly help to progress the field and increase its usefulness in criminal investigations.

Other areas greatly in need of development are the ongoing training and proficiency testing of both laboratory and crime scene staff. With increased international scrutiny of the field of forensic sciences as a result of a number of court challenges and government investigations, a proactive response from the forensic community to improve its procedures and standardise across jurisdictional borders is far preferable to a knee-jerk reaction to any potential legal challenge in the future.

Chapter 3:

Casework data

Chapter 3: Casework data

3.1 Introduction

Frustrations with the inability to access DNA success rates were noted across the Australasian region in the previous chapter. In many jurisdictions results must be collated manually, and understandably given the high workloads this is often seen as a luxury, falling second to casework. This phenomenon is felt personally by the author, having experienced the difficulty in accessing the results of casework samples, and the lack of information into the viability of certain sample types.

Presumably as a result of the highlighted problems, to date there has been no published review of trace DNA success rates in Australia. It is believed the only paper of this type internationally was a review of New Zealand DNA casework, published in 2008 [213]. This paper analysed the results of 908 samples expected to produce low levels of DNA, and included samples from saliva, as well as 259 swabs of handled items. Across all sample types, full or partial profiles were achieved in 35%. Of the handled items, 24% resulted in a full or partial profile, and 69% gave no profile. The benefit of a similar study of trace DNA samples in NSW was identified during this project.

Another motivation for this chapter was that as experimental work is 'staged', the accuracy of its representation of, and relevance to, casework are often unknown. However in casework as there are so many variables involved, it is difficult to assess the effect of individual factors on the final outcome. To balance the shortcomings of each approach, this project incorporated an assessment of casework data alongside the experimental work.

To assist the interpretation of the research data presented in Chapters 5 to 7, casework data from the NSW Police Forensic Services Group were assessed. 252 trace DNA samples from 201 burglary, robbery and drugs cases were compiled with respect to the type of sample, region where collected, the time lapse between the offence, sample collection and laboratory submission, and the DNA quantity and profile recovered. The samples had been analysed by a private Victorian forensic laboratory from March to June 2008, as has occurred for volume crime cases in NSW since 2007.

The samples were scrutinised according to the region they were collected, to determine if any significant differences occurred between certain areas. Like all Australian states, NSW is heavily urbanised, with 63% of the state's population living in its largest city (Sydney), which makes up only 1.5% of the total landmass of the state [214]. As the country areas of NSW are so remote and sparsely populated, it is often felt that they receive less funding, resources and training support than the Sydney area, where the majority of the population lives. It was therefore hypothesised that there may be differences between the number and results of samples submitted from country and Sydney regions. It was also expected that there might be a more lengthy delay in crime scene attendance and sample submission given the large distances in the country area.

In NSW there is a separation between the response to volume and major crime scenes. Volume Crime Examiners are civilian employees who only attend incidents such as burglary, recovered stolen motor vehicles, or minor theft. They are required to have a science degree prior to employment, preferably in the forensic field. Major Crime Examiners are in the majority sworn police officers, with several civilian employees employed in recent years. They attend all other crime incidents where a forensic response is required, such as murder, sexual assault, and arson. Science degrees are only required of the civilian employees, however all forensic police must complete a diploma in forensic science within five years of their secondment to forensic duties. The data was analysed to determine if there was any difference in the success rates of trace samples collected by each examiner group. Factors affecting these may be the scientific education of the examiner, or the investigative knowledge of police leading to more relevant and potentially more probative sample selection. The examiner groups are trained in trace DNA collection separately by individuals in their own section, which may contribute to variability in recovery rates.

The actual profiles from the casework samples could not be accessed during this study, and the only information available was a single descriptor as to the completeness of the profiles achieved (for example, 'mixture', 'full profile', 'amelogenin only'). Therefore it could not be determined whether the mixtures were interpretable and usable, which is a very limiting factor. As a result, in an effort to prevent a bias in the data and increase the usefulness of the study, steering wheel swabs were excluded from the survey, as they often produce mixed profiles due to high levels of the vehicle owner's DNA being present.

Subsets of the data were analysed in later chapters to provide comparison between certain sample types and the experimental data.

3.2 Methods

The samples had been collected by various forensic examiners from around NSW, using the double swab method described in Chapter 4. The swabs were then stored at room temperature until being sent to the Genetic Technologies Limited laboratory, Fitzroy, Victoria where DNA analysis was performed. At the laboratory, the swabs were stored at room temperature until their extraction using a Qiagen® spin column method on a BioRobot® 8000, and the 40µL extracts stored at -20°C until amplification. The extracts were not routinely concentrated, but if warranted by a review of results were concentrated to 20µL using the Qiagen® DNA MicroKit. The average final amount of extract across the samples was determined to be 40µL. The extracts were quantified using Quantifiler™ real-time PCR, and 10µL of extract (diluted if the concentration >0.125ng/µL) amplified in 25µL 28 cycle AmpFlSTR® Profiler Plus™ reactions. 2µL of the amplified product with 9µL sample mix was run on an ABI Prism 3130*xl* Genetic Analyser, at 5 seconds injection. The samples were amplified even if they gave a negative Quantifiler™ result. The profiles were assessed by qualified biologists within the company, with RFU thresholds of 50 and 250 for heterozygote and homozygote loci respectively. Peak height ratios within loci were required to be 50% or greater to be considered as originating from the same source.

The samples were grouped into six different categories;

1. Firearms
2. Packaging (generally plastic bags used to hold drugs)
3. Tools (screwdrivers, crowbars and other weapons such as knives)
4. Robbery items (bags, mobile phones and other items stolen during street robberies)
5. Points of entry (swabs taken from the points of entry of burglaries or robberies)
6. Other touched items (items or areas touched during an offence, not owned by the offender).

The data was extracted from spreadsheets provided by the DNA laboratory, and the Computerised Operational Policing System (COPS) of the NSW Police Force. The laboratory spreadsheets provided the NSW Police Force case identifier, the DNA quantity recovered, a descriptor of the level of completeness of profiles, and the date the sample was received by

the laboratory. No access was given to the actual profiles or Quantifiler™ data. The individual cases were then inspected on the COPS program to determine the sample and offence types, the region where collected, and the date and time of the offence and sample collection. Statistical analysis was performed using Microsoft Excel™ 2004 and Winks SDA (Texasoft, Cedar Hill, USA) software.

3.3 Results

The entire list of samples is contained in Appendix C.

The average amount of DNA recovered from all samples was 1.7ng in the total extract, with the highest amount recovered being 50.8ng from a mobile phone stolen during a robbery. In 41 samples (16%) no DNA was detected. Figure 3-1 displays the average amount of DNA recovered per sample type. Using Kruskal-Wallis non-parametric analysis and multiple comparisons [215, 216] significant differences were noted between the amounts of DNA recovered from robbery items and the points of entry samples, and between the tools and the points of entry samples.

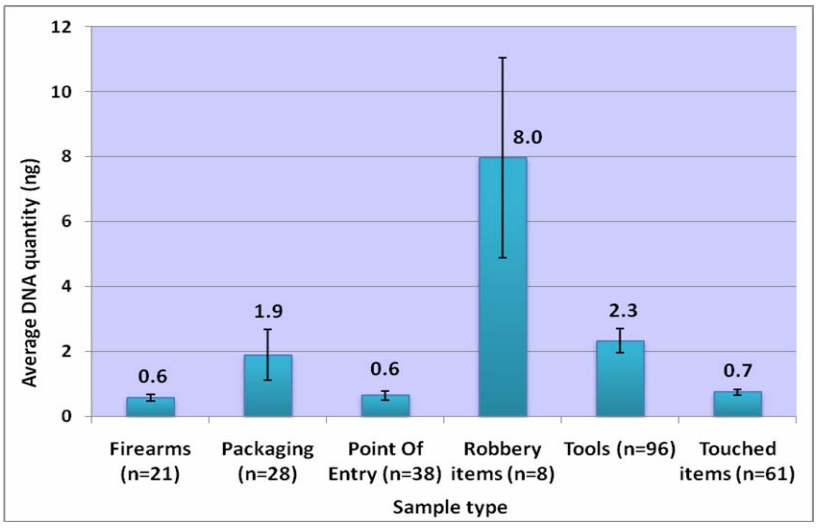

Figure 3-1. Average DNA quantity recovered by sample type. Negative samples were included in the calculation of the mean of each group.

111 of the trace DNA samples did not produce a profile, and only 19 samples gave a full profile. Figure 3-2 shows the level of completeness of the profiles achieved, and Figure 3-3 shows the profiles recovered from the various sample types. Excluding the mixtures, as their usefulness could not be determined from the data, 17% of the samples produced a profile

suitable for inclusion onto the NSW DNA database (ie. containing 12 or more alleles). As expected, the quantity of DNA in the sample did significantly affect the quality of the profile achieved, in that higher quantity samples were more likely to produce a full profile.

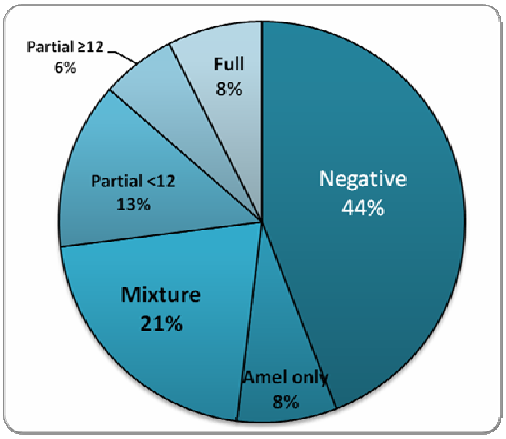

Figure 3-2. Completeness of profiles recovered from the casework data. The partial profiles were categorised as to whether they contained less or more than 12 alleles.

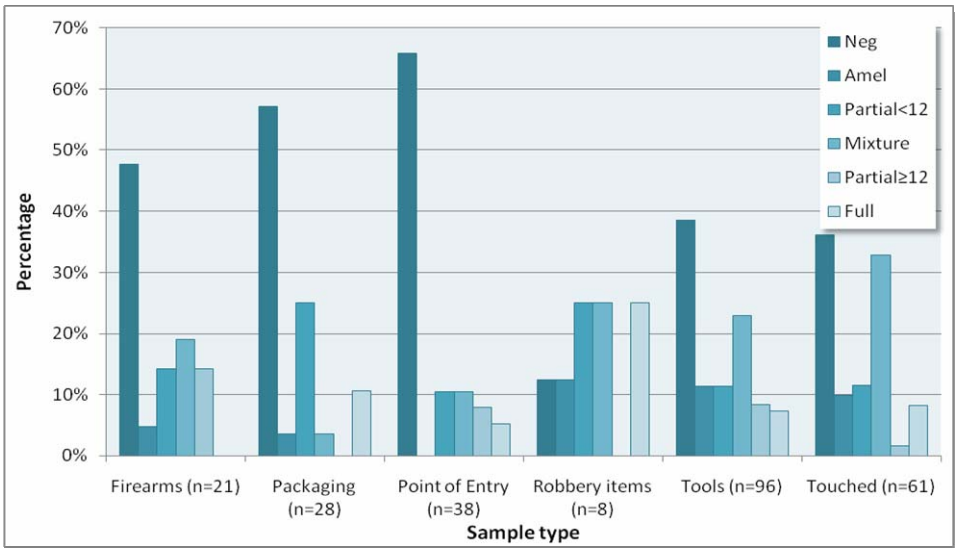

Figure 3-3. Completeness of profiles recovered by sample type.

The samples from points of entry gave the highest percentage of negative profiles, followed by the packaging and firearm samples. The robbery items and tools were the most successful, in terms of quantity and the highest percentage of profiles suitable for database use.

The samples came from 53 different policing regions. 138 samples came from the Sydney metropolitan area and 114 from country areas of New South Wales. Despite the initial hypothesis, no significant difference was noted between these regions in terms of the

number of submitted samples, or the quantity of DNA recovered (Figure 3-5). The majority of the trace DNA samples were collected by civilian Volume Crime Examiners (77%). Whilst the average quantity of DNA recovered from samples collected by volume crime examiners was higher than for major crime (1.8ng as opposed to 1.2ng), this difference was not significant (Figure 3-4).

Also, there were no significant difference in the time between the offence and the sample collection (16 days for Sydney, 17 days for the country areas). Somewhat surprisingly, the samples from the Sydney region took on average 13 days longer to reach the metropolitan DNA laboratory than the more remote country areas (Figure 3-5). This difference was however not statistically significant. The 88 samples that had been collected within one day of the offence were compared against the 51 samples that had been collected over two weeks after the offence, to determine if the time delay introduced any differences. Using the *t*-test, there was no statistically significant difference in the DNA quantity recovered between the two groups (p=0.67) or the completeness of profile (p=0.52).

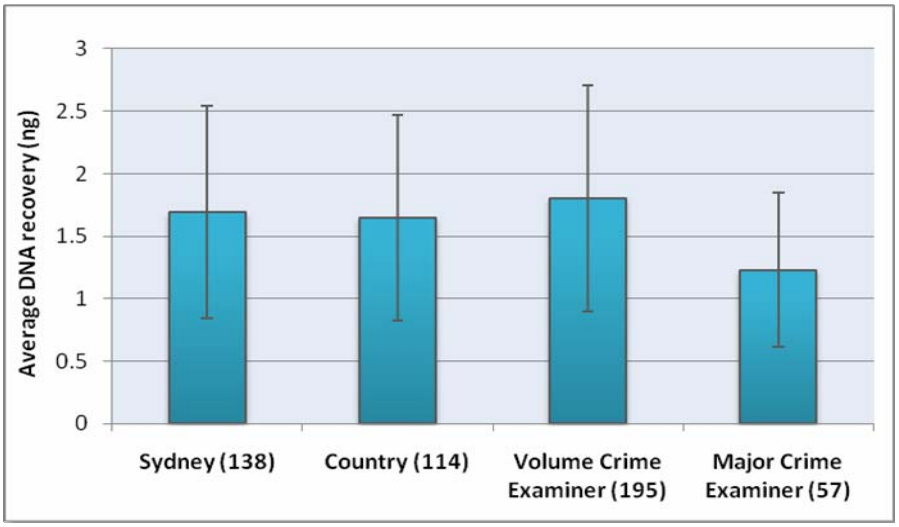

Figure 3-4. Average recovered DNA quantity by location and examiner type.

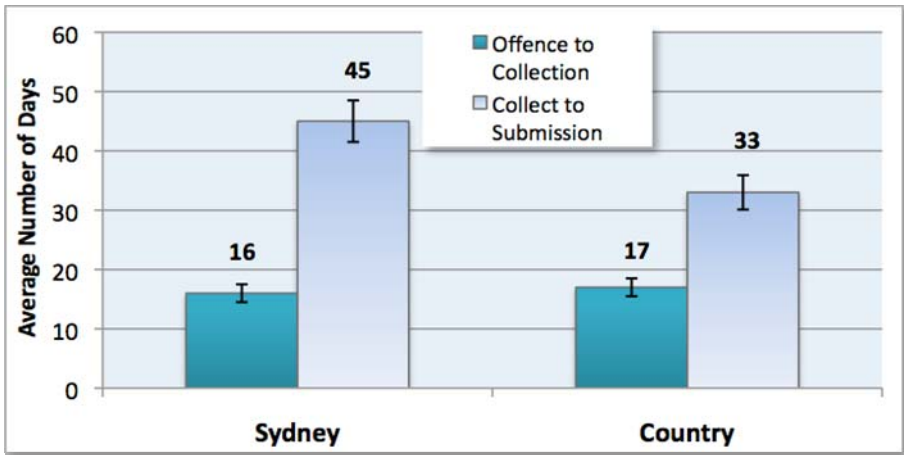

Figure 3-5. Time delays for sample collection and laboratory submission, by location recovered.

Whilst is was not possible to determine how many database hits resulted from these samples, the total number of DNA database 'cold' links from the 9622 NSW samples submitted to this laboratory stands at 3236, or 34% [217]. This includes all sample types, including blood swabs, cigarette butts and trace samples. As of April 2009, there were 304 convictions resulting from these cold links.

3.4 Discussion

The overall level of DNA recovered from these trace samples was quite low. It was a relatively similar result to those obtained in New Zealand in terms of the recovered profiles [213], with no profile resulting from 45% (NSW) and 69% (NZ), and full profiles from 6% (NSW) and 5% (NZ). Likewise, the New Zealand researchers estimated that 20% of 'low level' DNA samples produce a profile suitable for inclusion on a database, found to be 17% in this study. The New Zealand study did not produce quantitation data, so cross-comparison of this aspect is not possible. The fact that the results are so similar is interesting, given that the methods of extraction, quantitation and amplification were quite different between the two jurisdictions. The New Zealand study used an organic extraction method, Quantiblot® quantitation and AmpFISTR SGM Plus™ Amplification, as opposed to the Qiagen® extraction, Quantifiler® quantitation and Profiler Plus™ amplification used in the NSW samples. There is no apparent reason why one jurisdiction would have better quality forensic samples, therefore the methods used in each jurisdiction must be equivalent in their overall effectiveness.

The robbery samples gave the highest quantity of DNA of any group, however only contained eight samples. These samples are from types of items (for example wallets and mobile

phones) likely to be handled regularly by users. It is therefore possible that the DNA recovered from these items may be from the victim rather than the offender; however this could not be determined from the data. Tools were the second most successful sample type, again as expected given these items are thought to be in use and therefore handled for longer periods than other categories. The lowest quantities and least successful profiles were achieved from the points of entry, followed closely by firearms. Whilst the results of the points of entry were expected given the brief amount of time the surface would be handled, it was thought that firearms may have been more successful, as extensive handling is often required during their loading and maintenance. The NSW DNA laboratory (DAL) previously noted low success rates with firearms, which they postulated was due to the oils and lubricants used which may hamper the initial transfer of cells [158].

Mixtures were observed in one out of every five samples. These mixtures may still be useful for evidentiary purposes, particularly if elimination profiles were obtained from victims. If the case circumstances warrant, it may be beneficial to have a notification system in place that requires investigators to collect elimination samples from victims and relevant persons when a mixture is obtained from the crime scene sample. Considering the amount of time and money spent on DNA evidence, a relatively simple task such as this may have the potential to greatly increase the resulting number of useable profiles.

There was a further similarity between the New Zealand and NSW studies in that neither could determine the value of the DNA results to the investigation. The NZ study was able to identify the number of DNA database links generated from the trace samples, finding that around a third of all links resulted from trace samples, which was not possible in this study. The NSW database 'link rate' across all sample types was around 30%, but it could not be determined how many of these were from trace samples. It would seem a relevant exercise to determine how useful the DNA result was to each case, however this would be extremely labour intensive (requiring the scrutiny of each case with the assistance of another police department, review of court transcripts and results and possibly interviewing investigators) and was beyond the scope of this study. A future study could perhaps be dedicated to this cause.

The majority of samples from this data set were expected to come from volume crime scene examiners, as the outsourcing of sample analysis to the private laboratory was restricted to volume offences. However, the collection of trace DNA from volume crimes is relatively

discouraged in NSW, and preferred only from more serious offences in order to limit backlogs. The standard operating procedures for SOCOs state '*the following biological evidence types are **not to be** collected from scenes of volume crime:…. substrates touched by the offender'*, that is, trace DNA samples [218]. The number of trace samples submitted was therefore surprisingly high. The New Zealand study also found the majority of samples to result from volume crime scenes. It is interesting to see that both jurisdictions are allocating such large quantity of resources to volume crime investigation. This is reasonable if best value is being achieved, however considering that NSW does not conduct regular assessments of the results of these samples, one wonders if this funding is utilised effectively.

Another unexpected result from the data is that in many instances it took Sydney personnel longer to deliver samples to the Sydney-based DNA laboratory than their country counterparts. A possible explanation for this is that there is a contracted courier system available to country areas for the regular transport of evidence. Sydney staff must personally transport the samples to the laboratory, a task that can be delayed as other duties take precedence.

The time delay between the offence and sample collection was quite high, at an average of 17 days overall. This result was skewed towards the higher values as the median value was just one day. 89 samples (35%) were collected within 24 hours of the offence, and 169 (67%) within three days. It is believed that the samples with the longest time delay between the offence date and sample collection were from exhibits that had been collected from the scene, but their relevance and the necessity to sample for DNA was not determined until some time after the offence. This action is sometimes only deemed necessary after a court hearing, which may be years after the offence. It was expected that there may be some difference between the quality of samples collected shortly after the offence and those collected some time later, however no difference was noted in the data. This is discussed further in chapter 7.

This study highlighted the difficulties in easily identifying success rates. The data collation could not be conducted automatically by computer systems, and each case had to be manually searched in order to garner the necessary detail, a task that was intensively time consuming even for this relatively small data set. This also leaves the results open to human error and interpretation. A further hindrance was that the data came from two different organisations, and typographical errors, such as case number discrepancies, were regularly

noted between the two systems. This hampered the data analysis and causes concern if the data is be used in criminal trials, however this not currently the case and administrative reviews should prevent such errors reaching the court. It is clear why such statistics are not collected on a regular basis; however the benefit of this data in terms of policy direction (such as recommending the collection of certain sample types over others) and training needs (such as identifying staff with poor sampling technique) is evident. Another use not currently exploited is the ability for crime scene examiners or investigators to electronically check or be notified of the results of crime scene samples. This function would enable quick feedback to investigators and examiners, saving time by eliminating lines of enquiry if there is a negative result and allowing the investigation to proceed in a more timely matter. It was recommended to the organisation that consideration be given to the automation of this data collation and dissemination in future infrastructure upgrades.

The data contained in this chapter will be further dissected in the experimental section, assessing subsets of the data that are relevant to the particular experiments.

3.5 Conclusions

The results of 252 trace DNA samples collected from NSW crime were analysed. The following points arose out of this research;

- The average amount of DNA recovered from trace DNA samples collected in NSW Police Force casework was 1.7ng.
- Full or major (12 or more alleles) profiles were recovered from 14% of samples.
- Mixtures were recovered from over 20% of samples, presenting a case for the collection of more elimination profiles to enable more samples to be used for database purposes.
- There was no significant difference between the amount of DNA recovered from the various regions, or between volume and major crime scene staff.
- The difference in time delays between offence and sample collection, and collection and laboratory submission were not significant between the country and Sydney areas.

- Internationally the only available comparison to this data was from New Zealand, which was found to have similar results in terms of the profiles recovered from trace DNA samples, despite methodological differences.
- The research highlighted the difficulties in collecting data into the success rates of samples. Allowing computerised automation of this process would be extremely beneficial to policy development, training, and investigative usefulness.

Chapter 4:

Methods

Chapter 4: Methods

4.1 Introduction

The technical methods outlined in this chapter were used to conduct the majority of the experiments detailed in chapters 5, 6 and 7. Any variations to these methods or alternative methods are noted in the individual chapters. The methods were selected for their widespread use in Australian forensic laboratories, as established by the Methods Survey. Where possible, standard operating procedures from the NSW Police Forensic Services Group and the Division of Analytical Laboratories were followed. Given this project was conducted on a part-time basis over a number of years, new methods became available in that time and were implemented if in common use.

4.2 DNA Sampling

4.2.1 Double swab method:

As shown by the methods survey, this method is the most prevalent for sampling trace DNA. The double swab method was first published in 1996 [194], and a second study in 2007 [193] demonstrated that a single wet swab is not sufficient to maximise the recovery of DNA. The second, dry swab recovers cells re-hydrated by the wet swab and loosened from the surface. The method is outlined below.

- Sterile water was dropped onto a sterile cotton swab (type 150C, Copan, Brescia, Italy) so that it was completely wet.
- The wet swab was rolled over the surface of interest with firm pressure and using circular motions, traversing over the target area multiple times. If the target area was large, the swab was re-wetted during the swabbing process.
- A second, dry cotton swab was then immediately rolled over the surface using similar pressure and movements as the first swab, ‘mopping’ up all residual moisture on the surface.

4.3 DNA Extraction

4.3.1 5% Chelex method:

Chelex is a chelating resin with the ability to remove cellular components and metal ions from a sample that may interfere with subsequent DNA analysis. Reported in 1989 [219], it is still in common use today given its low toxicity, ease of use and relative effectiveness. However other extraction methods have proven to be more effective when inhibitors are present or for more degraded samples [220]. The method described below is derived from a modified method published in 1996 [221] and the NSW Police Forensic Services Group Methods Manual [222].

- The swab heads were cut from their sticks and teased apart, and both swabs of the double swab pair transferred to a 1.5mL microcentrifuge tube.
- 300µL of 5% chelex (Bio-Rad, Hercules, USA) and 10µL of proteinase K (20mg/mL, Promega Corporation, Madison, USA) was added to each tube, which was then vortex-mixed for 2 seconds. The tubes were incubated at 56°C for 90 minutes.
- After a 10 second vortex-mix, the tubes were then incubated at 100°C for 8 minutes.
- The tubes were then vortex-mixed for 10 seconds, then spun in a microcentrifuge at maximum speed for 3 minutes. The supernatant was then removed to a second tube, and the approximately 10-20µL of extract remaining with the chelex beads was discarded.

4.3.2 20% Chelex method:

The 20% chelex method detailed below is employed by the Division of Analytical Laboratories for epithelial cell extraction [223].

- The swab heads were removed from their sticks, and both swabs of the double swab pair transferred to a 1.5mL microcentrifuge tube.
- 200µL TE buffer (10mM Tris-HCl, 0.1mM EDTA, pH 8.0) and 10µL of proteinase K (20mg/mL) were added to each tube, then vortex-mixed for 2 seconds. The tubes

were incubated at 56°C for 1 hour, then vortex-mixed for 5 seconds, and centrifuged briefly.

- The swab heads were removed and placed into spin baskets in the tubes, then centrifuged at maximum speed for 3 minutes.
- The swabs were transferred to a new tube, and 50µL of 20% chelex added to the remaining extract. The extract was then incubated at 56°C for 30 minutes.
- The tubes were vortex-mixed for 5-10 seconds, and then heated at 100°C for 8 minutes.
- The tubes were again vortex-mixed for 5-10 seconds, and centrifuged at maximum speed for 3 minutes. The supernatant was then removed to a second tube (or if concentrating, into a Microcon® 100 filter unit), and the approximately 10-20µL of extract remaining with the chelex beads was discarded.

4.3.3 Microcon® 100 concentration:

As two swabs are used in the sampling of epithelial cells, a larger volume of extraction fluid is needed to fully immerse both swabs. Given that the amount of DNA present is likely to be small, the extract can be concentrated to a smaller volume, therefore increasing the DNA concentration and the likelihood of its detection. Microcon® 100 filter units (Millipore, Billerica, USA) are used by the Division of Analytical Laboratories [223] and the Australian Federal Police Forensic Biology section [224] to assist with the extraction of trace DNA samples. The method is described below.

- The Microcon® 100 filter unit was pre-rinsed by centrifuging with 100µL of sterile water and then 100µL of TE buffer for 3 minutes each.
- After the final extraction step, the supernatant of the extract was removed to a Microcon® 100 filter unit.
- The extracts were centrifuged at 2500rpm for 10 minutes.
- 200µL TE buffer was then added, and the tubes centrifuged at 2500rpm for 10 minutes. This step was then repeated.

- After the two rinses of the extract, sufficient volume of TE buffer was added to give a final volume of 60µL. The extracts were allowed to stand for 5 minutes, then inverted into new tubes and centrifuged at 2500rpm for 5 minutes.

4.3.4 FTA™ card buccal collection and extraction:

FTA™ cards (Whatman Ltd, Kent, UK) are coated with a proprietary mix of chemicals which act to preserve the DNA present at room temperature, by lysing inhibitors and preventing the growth of bacteria [225]. They provide a simple method for collecting buccal swab DNA profiles from donors, and are used in NSW for the collection of offender and elimination profiles for the national DNA database. The volunteers in this study signed a participation consent form and the collection of DNA profiles was authorised by the UTS ethics committee (03/98A). The following method is as per the NSW Police Force Forensic Services Group Methods Manual [226].

- The buccal swabs were self-administered by participants. The participants were instructed to rub the swab vigorously on the inside of their cheeks and gum line for approximately 30 seconds, ensuring that the swab was heavily coated with saliva. They then pressed one side of the swab firmly onto a circle on the FTA™ micro card, and squeezed so that the saliva was transferred on the card. This was repeated with the opposite side of the swab into the second circle on the card. The cards were sealed inside envelopes marked with the participant's code, and stored at room temperature until extraction. The swabs were discarded.

- Using a 1.2mm Micro-Harris punch and mat, a plug of the FTA™ paper was taken from the middle of the saliva stain and placed into a 0.5mL microcentrifuge tube. The punch and mat were cleaned between samples with methanol.

- 200µL of TE buffer was added to each tube, then vortexed gently and incubated at room temperature for 2-3 minutes. The tubes were again vortexed gently, and incubated at room temperature for another 2-3 minutes.

- The TE buffer was removed, and the wash procedure was repeated. The TE was again removed, and the FTA™ paper left to dry at 56°C. The tubes were then stored at 4°C until amplification.

4.4 DNA Quantitation

4.4.1 PicoGreen® quantitation:

The PicoGreen® dye is a sensitive nucleic acid stain, and is used for the quantitation of double-stranded DNA (dsDNA) in solution. When bound to dsDNA, the mixture emits fluorescence in the range of 502-523nm when excited by 480nm light. The dye is not human-specific, however it has been reported to have a sensitivity to concentrations as low as 25pg/mL [227]. The method below follows the NSW Police Forensic Services Group Methods Manual [228] and the product literature [229].

- On the day of the quantitation, a 200-fold dilution of the concentrated PicoGreen® dye (Molecular Probes® Inc, USA) was prepared in TE buffer (10mM Tris-HCl, 1mM EDTA, pH 7.5) to give sufficient volume for all standards and samples.

- A 2µg/mL stock solution of dsDNA standard was prepared in TE buffer, which was then diluted to give the following standard solutions; 200 ng/mL, 20ng/mL, 2ng/mL, 200pg/mL, 20pg/mL, and a blank.

- 200µL of the diluted PicoGreen® dye and 200µL of the each standard were added to disposable cuvettes, mixed well and incubated for 2-5 minutes at room temperature, protected from light.

- After incubation, the fluorescence of each standard was measured using the Versafluor™ fluorometer (BioRad #170-2402). The fluorometer was 'zeroed' using the blank standard, then the range set by measuring the standard with the highest quantity. The gain was adjusted when necessary to accommodate the lower fluorescence signals. A standard curve was later calculated using Microsoft Excel™ 2004 for each set of experiments.

- 50µL of the experimental samples (taken from the extracts prior to the 100°C incubation, to leave dsDNA) was added to 150µL of TE buffer. 200µL of the diluted PicoGreen® dye was added to each sample, then incubated for 2-5 minutes at room temperature, protected from light.

- The fluorescence of each sample was measured in the same manner as the DNA standard solutions. The DNA concentration of each sample was then calculated from the standard curve generated from the DNA standard solutions.

4.4.2 Quantifiler™ quantitation

The development of real-time PCR chemistry in the past decade has greatly increased the accuracy in quantitation of forensic DNA samples. The method is based on the measurement of the increase in fluorescence between each cycle of amplification, followed by comparison with a standard curve to determine quantity [230]. The Quantifiler™ kit (Applied Biosystems, Foster City, USA) utilises a fluorogenic probe (TaqMan®) that releases a fluorophore when degraded by the Taq polymerase during PCR extension [231]. Synthetic DNA included in the master mix acts as an internal control to allow for the detection of inhibition. The following method is as described by the manufacturer [232].

- The 200ng/µL DNA stock solution was diluted with TE buffer to give eight DNA standard solutions, ranging from 50ng/µL to 23pg/µL. The standards were mixed thoroughly.

- A master mix was prepared by mixing 10.5µL of Quantifiler™ Human Primer Mix and 12.5µL of Quantifiler™ PCR Reaction Mix per number of reactions. 23µL of master mix was transferred to each required well of a 96-well reaction plate.

- 2µL of sample, standard or TE buffer (for a blank) was added to the master mix in the appropriate well. The plate was then sealed using an optical adhesive cover, placed into an Applied Biosystems 7500 SDS instrument, and run using the provided software.

4.5 DNA Amplification

4.5.1 Profiler Plus™ Amplification

The Profiler Plus™ kit (Applied Biosystems, Foster City, USA) enables the simultaneous amplification of nine STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818,

D13S317, and D7S820) with a section of the Amelogenin gene, allowing sex determination [233]. The kit was validated and in use in Australia since the late 1990s [15] and is still the system currently used in Australia for analysis of samples to be included on the national DNA database (NCIDD). The method described below is a reduced volume reaction, validated in 2003 [234].

- 25µL AmpFlSTR® Profiler Plus™ reactions were used to amplify the samples. A master mix was prepared by mixing 10µL AmpFlSTR® PCR reaction mix, 5µL of AmpFlSTR® Profiler Plus Primer Set, and 0.5µL of AmpliTaq Gold™ DNA Polymerase, per number of reactions.

- Up to 10µL of extract (dependent on quantitation, to give up to 1ng of DNA in the reaction) was added to 15µL of the master mix and mixed thoroughly. In the case of FTA card extracts, the entire punch was added to the master mix with 8µL of TE buffer. The samples were amplified using a GeneAmp System 9700 thermocycler, using either 28 or 34 cycles (refer to individual experiments). Positive (AmpFlSTR® Control DNA 9947A) and negative (TE buffer) controls were also conducted per set of reactions.

The use of 34 cycle (or Low Copy Number/Low Template) DNA analysis is not currently common practice in Australian forensic laboratories, and in fact New Zealand is the only jurisdiction in the region to have implemented the practice in casework. This type of analysis requires stringent contamination prevention protocols and interpretation criteria as discussed in section 1.5.4.1. Whilst not utilised in this region for volume crime investigations currently, the technique has been used successfully for such offences in the United Kingdom in recent years. Therefore, the method was employed in this project in order to provide background information should it come into common usage in the future.

4.5.2 Monoplex Amplification

Early in the experimental work of this thesis, quantitation systems were not available. A screening method was required to determine which samples would be likely to produce a profile using Profiler Plus™. A monoplex kit utilising the D5S818 locus and JOE fluorescent

dye (Promega Corporation, Madison, WI) was used to screen samples, and if positive with this system they were then amplified with the Profiler Plus™ system.

- 25µL reactions were used to amplify the samples. A master mix was prepared by mixing 10µL nuclease-free water, 2.5µL Gold Star 10X buffer, 2.5µL of Primer mix, and 0.1µL AmpliTaq Gold™ DNA Polymerase per number of reactions.

- 10µL of extract was added to 15µL of the master mix and mixed thoroughly. The samples were amplified using a GeneAmp System 9700 thermocycler, using either 28 or 34 cycles (refer to individual experiments). Positive (AmpFlSTR® Control DNA 9947A) and negative (TE buffer) controls were also conducted per set of reactions.

4.6 Analysis

4.6.1 DNA analysis

The analysis of the amplified DNA occurs by the detection of the dye-labelled fragments of the Profiler Plus™ amplification, and a common method used is capillary electrophoresis. A dye-labelled size standard (GeneScan™ 500 ROX™) is included with the sample mix to enable the sizing of the sample fragments. Current is applied to move the samples along the capillary, and they are electrophoretically separated as they travel through the polymer in the capillary. A laser excites the fluorescent dye labels through a detector window at the end of the capillary. The emitted fluorescence captured by a CCD camera in digital form, which is then analysed by the provided software. The following method for the preparation of samples to be loaded onto the 310 instrument is from the NSW Police Forensic Services Group Methods Manual [222].

- 1.5µL of the amplified product was added to 25µL of deionised formamide and 0.5uL of GeneScan™ 500 ROX™ Size Standard.
- The mix was then denatured at 95°C for 3 minutes, and incubated at -20°C for a further 3 minutes.
- The samples were run for 30 minutes on an ABI Prism 310 Genetic Analyser, with 5 seconds injection. The results were analysed using the GeneScan™ and Genotyper™ software (Applied Biosystems, Foster City, USA).

- The relative fluorescence units (RFU) cut off values used were 50RFU for heterozygotes, and 75RFU for homozygotes. It should be noted that these cut off values are lower than those generally employed in casework.

4.6.2 Data analysis:

Statistical analysis of data collected from the methods survey, the casework data study, and the experimental work was performed to determine any statistically significant relationships or differences. To facilitate this, linear regression and *t*-test analyses were performed using Microsoft Excel™ 2004. One way analysis of variance (ANOVA) and Newman-Keuls multiple comparisons were performed using WINKS SDA 6.0 software (Texasoft, Cedar Hill, USA).

Chapter 5:

DNA Abundance

Chapter 5: DNA Abundance

5.1 Introduction

This chapter contains the details of a study investigating the background levels of DNA at crime scenes, to determine if there is a 'baseline' over which a profile may be interpreted. The extent of the contribution pre-existing DNA traces make to profiles recovered from scenes has yet to be fully investigated. There are limitless scenarios encountered in forensic casework, so to focus the experiment the two volume crime types of burglary and robbery were chosen. Similarly to studies investigating the background levels of other trace evidence such as glass or fibres on certain surface types [75, 77, 78, 80], this experiment aimed to provide data to be used in the denominator of a Bayesian formula, that is, the likelihood of finding an exploitable DNA profile at a crime scene by chance.

This chapter presents the methods and results of the two experimental sections separately, leading to a joint discussion of the results and conclusions.

5.2 Abundance – Burglary

Good sources of DNA, such as blood and saliva, are only encountered and recovered from a small percentage of volume crime scenes. Of the 28 600 burglaries attended in the Sydney metropolitan area in 2008, blood was recovered from 3-4% of scenes [111]. In order to increase the number of volume crime scenes where DNA may a be useful investigative tool, the Pathfinder study in the United Kingdom incorporated the collection of trace DNA from items such as tools and weapons that the offender left behind at the scene [101]. This doubled the percentage of scenes yielding DNA evidence from 6% to 12%. Fingerprints, however, were recovered at 28% of scenes, and in NSW are recovered at approximately 19%. In addition, these figures comprise only the fingerprints that were deemed to be of sufficient quality for comparison. The number of scenes where smudged finger and hand marks are located is likely to be much higher, as observed by the author in casework. At present the collection of swabs from these smudged marks is not permitted in the standard procedures of the NSW Police Force [218]. However there is a potential for this previously unusable evidence to become of use to investigations.

Conceivably, a good site for trace DNA sampling would be a location most likely to have been handled by the offender, in a low traffic area not regularly accessed by the occupants. However, the environmental survey of DNA levels in dust at a university found that human DNA was present even in low traffic areas [144]. This experiment aimed to determine the background level of human DNA in various residential locations, and whether this could interfere with the recovery of suspect profiles. As a result it was hoped that areas suitable for targeting offender's DNA might be identified.

5.2.1 Burglary Abundance - Method.

The experimental work into the level of background DNA on burglary surfaces took place in three parts.

1. An initial survey was conducted of 95 burglary offences in the inner Sydney area to determine which areas would be the most suitable place for trace DNA collection with the intention of identifying the offender, and the most common points of entry. The survey was completed by three Scenes of Crime Officers based in the Redfern Local Area Command.

2. The second section comprised experimental work and was conducted in 2004, at which time the quantitation methods later employed were not available or in common use. 29 residential premises were volunteered by tenants, and consisted of 12 units and 17 freestanding or terraced houses in a number of inner Sydney suburbs. The tenants completed a brief survey providing the following information;

- How many tenants reside at the address?
- How long have the current tenants lived there?
- Approximately how many visitors have attended the address in the last week?
- Approximately how many times in the last week has the target location been touched or accessed, and by how many people?
- How long ago was the target location cleaned and what was it cleaned with?

The surface type and material at the points of entry were also recorded.

Four to five locations in each of the premises, identified as common burglary entry points by the first section of this project, were then swabbed using the double swab method. Figure 5-1 shows examples of these locations. The swabs were extracted with the 5% chelex method

and concentrated using Microcon® 100 concentrators to approximately 60µL. The 20% chelex extraction method used by the NSW DNA laboratory (DAL) for trace samples was not used in this primary experiment, as it had not been disclosed to the author at this point.

As no quantitation method was available, the samples (n=150) were screened using a Promega monoplex D5S818 reaction at 28 and 34 cycles. Samples that gave a positive result with the monoplex amplification were then amplified in 34 cycle Profiler Plus™ reactions.

3. The third, smaller experiment was conducted when the Quantifiler reaction became available, in order to estimate the quantity of DNA present at common entry points. In addition the 20% chelex extraction method was used, with Microcon® 100 concentration as previously. Five residential premises were sampled in the same manner as the previous experiment, and surveys completed. The resulting 20 samples were extracted and quantitated, and samples showing that DNA was present were amplified in 28 and 34 cycle Profiler Plus™ reactions.

Once the samples were profiled, where possible buccal swabs were collected from the tenants of locations that gave positive samples. Extraction and amplification blanks were conducted during both experiments.

Figure 5-1. Examples of sampled entry points. The yellow labels (placed after the swabbing was completed) indicate the specific areas of swabbing.

5.2.2 Burglary Abundance – Results.

1. Initial Survey:

The first component of the initial survey of 95 residential burglaries asked the SOCO to list the area they determined most suitable for DNA collection, from their assessment of the scene and knowledge of DNA evidence. At 62% of the burglaries, the most suitable surface for DNA collection was deemed to be at the point of entry. The areas deemed most suitable for DNA collection that were not at the point of entry included jewellery boxes, an ashtray, a fence, and a candy wrapper. Other items which would be expected to be useful such as tools or clothing items left behind by the offender were not encountered at these burglaries.

At 9% of the burglaries there was no suitable surface for DNA collection identified; for example the offender entered through an open door, and therefore did not have to touch anything other than the stolen item. Only at one burglary was there another source of DNA present other than trace, in this case blood.

The second component of the survey assessed the points of entry of the burglaries (Figure 5-2). Nearly half were through a window, and 29% through a door.

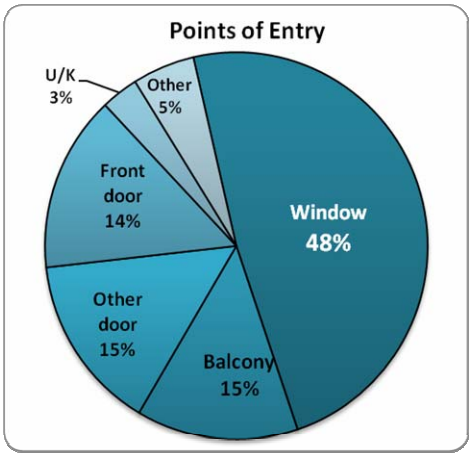

Figure 5-2. The location of points of entry from 95 residential burglaries

From these figures, it was determined that at each volunteer residence front, side or rear doors, and at least two windows or a balcony rail (if available) would be swabbed, adapted according to the characteristics of the individual premises.

2. Primary experimental work:

The 29 premises ranged from one to five tenants, and most tenants (75%) had resided there for more than one year. The sample locations were rarely recently cleaned (20%). The surface types were mainly painted or lacquered wood, aluminium frames, and plastic or metal handles.

A total of 150 locations were swabbed. 92 of these swabs were amplified using the monoplex kit at 28 cycles, however all proved negative. All 150 samples were then amplified using the monoplex kit at 34 cycles, and 46 produced alleles. These 46 samples were then amplified at 34 cycles in the Profiler Plus™ reaction, and 39 (26% of the total 150 samples) produced alleles. The 39 positive samples came from 20 different residential premises. Figure 5-3 and Figure 5-4 display the types of profiles recovered, and the location of the positive samples.

3. Secondary experimental work:

The five premises were occupied by either two or three tenants, ranging from one month to 32 years residency. Some of the surfaces had been cleaned one week prior, others never. The surfaces types were mainly painted wood, with some aluminium frames.

7 of the 20 samples (35%) were negative. The average quantity was 3.35ng in the total extract, and doors averaged 6.05ng, and windows just 0.05ng. All doors (n= 11) gave a positive result, only two of the nine (22%) windows did. This result is not statistically significant (p=0.08, *t*-test for unequal variances) but may prove to be if more samples were included.

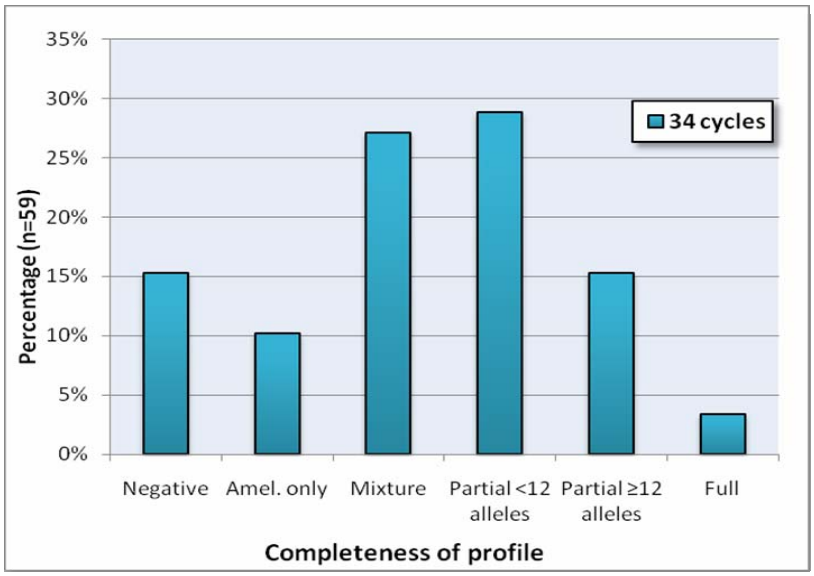

Figure 5-3. The types of profiles recovered from residential points of entry, at 34 cycle amplification

Figure 5-3 shows the types of profiles recovered at 34 cycles from the 59 samples collected during both experimental sections. Of the 13 samples amplified at 28 cycles in the second experiment, seven were negative, four showed the Amelogenin locus only, and the remaining two were partial profiles. Larger molecular-weight loci were less likely to be present in the profiles; for example alleles at the locus D18S51 appeared in just 11% of the profiles, compared with 74% for the smaller locus D3S1358.

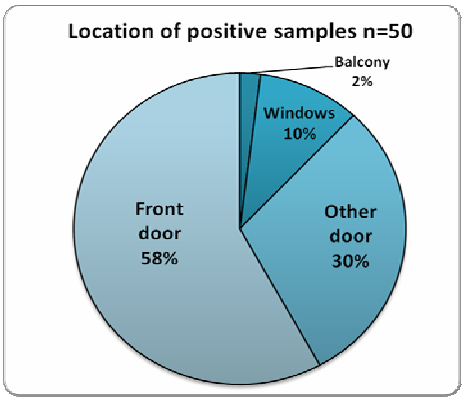

Figure 5-4. The location of positive samples from residential points of entry, at 34 cycle amplification

The majority of positive samples from both experimental sections came from a door (88%) as shown in Figure 5-4. In total, between the two experiments there were 50 positive samples (29% of the total 170 samples collected). The 50 positive samples came from 25 different premises.

Linear regression analysis (Microsoft Excel™) was conducted to determine if there was a correlation between the number of alleles in the Profiler Plus™ amplifications of both experiments and the following factors:

- The number of tenants
- The number of visitors
- How many times the surface had been handled
- The number of people who had handled the surface
- The length of residency
- The time since cleaning of the surface

This information had been self-disclosed by the volunteers in the survey. There was no evidence of a linear relationship between the number of alleles in the Profiler Plus™ profile and any of these factors (p values ranged 0.06 – 0.74), except for the number of tenants (p=0.008). However unexpectedly this was a negative relationship, in that the number of alleles decreased as the number of tenants increased ($R^2 = 0.12$).

Buccal swabs were obtained from the tenants of 13 of the 25 residences from which positive samples were recovered. The remaining volunteers either declined to provide a buccal swab or were unable to be contacted. 42% of the profiles recovered from these 13 premises showed alleles foreign to the residents (34 alleles in total, being 6% of the total number of alleles). 88% of the foreign alleles came from either a front door (47%) or another door (41%), and the remainder were found on a window and a balcony rail. There was no significant correlation between the number of visitors to the residence and the number of foreign alleles.

5.3 Abundance – Robbery

This component of the research is similar in premise and design as the previous; this time using the crime scenario of street robbery, or mugging. A pilot survey of 2892 robberies in the Sydney metropolitan area in 2008 found that personal items such as cash, credit cards, bags and mobile phones were stolen in 69% of occasions. Force was used in two thirds of robberies. Anecdotally it is known that bags and wallets stolen during a robbery may be recovered some time after the event, either dumped near the location of the robbery or even found in a search of suspect premises or vehicles [235].

Given that force is used in the majority of robberies, which would be expected to facilitate DNA transfer, it would seem feasible to submit recovered stolen personal items for DNA analysis. However, as in the previous experiment, the extent at which the background DNA of the victim may overwhelm any DNA transferred by the offender is unknown. If background DNA is likely to interfere with transferred 'offender' DNA in the majority of cases then it may not be an effective strategy to test this evidence.

In this study the background level of DNA on 20 personal items (wallets, purses and bags) was assessed. Two areas on each item were sampled, to ascertain whether particular areas have more or less DNA present. The two sampled areas were categorised as 1; the area used to carry the item (for example the handle or strap of a bag, or the overall exterior of a wallet or purse), or 2; the opening area of the item (whether zips, buttons, or the edges of the opening flap).

5.3.1 Robbery Abundance – Method.

20 volunteer subjects were asked to supply a personal item commonly stolen during a street robbery (for example a wallet, purse, handbag or backpack). The volunteers completed a brief survey prior to the experiment, which asked the following questions;

- How long have you owned the item?
- How often do you use the item?
- Does anyone else use the item, or has owned the item? If so, when was the last time they used it?
- How do you carry the item when you use it?
- Do you ever clean the item, and if so, when was the last time it was cleaned?

The type and material of the item were also recorded. The items were then swabbed using the double swab method in two locations as specified previously. Buccal swabs were collected from participants, and stored on FTA™ cards.

The swabs were extracted with the 20% chelex method and concentrated using Microcon® 100 concentrators to approximately 60µL. The extracts were quantitated using the Quantifiler™ reaction, and amplified with 28 and 34 cycle Profiler Plus™ reactions.

Extraction and amplification controls were also conducted.

5.3.2 Robbery Abundance – Results.

Eight bags and twelve purses or wallets were sampled during the experiment. Twelve of the items were leather, six were PVC or a similar synthetic material, one was canvas, and one was a combination of leather and vinyl.

The items had been owned from three months to thirty years, and most (80%) were used every day or several times a week. All of the items were owned and used solely by the volunteer, except for one, which belonged to the husband of the volunteer and had been borrowed for a weekend.

DNA was recovered from every item, with an average of 7.5ng and ranging from 0.9ng to 28.1ng in the 60µL extract. Figure 5-5 and Figure 5-6 show the amounts of DNA recovered from bags versus wallets and purses, and the carrying versus opening area.

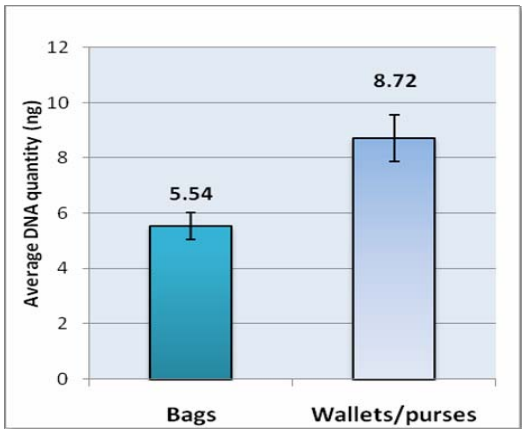

Figure 5-5. Comparison of the DNA recovery from bags versus wallets and purses.

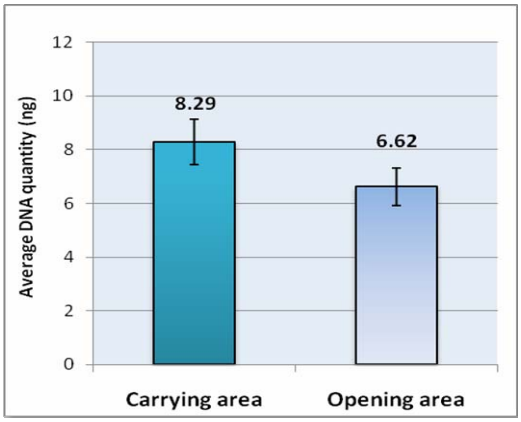

Figure 5-6. Comparison of the DNA recovery from the two sampled areas.

A preliminary test for the equality of variances for each of the comparisons was conducted, to determine the appropriate *t*-test to apply. Whilst the wallets and purses were found to have a larger amount of DNA present, the difference was not statistically significant using the *t*-test for unequal variances (p=0.1). Likewise, the difference between the areas swabbed was not statistically significant using the *t*-test assuming equal variances (p=0.5).

The items made of leather did not return significantly less DNA than other items (p=0.9, *t*-test assuming equal variances).

One-way ANOVA was performed to test whether the various methods of carrying the items had a significant effect on DNA recovery. The only significant difference (p=0.05) was noted between items that were carried in a pocket and in hand, and those carried over the shoulder, with average quantities of 13.7ng and 4.3ng respectively. No significant differences were found between groups according to how often the item was used.

Figure 5-7 shows the average amount of DNA recovered from the items according to how long they had been owned. Despite showing some positive correlation, linear regression analysis proved it was not statistically significant (p=0.06).

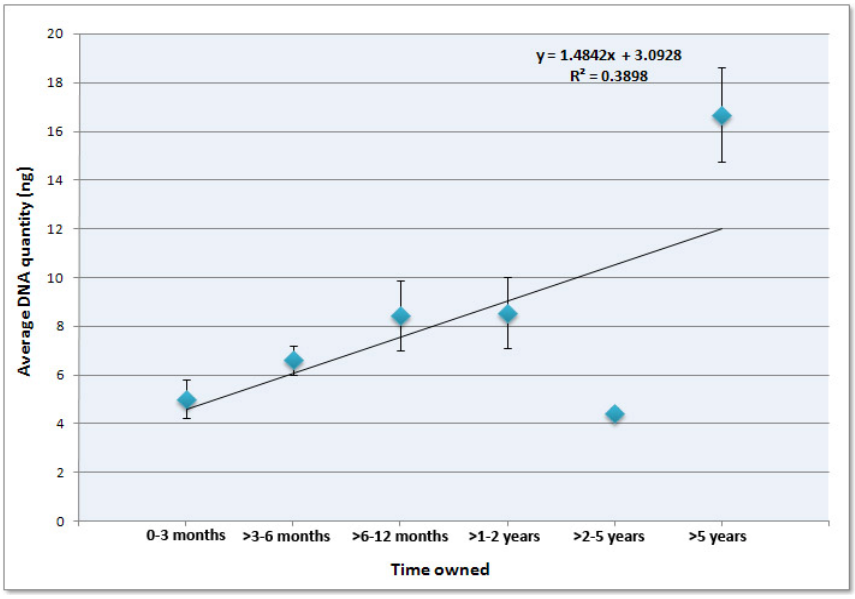

Figure 5-7. The amount of DNA recovered from personal items versus the length of time owned

The level of completeness of profiles recovered from the items is displayed in Figure 5-8, showing that the majority were partial profiles.

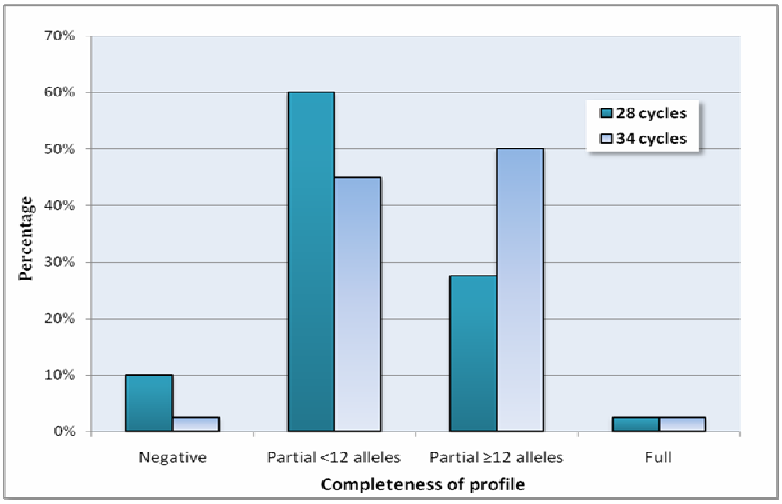

Figure 5-8. The level of completeness of profiles recovered from the personal items, at 28 and 34 cycle amplification

Every profile recovered was found to have the majority of alleles in common with the owner of the item. However, alleles foreign to the owner were found in 30% of the profiles at 28 cycles, and 48% of the 34 cycle profiles. There were 32 'non-owner' alleles in the 28 cycle profiles (8% of the total number of alleles), and 56 non-owner alleles in the 34 cycle profiles (12% of the total number of alleles). The number of extraneous alleles per profile ranged from 1 to 15, with an average of 3.2 alleles. Across all of the profiles the average number of extraneous alleles was 0.8 alleles (28 cycles) and 1.3 alleles (34 cycles). One bag accounted for 35% of the extraneous alleles, and this was the item that had been borrowed. However the regular user of the bag could be associated to only 11 of the 31 non-owner alleles in the 28 and 34 cycle profiles from this item. The profiles from this item were the only complex mixtures recovered, in all others the owner's profile could be readily established.

5.4 Discussion.

From the results it can be seen that there is a baseline level of background DNA present on typical surfaces encountered in forensic examinations. The amounts of DNA vary however, and as expected personal items such as bags and wallets hold more DNA than 'exposed' surfaces such as doors and windows. The average amount of DNA recovered during the robbery experiments was 7.5ng, more than double the average amount recovered from the burglary experiments (3.35ng). Again as expected, doors returned more DNA than windows.

Other factors that were expected to influence the amount of DNA recovered were not found to have a significant impact. The number of tenants or visitors, the times the surface had been handled, and the length of residency did not significantly increase the number of alleles recovered from the residential surfaces. The surface material of the robbery samples was equally insignificant, with leather items returning a similar quantity of DNA as synthetic materials. Leather is thought to be a PCR inhibitor [45], and so it was envisaged that leather bags and wallets may return inferior results. The only factor found to affect DNA recovery to a certain extent was the method of carrying, with items carried in the pocket and hand returning more DNA than those carried over the shoulder. A positive correlation was noted between the length of time the item had been owned and the quantity of DNA recovered, however this was not statistically significant.

A limitation of this study is that a quantitation reaction and the standard extraction method for trace samples were not available at the time the primary burglary experiment was conducted. It is therefore possible that negative samples in the first experiment may be due to inhibition rather than a low level of DNA, as no assessment of inhibition was possible. The quantitation data from points of entry is limited by the smaller number (20) tested in the secondary burglary experiment. The results of the primary experiment indicated that background levels of DNA on points of entry were not of concern when using 28 cycle PCR, but more so with 34 cycles. However alleles were recovered using 28 cycles in the second component of the experiment using the 20% chelex extraction and microcon concentration methods, indicating that the 5% chelex extraction method used in the primary experiment may not recover the same quantity and/or quality of DNA. Therefore background levels may prove to be an issue with 28 cycle PCR when using other extraction methods.

An aim of this part of the research was to determine if certain areas regularly hold lower levels of background DNA, and therefore could be targeted for sampling at crime scenes. For burglary offences, it is apparent that windows present the best option for trace DNA sampling. They comprise nearly half of the points of entry (Figure 5-2), and yet hold much less background DNA than other entry points. Just 50pg of DNA was recovered on average from windows. The personal items tested in the robbery experiment did not provide this clear distinction however, as the two areas targeted (‘carrying’ and ‘opening’) returned similar levels of DNA. Likewise, there was no significant difference between the two types of items swabbed; bags versus wallets and purses. A factor for consideration is that alleles at the larger molecular weight loci were rarely seen in the background DNA recovered from

residential premises. If a profile is recovered from a scene with these loci present, it may provide an indicator of a recent contact, rather than background DNA. Further work could be undertaken in this area to investigate this finding in more depth.

The most evident outcome of this study is that if trace DNA is to be targeted, elimination DNA profiles should be collected from victims wherever possible. The majority of the alleles present in background level DNA were found to be from the tenants or owners, and with elimination profiles the samples may still be interpretable and suitable for use on the database. However to complicate matters, small amounts of non-owner/resident DNA are present in around a third of cases. When there is extraneous DNA present there is an average of three alleles, which would seem insufficient to cause significant interpretative issues but to be considered nevertheless. These findings concur with previous research, where foreign alleles were found to be present on the skin [154] and under fingernails [146] of volunteers. It cannot be assumed that any foreign DNA present on a surface must belong to the offender.

This point is echoed in the casework data described in Chapter 3, where mixtures resulted from over one in five of the samples. These mixtures may be due to more than one offender handling the item, but can also possibly result from background traces of the victim present on the surface prior to the crime. Elimination buccal swabs from the victims may increase the ability of these profiles to be entered onto databases with the hope of identifying the offender.

Whether the amount of DNA transferred during the action of these crimes will be sufficient to be detected over the underlying background DNA remains to be seen, and will be investigated in the following chapter.

5.5 Conclusions.

5.5.1 Burglary

The baseline level of DNA from point of entry locations is low when using standard cycle numbers, but may become an issue if extended cycle regimes are employed. The majority of background DNA on entry points arises from the residents, not visitors, however small amounts of ‘non-resident’ DNA may be present on these locations.

If trace DNA is to be targeted at residential burglary scenes, windows (if utilised as an entry point) may be good surfaces for DNA sampling at burglary scenes, and conversely entry doors are relatively poor surfaces given the abundance of DNA present. Larger alleles are rarely present in background levels, and may provide an indicator of recent contact rather than background DNA.

5.5.2 Robbery

The levels of background DNA on items commonly stolen during a robbery could impact on the recovery and interpretation of offender DNA. There was no significant difference in DNA levels between the opening and carrying areas of the items. If these items are to be targeted for trace DNA evidence, it is possible that recently purchased items will produce less background DNA.

As an added complication, small amounts of 'non-owner' DNA are commonly present on these items, and therefore it cannot be assumed that 'non-owner' alleles belong to the offender. Elimination buccal swabs should be collected from victims and other legitimate parties wherever possible to ease the interpretation of the resulting profiles.

Chapter 6:

DNA Transfer

Chapter 6: DNA Transfer

6.1 Introduction

There have been a number of studies investigating DNA transfer, with conflicting results [35, 42, 149, 151, 152, 156]. There appear to be many variables involved in the transfer of DNA by skin contact, including the contact surface, the duration and type of contact, and physical characteristics of the donor skin. A comprehensive study of DNA transfer encompassing all potential variables is practically impossible. For this reason, this study empirically focussed on the context surrounding two specific crime types. The number of variables is thereby limited, with the hypothesis that the resulting data may be used in a Bayesian interpretation of trace DNA within the particular crime types, to assess the likelihood of trace DNA evidence given suggestions of particular transfer actions by either the prosecution or defence.

This chapter is presented in the same format as the previous, and presents the methods and results of the two experimental sections separately, and then discusses the results and conclusions concurrently.

6.2 Transfer - Burglary.

The previous chapter investigated the level of background DNA present on the surfaces of residential point of entries, and found the level was not insignificant. This experiment seeks to answer the questions; how much DNA is likely to be transferred during the act of breaking into a home, and will this be sufficient to be detected above the level of background DNA?

The level of DNA transferred during a burglary may be linked to the amount of force and effort required to enter the property. The recent study by the National Institute of Justice in the USA found that "*crime scenes in which the property was unlocked (and therefore did not require the suspect to break a window or pry open a door) were less likely to yield a probative sample*" [109]. Research suggests that a burglary entry would not take longer than 60 seconds [236]. For consistency across the experiment, the methodology in this project assumed a forced entry of a door surface taking 30 seconds.

Previous DNA transfer studies have controlled the 'hand-washing status' of participants, as one study found that a time period of 15 minutes post hand-washing gave the greatest variance in amount of DNA transferred [151]. In this experiment, participants were not specifically asked to wash their hands prior, but were questioned as to the last time they had. This was to enable a more accurate representation of the general population.

In order to compare the experimental data to real samples, a subset of 38 samples from the casework data in chapter 3 was selected. In each of these cases the sample was known to have come from the point of entry of a volume crime offence. The data was scrutinised to assess the level of DNA transfer in casework situations.

6.2.1 Burglary Transfer – Method.

20 volunteer subjects, 10 male and 10 female, participated in the experiment, ranging in age from 23 to 94 years. The subjects completed a brief survey prior to experiment, answering the following questions;

- When did you last wash your hands?
- What did you wash your hands with? (For example water only, hand soap and water, or other soap)
- What skin type are your hands? (Either dry, oily, normal or sensitive)
- Do you have any skin conditions on your hands such as dermatitis?

The volunteers were asked to forcefully grab onto a door surface for 30 seconds in a simulation of a burglary entry. The surface was cleaned prior to the experiment with 10% bleach and 70% ethanol. Several different door surfaces were used in this experiment, selected to be most convenient to the volunteer, however all were a similar painted or lacquered wood surface. Each volunteer participated only once during the experiment.

The surface was swabbed using the double swab method immediately after the burglary simulation, to negate any effect of persistence of the DNA. The surfaces were cleaned between 'grabs' if more than one volunteer was grabbing that surface occurring during a specific session. Buccal swabs were collected from the participants, stored on FTA™ cards. Surface blanks were taken from the surface using the double swab method, after cleaning and prior to handling by the volunteer.

The swabs were extracted with using the 20% chelex method, and concentrated using Microcon® 100 concentrators to approximately 60µL. The extracts were quantitated using the Quantifiler™ reaction, and amplified in 28 and 34 cycle Profiler Plus™ reactions. Extraction and amplification controls were also conducted.

6.2.2 Burglary Transfer – Results.

Seven of the volunteers stated they had dry skin on their hands, ten believed they had normal skin, one sensitive, one oily, and one between dry and normal. Two of the volunteers had a 'bit of dermatitis' on their hands, and one stated to have eczema.

The time since hand washing ranged from as recently as five minutes up to four hours prior to the experiment, using in the majority either hand soap and water (60%) or water only (25%).

DNA was recovered from 19 of the 20 transfers. The quantity ranged from 0ng (29 year old male, normal skin type, 30 minutes since washing) to 10.9ng (23 year old female, normal skin type, unknown time since washing). The average amount transferred was 2.5ng. Figure 6-1 displays the completeness of profiles achieved at 28 and 34 cycles. The majority of profiles contained 12 or fewer alleles; however two full profiles were recovered after 34 cycle amplification.

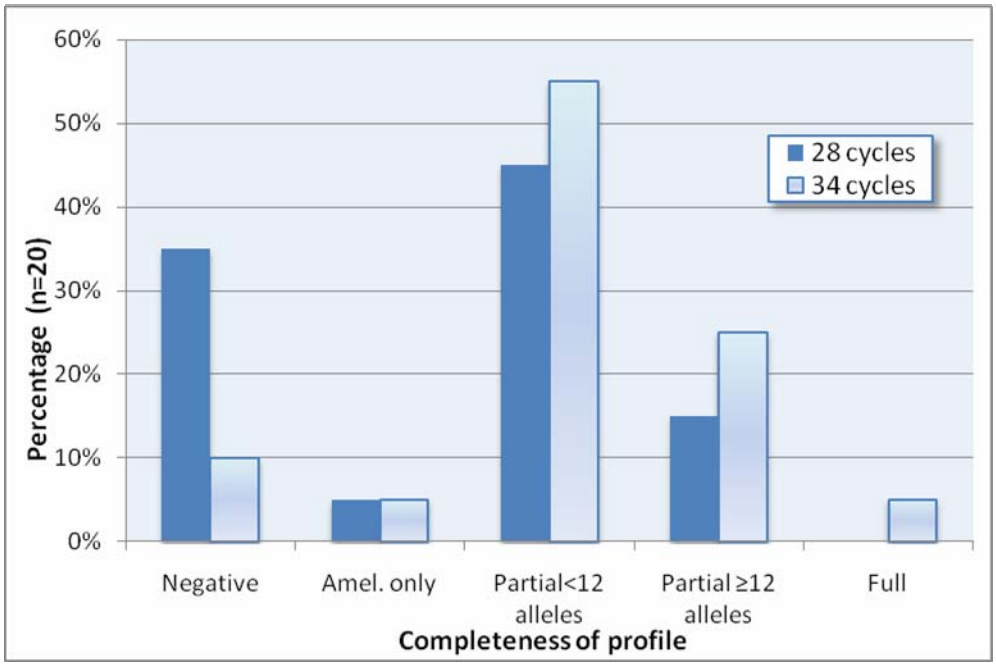

Figure 6-1. Completeness of profiles recovered from the burglary transfers, at 28 and 34 cycle amplification.

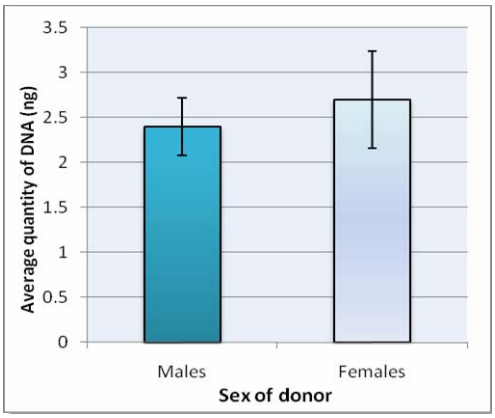

Figure 6-2. Average quantity of DNA according to sex of donor.

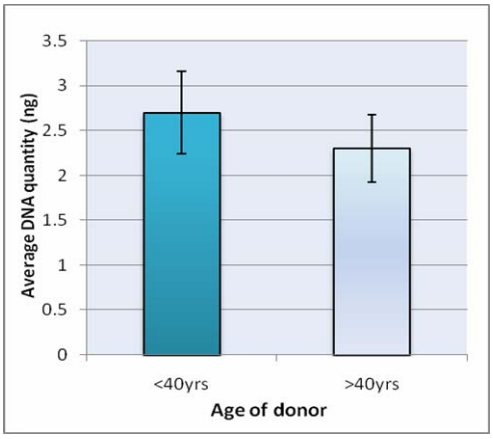

Figure 6-3. Average quantity of DNA recovered by age of donor.

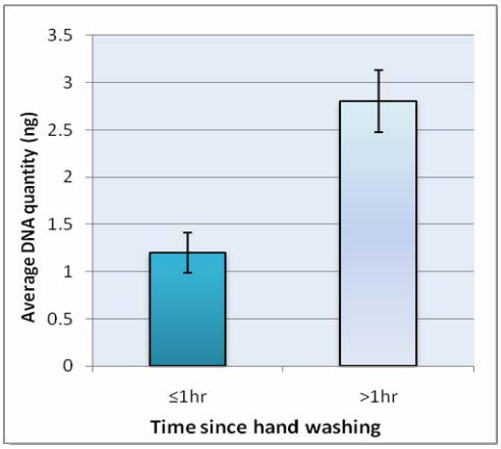

Figure 6-4. Average quantity of DNA recovered by time since hand washing.

Figure 6-2, Figure 6-3 and Figure 6-4 show the effect of the sex and age of the donor, and the time since hand washing on the recovery of DNA. A preliminary test for the equality of variances for each of the comparisons was conducted, to determine the appropriate *t*-test to apply. The difference between males and females, and whether the donor was older than 40

years was not statistically significant using the *t*-test for equal variances (p=0.8 in both cases). Whilst still not statistically significant (p=0.08), donors who had washed their hands within an hour of the experiment returned less DNA than those with longer time periods. No significant differences were noted between different skin types, or those with skin conditions.

DNA retrieved from each of the transfers gave a profile that matched the respective volunteer. However, additional alleles foreign to the volunteer were found in two of the 28 cycle profiles (10 alleles in total) and 11 of the 34 cycle profiles (33 alleles). One profile appeared to be contaminated by the previous volunteer to handle the surface, as six common alleles were in both the 28 and 34 cycle profiles. These two volunteers were a married couple, and it is a possibility that there was prior contact between them causing secondary transfer of DNA. However, three of the surface blanks (collected from the surface prior to handling by the volunteers) gave a small amount of DNA, and it is possible that the cleaning method did not adequately remove DNA from the surface on every occasion. The profiles generated from the three surface blanks contained less than 6 alleles, and could not definitely be attributed to any of the volunteers. There was no correlation between the length of time since hand washing and the number of extraneous alleles present in the profiles (R^2 = 0.0097).

6.2.2.1 Casework data

Table 6-1 displays the information collated regarding the 38 trace DNA casework samples collected from points of entry, arranged sequentially according to the quantity of DNA recovered. The DNA quantity is given as the Quantifiler™ output in nanograms per microlitre, and an estimation of the total DNA quantity in the extract.

The average amount transferred to points of entry across all of the samples was 0.6ng, but ranged from 0 to 10.3ng. Two-thirds of the samples did not result in a profile, and only two samples gave a full profile. There were four mixtures in the 38 samples. According to the laboratory's determination, mixtures and profiles with less than 12 alleles are not suitable for input onto the national database. Therefore, the percentage of these samples suitable for database comparison is 13%. It should be noted that the mixtures and partial profiles might still have probative value in terms of inclusions or eliminations, or other intelligence use.

Table 6-1. Casework samples from points of entry.

Sample	Offence	DNA quantity (ng/µL)	Estimated total DNA in extract (ng)	DNA profile result*
FPs on window**	Burglary	0	0	No result
Earprint on door	Burglary	0	0	No result
FPs on windowsill	Burglary	0	0	No result
FPs on window glass	Burglary	0	0	No result
Earprint on door	Burglary	0	0	No result
Earprint on door	Burglary	0	0	No result
FPs on window	Burglary	0	0	No result
FPs on front door	Burglary	0	0	No result
Forehead marks on window	Burglary	0	0	No result
Window security screen	Attempt Burg.	0	0	No result
Earprint on exterior of front door	Burglary	0	0	No result
Earprint on exterior of front door	Burglary	0	0	No result
Earprint on exterior of front door	Burglary	0	0	No result
Ear/face mark, exterior of front door	Burglary	0	0	No result
FPs on window flyscreen	Burglary	0.001	0.04	No result
Bolt (Vending machine POE)	Burglary	0.001	0.04	No result
Earprints on ext front door	Burglary	0.001	0.04	No result
FPs on interior window frame	Burglary	0.001	0.04	No result
Earprint on door	Burglary	0.002	0.08	No result
Earprints on exterior front door	Burglary	0.002	0.08	No result
FPs on interior aluminium doorframe	Burglary	0.002	0.08	No result
Earprint on door	Burglary	0.003	0.12	Partial <12
Downpipe at POE	Burglary	0.003	0.12	No result
Forehead mark on exterior of window	Burglary	0.003	0.12	No result
FPs on padlock at POE	Burglary	0.005	0.2	No result
FPs on interior door frame	Burglary	0.007	0.28	No result
Front flyscreen doorhandle	Attempt Burg.	0.01	0.4	Partial <12
FPs on exterior of door	Burglary	0.02	0.8	Partial ≥ 12
Earprint on exterior of front door	Burglary	0.02	0.8	Partial ≥ 12
Exterior car doorhandle (POE)	Robbery	0.022	0.88	Mixture
Point of exit, interior front doorhandle	Burglary	0.022	0.88	Mixture
FP on inside door	Armed Robbery	0.025	1	Partial <12
FPs on window frame	Burglary	0.028	1.12	Partial <12
Exterior sunroom window	Burglary	0.029	1.16	Full Profile
FPs on window sill	Burglary	0.033	1.32	Mixture
Lip/chin print on exterior sliding door	Burglary	0.046	1.84	Partial ≥ 12
Rear loading dock door	Armed Robbery	0.066	2.64	Mixture
FPs on interior of doorframe	Burglary	0.258	10.32	Full Profile

**Neg = No profile, AmeI Only = Only the Amelogenin locus present in the profile, Partial<12 = less than 12 alleles in the profile, Partial ≥12 = 12 or more alleles in the profile but less than a full profile, Mixture = A mixture of more than one person's DNA in the profile.*
***FPs = fingerprints*

6.3 Transfer – Robbery.

This component of the study aimed to investigate two aspects of DNA transfer during robbery offences; the amount generally transferred onto stolen items, and the length of time it takes for the offender's DNA to overtake the background DNA of the victim present on the item.

The only similar study that could be found in the literature was conducted by Murray et al. using wrist watches and volunteers of different shedder type [150]. Good shedders were found to completely replace the original wearer's DNA in two to three weeks, and became a major component of the profile after several days. Poor shedders took approximately two weeks to comprise a major component.

Rather than to base the experiment on good and poor shedder pairs, the experiment conducted for this project did not perform a prior assessment of shedder status. Volunteers were chosen randomly to give a general population survey of transfer, as it was felt this would reflect casework more accurately given the shedder status of an offender would rarely be known.

As for the previous experiment, casework data was also analysed to provide a comparison to the experimental work. The sample size was limited however, as only eight of the 252 casework samples could be identified as coming from personal items stolen during a robbery.

6.3.1 Robbery Transfer – Methods.

New, unused PVC wallets and coin purses were purchased for the experiment (Figure 6-5), and were exposed to shortwave ultraviolet light for 45 minutes prior to the experiment. Four of the wallets were then swabbed as surface blanks.

Figure 6-5. Wallets used for robbery transfer project.

Three groups of volunteers were recruited for this experiment.

The first group was used to assess the level of DNA transfer during robbery offences. The volunteers in this group were each provided a wallet. They were asked to grab the wallet, rummage through it simulating a robbery, and then retain and use the wallet for one minute, one hour, or one week. There were three volunteers per time period, and after the initial 'theft' were asked to handle the wallets as often and in a similar manner to how they would use their own wallets. The three time periods were selected after discussion with NSW Police Force investigators, who mentioned that after a street robbery the offender may either discard the item quickly after removing the valuables, or may retain the item for some time, as personal belongings from robberies have been found in searches of suspect vehicles or premises [235].

The second and third groups were constructed to assess the ratio of offender to victim DNA over time. The volunteers in the second group were given a wallet each and asked to use them in a normal manner for one week. At the end of that week, the first group of participants 'robbed' the 'victims' of their wallets. The 'robbers' then retained the wallets for either one minute, one hour, or one week with three replicates at each time period.

The third group were treated in the same manner as the second group, with the difference that the wallets were retained and used for two weeks prior to the 'robbery'. Only two replicates per time period were able to be conducted in this category. Buccal swabs were collected from all volunteers and stored on FTA™ cards.

Table 6-2 demonstrates the time periods and replicate numbers of the three groups in this experiment.

Table 6-2. Three groups used in the robbery transfer experiments.

Group 1			Group 2			Group 3		
Victim	**Robber**	**Reps.**	**Victim**	**Robber**	**Reps.**	**Victim**	**Robber**	**Reps.**
-	1 min	3	1 week	1 min	3	2 weeks	1 min	2
-	1 hour	3	1 week	1 hour	3	2 weeks	1 hour	2
-	1 week	3	1 week	1 week	3	2 weeks	1 week	2

After the scenarios had been completed, the wallets were collected and swabbed using the double swab method. The swabs were extracted with the 20% chelex method, and concentrated using Microcon® 100 concentrators to approximately 60µL. The extracts were quantitated with the Quantifiler™ reaction, and amplified in 28 and 34 cycle Profiler Plus™ reactions. Extraction and amplification blanks were also conducted.

6.3.2 Robbery Transfer – Results.

An average of 11.7ng was recovered from the wallets, with a range from 3.1ng to 33.0ng. The average of the first group transfer was 7.6ng (range 3.1ng to 15.4ng), which gives an indication of the level of transfer likely to occur during a robbery. Even those only held for one minute averaged 4.3ng. Figure 6-6 shows the average amounts of DNA recovered from each time period in the first group. There was some positive correlation between the length of time the wallet was held and the amount of DNA recovered, but was not statistically significant (p=0.1).

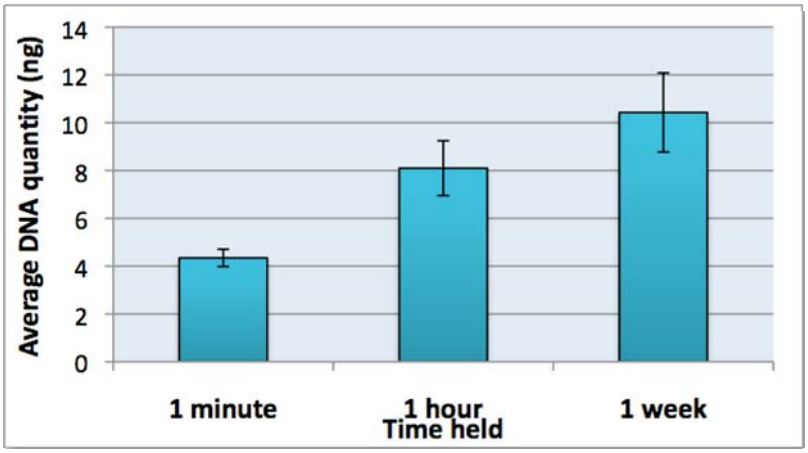

Figure 6-6. The average amount of DNA recovered from the three time periods of transfer, Group 1.

Figure 6-7 shows the completeness of profiles recovered from the first group, demonstrating the profiles that may be recovered from DNA transferred during a robbery. One full profile was recovered, the majority being partial with 12 or more alleles.

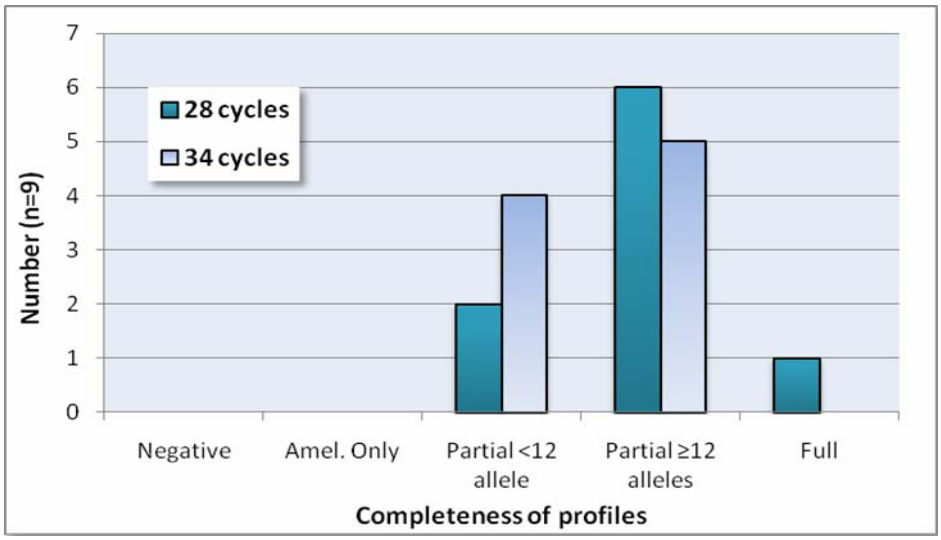

Figure 6-7. The completeness of profiles from Group 1, transfer only.

90% of the 30 profiles (28 and 34 cycles) resulting from the transfer pairs in Groups 2 and 3 were mixtures. Two of the single source profiles came from a pairing involving a one week time period (victim) followed by a one minute contact with the robber, showing only the victim's DNA at both 28 and 34 cycles. The third single source profile resulted from a pairing involving a one week time period (victim) followed by a one hour contact with the robber, showing only the robber's DNA at 28 cycles. The 34 cycle profile from this pair showed two alleles from the victim. Table 6-3 shows the results of the transfer pairs at 28 cycles. Similar results were achieved from the 34 cycle profiles.

Table 6-3. Results of the transfer pairs, Groups 2 and 3, 28 cycles.

Victim	1 week	1 week	1 week	2 weeks	2 weeks	2 weeks
Robber	**1 minute**	**1 hour**	**1 week**	**1 minute**	**1 hour**	**1 week**
	Majority Victim	**Robber**	Majority Robber	Majority Victim	Majority Victim	Majority Robber
	Majority Robber	Majority Robber	Even mixture	Majority Victim	Majority Victim	Majority Robber
	Victim	Majority Victim	Even mixture			

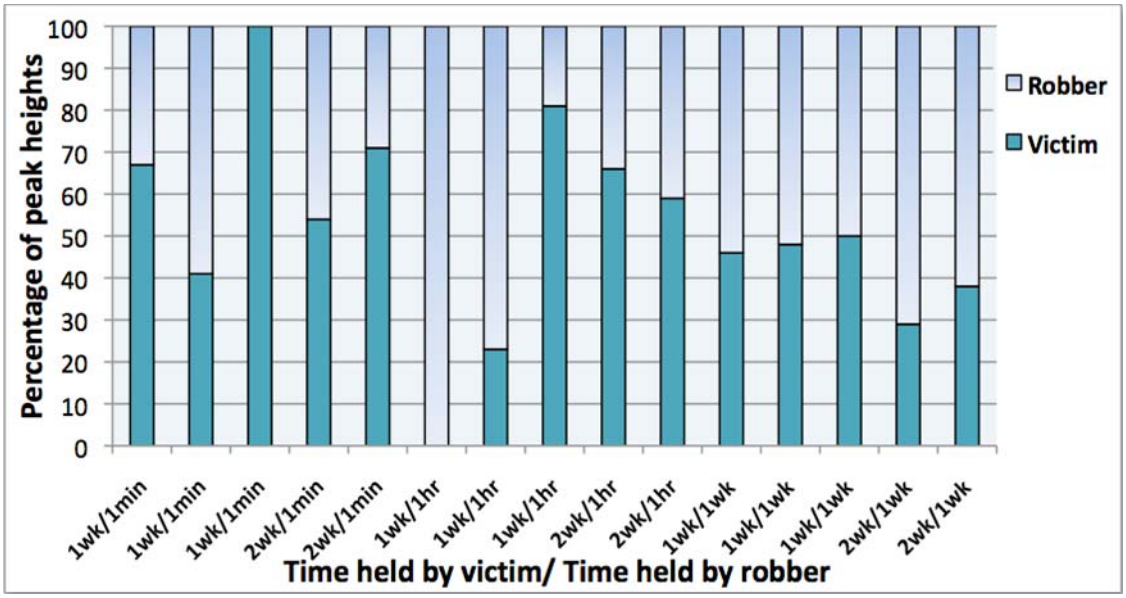

Figure 6-8. The ratio between the peak heights of the robber's DNA versus the victim's, 28 cycles.

As shown by Figure 6-8, there were no clear trends in the transfer pairs of groups 2 and 3. The amount of time that the victim held the wallet prior to the robbery (either one or two weeks) did not significantly affect the peak height percentage of the victim (p=0.9, *t*-test for equal variances). Likewise, the amount of time that the robber held the wallet after the robbery (either one minute, one hour or one week) did not significantly affect the robber's peak height percentage (p=0.3, *t*-test for equal variances).

A small number of extraneous alleles were noted in the profiles; three in the 28 cycle profiles and 15 in the 34 cycles profiles (0.8% and 4% of the total number of alleles respectively). These could either be due to contaminants on the hands of participants, or possibly from contaminants on the wallets themselves. The surface blanks showed there were very small quantities of DNA present, in the order of $1x10^{-7}$ng as shown in the Quantifiler^{TM} output, which may be an artefact given the minute amount. However alleles were noted in the amplification of the surface blanks, despite the wallets being newly purchased and treated with shortwave ultraviolet light prior to their sampling. Only two of these alleles could account for extraneous alleles present in the sample profiles, nevertheless it demonstrates that the cleaning procedure was not entirely effective.

6.3.2.1 Casework data

Table 6-4 shows the eight samples from the casework data that had come from personal items stolen during a robbery or burglary. DNA was recovered from all samples, and all but one provided some profile information. 20% provided a profile suitable for database inclusion.

Table 6-4. Casework samples - stolen personal items.

Sample	Offence	DNA quantity (ng/μL)	Estimated total DNA in extract(ng)	DNA profile result*
Debit card	Fraud	0.0080	0.32	No Result
Blackberry case	Burglary	0.016	0.64	Partial <12
Handbag	Robbery	0.017	0.68	Partial <12
Purse	Robbery	0.024	0.96	Amel. Only
Handbag	Robbery	0.038	1.5	Mixture
Purse	Robbery	0.070	2.8	Full Profile
Debit & bank cards	Theft	0.15	6.0	Mixture
Mobile phone	Theft	1.3	51	Full Profile

**Neg = No profile, Amel Only = Only the Amelogenin locus present in the profile, Partial<12 = less than 12 alleles in the profile, Partial ≥12 = 12 or more alleles in the profile but less than a full profile, Mixture = A mixture of more than one person's DNA in the profile.*

6.4 Discussion.

The level of DNA transfer found in these experiments was quite high, up to 10.9ng in the 30 second transfers of the burglary transfers, and up to 15.4ng in the single transfers of the first group of robbery experiments. The increase in the time the wallets were held showed an increase in amount of DNA; however this increase was not statistically significant. The level of transferred DNA was highly variable, showing a ten-fold difference across the spread of DNA quantities in both experiments. This variability is also evident in the casework data. The percentage of profiles suitable for database use (showing 12 or more alleles) was also similar between the experimental and casework samples, at around 10 to 20%.

The variation in the results is in contrast to some of the previous studies of DNA transfer. There were no clear trends in the amount of time the wallets were held and the likelihood of recovering either the victim's or robber's DNA. Murray et al. [150] found more consistent results in that good shedders reliably replaced the original wearer of a wrist watch in a short time period, and Lowe et al. [151] found that certain volunteers were consistently good shedders of DNA. During the course of the experimental work for this thesis volunteer

subjects were used a number of times across the different experiments, and no clear 'good' shedders were identified; in that no volunteer consistently become the majority profile or produced full profiles in single transfers. This was a similar result to Phipps and Petricevic [152], who found no good shedders amongst a group of 60 volunteers and suggested that perhaps the difference between good and bad shedders is more subtle, and may be difficult to detect above other environmental and influencing factors. It is possible that the variability between depositions from the same individual may be greater than the variability between individuals.

One aspect of the work that tends to concur with the prior studies of Lowe et al. [151] is the significance of hand washing on the transfer of DNA. The burglary transfer experiments afforded an assessment of this factor, and less DNA was transferred from those volunteers who had washed their hands more recently. Whilst the noted difference between the two groups was not statistically significant (Figure 6-4), it may prove to be so with greater sample numbers. This finding echoes the previous research that indicated that a longer period since hand washing will result in a greater amount of DNA. Interestingly, here the longer time since hand washing did not result in a greater amount of alleles foreign to the volunteer in the resulting profile.

The average level of transfer in the first group of robbery experiments was 7.6ng, which is very close to the level of DNA recovered from handbags and wallets in the abundance experiments (7.5ng). This indicates that the second component of the experiment was relatively accurate in mimicking the amount of 'victim' DNA likely to be present on these items prior to a robbery. Despite the fact that a reasonable amount of DNA was recovered from the robbery transfers, the majority resulted in partial profiles. It may be that the percentage of extract used in the amplification, or the percentage of amplified product in the capillary electrophoresis master mix was insufficient to produce full profiles.

The level of DNA transferred during this experimental work is higher than was found in the casework data. This is likely to be due to several factors; the experiment is somewhat contrived in that the subject grabbed the same location for a period of time, whereas in a real situation the offender may not be so focussed on one area. Also, the exact location of contact was known in the experimental work, whereas again in casework the location is not known (other than if screening with fingerprint enhancement), and a larger area may be swabbed rather than concentrating on a smaller location. Different extraction and analysis methods

were used between the experimental and casework samples, which also could contribute to the differences noted. Additionally, the time between deposition and sampling was shorter than what would be possible in real life situations. Further work could be conducted to more accurately represent casework, such as blind studies.

As a side issue, given the amount of publicity that forensic science has attracted in recent years, criminals are becoming more aware and often take precautions to prevent leaving fingerprints by wearing gloves. There have been no studies to determine exactly how often this is occurring, so in the process of conducting this research a small survey was undertaken to determine how often armed robbery offenders wear gloves. The crime of armed robbery on commercial premises was chosen because of the availability of CCTV footage and witness statements. Of 100 armed robberies where CCTV footage was available and viewed, at least one of the offenders wore gloves at 53% of the robberies. The most common types of gloves were fabric gloves such as cotton or wool, followed by latex (Figure 6-9). The wearing of gloves is therefore common, and is likely to prevent the deposition of fingerprints. It is feasible though that an offender may rub his face with the gloves or bite the tips of the gloves when removing, which may transfer DNA to a glove-handled surface, and thereby presenting another opportunity to obtain forensic information.

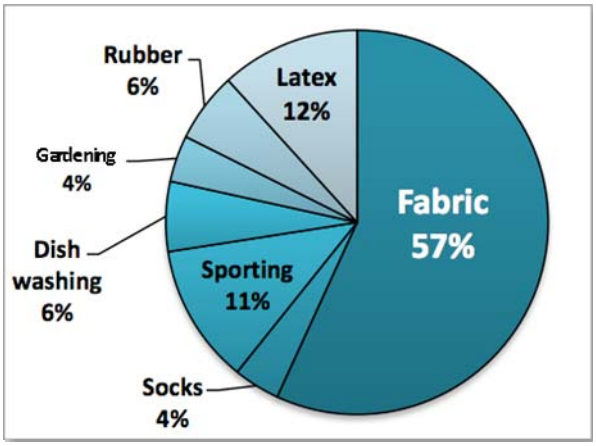

Figure 6-9. Types of gloves worn during 53 Sydney armed robbery offences.

An honours project was conducted as an adjunct to this thesis to test if DNA can be recovered from glove prints [237]. The study also aimed to test if someone wears another's gloves, will secondary transfer result? Cotton and latex gloves were worn by individual volunteers for three set time periods per glove type; either one hour, one hour per day for one week, or one hour per day for two weeks (cotton gloves), and 20 minutes, 40 minutes or one hour (latex

gloves). A sterilised polyethylene tube was then handled for five minutes and the tube sampled. To test secondary transfer, two different donors wore the gloves sequentially for different time periods, after which the second donor held a plastic tube for five minutes. The first wearer times were as for the previous experiment, and the second wearer times were either one hour, 30 or 15 minutes for cotton gloves, and five, 15 or 30 minutes for latex gloves.

DNA was recovered from 75% of the glove-handled tubes, ranging from 0.008-0.4ng from the cotton gloves, and 0-0.1ng from the latex gloves. More DNA was recovered from the cotton gloves, but the length of time the gloves were worn did not significantly affect the quantity recovered. Secondary transfer was detected in the second component of the experiment. A mixed profile was obtained from cotton gloves that had been worn for one hour per day for a week, and then worn by a second person for 15 minutes, with a major component of the first wearer and a minor component of the second wearer. A pair of latex gloves worn for one hour then 30 minutes deposited a profile with major component of the second wearer, and a minor component of the first wearer. These results show that profiles can be recovered from glove prints, however caution should be taken in the interpretation of results, as secondary transfer of DNA is possible.

In summary, there is considerable variation in the amount and quality of DNA transferred during burglary and robbery offences. No consistently good shedders of DNA were identified during these experiments; however DNA was transferred in sufficient quantities to produce profiles suitable for inclusion on DNA databases.

6.5 Conclusions.

6.5.1 Burglary

There is sufficient DNA transferred during the action of a burglary to produce a profile of the offender suitable for database purposes; however the chance of a successful profile will be limited by the detection and appropriate sampling of the target area, and the amount of background DNA on the surface. The average amount of DNA transferred during the action of a burglary (2.5ng) is;

- more than the average amount of background DNA on windows (0.05ng), and
- less than the average amount of background DNA on entry doors (6.05ng).

Considerable variation was noted in the amount of DNA recovered from the 20 donors and in the completeness of the profiles achieved, however no significant differences were observed according to the age or sex of the donor. Whilst not found to be statistically significant in these experiments, a difference was observed in the DNA recovered according to the time since hand washing.

6.5.2 Robbery

The amount of DNA transferred to wallets during the action of a robbery is variable (ranging from 3.1ng to 15.4ng), and is likely to be similar to the amount of background DNA present on these items (average 7.5ng).

There were no clear trends as to the length of time needed after a robbery for the 'robber's' DNA to become a major component of a profile recovered from the stolen item. Mixtures were recovered in all but three of the transfer pairs, however the robber was a major component of the mixture or a single source profile in 40% of the profiles. This indicates that the analyses of recovered items stolen during a street robbery may provide usable information as to the identity of the offender, despite the level of background DNA on these items.

Chapter 7:

DNA Persistence

Chapter 7: DNA Persistence

7.1 Introduction

The following chapter focuses on the issue of trace DNA persistence, aiming to determine how long DNA will persist in certain environments after an offence. Similarly for the transfer chapter, this work aimed to produce data to assess the probability of trace DNA evidence given suggestions of activity proposed by the prosecution or defence.

As for previous chapters, the experiment was constructed to mimic the two offence types of residential burglary and street robbery. Unlike the previous sections, the experimental work for the two crime types was performed concurrently and so the methods and results are jointly presented here.

Whilst the focus of this thesis was volume crime, the two crime types selected provide scenarios that could be applicable to a variety of other investigations including serious crime. The results of this study were used to assist a particular homicide enquiry that occurred in late 2003. An armed robbery of a petrol station (Figure 7-1) became violent and the victim was murdered in the process. Security cameras inside the shop revealed that the offender had pulled shut the entry door during the offence, and opened it on leaving the premises (Figure 7-2). A DNA profile was recovered from the outside and edge of the door, and matched a suspect. However the suspect had visited the petrol station two weeks prior to the offence, and the question was asked, could the DNA profile recovered from the crime scene have come from this innocent visit? Intuitively this assertion seems unlikely, however at the time there was limited research to give weight to a theory in court. Circumstances such as this provide a direct justification for the relevance of this research.

Given the stochastic nature of trace DNA it is often difficult to separate the effect of one variable from the many that affect its recovery. Therefore this study aimed not to exactly replicate crime scene trace DNA samples, but instead to determine the effect of crime scene environments on pristine DNA samples of known concentration. As the experimental set up was somewhat removed from 'real life' circumstances, analysis of the data from casework trace DNA samples in Chapter 3 is provided to complement and provide a comparison with the experimental work.

Figure 7-1. The exterior of the service station and entry door.

Figure 7-2. CCTV footage still and closeup showing the offender closing the entry door.

7.2 Methods.

This study consists of two parts; experimental work and the analysis of casework data.

7.2.1 Experimental.

7.2.1.1 Subject

Using hand contact as the DNA deposition method in experiments would prevent a robust quantitative analysis, due to the known variation between shedder types, and other factors

such as time since the hands were washed [151, 152]. Therefore, buffy coat (the white blood cell and platelet layer of whole blood) with known cell amounts was selected as the DNA source for these experiments. The buffy coat cells used were purchased commercially, purified, and quantitated by direct haemocytometer count and DNA quantitation methods. Cell stocks were stored in 500µL volumes at -80°C until use. 3µL aliquots of buffy coat were spread onto the surfaces with pipette tips over an area approximately 5mm^2.

For further accuracy in assessing the quantity of DNA recovered, 3µL aliquots (387ng) of control DNA solution (9947A, Promega Corporation, Madison, WI) was also used in one of the experiments. However it was envisaged that this 'naked' DNA would degrade more rapidly than the buffy coat DNA protected inside cells, and, therefore, may not be a true representation of the DNA found at crime scenes.

7.2.1.2 Substrates

To model burglary offences, outdoor window frame surfaces in a residential unit building were chosen, being common entry points [238, 239]. These surfaces were gloss-painted wooden window frames on a patio, under cover of a one-metre brick balcony above. This set of samples will be referred to as the 'house' samples hereinafter. For street robbery offences, vinyl, a common handbag material [240] was purchased and cut into 3 x 3cm swatches. This set of samples will be referred to as the 'bag' samples. The experiment took place in November and December, which in Sydney, Australia, provides average temperature and relative humidity of 24.1°C, 63% (day) and 18°C, 71% (night) [241]. The surfaces were in a partly shady location, and did not receive direct sunlight (Figure 7-3).

As a control set, glass microscope slides were selected as a substrate and stored in the dark in the laboratory in a sterile container, at ambient temperature. This final set will be referred to as the 'laboratory' samples.

All surfaces were pre-cleaned with 10% bleach and 70% ethanol solutions and surface blanks taken prior to the experiment.

Figure 7-3. Experimental setup of the persistence experiments.

7.2.1.3 Sampling

One set of placements was swabbed within 15 minutes of placement, using the double swab method [194]. The following sets were swabbed one day, three days, one week, two weeks, four weeks and six weeks after placement. Three replicates were conducted in each set. Additional to the surface blanks taken after cleaning the surfaces but prior to the placement of the samples, surface blanks were also collected from the 'house', 'bag' and 'laboratory' samples at the two week and six week time periods to determine if extraneous DNA was present.

7.2.1.4 DNA analysis

The samples were extracted using the 20% chelex method to a final volume of 260µL.

An initial experiment was conducted with 'house' samples only using PicoGreen® quantitation. When the Quantifiler™ method became widely available and validated for use in Australian forensic laboratories, the experiment was re-conducted using this method with the three sample types.

The samples with the highest quantity from each set of buffy coat samples at time=0, one, two, four and six weeks were amplified in 28 cycle AmpFlSTR® Profiler Plus™ reactions.

7.2.2 Casework data.

To assist the interpretation of the research data, a subset of the casework data presented in chapter 3 was analysed. 50 samples were identified as resulting from brief handling of an object, (for example the handling of a point of entry, or a cash register handled during a robbery) as opposed to items such as tools and weapons that may have been owned by the offender and handled over a long period of time. The time delays between their recovery from the scene, and submission to the laboratory were analysed to determine if there was any correlation in the amount of DNA recovered and if a profile resulted.

7.3 Results.

7.3.1 Quantifiler™ quantitation.

Figure 7-4 and Figure 7-5 show the results of the main experiment conducted using buffy coat DNA and control DNA solution on 'House', 'Lab', and 'Bag' surfaces, and Quantifiler™ quantitation. The results are displayed as a percentage of the amount recovered at time = 0, with the average of the three replicates at each time period.

Regarding the buffy coat samples (Figure 7-4) it is apparent that for all but the laboratory samples the amount decreased significantly after two weeks, to a negligible amount recovered after 6 weeks. The decline in DNA recovery across the six-week period was found to be statistically significant using linear regression analysis for the house and bag samples (p=2.5x10^{-3} and 7.0x10^{-3} respectively), but not for the laboratory samples (p=0.25). The average amount of DNA recovered at t=0 was 38.9ng, 20.4ng, and 96.3ng for the laboratory, house and bag samples respectively.

The DNA control solution samples did not decline as rapidly as expected (Figure 7-5). The laboratory samples did not decline below 100% of the starting time period, and the bag samples declined by 50% over the six week period. Only the house samples were found to decrease significantly in quantity (p=4.6x10^{-2}).

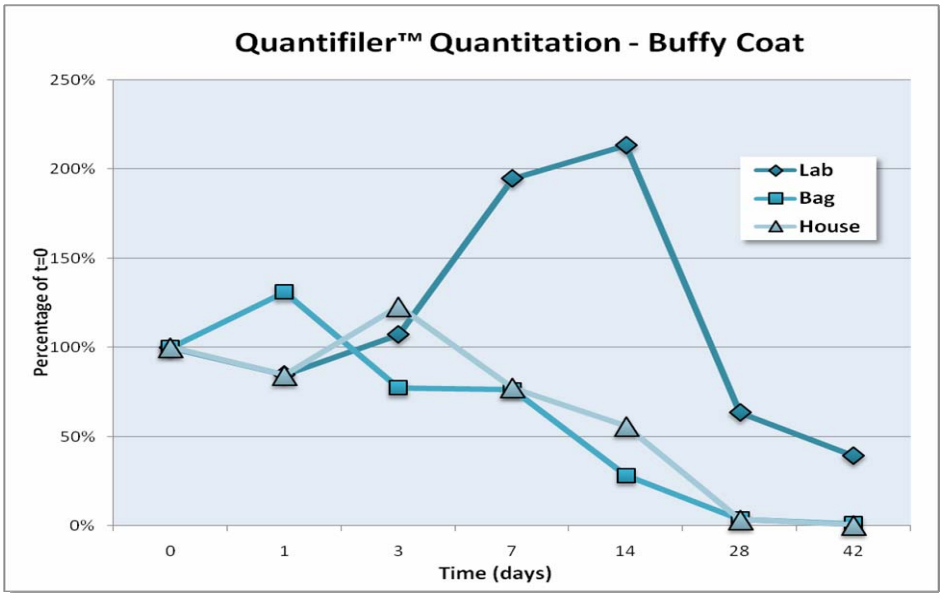

Figure 7-4. Quantifiler™ quantitation of DNA from three swabbed surfaces at various time intervals up to 6 weeks, after application of a standard amount of human Buffy Coat cells, presented as a percentage of the amount recovered at t=0.

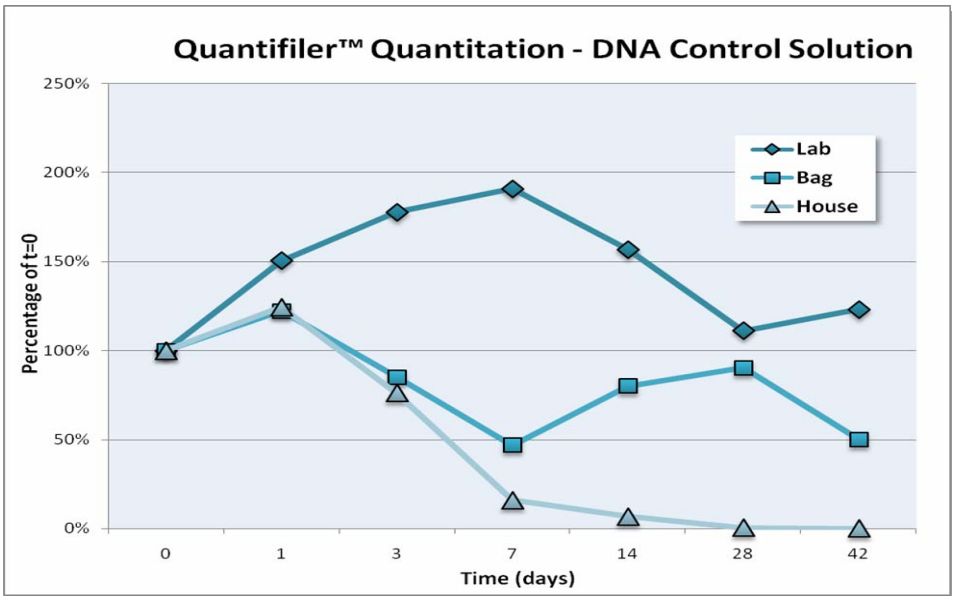

Figure 7-5. Quantifiler™ quantitation of DNA from three swabbed surfaces at time intervals up to 6 weeks after application of DNA control solution, presented as a percentage of the amount recovered at t=0.

7.3.2 PicoGreen® quantitation.

Figure 7-6 shows the results of the initial experiment conducted using buffy coat DNA on 'House' surfaces and PicoGreen® quantitation. The results are presented as a percentage of t=0, with the average of the three replicates at each time period. It should be noted that samples were not collected at the one day time period in this experiment. After this initial

experiment was conducted, it was decided to also swab after one day to provide more information at the early stage of the process.

The decline in DNA recovery from the 'house' samples across the six-week period was found to be statistically significant using linear regression analysis (p=1.8x10^{-2}).

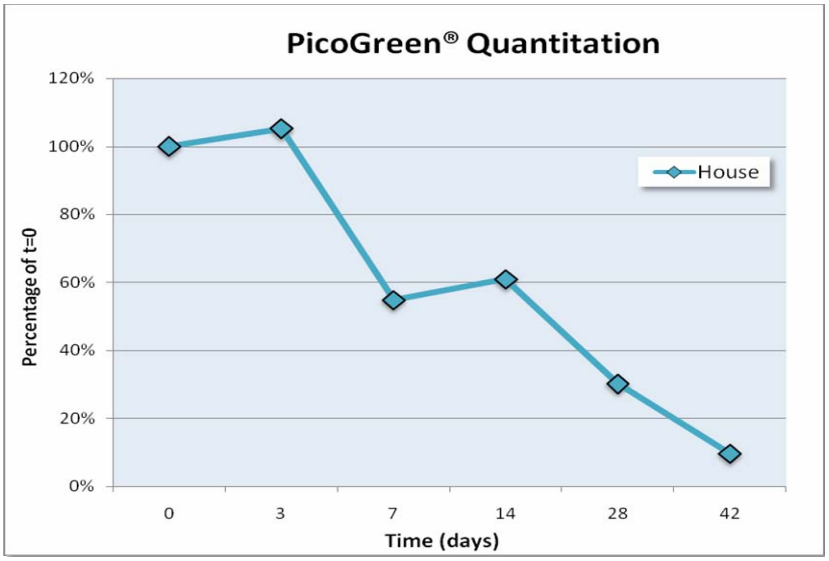

Figure 7-6. PicoGreen® quantitation of DNA from swabbed 'House' surfaces at various time intervals up to 6 weeks, after application of a standard amount of human Buffy Coat cells, presented as a percentage of the amount recovered at t=0.

7.3.3 Profiler Plus™ amplification.

Figure 7-7, Figure 7-8 and Figure 7-9 show the Profiler Plus™ amplifications of selected samples from each set of buffy coat samples at time = 0, 1 week, 2 weeks, 4 weeks and 6 weeks. All profiles are displayed at the same scale. No extraneous alleles were located in any of the profiles, indicating that contamination had not occurred. Quantitation of the surface blanks showed that no DNA was present on the surfaces prior to the experiments, and that no additional DNA had been deposited on the surface after the two and six week time periods.

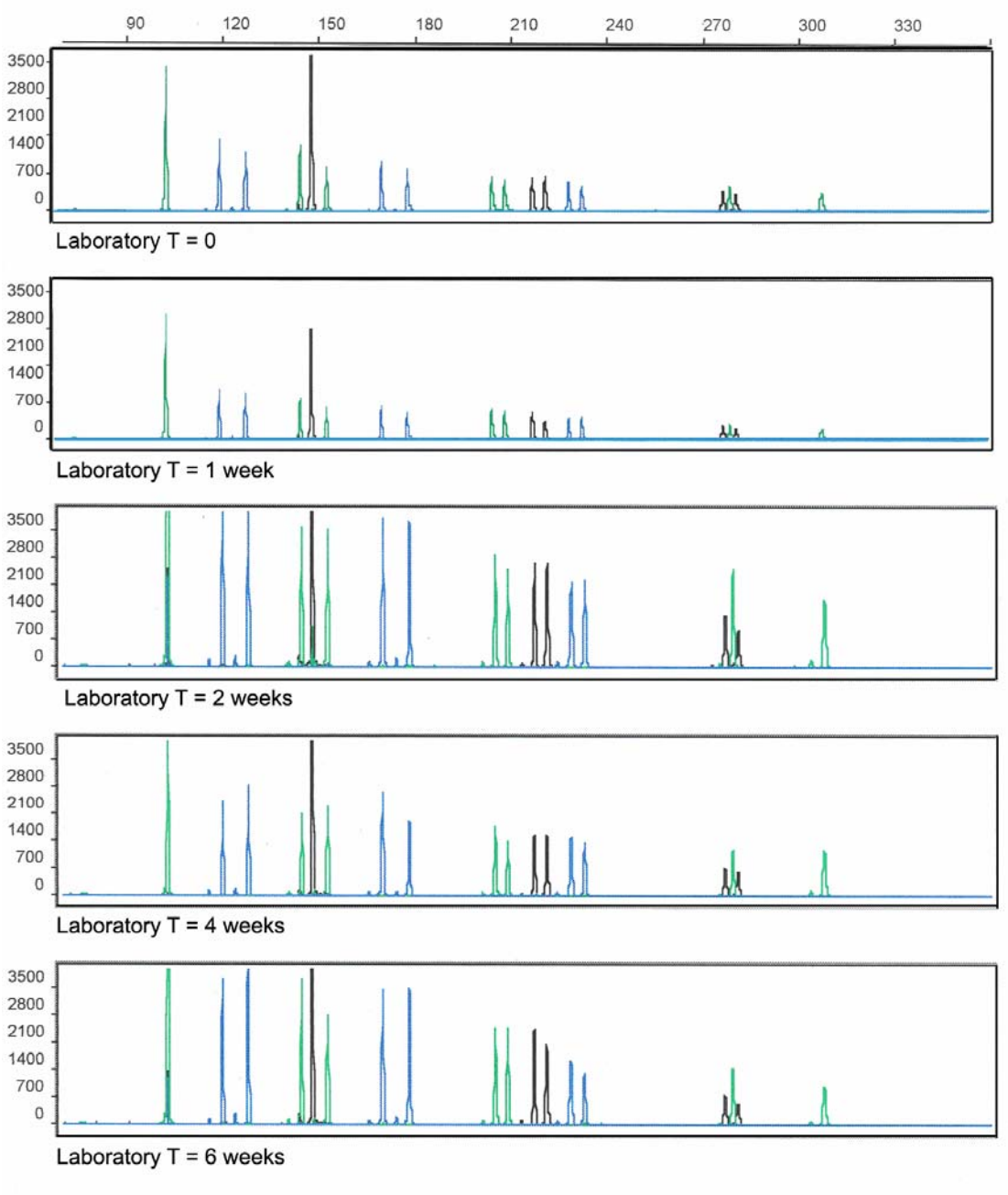

Figure 7-7. Profiler Plus™ profiles of selected Buffy Coat 'laboratory' samples over 6 weeks.

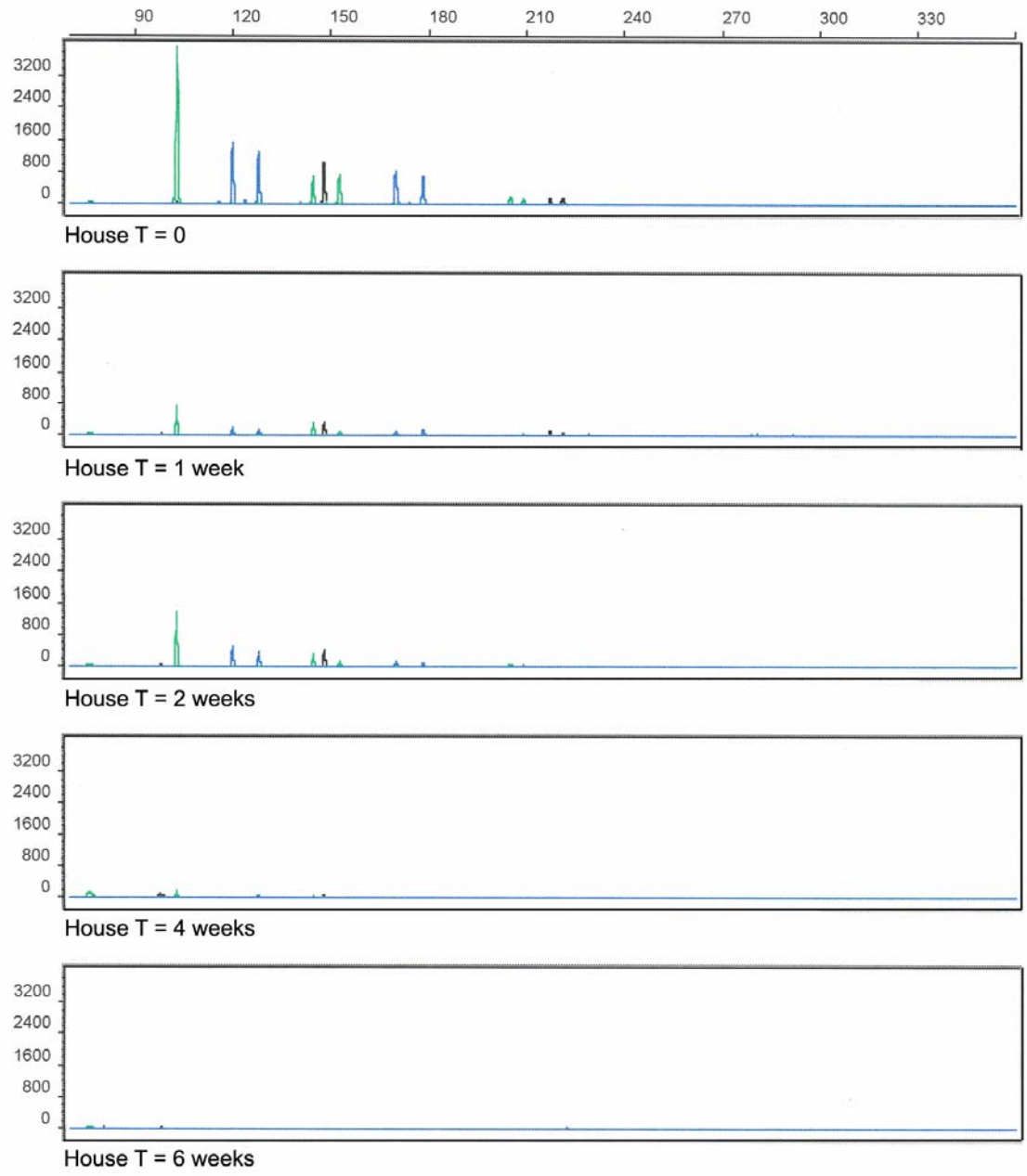

Figure 7-8. Profiler Plus™ profiles of selected Buffy Coat 'house' samples over 6 weeks.

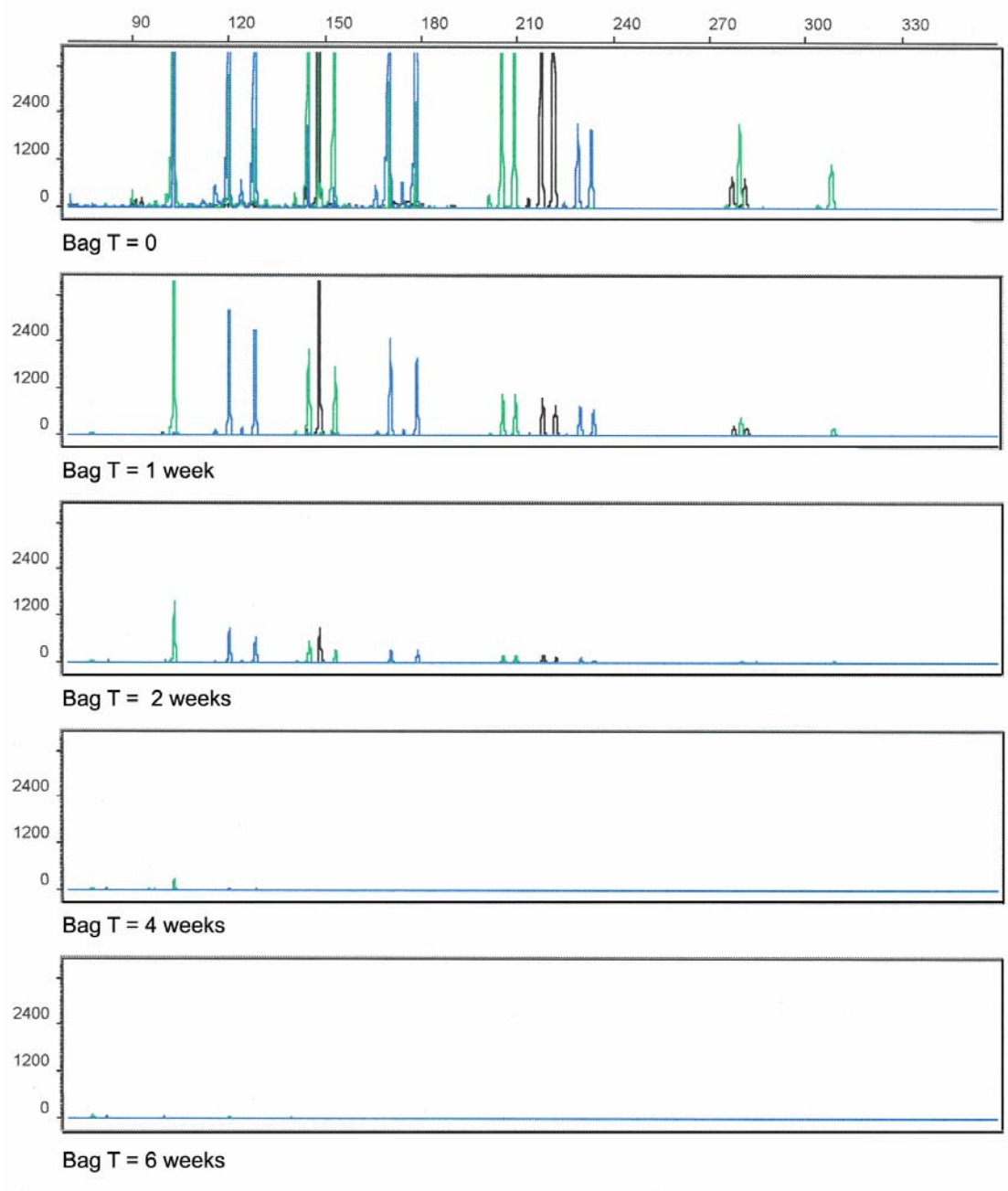

Figure 7-9. Profiler Plus™ profiles of selected Buffy Coat 'bag' samples over 6 weeks.

7.3.4 Casework data.

Table 7-1 displays the information collated regarding the 50 trace DNA casework samples, arranged sequentially according to the time difference between the offence and the sample collection. The time between the collection of the sample from the crime scene and the submission of the sample to the laboratory is also shown in days. This time delay ranged from four days to over one year (383 days). The DNA quantity is given as the Quantifiler™ output in nanograms per microlitre, and an estimation of the total DNA quantity in the extract. Figure 7-10 displays the percentage of each profile type produced from the samples. The laboratory determined that the mixtures recovered in these cases were not suitable for input onto the national database. It should be noted that these mixtures might still have significant value in terms of inclusions or eliminations, or other non-database use.

There was no evidence for a linear relationship between the time delay and quantity of DNA recovered in the DNA casework data (R^2<0.03). Likewise, no significant reduction in the quality of profile recovered was noted as the time delay between the offence and sample collection increased. Despite lengthy time delays between the sample collection and laboratory submission, there were again no significant decreases in the DNA quantity and profile quality (p=0.86 and 0.28). Figure 7-11 shows the spread in DNA concentration across five time periods between the offence and the DNA sample collection. Whilst the samples of highest concentration tended towards the lower time frames, there is a large range at each time period.

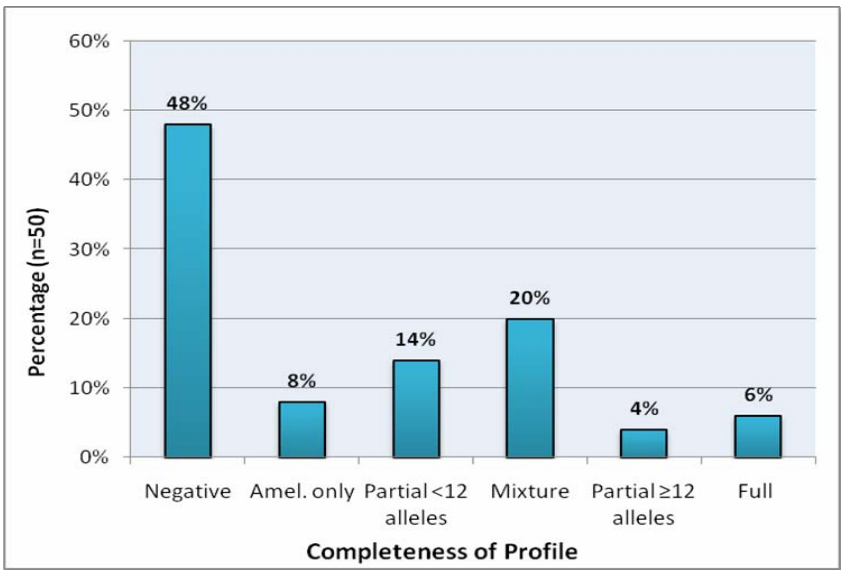

Figure 7-10. Completeness of profiles recovered from casework trace DNA samples.

Table 7-1. Results from trace DNA casework samples, sorted by the time difference between the offence and sample collection

Time between offence & collection	Time between collection & lab receipt (days)	Sample	Offence	DNA quantity (ng/µL)	Estimated total DNA in extract (ng)	DNA profile result*
1hr40min	225	FPs** at point of entry	Burglary	0	0	Neg
1hr40min	33	Earprint on door	Burglary	0.003	0.12	Partial <12
1hr40min	15	FPs on counter	Armed robbery	0.045	1.8	Mixture
1hr45min	39	Register note clips	Armed robbery	0.002	0.08	Partial <12
2hr15min	11	Handmark on counter	Armed robbery	0.017	0.68	Amel Only
2hr19min	37	Service counter	Armed robbery	0.025	1.0	Amel Only
2hr23min	383	FPs at point of entry	Armed robbery	0.025	1.0	Partial <12
2hr23min	383	Security wire above counter	Armed robbery	0	0	Neg
2hr40min	9	Cash register, FPs	Armed robbery	0	0	Neg
2hr40min	22	Arm mark on counter	Armed robbery	0.002	0.08	Mixture
2hr40min	22	Arm mark on counter	Armed robbery	0.008	0.32	Full Profile
2hr52min	7	Display mat on counter	Armed robbery	0.056	2.24	Mixture
3hr10min	13	Perspex partition	Armed robbery	0.046	1.84	Mixture
3hr30min	230	Shopping basket	Armed robbery	0.178	7.12	Mixture
3hr30min	230	Freezer door	Armed robbery	0.007	0.28	Partial <12
3hr30min	230	Rear loading dock door	Armed robbery	0.066	2.64	Mixture
3hr50min	169	FPs on window sill	Burglary	0.033	1.32	Mixture
4hr5min	4	Register keyring	Theft	0.004	0.16	Amel Only
5hr15min	29	Area around reg. plates	Theft	0	0	Neg
5hr15min	29	Area around reg. plates	Theft	0.001	0.04	Neg
5hr40min	29	Computer harddrive	Burglary	0.002	0.08	Partial <12
5hr50min	19	Plant pots	Burglary	0	0	Neg
8hr45min	7	Screwdriver handle	Burglary	0.18	7.2	Partial ≥12
9hr25min	31	Earprint on door	Burglary	0	0	Neg
10hr5min	173	FPs at point of entry	Burglary	0	0	Neg
10hr42min	24	Safe handle	Burglary	0.002	0.08	Neg
11hr35min	121	Glovebox handle	Robbery	0.014	0.56	Mixture
11hr35min	144	FPs on security camera	Arson	0.003	0.12	Neg
14hr25min	24	FPs at point of entry	Burglary	0.02	0.8	Partial ≥12
14hr58min	5	FPs at point of entry	Burglary	0.009	0.36	Neg
16hr	36	FPs on bumper	Theft	0.001	0.04	Neg
17hr31min	66	FPs at point of entry	Burglary	0	0	Neg
19hr26min	14	Earprint on door	Burglary	0	0	Neg
19hr31min	35	FPs at point of entry	Burglary	0.028	1.12	Partial <12
19hr55min	12	Earprint on door	Burglary	0.002	0.08	Neg
20hr55min	131	Auto gearshift	Vehicle offence	0.001	0.04	Neg
21hr10min	226	Earprint on door	Burglary	0	0	Neg
1d	16	Wallet	Burglary/SMV	0.074	2.96	Amel Only
1d	219	FPs at point of entry	Burglary	0	0	Neg
2d	13	FPs at point of entry	Burglary	0	0	Neg
3d	14	Partial FP on camera	Burglary	0	0	Neg
3d	6	Gas bottle handle	Drugs	0.032	1.28	Mixture
3d	241	FPs at point of entry	Theft	0.001	0.04	Neg
5d	17	Passenger doorhandle	Assault	0.022	0.88	Full Profile
9d	304	Handbag	Robbery	0.002	0.08	Neg
11d	142	Cheque book	Theft	0.004	0.16	Partial <12
22d	180	Glucodin powder box	Drugs/firearms	0.004	0.16	Neg
55d	32	Bag	Drugs	0.105	4.2	Full Profile
62d	39	Ziplock bag	Drugs	0.001	0.04	Neg
62d	8	FPs on laptop	Burglary	0.032	1.28	Mixture

**Neg = No profile, Amel Only = Only the Amelogenin locus present in the profile, Partial<12 = less than 12 alleles in the profile, Partial ≥12 = 12 or more alleles in the profile but less than a full profile, Mixture = A mixture of more than 1 person's DNA in the profile.*

***FPs = fingerprints.*

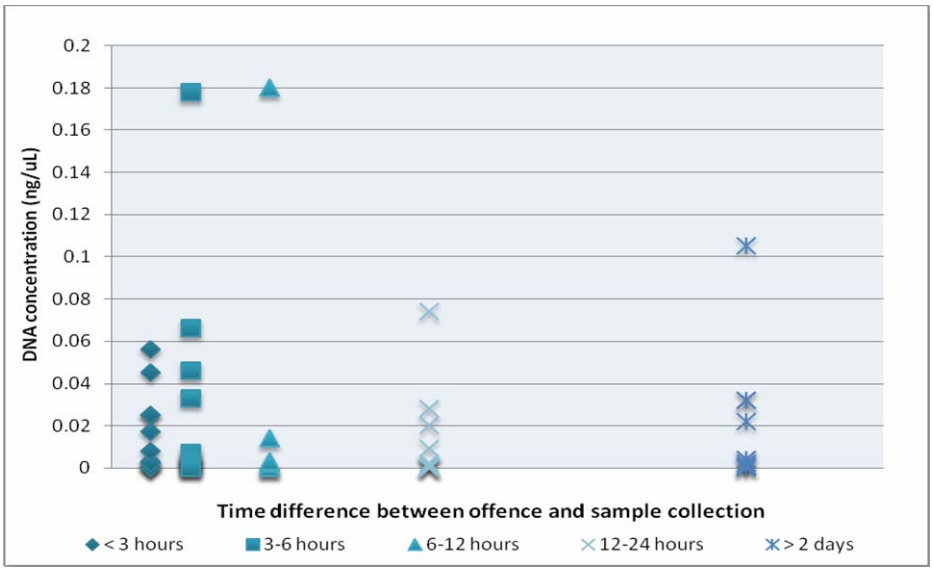

Figure 7-11. Concentration of DNA recovered from casework trace DNA samples, grouped in five time categories of the delay prior to the sample collection.

7.4 Discussion.

The experimental data support the hypothesis that the chance of recovering DNA from an outdoor surface decreases significantly over time. If a DNA profile is recovered from a similar location, it is likely to be from a recent contact. The quantity of DNA deposited in this experiment is up to 300 000 times greater than the amount left during a hand contact, and therefore it is expected that DNA left through hand contact would be undetectable in a much shorter time period. For example, if 150pg of DNA were left after a hand contact on a bag (it has been estimated that 5 nucleated cells are present per fingerprint [63]), after two weeks there would be 27% available for recovery. Assuming that there is 100% recovery of the cells, this would leave only 40.5pg. Whilst this may be feasible in research scenarios, recovery of such a small amount of DNA at a crime scene in routine conditions would be unlikely.

Whilst these results are preliminary and further data would be required to confirm this, the decline of trace DNA appears to follow a linear trend, rather than a strong drop off in the first few days. This is contrary to the persistence of other trace evidence such as fibres, which generally follow an exponential decrease with significant loss in the first hours after the transfer [242].

As expected, the laboratory-stored samples proved to be more robust than the samples left outdoors. Whilst the amount of DNA declined, full profiles were recovered over the entire six-week period. The results of the laboratory samples indicate that if crime scene samples are left in an environment that is cool, dark and in a low traffic area, profiles may be recovered for a longer period of time.

Three points of interest in the experimental data are: the differences in the amount of DNA recovered at t=0 between the surfaces; the spike in recovery of DNA from the 'laboratory' samples at one and two weeks; and the insignificant decline in the 'laboratory' and 'bag' DNA control solution samples (Figure 7-4 and Figure 7-5).

These anomalies may be explained in part by an uneven distribution of white blood cells in the buffy coat preparations. Two separate aliquots were each quantitated twice to ascertain the quantity of DNA present, and produced differences of up to 40ng within and between separate 20µL aliquots (data not shown). This provides an explanation why the 'bag' samples returned significantly more (p=0.03) DNA than the 'laboratory' samples in the first week, and for the spike in recovery of the 'laboratory' samples at one and two weeks. In addition, at the one and two week time periods the deposit became clearly visible as a dried white spot and therefore was simple to target, whereas prior to this it had not been as easily discernable. The 'house' and 'bag' samples did not show this spike, and therefore the effect of the outdoor environment on these samples may have negated any targeting advantage provided by the deposits becoming visible.

It is supposed that the variation between the 'house' and the 'bag' samples (Figure 7-8 and Figure 7-9) may be due to the deposition method. As the house surface was vertical it was more difficult to deposit the fluid sample. Conversely, the 'bag' samples were stored horizontally preventing the deposit from spreading, allowing an easier recovery leading to higher quantities and stronger profiles.

The casework data in Table 7-1 indicate the difficulties encountered in forensic trace DNA analysis. The average amount recovered from the trace samples was fairly low at 35pg/µL or 1.4ng in the total extract, despite the majority of samples (74%) being recovered within 24 hours of the offence. Full profiles were only recovered in ten cases (8%), with no profile recovered in approximately half of the cases (Figure 7-10).

Linear regression analysis shows that the time delay prior to sample collection did not significantly affect the quantity of DNA recovered. This may be due to the limited number of samples in this study with a lengthy time delay, and the effect may prove more influential if further cases could be included. However in the assessment of the total 252 samples in chapter 3 (page 91), no difference was noted between samples collected within one day and those collected over two weeks after the offence. The time delay between the sample collection and the laboratory submission also proved insignificant, despite a third of the samples being held for over three months prior to submission. This concurs with a 2006 study [128] that found no decrease in DNA recovery from swabs stored for different time periods.

The large number of variables affecting the recovery of DNA from casework samples (such as different donors, differing hand contact, surface types and sampling techniques) greatly inhibits the accurate determination of the effect of a single variable, such as time. These variables are difficult, if not impossible, to ascertain or control in casework, emphasising the inherent variability of forensic trace DNA analysis. Whilst all efforts were made to reduce the number of variables in the experimental work, differences were still noted in the outcome. This highlights the importance of criminalistic consideration of these factors through research, which in combination with the experience of the forensic scientist will allow the interpretation of casework results in the light of propositions put forward by legal parties. With ongoing research and casework data, guidelines can be offered to assess the likelihood of case results given a suggested scenario, with the potential for Bayesian analysis.

This study was used to assist the court's interpretation of DNA evidence in a murder trial, discussed in the introduction. The defence asserted that their client's DNA profile might have been recovered from the crime scene as a result of an innocent visit two weeks prior to the offence. A statement was prepared stating that the ability to recover analysable DNA from outdoor surfaces decreases rapidly over several weeks. With this report countering their argument, and other circumstantial evidence, the accused plead guilty to the murder.

7.5 Conclusions.

Human cells deposited on an outdoor surface such as a window frame or bag will deteriorate significantly ($p < 0.05$) over the course of six weeks through environmental conditions, to such an extent that the chance of recovering a DNA profile is substantially reduced over this time. However if the cells are deposited and stored undisturbed in a cool and dark location, as in a laboratory, profiles may still be recovered after six weeks.

It should also be noted that these experiments were conducted with a large amount of human cells. Contact between a person's hand and an object tends to leave far less DNA on the object, as shown by casework data, which would exacerbate the difficulty of recovering a DNA profile over time. It is therefore imperative that trace evidence is collected expeditiously to give the best chance of a successful outcome.

This research provides an initial look at the extent of the persistence of DNA in the context of volume crime offences, and the results provided a more objective approach to the interpretation of DNA evidence in a criminal trial. Whilst this is a limited study, it demonstrates that research into the trace evidence characteristics of DNA offers a criminalistic approach to biological evidence, of particular importance when the identification of the DNA profile is not in question but the activity leading to its deposition remains uncertain.

Chapter 8:

Discussion and Conclusions

Chapter 8: Discussion & Conclusions

This chapter is divided into sections that assess the findings against the aims of the project. The first section comprises a summary and overall discussion of the results. In this section the results of the methods survey are reviewed, and then the casework data of chapter 3 and the experimental results of chapters 5 to 7 are examined. The limitations of the research and potential areas for further work are discussed in the final component of this section. The second section of the chapter sees the results given a practical context. The overall findings of the project are applied to an interpretive framework for trace DNA in volume crime casework, and the viability of the use of this type of forensic evidence is examined incorporating an assessment of the costs versus benefits. Thirdly the outcomes and recommendations resulting from the project are offered, followed by concluding remarks.

8.1 Summary and discussion of the data

8.1.1 Learnings from the Methods Survey

The first aim of the project was to investigate current methods and practices in trace DNA in the Australasian region, and from this identify areas for improvement. The impetus for the methods survey was that even within the relatively small Australasian forensic community there was little communication between laboratories and organisations earlier in the decade. This has found to be slowly growing with increased information technology enabling more rapid communications and further meetings facilitated through the overseeing national body of the National Institute of Forensic Science (NIFS; now part of the Australian and New Zealand Policing Advisory Agency, ANZPAA). However, from personal experience it is often found that agreements and working groups formed during meetings become secondary in importance when participants have to return and cope with their considerable casework loads. The integration between the various arms of forensic science (police crime scene/laboratory, fingerprints/DNA) is gradually increasing though still has a way to go to be fully effective. Encouragingly it appears individuals at least may be taking a more holistic view of forensic science than the compartmentalised versions of the past, which hopefully will lead to more unified forensic organisations.

The methods employed across the various organisations were found to be similar in the larger processes such as extraction, quantitation and amplification kits, no doubt due to shared aims and the consequently small forensic commercial market, but varied in the finer details. In the 2004 survey deficiencies were noted in contamination prevention procedures, but fortunately by 2009 participants stated stricter measures had been enforced.

The opinion of the value of trace DNA as evidence held by the three groups ranged from average to high, with some attributing a low significance due to delays in processing. Many respondents recognised the investigative and intelligence value of trace DNA, however it is unknown how well this is explained to police investigators. These emerging applications of DNA evidence have yet to be fully exploited in Australian jurisdictions. To date they have been hampered as interstate comparison of DNA databases has only been implemented in recent years. It is also apparent from the answers of participants in this survey that the use of DNA evidence is still very much the justice-based approach, with the focus on individual convictions rather than a broader integration of forensic science information into a national security model.

Technology has progressed in the five years between the surveys, with major advancement in automation and high throughput technologies. These advances will greatly increase the capacity of laboratories and hopefully reduce backlogs. Respondents to the 2009 survey reported in the main that the numbers of trace samples submitted to the laboratory had not changed since 2004. With increased capacity and similar sample numbers it logically follows that backlogs should be reduced and not reach levels seen previously. Several jurisdictions also reported that they had reduced the number of trace samples submitted from volume crimes. Laboratories have been shown to investigate and implement new methods of collection and extraction (although the purpose of these developments may be more for backlog reduction than increased success), and have anecdotally reported an increase in the success of low level samples. Despite these positive indications, proficiency testing and refresher training are still not regularly conducted with regards to trace DNA. The findings of international reports such as the National Academy of Sciences [34] and the Caddy review of low template DNA analysis [211] greatly emphasise the need for scientific transparency and the importance of standardised and ongoing education and training programs. The Australasian region must improve in this area, and should investigate the development of national training and proficiency testing regimes for trace DNA.

One of the greatest needs in forensic DNA analysis is for automated results gathering and dissemination, with frustrations evident in the completed surveys from both within the laboratory and out in the field. The computer technology to provide this has been available for many years, but it requires some development to fit both the laboratory and police force requirements. Biologists do not have time to manually collate statistics, and as found during the collation of the casework data chapter it can be extremely complex and time consuming given the numerous systems and data types in use between forensic organisations. Such collation is vital to ensure best value is achieved, and to guide policies relating to specific sample types. For example, if a particular sample type is proven to be so rarely successful the organisation may be able to limit its submission for certain crime types, whilst ensuring there is no other valid reason for the low success rate. Enabling cross-jurisdictional comparison of results would be helpful in identifying if certain organisations are obtaining better or worse results. The relatively small forensic community of Australasia is also in a good position to share research into new methods, thereby preventing wasted time repeating experiments. A further benefit of improved statistical collation is for training and assessment purposes – crime scene examiners with poor technique may be identified and corrected to ensure value for money and best practice is being achieved. In addition to the benefits to individual cases, forensic intelligence uses and offence linking may be greatly enhanced through the immediacy of the data and potential for analytical processing.

It must be noted however that the problem of results dissemination is not solely IT based, instead a shift must also occur in the philosophy of forensic organisations. As stated previously and as highlighted by Ribaux et al. [69] the current mindset of forensic science is the presentation of evidence on a case-by-case basis, instead of a 'big picture' view. The industry is somewhat hamstrung by its preoccupation with ensuring the acceptance of evidence in court, rather than broadening the scope to increase the viability of the intelligence use of the evidence. This change is unlikely to happen quickly, but a recommendation of this project is that prior to logistical developments, forensic organisations should conduct thorough reviews to consider improvements in the area of forensic intelligence, and to ensure information flows effectively to all stakeholders.

The problems highlighted from the methods survey were aptly summarised in Wickenheiser [243], "*the work of the most dedicated, skilful, and highly motivated investigators, supervisors and forensic scientists can be defeated by the lack of effective case management systems and the lack of systems to ensure communication and co-operation among law enforcement*

agencies". This quote was taken from a Canadian judicial inquiry into a murder case that may have been prevented, had DNA evidence been processed in a more timely manner. As stated previously, the primary role of forensic DNA laboratories is to assist criminal investigations through the reporting of DNA links or exclusions. If these reports are excessively delayed or mislaid due to ineffective systems then the value of that organisation is greatly diminished.

Further to this point, commentators have noted that the focus of research and funding in forensic science has largely been decided without consultation of the end-users [99, 244, 245]. As such, the bulk of research has involved the technology rather than the output. Conversely, a Finnish survey of police investigators found that no responses requested better technology, but instead wanted improved reporting procedures and presentation of evidence [244]. A case is therefore made for new lines of research in forensic science to focus on its interaction with the legal and police communities, incorporation into broader intelligence-led policing methods, and the end product of the technology, rather than the technology itself.

8.1.2 The casework data

The second aim of the project was to investigate casework data regarding trace DNA to gain an understanding of current success rates and factors affecting results in casework. The overall success rate for trace DNA samples collected in NSW casework was found to be 14%, with the potential to increase if some of the 21% of samples resulting in mixtures could be utilised. Organisations considering the use of trace DNA in casework must accept that only around 1 in 7 samples may produce a result. In order to maximise this percentage, organisations should give staff thorough training and proficiency tests in trace DNA collection and analysis, and the knowledge to target the best samples. This factor is discussed further in section 8.2.

The level of DNA recovered from the experimental work was somewhat higher than was recovered from the casework samples. This is likely to be caused by the experimental set up; the location of contact was known, the samples were collected soon after their deposition, and the volunteers may have handled the surfaces more enthusiastically than what would occur in a crime situation. If exact replication of crime scenarios is required, future studies could incorporate blind testing. An additional point of difference between the experimental and casework studies was the threshold cut-offs for homozygote peaks, which were lower for the experimental samples.

It was interesting to note that whilst the standard procedures of the NSW SOCOs state that trace DNA is not to be collected from volume crime scenes, such samples are nevertheless submitted and analysed by the laboratory. The reason for this may be that the organisation tacitly allows the submission of the samples, but does not want to overwhelm the system by specifying their collection in standard procedures. Alternatively, the organisation does not have a system in place to reject these samples, or to notify the SOCO's supervisor that they are not following standard procedure. In either regard, the organisation does not seem to have effective control over the submission of samples. Yet again, the need for more efficient computerised data systems is highlighted, which would give forensic organisations more control to manage their policies. In a recent conference presentation, Himberg [244] noted that the number of DNA samples submitted to the Finnish forensic laboratory has increased exponentially in the last ten years. The question was asked; who is managing this change? The provided answer was that it does not seem to have been instigated or facilitated by the forensic organisations. The deficit of effective management and utilisation of forensic evidence is apparently a global issue.

Authors have called for a greater scrutiny of DNA evidence than has been conducted in the past [99, 100, 246], a rational suggestion when the immense funding required to implement and facilitate DNA evidence is considered. Whilst complex and time consuming to achieve, a complete review of the effect and value of trace DNA evidence in the criminal justice system is warranted.

8.1.3 The experimental results

The third aim of the project was to conduct preliminary experiments into the trace evidence characteristics of DNA. The purpose of this experimental component was to provide initial data to further our understanding of the 'behaviour' and activity of DNA as a trace, and to investigate whether such data collation is practical and useful to criminal investigations. Trace DNA is not visible to the human eye, and therefore it is difficult to definitively state how it came to be present on a surface. These experiments were designed to assist the interpretation of trace DNA evidence, so that forensic scientists may be of more assistance to the court when questions of the activity leading to the deposition of the DNA arise.

The level of background environmental DNA on surfaces tended to concur with what would intuitively be expected; surfaces handled more regularly or in more concentrated areas

tended to hold more background DNA. The differences between the levels of background DNA on surfaces and the level of transferred DNA were quite informative in particular instances. For example, the average amount of DNA transferred during the action of a burglary (2.5ng) is *more* than the average amount of background DNA on windows (0.05ng), but *less* than the average amount of background DNA on entry doors (6.05ng). From the robbery abundance experiments, the level of background DNA present tends to be similar to the level of DNA transferred during a robbery. Despite this, informative profiles can still result with around 40% of profiles from the robbery pairs having the robber as a major component. Another interesting finding noted during the abundance experiments were that small amounts of non-owner DNA are present on many surfaces, and therefore it cannot be assumed that any DNA present must belong to the offender.

The most evident outcome of the abundance experiments is the need for elimination samples to be collected wherever possible, to assist the interpretation of profiles and gain maximum benefit from the investment. This would also prevent meaningless samples (those of victims) being entered onto criminal databases. Previous work [99] has found that DNA databases are most effective when carefully managed and targeted to ensure only quality data is present. High numbers of irrelevant samples reduces the efficiency of the database, and increases the chance of adventitious matches.

In the transfer experiments, clear and definitive examples of shedder status were not observed, unlike some prior studies [53, 150, 151] but concurring with another [152]. It appears there are many factors that influence an individual's shedder status. Transfer is one of the most commonly contested and least understood issues regarding trace DNA evidence [99], and more work is still needed in this area to ensure that correct information is being presented to the court. Future work could determine 'average' transfer levels, as the extreme limits of transfer have already been identified in selected studies of 'good' and 'poor' shedder pairs. A recent novel study by Goray et al. [201] may help to indicate how much DNA would need to be present for an assertion of secondary transfer to be likely.

Like the abundance experiments, the persistence experiments also followed prior expectations. The persistence of DNA was found to be low in outdoor environments, however when in indoor, sheltered locations, the DNA could be recovered for at least six weeks. The results further emphasise the need to expedite attendance at crime scenes to minimise loss of evidence.

Some may question the relevance of this type of research seeing as the results followed so closely to the lines of common sense – is it in fact needed? As proven by the court case outlined in chapter 7, whilst courtroom assertions of certain actions may intuitively seem unlikely, there has been little research to refute or confirm our intuition. Following the hierarchy of propositions as outlined by Cook et al. [185], courts now more often want an answer to the question of activity (how did the DNA get there?) rather than source (from whom did the DNA come?). This was definitely the case in the Omagh bombing trial (see 1.5.4.1), where the court wanted a clearer guiding from the scientists as to the most likely activity that caused the defendant's profile to be recovered from the bomb components, whether through contamination, secondary transfer, or bomb manufacturing. The case scientist was not given the forum to properly explain the evidence, and did not have any data to assist the court with this question [247]. Some scientists suggest that the question of activity may be more for the court to decide rather than the realm of the scientist [168]. However the court is unlikely to have the knowledge to determine how trace DNA transfers and persists without assistance from the scientist. With further research in the field of DNA criminalistics, scientists will be able to offer greater assistance to the court. Given the sheer number of variables involved in trace DNA evidence it is unlikely that definitive answers may ever or should ever be provided, but research can give indications of the probability of obtaining a set of results given activities proposed by investigators and legal members.

Ideally, case-based research projects should be conducted for every case where questions of activity arise, however this is obviously unlikely to occur given the stretched resources of forensic laboratories. Therefore studies such as the experiments described in this thesis become useful, by providing general trends and some limits to support or oppose certain arguments. For less extreme suggestions of activity, the data provide guidance to assist the scientist to formulate a qualified opinion.

Viewing the experiments holistically, a better understanding is provided of the timeline of trace DNA in the context of a specific crime type; from the background levels of DNA on the surface, to the transfer during the crime, and the persistence of the DNA following the event. The aim of the experimental component of the project was to demonstrate that collating data on trace evidence characteristics of DNA is possible and useful. Whilst areas for further work are clearly evident, the application of the results of the persistence study to a criminal trial demonstrates the relevance of this research to casework.

8.1.4 Limitations and areas for future research

There are a number of limitations in this research that must be taken into consideration and highlight areas for further research, some of which have previously been discussed. Several of the shortcomings arise from the complexity of the data collected by forensic DNA laboratories, and the lack of a consistent approach to DNA data collation across the region. Highlighted by the methods survey, a major deficiency in the data collation was the inability to determine the success rates of trace samples from the range of jurisdictions. The field would greatly benefit from the development of a standard definition of DNA success rates that can be applied for cross-comparison. In chapter 3, the inconsistencies between the various IT systems, even within NSW, prevented the value of DNA evidence in criminal justice system from being fully determined. As noted by Briody et al. [100], if a profile is achieved from a sample it does not always follow that a suspect is arrested or convicted, and it was beyond the scope of this project to follow the profiles through to determine their usefulness to the investigation. The value of the mixed profiles could also not be determined. A future study could be undertaken to assess the value of trace DNA samples, from obtaining an exploitable profile through to their influence on the investigation in terms of arrest rates, convictions, and sentence lengths.

The development of the surveys was a difficult task, to ensure that all possible information could be gathered whilst still being of practical length for the participants. Problems were also encountered when attempting to collect an even response from every jurisdiction, and in the follow-up study one jurisdiction failed to return any surveys. This may affect the results in that they may have been skewed to the answers from the jurisdictions with the highest number of responses, however effort was made to avoid this by comparing the jurisdictions rather than averaging the total responses. In hindsight and despite completing 'test runs' of the survey, some of the questions did not gather all the desired information and were perhaps poorly worded, as it was not clear from the responses whether they had been interpreted as intended. Much was learned from the first survey however, and questions were rephrased and the follow up survey format devised in such a way to elicit responses and ease data collation.

Regarding the experimental work, the size of the experimental component limits the conclusions that can be made as to the extent of their effect on DNA recovery. As discussed in the introduction, secondary transfer is often proffered by the defence as the reason their

client's DNA came to be present at the crime scene. Previous studies have shown that this can occur in 'best-case' scenarios [151, 156-158], but a large scale study of transfer would be beneficial to determine how *likely* it is to occur across a general population.

To provide a more accurate quantitation in the persistence experiments, buffy coat and DNA control solutions were utilised, which may not accurately represent trace DNA as the level of transferred DNA would be much lower. Nevertheless it is believed that the results can be used to infer a similar decline from a lower starting amount. Trace DNA research creates a 'catch-22' situation; it is difficult to ever accurately represent case scenarios, which is the reason why casework data was analysed in this project as a complement. However with casework data the large number of variables involved cannot be separated to determine the effect of one on the final result.

Another issue with the experimental work was that the methods were selected early in the project from methods that were in use at the time. Due to the length of the project conducted on a part-time basis, the methods in forensic laboratories changed over time, and it was difficult to achieve the best results whilst maintaining relevancy and consistency across the experiments. Examples of these issues include the quantitation methods; first none were available, then PicoGreen® and Quantifiler™ became readily used; and the concentration of amplified DNA in the capillary electrophoresis run is less than currently used (1.5µL DNA in a total 27µL of master mix in these experiments, now may be increased to 2µL in 11µL). However despite differences in the methods used between the casework data and the experimental component, similar results were achieved in terms of the quantity of DNA recovered from trace samples. It may be that these variables only make up a small contribution to the overall recovery of a useable DNA profile.

8.2 Practical applications of the data

The fourth aim of the project was to investigate whether the data from the experiments can assist with an interpretive framework of trace DNA and aid court presentation. The following sections revolve around a discussion of this aim.

It has been demonstrated that the effectiveness of DNA databases is dependent on the quality of the person and crime scene samples it contains [99]. The triaging of samples collected from serious offences generally occurs some time after the crime scene

examination, by group consultation between investigators and forensic personnel. Given the sheer number of volume crimes, it is important to triage samples out in the field at these scenes to prevent excessive backlogs of unnecessary samples and to ensure only probative samples are entered onto DNA databases. However to perform this triage effectively SOCOs need to be provided the knowledge to target the most appropriate samples.

In a practical context, the data collated during this project may be able to be used by SOCOs to assess the value of evidence whilst they are at the crime scene. There is the potential to produce decision matrices or 'cut off' values to be used in training, or even in the field to assist SOCOs to determine the samples most likely to produce a good result. In NSW there are several hundred SOCOs deployed around the state, often in remote locations. As evidenced by the methods survey consistent training is difficult to provide, and very little training appears to be given specifically in regards to trace DNA. Therefore, many SOCOs may not have access to all the available research and data in their decision-making.

An example of a decision matrix based on street robbery offences is demonstrated by Table 8-1; the table is divided into columns representing a number of variables that contribute to the likelihood of a successful result. The circumstances under which each variable may be encountered in casework as listed in each column, progressing from those detrimental to a successful result through to more favourable conditions. As an example; a wallet that had been owned by the victim for a month is stolen during a street robbery. It is found two hours after the offence in a known dumping ground for stolen items, in a relatively protected location. The wallet has been extensively handled by the offender as all the cards are missing, and according to the victim a fair amount of force is required to pull the cards from the wallet. According to the decision matrix this would be a targeted item for trace DNA given the favourable circumstances of the event. In a second scenario; a handbag owned for several years and used regularly by the victim was stolen. It was found dumped a short distance away from the robbery over three weeks after the offence. Only the wallet has been removed from the bag indicating that it was not extensively handled by the offender. It could be recommended that this bag not be sampled for DNA, but instead only examined for fingerprints (a cheaper option).

Table 8-1. An example decision matrix for street robbery offences.

Variable	Chance of success	Location where item was found	Time since offence	Type of handling by offender	How long owned by victim?	How often used by victim?	Victim buccal swab?
Responses	**Low**	Outdoors–unprotected location	>1mth	Light, eg only banknotes missing from wallet	>2 years	Every day, extensively handled	No
		Outdoors – protected location	2-4 weeks	Moderate, several items missing	1-2 years	Every other day, extensively handled	Yes
	High	Indoors	1-2 weeks	Extensive, item has been rummaged through, lots of items missing	6-12mths	Every other day, not extensively handled	
			1-7 days		1-6mths	Weekly	
			<1 day		<1 month	<Weekly	

Whilst these guidelines are unlikely to be definitive, they nevertheless demonstrate that the data from the experiments conducted during this project can be applied to assess the value of a sample and the likelihood of a usable result. It may even be possible to take this example further, by assigning values to each of the variables with the potential to develop objective cutoff levels for samples; If they do not reach X points, the sample is not collected. The variable columns could be weighted according to the extent of their effect on a successful outcome. This in turn could be ranked against the organisation's priority on certain offence types. It may be impractical for a SOCO to calculate such figures out in the field, but these threshold values may be used in training to demonstrate the principle. By implementing such models into training packages, forensic organisations will have greater control and management over the samples they will eventually process.

An important aim of this project was to develop an interpretive framework to assist the presentation of trace DNA in criminal trials. Given the expense involved in DNA analyses, for trace DNA to be even considered for volume crime investigations its value must be maximised. The interpretive difficulties involved in trace DNA, such as mixture interpretation and determining the significance of a crime scene profile, are considerable and in many jurisdictions may be sufficient for the evidence to be unviable in volume crime investigations. If these problems can be eased, through projects such as this, there is the potential for an increased forensic response to these ubiquitous crimes.

Criminological research on the incapacitation effect of prison on burglary rates found it was not inconsiderable [248]. The article also suggested that "*the incapacitation effect of prison*

on burglary will also increase if either (a) police improve their clear up rate for burglary or (b) prosecutors become more successful at convicting those they charge with burglary". It was noted that the resolution of burglary offences was "*quite low and might be higher if police had the resources required to investigate each burglary more thoroughly*." Trace DNA offers a relatively untapped avenue of investigation, and with a solid interpretive framework and a greater understanding of its trace evidence properties may provide police with a stronger ability to resolve volume crime offences.

8.2.1 An interpretive framework

The presentation of forensic evidence generally requires an assessment of its value, based on the scientist's opinion. To give a more objective approach to what may be quite subjective interpretation, forensic statisticians have battled with various approaches. Two approaches that have been applied to forensic DNA interpretation are the frequentist approach and Bayesian (or logical) framework.

The frequentist approach is the most common currently used to interpret a DNA profile. Only one proposition is considered, usually of the prosecution, and the output is generally the frequency of that profile in a given population as derived from genetic databases. An example of a statement assessing the value of a DNA profile using this approach would be, '*this DNA profile occurs in about one person in 1 000 000 of the population'*. The benefit of the frequentist approach is that it is somewhat simpler to present and understand, although it still has potential to be misinterpreted. The so-called 'prosecutor's fallacy' can turn the above stated conclusion into a one in a million chance that the accused is innocent. Because of its simplicity, it is suitable for simple profiles from good sources of DNA such as blood, but is less effective when mixtures, paternity cases and trace DNA are involved as only one proposition can be considered.

The Bayes theorem is a model based on logic and probability theory, first described by Thomas Bayes in the mid 1700s, and applied in a legal setting in France [249] over a century ago. The approach considers the competing hypotheses of both the prosecution and defence, and the full model incorporates all the evidence involved in the case, heard before and after the DNA evidence. The theorem models the thought process of the judge and jury; it enables the revision of a prior estimate of guilt, based on the evidence currently being presented. The Bayes Theorem is expressed formulaically as follows;

$$\frac{\Pr(H_p \mid E,I)}{\Pr(H_d \mid E,I)} = \frac{\Pr(E \mid H_p,I)}{\Pr(E \mid H_d,I)} \times \frac{\Pr(H_p \mid I)}{\Pr(H_d \mid I)}$$

Posterior Odds = Likelihood Ratio X Prior Odds

Where H_p = the prosecution hypothesis

H_d = the defence hypothesis

E = the evidence

I = the background information relevant to the case.

The likelihood ratio is seen as the domain of the forensic scientist, however there is some debate as to the extent the scientist should incorporate knowledge of the prior odds into their assessment of the evidence [247, 250]. It may be that in certain circumstances knowledge of the case details is essential to proper interpretation of the evidence. A full Bayesian approach incorporates an assessment of the prior and post odds, whereas often a modified Bayesian approach is employed using only the likelihood ratio – referred to as the 'logical' approach. To provide an explanation to the court regarding the value of the finding, the UK Forensic Science Service developed a verbal scale (Table 8-2) for use in reports, containing subjectively assigned statements corresponding to values from the likelihood ratio [251].

Table 8-2. Forensic Science Service verbal scale for the likelihood ratio.

Likelihood Ratio	**Verbal Scale**
>1 to 10	Limited evidence to support
10 to 100	Moderate evidence to support
100 to 1000	Moderately strong evidence to support
1000 to 10 000	Strong evidence to support
>10 000	Very strong evidence to support

Numerous articles have been written applying the Bayes Theorem to DNA evidence [252-259], yet the full approach is still rarely used to present DNA evidence in court. In a 2002 study of 19 European laboratories [249], only two were employing a Bayesian approach to the presentation of DNA evidence. Practitioners tend to avoid this method, as it may be a difficult concept to accurately present to a jury without fear of misinterpretation. Nevertheless, Bayes interpretation has been successfully used to present glass and paint

evidence in New Zealand and the United Kingdom. Is it possible for it to be used to aid interpretation of *trace* DNA, just like other trace evidence?

A major criticism of the practical application of Bayesian analysis, especially in trace evidence areas, is the lack of data needed to give a numerical output. Glass evidence has pioneered the application of the Bayesian framework in trace evidence because the glass features used in forensic comparisons are limited and discrete, and there is an abundance of research into their trace evidence properties [73-75, 77, 78, 80, 160], enabling data to be entered into the equations. Trace DNA has presented difficulties for forensic biology practitioners because there are a greater number of variables involved in its interpretation than for visible sources of DNA such as blood, additional to the frequency of that profile in the population. As demonstrated by the experimental work in this project, trace DNA behaves more like any trace evidence. In fact, it could be argued that the interpretation of trace DNA may be very similar to that of glass: a limited number of discrete features used for the analysis in combination with trace evidence behaviour such as background levels, transfer and persistence.

The complex nature of circumstances surrounding trace evidence requires a rugged interpretive framework. Bayesian networks (BNs) have been used to graphically dissect all variables involved in the recovery of the evidence, providing a tool for the interpretation of the probabilistic relationships between a set of variables. Evett et al. have applied BNs to the interpretation of trace DNA samples [255], and were able to include some data on the variables thereby resulting in a numerical output. Evett et al. conceded that BNs may not be able to be presented in court, but note they allow the scientist to grasp the fundamental issues within a case. As put by the authors, '*the presentation of scientific evidence…particularly in complex cases,… can descend to a welter of ifs, buts and maybes'.* By employing BNs during the interpretation of the evidence, there will be a solid grounding to their conclusions and confidence in the value of the evidence.

In recent years there has been a considerable amount of research into trace DNA, which may contribute to numerical data in a Bayes interpretation. The following example will demonstrate how the data gleaned from the experiments undertaken in this project may be applied to the likelihood ratio.

8.2.1.1 Likelihood ratio example

Readers should note that this is a very simplistic demonstration, and the author defers to forensic statisticians for a thorough mathematical derivation, and indeed the paper by Evett et al. [255] provides an extensive insight. This example serves merely to illustrate that data into the trace evidence characteristics of DNA can be used to provide a numerical, objective assessment of the value of such evidence.

A suburban house is broken into during the day and numerous items have been stolen. The point of entry was through a ground floor window, where the frame was jemmied. It appears the offender entered and exited through this window as the doors were deadlocked. The premises are examined about 24 hours after the offence, and smudged fingerprints unsuitable for comparison are developed on the window frame. A full DNA profile is later recovered from swabs of these marks, which is linked to a person on the DNA database. The suspect is arrested and charged with the offence. In his defence, he states that he was interested in moving into the area, and that he 'looked in that window', without touching it, two weeks prior to the offence. The window is in an unsheltered location with partial sunlight.

The judicial question is one of activity and therefore; what is the probability of, respectively, the prosecution and the defence propositions given the evidence? The court would be unlikely to have the scientific knowledge to answer this question without assistance from forensic experts. Using the Bayes theorem, the judicial question is translated into a scientific question.

The proposition of the prosecution (H_p) is that the accused transferred his DNA profile onto the window during the action of breaking into the home.

The proposition of the defence (H_d) is that the accused transferred his DNA profile onto the window when he glanced inside the home two weeks prior to the event.

Likelihood ratio = $\frac{T_b P_{1d} B}{T_i P_{2w} B}$

T_b = The probability that DNA will transfer during the action of burglary

P_{1d} = The probability that the DNA will persist one day after the offence

B = The probability that the offender's DNA will override existing background DNA on the window

T_i = The probability that DNA will transfer during the action of looking into the window

P_{2w} = The probability that DNA will persist two weeks after the innocent visit

Now to input data into the likelihood ratio;

T_b From the burglary transfer experiments (chapter 5), DNA was transferred in 19 out of 20 occasions, therefore this probability can be estimated at **0.95**

P_{1d} From the persistence experiments (chapter 6), this probability is close to 1, say **0.9**

B From the burglary abundance experiments (chapter 5), very little background DNA was recovered from windows, therefore this probability is **close to 1** (and in any regard is cancelled out of the equation)

T_i The mere action of looking into the window would be less likely to transfer DNA onto the window frame than the forcible action of breaking into the window. Therefore this probability is estimated at **0.1**

P_{2w} From the persistence experiments, the probability of trace DNA persisting for two weeks in an exposed location is close to 0, or an estimate of **0.001**

Therefore;

LR = (0.95 x 0.9) / (0.1 x 0.001) **= 8850**.

Following the verbal scale (Table 8-2), this evidence therefore gives "strong evidence to support" the prosecution proposition, rather than the defence proposition. An alternative presentation is that whatever odds were placed on the offender's guilt prior to this evidence, the trace DNA evidence multiplies that by 8850.

Given the number of variables involved in trace DNA evidence, it is probably unlikely that all the relevant data will ever be researched and known. However if it is known that the trace DNA evidence is in contention, experiments can be devised to assess the contentious issue prior to trial as was performed in the persistence experiments. Also, many of the variables in volume crimes such as burglary have common characteristics and may be able to be encompassed by a bulk study. Even if these devised numerical values are never presented in court, they can help the scientist to evaluate the evidence prior to testimony.

8.2.2 The value of trace DNA in volume crime investigation

The fifth and final aim of the project was to provide an estimate of the value of trace DNA in volume crime investigations in Australia. With further data to assist the interpretation of trace DNA evidence, it may prove to be more broadly applied to criminal investigations. However is it really worth the considerable investment needed to apply it to volume crimes, and will the costs outweigh any benefits in terms of retribution and crime reduction?

Previous cost benefit studies have been used to assess whether the cost of processing DNA is worth the investment in terms of arrests and crime prevention. Tracey & Morgan [246] first attempted a brief assessment of the cost-effectiveness of DNA evidence in 2000, somewhat in response to the public fanfare associated with databases at the time. The authors felt that the massive cost involved in sample processing and database administration was not justified given what they saw as a mediocre return on investment. A more thorough investigation of the cost-benefits of DNA evidence in sexual assault cases in one US laboratory was undertaken in 2004 [243]. Contrary to the previous review, the study found there was 'an extraordinary return on investment' by the application of DNA to sexual assaults, largely because of the considerable cost incurred by the victims of sexual assault in terms of trauma and reduced quality of life.

The first thorough assessment of the value of DNA evidence in volume crime cases was also conducted in the USA, from 2005-2007, where over 1000 cases with DNA evidence were compared to over 1000 cases without DNA evidence, from five different jurisdictions [109]. The study found that twice as many suspects were identified and arrested, and more than twice as many cases accepted for prosecution in cases were DNA evidence was utilised. The study assessed the cost of DNA evidence above the cost of traditional policing, which averaged at US$14169 (approximately AU$15600) per arrest. There was considerable variance between the five jurisdictions, and the cost per arrest ranged from AU$4570 to $34000. The study made no attempt to assess this against the value of the evidence in terms of prevented crimes or retribution, which is an obvious limitation.

There is considerable cost in the set up of forensic laboratories and implementing and maintaining a DNA database – but what value do we place on solving and preventing crime? Logically, the value in apprehending the offender of a burglary is far less than a murderer or rapist, but does the sheer number of volume crimes increase the importance of their

resolution and potential prevention? And as discussed in the introduction, offenders may progress to more serious offences, or be simultaneously involved across the crime spectrum, so interception early in their criminal career becomes much more valuable. From a national security model, the disruption of volume crime offenders may even be calculated as more valuable to society than the apprehension of a murderer who may be unlikely to reoffend. Some studies are sceptical of the ability of DNA evidence to reduce crime rates [100, 246], despite the fact that this effect was offered by early proponents of DNA databases as a primary justification for their existence. There is no conclusive research that suggests any type of forensic evidence helps to reduce crime, but this is a difficult matter to investigate given the number of variables involved. To date, most models applied to capture this information have been too reductive, primarily considering identification and arrests instead of the broad disruption and prevention of criminal activity. The end result may underestimate the actual value of forensic science in general, and DNA in particular.

A small assessment of the costs involved in DNA processing in volume crime cases in NSW is presented here. The costs below are either a specified cost (for example the amount charged to the NSW Police Force for processing each sample) or estimated from the author's knowledge of volume crime investigations and communication with police investigators.

The current price of processing a crime scene sample for DNA in NSW averages at $150, and a person sample $70 [217]. Therefore the cost of analysing DNA evidence for a single volume crime scene would be approximately $410; including two crime scene samples, an elimination sample from the victim, and around an hour of additional work by the SOCO (including the collection at the scene, and administrative work involved in recording the collection and organising transport to the laboratory). Once a database link is received, NSW legislative requirements mean that an additional buccal swab must be collected from the suspect; a further $70 charged to the police for the sample processing, and around an hour's work for investigators to conduct the forensic procedure to collect the sample ($40). The administrative costs to investigate a database match is estimated at $1080; several day's work given a simple case involving brief preparation and statement gathering. The cost to have a DNA expert in court for one day is around $400. Therefore the total cost for use of DNA evidence in a volume crime case is estimated at $2000, which is less than the proffered cost of a burglary event to society at $2700 [84]. This data is demonstrated in Table 8-3. Additionally, the benefit to society of the retribution for the offence is probably immeasurable.

Table 8-3. Estimated costs of DNA evidence in volume crime investigations

Action	*Estimated Cost*
Two crime scene samples	$300
Elimination sample from victim	$70
Additional work by SOCO in collection/admin	$40
Additional reference sample from suspect	$70
Additional work to collect reference sample	$40
Brief preparation	$1080
DNA Expert in Court	$400
Total	**$2000**

If trace DNA were collected from volume crime scenes, it is estimated that 30% of burglaries could produce a DNA sample, increasing from the 5% of scenes where blood is currently located. This estimate is reached from the surveys conducted with SOCOs (see chapter 5), asked to assess potential areas for trace DNA collection. From these samples, a profile is achieved in 20% of samples (from the casework data in chapter 3; 14% of profiles were suitable for inclusion on the database, plus an estimated further 6% percent from the mixtures that could be usable). Therefore; of 1000 burglaries, 300 produce a DNA sample; 60 of these samples give a usable profile, and 20 of those match a person on the database [217]. So for the cost of collecting and analysing DNA samples from 300 burglaries, 20 arrests will result, a cost of $7840 per arrest (see Table 8-4). This is less than the average American estimate of AU$15600 per arrest, which appears to be due to wage structures and American outsourcing costs.

Table 8-4. Total costs of DNA evidence in volume crime investigations

Event	*Costs per event*	*Total*
1000 burglaries		
300 produce a DNA sample	$300 (2 crime scene samples) + $70 (victim elimination) + $40 (additional work required)	$123000
60 DNA samples give a useful profile	$70 (offender buccal swab)	$4200
20 match a person on the database & are arrested	$1080 (administrative costs for brief preparation) + $400 (DNA expert in court)	$29600
17 found guilty		
8 result in a prison sentence		
Total cost for 20 arrests, and 8 prison sentences		**$156800**
Cost per arrest		**$7840**

From the NSW court statistics, of these 20 arrests on average 17 are found guilty (87.3%) and 8 (48.5%) result in a prison sentence [97]. The average prison sentence for burglaries is 8.5 months [97], therefore a total of 68 months would be spent in prison by these 8 individuals. During these 68 months, 216 burglaries would be prevented according to Weatherburn et al.

[248], who found that an average of 38.1 burglaries was conducted per burglar per year. Therefore for DNA costs of $156800, an estimated $583200 would be saved from 216 prevented burglaries (costing society $2700 per burglary [84]), representing a saving of 73%. There is also no current research in NSW to suggest whether DNA evidence has any effect on sentence length, or whether criminal trials incorporating DNA evidence are more likely to produce guilty verdict, although the research by Briody suggests that any effect is minimal [105].

It should be noted that these cost-benefit analyses take a simplistic view and make many assumptions, such as that these offenders would not have been caught by traditional policing methods. The estimates of administrative costs are conservative, including only those that are directly incurred as a result of the DNA evidence, additional to standard investigation costs. It is assumed that the DNA database links are relevant to the case and would result in an arrest. However the analysis was conservative in that it only took into consideration database links, and not the potential for profiles to match suspects not present on the database. The assessment solely tested the effect of the incapacitation of offenders in prison, and not any deterrent effect on crime that may result, as this has been proven to be difficult to assess in prior studies [248]. Also not included are the costs incurred from the incarceration of offenders. Other complicating factors include whether offenders actually increase their rate of burglaries after a prison sentence, but this has been thought to be cancelled out by the effect of rehabilitation in prison [248].

As stated, there have been no thorough cost-benefit analyses of the use of trace DNA evidence in Australia. However in 2009, the NSW Police Force undertook a small study into the value of collecting more than one sample per volume crime scene [260]. In NSW in recent years, an attempt to prevent large DNA backlogs gave rise to a policy whereby SOCOs were permitted to submit one item only from each volume crime scene for DNA testing. This was an arbitrary value and no assessment had been made as to the potential effects of this policy. In the recent cost-benefit survey of this policy, SOCOs from four selected localities were permitted to submit more than one DNA sample per volume crime, using their judgement to decide when this would give best value (for example witness statements suggested more than one offender was involved, or cigarettes with different brands were discovered). The study attempted to discover how often the organisation might be missing the identification of a second offender by limiting sample submission.

Of the 670 volume crime cases surveyed during the study, 120 contained more than one DNA sample for analysis. In 22% of two-sample cases two different DNA profiles were obtained, and in 53% (8) of the three-sample cases there were at least two different profiles. The study concluded that if the number of DNA samples permitted to be submitted from volume crime cases was increased to two, a minimum of 36 additional database links would be achieved annually, at a cost of between $4527 and $5173 per link. The NSW Police Force now permits the collection of more than one DNA sample per volume crime scene, provided there are mitigating circumstances and permission is obtained from a supervisor.

Regardless of the costs involved, the value of DNA evidence greatly decreases if there are excessive time delays in processing, and notification of results and database links. With resources permitting, DNA samples can be processed in 48 hours. However particularly for volume crime, results may not be obtained for months or years. As quoted by one participant in the 2009 method survey, '*turn-around times are so long that identifications are irrelevant'*. A second participant suggested their own cost-benefit analyses of DNA evidence; '*if the total value of the lost goods from the crime is less than the cost of processing the samples then don't collect them'.* In major crime cases such as murders and sexual assaults, identification are always relevant as cases can and will be investigated many years after the offence. However in volume crime cases expediency is paramount, as victims may move on or be unwilling to assist police so long after an offence and the value in pursuing the matter may be low.

The question then arises; what is the point of spending the money processing trace DNA samples if the backlogs and time delays render any result worthless? It would seem good business management for forensic organisations to carefully assess their capabilities and set clear turnaround time targets. If these targets cannot be met, then the number of samples submitted for analysis should be cut back if they cannot be achieved in a timely manner, particularly for volume crime. As noted by the 2009 component of the methods survey, several jurisdictions in Australia have reviewed their policies for volume crime, and no longer collect samples such as vehicle swabs for less serious offences. There is still potential to collect as many samples as relevant from the crime scene, but only submit the most probative. The additional samples can be analysed at a later date if still deemed relevant and extra funding and staff become available.

A further consideration in this matter is that delays mean offenders are likely to be committing extra offences in that time. What consolation is there to the victim when it is realised that had DNA samples been processed more quickly, the offence committed against them may not have occurred? The 2003 report on DNA evidence in the United States graphically demonstrates crimes that could have been prevented had DNA analysis been conducted sooner, including the details of 21 murders and 105 sexual or other assaults [261]. From a purely economic point of view, the cost-effectiveness of DNA evidence is greatly reduced by any delays in processing, as one of the major economic benefits comes from the value of the prevented crimes.

It is understandable that jurisdictions want to implement new techniques quickly in the hope that more crimes will be solved. However often this is without full consideration of the value of the technique versus its cost, and the organisation's capability to deal with the additional information and processes. As a result, and as we have seen with DNA evidence in many jurisdictions [21, 262], large backlogs result which greatly devalue the evidence. Whilst the United States may appear to be lagging behind other countries such as the United Kingdom in terms of their application of DNA evidence to volume crime, their approach to thoroughly investigate the worth of such a large investment prior to its application is admirable. Even though cost-benefit analyses may tend to indicate the value of DNA evidence in volume crime investigations; if there is insufficient funding, staffing and resources to cope with the work then it may not be justified.

8.3 Outcomes and recommendations

The project was broad in scope and varying aspects of trace DNA evidence were investigated, from the current state of play in the casework analysis of the evidence in the Australasian region, to preliminary experimental work into the trace evidence characteristics of DNA. The project highlighted several areas for improvement, which if addressed would greatly assist the relevance and effectiveness of trace DNA and forensic science as a whole. These areas fall into three general categories;

8.3.1.1 Interpretation

It is evident from this project that more work is still needed in the field of trace DNA interpretation. To date, the primary focus of research in this field has been the improvement of technology, and as we are now able to analyse such minute quantities a Pandora's box of interpretive issues is opened. In recent decades there has been a philosophical shift away from the forensic generalists of the past, and a move to keep the forensic scientist closeted in the laboratory away from the context of the crime for fear of seeming biased. This has especially been the case for DNA laboratories where most of the interpretative process so far has focused on the 'who' question (identification). This situation contributed to a general loss of a holistic view of the overall forensic case by forensic scientists. The legal community is now demanding more information and interpretation from experts to assist the judicial process. Experiments designed to mimic casework scenarios, such as those described in this project, and a revisitation to the basic criminalistic concepts may provide more informative evidence for the court rather than, to paraphrase Evett et al. [255], descending into a mire of ifs, buts and maybes.

RECOMMENDATION 1: That further work is conducted into the provision of data for Bayesian analysis of trace DNA evidence, and to assist investigative and legal inquiries into the activity level of the evidence.

8.3.1.2 Review

The value of trace DNA in volume crime investigation should be thoroughly assessed in each jurisdiction. Only the individual stakeholders can assess what value is placed on the resolution of volume crime offences, and their capabilities in dealing with the resulting

samples. Similarly, assessment of a jurisdiction's systems and processes should incorporate the investigation of the intelligence use of DNA evidence. The identification of an offender of a single crime event is just one aspect of the use of DNA evidence, whereas intelligence-led applications can open a world of information relevant to criminal investigation and national security. However intelligence processing can be resource and time intensive, and without prior review of the information output and dissemination systems, the full potential of the information may be lost.

The division of response to volume and serious crime that occurs in forensic organisations is largely based on criminal law. By taking a more global approach to crime and recognising the interaction of criminals across the crime spectrum, organisations may be able to allocate their forensic response according to the best value achieved, rather than to somewhat arbitrarily categorised crime types. However, whilst disappointing for victims of crime and for national security, it may be acceptable for some organisations to draw the line and eliminate the examination of trace DNA samples for certain offences if they are unable to cope with the information and unacceptable backlogs result. If this decision is made, the organisation should take the opportunity to review its processes and invest in research to streamline procedures and reduce turnaround times, so that these samples may be able to be utilised in the future.

RECOMMENDATION 2: That forensic organisations should clearly outline their goals and focus, and conduct broad-reaching reviews to ensure the full potential (both in terms of criminal convictions and intelligence applications) of trace DNA evidence is realised.

8.3.1.3 Logistical improvements

To facilitate the previous points, and once thorough review has occurred, logistical improvements need to be made. The implementation or improvement of automated data management systems would assist intelligence gathering, expedite results, identify training needs and facilitate best practice. Organisations also need to provide effective and ongoing training to staff to ensure quality in samples and analysis, and review, implement and enforce standard operating procedures to maximise the benefits of the evidence.

RECOMMENDATION 3: To assist intelligence applications and to ensure best value is achieved, forensic information flow should be effective and easily accessible to all stakeholders.

RECOMMENDATION 4: Training and proficiency tests in trace DNA analysis should be standardised across jurisdictions, and conducted on an ongoing basis. They should aim towards the professionalisation of the discipline through a moral contract involving employers, employees, and training/proficiency service providers.

8.4 Conclusions

The criminalistic properties of trace DNA demonstrate its inherent variability, but can be investigated in a similar manner to other trace evidence types such as fibres and glass to give a better understanding of its behaviour. Background levels of DNA are present on surfaces commonly encountered in forensic scenarios, and may be sufficient to interfere with the detection of the offender's DNA. DNA foreign to the owner or user of an item may also be found in swabs taken from such an item. Trace DNA transfer is variable, ranging from negligible to high quantities and it appears there are many factors involved. In this research, DNA was found to persist for only short periods in exposed locations, but at least six weeks in sheltered environments. The collection of elimination buccal swabs from victims will greatly assist the interpretation of results, and increase the chance of relevant database links.

The experimental work showed that once the complicating factors of trace DNA evidence such as background levels, transfer and persistence are better understood the evidence increases in value to investigations. Conducting experiments that mimic the case circumstances to ease interpretation may also answer questions of activity arising in court, and during the course of this project greatly assisted an actual murder trial. Data from these and future experiments may be used in Bayesian analyses of trace DNA evidence. In addition, the knowledge gained through these experiments can be used to better educate crime scene personnel and investigators to ensure only samples with the most value are collected and submitted.

Trace DNA has been proven to have value in the resolution of volume crime offences, and the success rate of trace DNA samples in the Australian context is in the order of 15%. This success rate may rise if mixtures can be resolved and interpreted through the collection of

elimination samples, and if effective training is in place to ensure only the most viable samples are collected. However if the collection of trace DNA samples from volume crimes is beyond the jurisdiction's capability, both in terms of backlogs and also sufficient numbers of trained police to investigate the links, then its value may be reduced as timeliness is a pivotal factor. Trace DNA needs to be targeted intelligently; collected by highly trained personnel, analysed using the most effective methods, interpreted with rigorous protocols, and results disseminated in a timely and efficient manner.

Individual jurisdictions should assess the cost of trace DNA evidence against its value in volume crime investigation. If the jurisdiction places a strong emphasis on solving volume crime, then trace DNA may be an effective tool. The use of trace DNA in forensic intelligence applications should also be considered and exploited where possible. However forensic organisations should carefully assess their capabilities and set clear turn-around targets. To this end, it is highly beneficial for forensic organisations to implement effective computerised data management systems so results can be easily disseminated and dissected. Only with thorough review and critique can the field of forensic science move forward. As a final comment; once we come to the general realisation that after all DNA is another type of trace evidence which, as indicated by Ribaux et al. [69], can be considered as the most basic 'material or physical' information on crime, we can enhance the quality of interpretation and therefore the relevance of this evidence to criminal investigations.

"In short, there exists in the field of criminalistics a serious deficiency in basic theory and principles, as contrasted with the large assortment of effective technical procedures…… Criminalistics is an occupation that has all of the responsibility of medicine, the intricacy of the law, and the universality of science. Inasmuch as it carries higher penalties for error than other professions, it is not a matter to take lightly, nor trust to luck. Great divergence of philosophy and opinion exists; we often travel separate roads; the goal is not always clearly recognised. When answers are incomplete, restatement of the question is useful. Where is criminalistics, forensic science, or whatever it may be called, going? Is it not time to make a serious effort to define a goal, so that we may all talk about the same thing and move in similar directions, in order that the field will command greater respect, and generate more pride in its accomplishments?"

- Paul L. Kirk, 1963 [263]

Appendices

Appendix A: Methods Surveys – 2004 and 2009

TRACE DNA ANALYSIS:

Australian and New Zealand Methods Survey 2004.

PART 1 - Collection of trace DNA at crime scenes.

To be completed by crime scene officers or equivalent.

This survey is being conducted as part of a PhD project at the University of Technology, Sydney, and has the support of the National Institute of Forensic Science. It aims to benchmark the current methods and practices utilised in trace DNA analysis, and share this information across the jurisdictions of Australia and New Zealand.

Please answer these questions as accurately as per your current work practices, in as much detail as possible. The survey can be anonymous and will not be used to assess individual performances. Tick as many boxes as appropriate for each question.

Some sections may not be directly relevant to your duties, so please complete only those sections pertaining to tasks you would routinely perform. If your sole function in crime scene is fingerprinting, please complete only those questions that have been marked with a star.

The survey is targeting trace or contact DNA, and the questions should be answered specifically with regard to trace, and not gross (visible) DNA samples and protocols. Trace DNA is taken to mean DNA deposited through handling or wearing items, and **does not include blood, semen, or saliva from cigarette butts.**

Please complete the survey within two weeks of receipt, and return to:

Ms Jennifer Raymond
Redfern Police Station
30 Turner St Redfern
NSW 2016
Ph: (02) 9690 4617
Fax: (02) 9690 4650

TRACE DNA ANALYSIS:
Australian and New Zealand Methods Survey 2004.

SUBJECT DETAILS

Name (optional):……

Email (optional):……

***Position and brief description of duties:**……
……
……
……
……

***Organisation:**……

***State:**……

** = Required fields*

1. FINGERPRINT EXAMINATION (if applicable):

***1.1 What method/s do you routinely use for fingerprint examination at crime scenes, and for what surfaces or situations would you use them?**

□ Standard powder Uses:……..
□ Other powder Uses:……..
□ Cyanoacrylate Uses:……..
□ Cyanoacrylate + stains Uses:……..
□ Iodine/benzoflavone Uses:……
□ Other (please detail and list uses):……

***Which of the above do you use the most?**……

***1.2 When using powder methods, what kind of applicator do you use? If used in different situations, please detail.**

Squirrel or synthetic □Yes □No Uses:……
Fibreglass □Yes □No Uses:……
Magnetic wand □Yes □No Uses:……
Other (specify):…… Uses:……

***Which of the above do you use the most?**……

***1.3 How long are your fingerprint powder brushes kept in use?**

□ Single use/disposable □ 1 week □ 1 month □ 6 months □ > 6 months

***1.3 Do you clean your powder brushes, and how often?**

□ Never □ Occasionally □ Weekly □ Daily

2. DNA COLLECTION (if applicable):

2.1 What method do you use for collection of trace DNA?

□ Cotton swab □ Foam swab □ Tapelift □ Collect whole exhibit
□ Method varied according to target area (please detail):……

2.2 If your method is swabbing, what specific method do you employ?

□ Single dry swab □ Single wet swab □ Two swabs (1st wet, 2nd dry)
□ Two swabs (other combination – please detail):……
□ Other (please detail):……
□ Method varied according to target area (please detail):……

2.3 What solution do you use for swabbing for trace DNA?

□ Sterile water □ Ethanol or % solution of (specify):……..
□ Other (please detail):……

2.4 What action do you use when swabbing an average sized exhibit?

□ Maintain swab in fixed orientation (DNA concentrated on one side)
□ Continual rotation of swab
□ Changing sides/orientation of swab at set times during swabbing
□ Other (please detail):……

2.5 Approximately how many times do you pass over the target area when swabbing an average sized exhibit?

□ 1-2x □ 3-5x □ 5-10x □ 10-20x □ > 20x

2.6 If you tapelift samples for DNA, how many times do you press the tape on the target area?

□ Once
□ A set number of times: please specify……
□ Multiple times till the tape is no longer sticky
□ Other (please detail):……

2.7 When tape-lifting, how is the tape submitted for DNA analysis?

□ Left whole and placed in tube, trying to avoid scrunching up
□ Scrunched up and placed in tube
□ Cut up into a few strips
□ Cut up into several small fragments
□ Placed on an acetate sheet (or similar)
□ Other (please detail):……

3. CONTAMINATION PREVENTION:

Complete all sections relevant to your duties.

***3.1 Do you wear gloves whilst conducting fingerprint examinations?**

□ Never □ Always □ Only for specific situations (please detail):……
**If worn, how often do you change gloves during examinations?*
□ >Once per scene □ Per scene □ Daily □ 1 week □ >1 week

3.2 Do you wear gloves during DNA collection?
☐ Never ☐ Always ☐ Only for specific situations (please detail):……

3.3 What type of gloves do you wear at a scene during DNA collection?
☐ Latex ☐ Cotton ☐ Two pairs latex ☐ Other (please detail):……
If worn, how often do you change gloves during DNA collection?
☐ More than once per exhibit ☐ Per exhibit ☐ Per scene/case ☐ Less frequently

***3.4 Do you wear a face mask whilst conducting fingerprint examinations?**
☐ Never ☐ Always ☐ Only for specific situations (please detail):……
……
**If worn, how often is the mask changed during examinations?*
☐ >Once per scene ☐ Per scene ☐ Daily ☐ Weekly ☐ Monthly
☐ Less frequently

3.5 Do you wear a face mask during DNA collection?
☐ Never ☐ Always ☐ Only for specific situations (please detail):……
If worn, how often is the mask changed during DNA collection?
☐ >Once per scene ☐ Per scene ☐ Daily ☐ Weekly ☐ Monthly
☐ Less frequently

3.6 Do you wear other protective apparel, in addition to your standard work wear, during DNA collection?
☐ No ☐ Hairnet ☐ Overalls ☐ Other full body covering ☐ Lab coat

If yes, how often is the apparel replaced/washed?
☐ >Once per scene ☐ Per scene ☐ Daily ☐ Weekly ☐ Monthly
☐ Less frequently

4. EXHIBIT STORAGE AND TRANSPORT:
Complete if relevant.

4.1 How do you package trace DNA samples?
- Swabs:
☐ In swab container ☐ Paper bag ☐ Plastic container ☐ Box
☐ Other (please detail):……..
If placed in a swab container, is it closed off or with an opening?……

- Other trace items:
☐ Paper bag ☐ Plastic container ☐ Plastic bag ☐ Box
☐ Varying containers dependent on sample (please detail):……
☐ Other (please detail):……

4.2 How do you store trace DNA exhibits?
☐ In fridge ☐ In freezer ☐ At room temperature

4.3 On average, approximately how long would you keep trace DNA exhibits prior to sending to the laboratory?
☐ 1 day ☐ 1-3 days ☐ 3-5 days ☐ 1 week ☐ 2 weeks ☐ Longer

5. GENERAL PRACTICES:
Complete to the best of your knowledge.

5.1 Do you collect trace DNA samples when a potentially identifiable fingerprint has already been obtained from the scene/exhibit?
☐ Never ☐ Often ☐ Only in specific situations (please specify) ……..

5.2 Do you collect trace DNA samples when a good blood, saliva or semen sample is also available from the scene?
☐ Never ☐ Often ☐ Only in specific situations (please specify) ……..

5.3 On average, how many trace DNA samples would you collect per week?
☐ 0-1 ☐ 1-2 ☐ 2-5 ☐ 5-10 ☐ 10-20 ☐ >20

5.4 Do you consider trace DNA for volume crime investigation? (Eg. stolen vehicles, burglaries)
☐ Never ☐ Often ☐ Only for more serious volume crime offences

5.5 Approximately how often would you collect trace DNA for volume crime?
☐ Never ☐ Rarely ☐ Once per month ☐ Once per week ☐ Daily ☐ >Once per day

5.6 For motor vehicles, which parts of the vehicle would you swab for trace DNA?
☐ Steering wheel whole ☐ Steering wheel part (please detail):……
☐ Automatic gear shift ☐ Manual gear shift ☐ Ignition areas ☐ Seatbelts
☐ Other (please detail):……

5.7 From the total trace DNA samples you collect, can you give the approximate percentage of samples coming from the following types of exhibits?

- Motor vehicles ☐**0-5%** ☐**5-10%**☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(steering wheel, gear shift, seatbelt etc)
- Food/drink items ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(bottles, straws, spoons, partially consumed food etc)
- Guns ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Knives/weapons ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Tools ☐**0-5%** ☐**5-10** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(hammers, screwdrivers, crowbars etc)
- Clothing fabric ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(jumpers, underwear, caps, balaclavas etc)
- Clothing hard ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(shoes, belts)
- Watches/jewellery ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Reading/sunglasses ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Packaging ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
(Plastic bags, adhesive tape, drug packaging etc)
- Ropes and wire ☐**0-5%** ☐**5-10%** ☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Paper ☐**0-5%** ☐**5-10%**☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Other touched items ☐**0-5%** ☐**5-10%**☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**
- Other (specify)**.....** ☐**0-5%** ☐**5-10%**☐**10-25%** ☐**25-50%** ☐**50-75%** ☐**75% +**

5.8 In your opinion, how significant are trace DNA samples as items of evidence in the cases you examine?

☐ Highly significant, of great value
☐ Average significance, of average value
☐ Highly insignificant, of little value

6. TRAINING AND EXPERIENCE:

***6.1 What is your highest level of education?**

☐ High School ☐ Certificate ☐ Diploma ☐ Undergraduate degree
☐ Honours degree ☐ Masters degree ☐ PhD

**If you have completed tertiary education, in what field?*

☐ Chemistry ☐ Molecular biology/Genetics ☐ Other biology (specify):……
☐ Policing ☐ Other science (specify):……
☐ Other non-science (specify):……

6.2 How long is it since you were originally trained in trace DNA collection?

☐ <6 months ☐ 6 – 12 months ☐ 18 months ☐ 2 years ☐ >2 years

6.3 What format was the training you received in trace DNA collection?

☐ One-on-one ☐ Group tutorial ☐ Lecture only
☐ Lectures and practical ☐ Practical only

Length of training (full time equivalent):

☐ 1-2 hours ☐ Half-day ☐ Full day ☐ Week course ☐ Longer

6.4 How were you assessed in trace DNA collection?

☐ Practical test ☐ Written exam ☐ Oral exam ☐ No official assessment

6.5 Do you receive refresher courses in trace DNA collection?

☐ No ☐ Every 6 months or less ☐ Once yearly ☐ > Once yearly

***6.6 How long have you been employed as a crime scene officer (or equivalent)?**

☐< 3 months ☐ 3-6 months ☐ 6-12 months ☐ 1-2 years ☐ 2-5 years ☐ >5 years

TRACE DNA ANALYSIS:
Australian and New Zealand Methods Survey 2004.

Part 2 – Laboratory Analysis.

To be completed by laboratory scientists.

This survey is being conducted as part of a PhD project at the University of Technology, Sydney, and has the support of the National Institute of Forensic Science. It aims to benchmark the current methods and practices utilised in trace DNA analysis, and share this information across the jurisdictions of Australia and New Zealand.

Please answer these questions as accurately as per your current work practices, in as much detail as possible. The survey can be anonymous and will not be used to assess individual performances. Tick as many boxes as appropriate for each question.

There are a number of sections within this part of the survey. The sections are divided according the individual processes of sample collection, DNA extraction, quantitation, typing, analysis and results. Your duties may only include a subset of these processes, therefore please complete only those sections that are specific to your work. In addition, please complete the training and education section at the end of the survey.

The survey group would appreciate full protocols, which can be attached to the survey and returned. If further space is required, please use the final page.

The survey is targeting trace or contact DNA, and the questions should be answered specifically with regard to trace, and not gross (visible) DNA samples and protocols. Trace DNA is taken to mean DNA deposited through handling or wearing items, and **does not include blood, semen, or saliva from cigarette butts.**

Please complete the survey within two weeks of receipt, and return to:
Ms Jennifer Raymond
Redfern Police Station
30 Turner St Redfern
NSW 2016
Fax: (02) 9690 4650

Queries about the survey may be directed to raym1jen@police.nsw.gov.au

TRACE DNA ANALYSIS:
Australian and New Zealand Methods Survey 2004.

SUBJECT DETAILS

Name (optional):……

Email (optional):……

***Position and brief description of duties:**

……
……
……
……

***Organisation:**……

***State:**……

***Date of survey completion:**……

** = Required fields.*

1. SAMPLING:
To be completed if applicable to your duties.

1.1 How do you sample trace DNA exhibits in the laboratory? Tick all that apply, and specify the types of surfaces/exhibits for which each method would be employed.

□ Substrate cut up *List surface types:*……
□ Tape lift *List surface types:*……
□ Single dry swab *List surface types:*……
□ Single wet swab *List surface types:*……
□ Two swabs (1 wet, 1 dry) *List surface types:*……
□ Two swabs (other combination – *please detail and list surface types*):……
□ Other (*please detail and list surface types*):……

1.2 What solution do you use for swabbing for trace DNA?
□ Sterile water □ Ethanol (or % solution) □ Other (please detail):……

1.3 What type of swab do you use?
□ Foam swab □ Cotton swab □ Branded swab or other (please detail):

1.4 What action do you use whilst swabbing an average-sized exhibit?
□ Maintain swab in fixed orientation (DNA concentrated on one side)
□ Continual rotation of swab
□ Changing sides/orientation of swab at set times during swabbing
□ Other (please detail):……

1.5 Approximately how many times do you pass over the target area during swabbing of an average-sized exhibit?
□ 1-2x □ 3-5x □ 5-10x □ 10-20x □ > 20x

1.6 When tape-lifting a sample for DNA (if applicable), what type of tape do you use?
Please specify type and brand……

1.7 When tape-lifting, how much pressure do you apply?
□ Just allow contact
□ Press firmly with fingers once
□ Press firmly with fingers multiple times - Approx_____times.
□ Other (please detail):……

1.8 How many times do you press the tape on the target area?
□ Once
□ A set number of times: please specify……
□ Multiple times till the tape is no longer sticky
□ Other (please detail):……

1.9 How do you prevent the tape sticking onto itself, or to the inside wall of the tube?
……
……
……
1.10 When tape-lifting, how is the tape submitted for DNA analysis?
□ Left whole and placed in tube, trying to avoid scrunching up
□ Scrunched up and placed in tube
□ Cut up into a few strips
□ Cut up into several small fragments
□ Other (please detail):……
……

2. CONTAMINATION PREVENTION DURING *COLLECTION*
To be completed if applicable to your duties.

2.1 Do you wear gloves during exhibit examination and DNA sampling?
□ Never □ Always □ Only for specific situations (please detail):……
……

2.2 What type of gloves do you wear during DNA sampling?
□ Latex □ Two pairs latex □ Other (please detail):……

Approximately how often do you change gloves during DNA sampling?
□ More than once per exhibit □ Per exhibit □ Per scene/case
or is it time related; □ per hour □ per day □ other (please specify) ……..

2.3 Do you wear a face mask during DNA sampling?
□ Never □ Always □ Only for specific situations (please detail):……
……
If worn, how often is the face mask changed during sampling?
□ Per exhibit □ >Once per case □ Per case □ Daily □ Weekly □ Monthly
□ > Monthly

2.4 Do you wear other protective apparel during DNA collection?
□ No □ Hairnet □ Full body covering □ Overalls □ Lab coat

If yes, how often is the apparel replaced/washed?
□ >Once per case □ Per case □ Daily □ Weekly □ Monthly □ > Monthly

3. EXTRACTION:
To be completed if applicable to your duties.

3.1 What proportion of the swab do you use?
□ Whole □ Most □ Half □ < Half

3.2 In what condition is the swab prior to extraction?
□ Wet □ Moist □ Dry

3.3 Do you perform any of the following on the swab during extraction?
□ Cut into many small fragments □ Cut up slightly
□ Teased apart □ None

3.4 What type of tube do you used during extraction?
□ Standard 1.5mL eppendorf □ 10mL tube
□ Other (please detail):……
If more than one type specify when each type is used:……

3.5 What extraction procedure do you follow for trace DNA samples?
Please attach detailed protocol if possible.
□ 5% Chelex □ Organic □ Brand kits (please specify):……
□ Other (please detail):……
□ Different methods used for different sample types (please detail):……

If chelex procedure is used:
Volume of chelex used:……..
Incubation time at 56°C:……..
Incubation method at 56°C:
□ Water bath □ Shaking water bath □ Heat block □ Incubator
Incubation time at 100°C:……
Incubation method at 100°C:
□ Water bath □ Shaking water bath □ Heat block □ Incubator
Is the sample vortexed;
□ Prior to 56°C incubation □ Prior to 100°C incubation □ After 100°C incubation
Time vortexed:…….
Are tubes centrifuged, if so, at what point and for how long?……

3.6 How do you isolate the extract?
□ Remove swab from tube □ Remove extract and place in second tube

3.7 Please list any variations to standard protocols which may be used:

3.8 Are any cleanup or concentration techniques employed?
□ Centricon □ Microcon □ QIAquick □ Ethanol precipitation
□ Brand kits or other (please specify):……

How often are cleanup and/or concentration techniques used?
□ Always □ Never □ For certain samples (please detail):

Is variation/experimentation in your standard methods allowed for difficult samples?

---

4. CONTAMINATION PREVENTION DURING *EXTRACTION*
To be completed if applicable to your duties.

4.1 Do you wear gloves whilst performing DNA extraction?
□ Never □ Always □ Only for specific situations (please detail):……
4.2 What type of gloves do you wear whilst performing DNA extraction?
□ Latex □ Two pairs latex □ Other (please detail):……..
Approximately how often do you change gloves whilst performing DNA extraction?
□ After touching any tube
□ After performing a specific step in the protocol (please detail):……
or is it time related;
□ Every 15 minutes □ Every half hour □ Every hour □ Per day
□ Other (please detail):……

4.3 Do you wear a face mask whilst performing DNA extraction?
☐ Never ☐ Always ☐ Only for specific situations (please detail):……
……
If worn, how often is the face mask changed during sampling?
☐ Per series of extractions ☐ Daily ☐ Other (please detail):……..

4.4 Do you wear other protective apparel whilst performing DNA extractions?
☐ No ☐ Hairnet ☐ Full body covering ☐ Lab coat
If worn, how often is the apparel replaced/washed?
☐ > Once per case ☐ Per case ☐ Daily ☐ Weekly ☐ > Weekly

5. QUANTITATION:

To be completed if applicable to your duties.

5.1 What DNA quantitation methods do you employ for trace samples?
☐ Quantiblot ☐ Real-time PCR ☐ None for trace
☐ Other (please detail):……

5.2 What volume of the DNA extract do you use for quantitation? ……µL

5.3 What percentage is this of the extract? ……..%

5.4 Do you report the estimates only as equal to one of the standards, or a specific amount or concentration?

5.5 Do you repeat all negative samples if the lowest standard is not detectable? ……

5.6 Do you amplify samples with a negative Quantiblot result?
☐ Never ☐ Always ☐ For certain cases (please detail):……
……

5.7 Are you happy with the results of your quantitation method, and is it relevant or effective with trace samples?

---

6. PCR:
To be completed if applicable to your duties.

6.1 What type of PCR multiplex do you use for trace samples?
☐ Profiler Plus™ ☐ Profiler Plus/Cofiler™ ☐ Powerplex®1.1/1.2 ☐ Powerplex®16
☐ SGM Plus™ ☐ Other (please detail):

6.2 What reaction volume do you use?
☐ 50µL ☐ 25µL ☐ 15µL ☐ 10µL ☐ Other (please detail):……..

6.3 How many PCR cycles do you run?……..
……

6.4 Do you use any variations to the manufacturer's methods (eg BSA addition etc)?
……
……
……
……
6.5 Do you set up PCR amplification in a dedicated hood/cabinet?……

6.6 What thermocycler do you use?……

6.7 Is the thermocycler in a purpose committed area?……

6.8 Is the amplified product used and retained in a purpose committed area?……

6.9 Have you tried, or are you aware of Low-Copy Number (LCN) analysis? Please comment.
……
……
……
……

7. TYPING:
To be completed if applicable to your duties.

7.1 What electrophoresis platform do you use for the analysis of trace DNA samples?
□ ABI 377 □ ABI 310 □ ABI 3100
□ Other (please detail):

7.2 What volume of amplified product do you add to the sample loading mix?___µl
7.3 What is the total volume of the sample loading mix? ___µl
ABI 377 or equivalent
Volume of sample mix loaded per well: ___ µl

ABI 310/3100 or equivalent
Injection time:……
Run time:……
Voltage:……
Internal Standard used:……

8. ANALYSIS:
To be completed if applicable to your duties.

8.1 What is your criteria for calling an allele?……
……
Minimum limit for heterozygote alleles:……
Minimum limit for homozygote alleles:……..

8.2 Do you repeat sample amplification?
□ Never □ Always □ For certain cases (please detail):……

8.3 Do you ever use up all of the available sample to obtain a result?……

9. TIME AND STORAGE:
Provide estimates for those stages relevant to your duties.

9.1 Please approximate the general time intervals for the following stages:

1. Lab receipt to examination
□ < 24 hrs □ 1-6 days□ 1 week – 1 month □ 1-6 month □ > 6 months
2. Examination to extraction
□ < 24 hrs □ 1-2 days□ 2-6 days□ 1 week – 1 month □ > 1 month
3. Extraction to quantitation
□ < 24 hrs □ 1-2 days□ 2-6 days□ 1 week – 1 month □ > 1 month
4. Quantitation to amplification
□ < 24 hrs □ 1-2 days□ 2-6 days□ 1 week – 1 month □ > 1 month
5. Amplification to typing
□ < 24 hrs□ 1-2 days□ 2-6 days□1 week – 1 month □ > 1 month

9.2 What are the storage conditions of samples at the following stages?
1. Exhibit prior to DNA sampling
□ Room temp □ Fridge □ Freezer –15°C □ Freezer –70°C
□ Different temps for different exhibit types (please detail):……..
……
2. Extracted DNA prior to amplification
□ Room temp □ Fridge □ Freezer –15°C □ Freezer –70°C
3. Extraction DNA after amplification
□ Room temp □ Fridge □ Freezer –15°C □ Freezer –70°C
4. Amplified product prior to typing
□ Room temp □ Fridge □ Freezer –15°C □ Freezer –70°C
5. Amplified product after typing
□ Room temp □ Fridge □ Freezer –15°C □ Freezer –70°C

10. RESULTS:
Complete to the best of your knowledge.

10.1 Approximately how many trace DNA samples (and/or exhibits) would you personally process per week?
□ 0-1 □ 1-2 □ 2-5 □ 5-10 □ 10-20 □ 20-50 □ >50

10.2 Can you give the approximate percentage of these trace DNA samples coming from volume crime offences (eg burglaries, stolen motor vehicles)?
□ 0-5% □ 5-10% □ 10-25% □ 25-50% □ 50-75% □ 75% +

10.3 Can you give the approximate percentage of these trace DNA samples coming from the following types of exhibits?

Motor vehicles □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
(steering wheel, gear shift, seatbelt etc)
Food/drink items □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
(bottles, straws, spoons, partially consumed food etc)
Guns □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
Knives/other weapons □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
Tools □0-5% □5-10% □10-25% □25-50%□50-75% □75% +
(hammers, screwdrivers, crowbars etc)
Clothing fabric □0-5% □5-10% □10-25% □25-50%□50-75% □75% +
(jumpers, underwear, caps, balaclavas etc)
Clothing hard □0-5% □5-10% □10-25% □25-50%□50-75% □75% +
(shoes, belts)
Watches and jewellery □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
Reading/sunglasses □0-5% □5-10% □10-25%□25-50% □50-75% □75% +
Packaging □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(Plastic bags, adhesive tape, drug packaging etc)
Ropes and wire □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Paper □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Other touched items □0-5%□5-10% □10-25% □25-50% □50-75% □75% +
Other (specify)…… □0-5%□5-10% □10-25% □25-50% □50-75% □75% +
……

10.4 In your opinion, overall and/or per sample type, what proportion of trace DNA samples provide a result that is suitable for use in the particular case or through the DNA database?

Overall □0-5% □5-10% □10-25%□25-50%□50-75% □75% +
- Per sample type:
Motor vehicles □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(steering wheel, gear shift, seatbelt etc)
Food/drink items □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(bottles, straws, spoons, partially consumed food etc)
Guns □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Knives/other weapons □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Tools □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(hammers, screwdrivers, crowbars etc)
Clothing fabric □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(jumpers, underwear, caps, balaclavas etc)
Clothing hard □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(shoes, belts)
Watches and jewellery □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Reading/sunglasses □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Packaging □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
(Plastic bags, adhesive tape, drug packaging etc)
Ropes and wire □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Paper □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Other touched items □0-5%□5-10% □10-25% □25-50%□50-75% □75% +
Other (specify)…… □0-5%□5-10% □10-25% □25-50% □50-75% □75% +
……

10.5 In your opinion, how significant are trace DNA samples as items of evidence in the cases you examine?
□ Highly significant, of great value
□ Average significance, of average value
□ Highly insignificant, of little value

11. TRAINING AND EXPERIENCE: **-** *All to complete.*

11.1 What is your highest level of education?

□ High School □ Certificate □ Diploma □ Undergraduate degree
□ Honours degree □ Masters degree □ PhD

- If you have completed tertiary education, in what field?

□ Chemistry □ Molecular biology/Genetics □ Other biology (specify):……
□ Policing □ Other science (specify):…….
□ Other non-science (specify):……

11.2 How long is it since you were originally trained in trace DNA collection?

□ <6 months □ 6 – 12 months □ 18 months □ 2 years □ <2 years

11.3 What format was the training you received in trace DNA collection?

□ One-on-one □ Group tutorial □ Lecture only
□ Lectures and practical □ Practical only
□ 1-2 hours □ Half-day □ Full day □ Week course □ Longer

11.4 How were you assessed in trace DNA collection?

□ Practical test □ Written exam □ Oral exam □ No official assessment

11.5 Do you receive refresher courses in trace DNA collection?

□ No □ Every 6 months or less □ Once yearly □ > Once yearly

11.6 How long have you been employed as a laboratory scientist (or equivalent) and been collecting trace DNA samples?

□< 3 months □ 3-6 months□ 6-12 months □ 1-2 years□ 2-5 years□ > 5 years

TRACE DNA ANALYSIS:
Australian and New Zealand Methods Survey 2004.

Part 3 – Management, Training, Research and Development.

To be completed by managers of staff collecting and/or profiling trace DNA samples.
This survey is being conducted as part of a PhD project at the University of Technology, Sydney, and has the support of the National Institute of Forensic Science. It aims to benchmark the current methods and practices utilised in trace DNA analysis, and share this information across the jurisdictions of Australia and New Zealand.

Please answer these questions as accurately as per your current policing and/or laboratory arrangements, in as much detail as possible. The survey can be anonymous. Tick as many boxes as appropriate for each question. If further space is required, please use the final page.

The survey is targeting trace or contact DNA, and the questions should be answered specifically with regard to trace, and not gross (visible) DNA samples and protocols. Trace DNA is taken to mean DNA deposited through handling or wearing items, and **does not include blood, semen, or saliva from cigarette butts.**

Name (optional):……
Email (optional):……
Position:……
Organisation:……
State:……..

Date of survey completion: / /

Please complete the survey within two weeks of receipt, and return to:
Ms Jennifer Raymond
Redfern Police Station
30 Turner St Redfern NSW 2016
Ph: (02) 9690 4617
Fax: (02) 9690 4650

Queries about the survey may be directed to raym1jen@police.nsw.gov.au

i) How many staff are in the group that you supervise?……
ii) How many of these are able to collect trace DNA samples?……
iii) How many are able to analyse/interpret trace DNA samples?……
iv) Please provide a brief outline of the setup of your laboratory; eg. how many teams and what type of duties they perform, and how the workload is divided etc.

……
……
……

1. TRAINING AND ASSESSMENT:

1.1 What is the minimum level of education your biologists and/or crime scene officers must hold?
□ High School □ Certificate □ Diploma □ Undergraduate □ Honours □ Masters □ PhD

1.2 What type of degree do your biologists and/or crime scene officers generally hold?
□ Molecular biology/Genetics □ Other biology (please detail):……
□ Other science (please detail):……
□ Other non-science (please detail):……

1.3 What training in trace DNA (theory and/or practical) do you provide for staff?
□ Accredited course □ Lectures/tutorials □ On-the-job, extensive
□ On-the-job, limited □ None

1.4 Do you provide ongoing refresher courses (in relation to trace DNA)?
□ Often □ Occasionally □ Only as a response to specific needs □ Never

1.5 If refresher courses are provided, how regularly?
□ <6 months □ Yearly □ Every 2 years □ > 2 years

1.6 Do you conduct proficiency assessments (specifically relating to, or incorporating trace DNA) of your staff?
□ Blind testing □ Random testing □ Regular notified testing □ None

1.7 If such proficiency assessments are conducted, how regularly?
□ 2 months □ 2-6 months □ 6-12 months □ Every 2 years □ >2 years

2. METHODOLOGY

2.1 In your laboratory, is variation or experimentation in standard trace DNA analysis methods permitted for difficult or unusual samples?……
……
……
……

3. RESEARCH AND DEVELOPMENT:

3.1 Are you currently investigating alternative procedures and/or methods in the following steps of analysis;

- Sampling: □ Yes □ No
If yes, please briefly describe:……
……
……
……
- Extraction: □ Yes □ No
If yes, please briefly describe:……
……
……
……**Amplification:** □ Yes □ No
If yes, please briefly describe:……
……
……
……
- Low Copy Number Techniques: □ Yes □ No
If yes, please briefly describe:……
……
……
- Typing/Analysis/Interpretation: □ Yes □ No
If yes, please briefly describe:……
……
……

4. RESULTS:

4.1 Do you routinely collect and maintain statistical records on:

Type and number of trace samples collected	□ Yes	□ No
Number of trace samples submitted for DNA extraction	□ Yes	□ No
Number of these providing sufficient DNA for amplification	□ Yes	□ No
Number of these providing partial or full profiles	□ Yes	□ No

4.2 On average, approximately how many trace DNA samples (and/or exhibits) does your team analyse per week?
□ 0-1 □ 1-2 □ 2-5 □ 5-10 □ 10-20 □ 20-50 □ 50+

4.3 What is the approximate proportion of all the DNA samples that you analyse, from trace DNA samples?
□ 0-5% □ 5-10% □ 10-25% □ 25-50% □ 50-75% □ 75% +

4.4 Can you give the approximate percentage of these trace DNA samples coming from volume crime offences (eg burglaries, stolen motor vehicles)?
□ 0-5% □ 5-10% □ 10-25% □ 25-50% □ 50-75% □ 75% +

4.5 Can you give the approximate percentage of these trace DNA samples coming from the following types of exhibits?

Motor vehicles *(steering wheel, gear shift, seatbelt etc)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Food/drink items *(bottles, straws, spoons, partially consumed food etc)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Guns	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Knives	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Other weapons	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Tools *(hammers, screwdrivers, crowbars etc)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Clothing fabric *(jumpers, underwear, caps, balaclavas etc)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Clothing hard *(shoes, belts)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Watches and jewellery	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Reading/sunglasses	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +
Packaging *(Plastic bags, adhesive tape, drug packaging etc)*	□0-5%	□5-10%	□10-25%	□25-50%	□50-75%	□75% +

Ropes and wire □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Paper □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Other touched items □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Other (specify)…… □0-5% □5-10% □10-25% □25-50% □50-75% □75% +

4.6 In your opinion, overall and/or per sample type, what proportion of trace DNA samples provide a result that is suitable for use in the particular case or through the DNA database?

Overall □0-5% □5-10% □10-25% □25-50% □50-75% □75% +

- Per sample type:
Motor vehicles □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(steering wheel, gear shift, seatbelt etc)
Food/drink items □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(bottles, straws, spoons, partially consumed food etc)
Guns □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Knives □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Other weapons □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Tools □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(hammers, screwdrivers, crowbars etc)
Clothing fabric □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(jumpers, underwear, caps, balaclavas etc)
Clothing hard □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(shoes, belts)
Watches and jewellery □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Reading/sunglasses □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Packaging □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
(Plastic bags, adhesive tape, drug packaging etc)
Ropes and wire □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Paper □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Other touched items □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
Other (specify)…… □0-5% □5-10% □10-25% □25-50% □50-75% □75% +
……

4.7 Are the answers to questions 4.2 – 4.5 based on:
□ Detailed stats □ Some general stats □ General impression

4.8 In your opinion, how significant are trace DNA samples as items of evidence in the cases you examine?
□ Highly significant, of great value
□ Average significance, of average value
□ Highly insignificant, of little value

Any additional comments:

TRACE DNA ANALYSIS:

2004 Australian and New Zealand Methods Survey – 2009 follow up.

This survey is the successor of a survey conducted in 2004 as part of a PhD project at the University of Technology, Sydney. The 2004 study aimed to benchmark the current methods and practices utilised in trace DNA analysis, and share this information across the jurisdictions of Australia and New Zealand. The results can be found in the article '*Trace DNA Analysis; Do you know what your neighbour is doing? A multi-jurisdictional survey.'* FSI:Gen, 2(1) 2008, 19-28.

Please read the questions carefully and answer them as accurately as per your current work practices. The questions are mainly 'tick a box' style, but please add any further detail if necessary. Tick as many boxes as appropriate for each question. The survey can be completed anonymously, and should not take more than 30 minutes to complete. The form can be completed electronically (preferred), or printed and completed by hand.

The survey is targeting trace or contact DNA, and the questions should be answered specifically with regard to trace, and not DNA from blood, saliva or semen. Questions not relevant to your duties may be skipped over.

Whilst a collation of data from this survey may be published, names of participants and their institution will not be disclosed. Any collated data will be made available to participants.

Please complete the survey within two weeks of receipt, and return to Ms Jennifer Raymond by fax, email or post:

Fax: (02) 9688 9211
Email: raym1jen@police.nsw.gov.au
Post: Mark Attention: Jen Raymond
NSW Police Forensic Science Services Branch
6-20 Clunies Ross St, Pemulwuy
NSW 2145

Thank you for your assistance and participation in this survey.

Kind regards,

Jen Raymond
Supervisors: Dr Roland van Oorschot, Prof Claude Roux, Mr Simon Walsh.

SUBJECT DETAILS

Name (optional):
Email (optional):

Please tick the boxes that reflect your *current* duties and/or position in relation to trace DNA:

Scene based:
☐ You collect trace DNA samples from scenes

Laboratory based:
☐ You collect trace DNA samples from exhibits in the laboratory
☐ You extract DNA from trace DNA samples
☐ You amplify and run trace DNA samples
☐ You type profiles generated from trace DNA samples
☐ You use generated profiles from trace DNA samples to assist the interpretation of case scenarios and/or database matches
☐ You report trace DNA profiles interpretations for court purposes

Management:
☐ You manage a work unit that collects trace DNA samples from scenes
☐ You manage a work unit that collects trace DNA samples from exhibits in the laboratory
☐ You manage a work unit that extracts DNA and/or generates genetic profiles
☐ You manage a work unit that interprets profiles generated from trace DNA samples
☐ You manage a work unit that uses the interpreted profiles to assist investigations

***Organisation:**

***State:**

***Date of survey completion**:

** = Required fields. Please note that organisation details will not be disclosed in any publication.*
Note: The questions highlighted in red are for laboratory based scientists only. All other questions relate to all survey participants.

---

1. METHODS & PROTOCOLS:

This section relates to the procedures used in the collection and analysis of trace DNA samples. Please skip over the questions that do not relate to your duties.

1.1 Have any of your methods for collecting trace DNA samples changed since 2004?
If yes, please briefly detail.

☐ Yes ☐ No ☐ Not relevant to my duties

Details:

1.2 Have any of your methods for trace DNA analysis changed since 2004 in the following areas?
If yes, please briefly detail.

	Yes	No	Detail:
- Sampling	☐	☐	
- Extraction	☐	☐	
- Quantitation	☐	☐	
- Amplification	☐	☐	
- Analysis	☐	☐	

1.3 Are you currently using robotics for any aspect of trace DNA analysis?

	Yes	Are currently implementing	Are considering	No
- Extraction	☐	☐	☐	☐
- Quantitation	☐	☐	☐	☐
- Amplification	☐	☐	☐	☐
- Analysis	☐	☐	☐	☐

Details:

1.4 Has the total number of trace DNA samples permitted to be collected at a scene or in the laboratory changed since 2004?

☐ Yes has *increased* for volume crime scenes
☐ Yes has *decreased* for volume crime scenes
☐ Yes has *increased* for major crime scenes
☐ Yes has *decreased* for major crime scenes
☐ No has remained the same
☐ Unsure

Details:

1.5 Has there been a significant change in the type of items from which trace DNA samples are collected?

☐ Yes, samples from certain offence types are no longer collected or processed
Detail:
☐ Yes, samples from certain objects are no longer collected or processed
Detail:
☐ Yes, now collecting or processing samples from additional offence types
Detail:
☐ Yes, now collecting or processing samples from additional objects
Detail:
☐ No
☐ Unsure

1.6 If there has been a change in the number or type of trace samples analysed in your jurisdiction, in your opinion what is the reason for this change? Tick all appropriate.

☐ Because of a change in submission policy created from internal lab research and validation
☐ Because of a change in submission policy created from external research/validation
☐ Because of a change in submission policy for cost saving reasons
☐ Because of a change in submission policy for backlog reduction needs
☐ Because of a change in methods (eg robotics)
☐ Because of a change in lab staff numbers (greater or fewer)
☐ Because of a change in crime scene officer numbers (greater or fewer)
☐ Because of a change in crime rates

Comments:

2. COMMUNICATION & REPORTING

These questions relate to the collation and dissemination of the results from **trace DNA samples** and analyses. Please answer to the best of your knowledge, and as before, skip over questions that do not relate to your duties.

2.1 Has your organisation implemented or improved an electronic information management system since 2004?

☐ Yes our system has improved a great extent
☐ Yes our system has improved somewhat
☐ We did not previously have an electronic management system but have since implemented one
☐ No, our system is still the same as in 2004
☐ Unsure / Other

Comments:

2.2 If applicable, does your electronic management system allow the collection of statistics (automated or manual) in the following areas?

Data	Yes, automated by the system	Yes, manually without too much difficulty or time	Yes, manually with considerable difficulty or time	No, it is not possible to readily collect	I don't know
No. of trace samples submitted to lab	☐	☐	☐	☐	☐
Types of trace samples submitted (eg trace swabs of steering wheel etc)	☐	☐	☐	☐	☐
Region/suburb where sample was collected	☐	☐	☐	☐	☐
Name of person who collected sample	☐	☐	☐	☐	☐
Quantity of DNA in sample	☐	☐	☐	☐	☐
Percentage of successful analyses of trace samples, per sample type	☐	☐	☐	☐	☐
Types of profiles recovered (eg full profile, partial, negative)	☐	☐	☐	☐	☐
Turn-around times for trace DNA sample analysis (time from lab submission to receipt of results)	☐	☐	☐	☐	☐
No. of database hits from trace samples	☐	☐	☐	☐	☐
No. of cases in which the result was of relevance to the investigating officer and/or the courts	☐	☐	☐	☐	☐

2.3 Are any of these data collated on a regular basis?

Data	Yes, ≤ weekly	Yes, monthly	Yes, every 6-12 mths	Sporadically, when research is needed	No, never	I don't know
No. of trace samples submitted to lab	☐	☐	☐	☐	☐	☐
Types of trace samples submitted (eg trace swabs of steering wheel etc)	☐	☐	☐	☐	☐	☐
Region/suburb where sample was collected	☐	☐	☐	☐	☐	☐
Name of person who collected sample	☐	☐	☐	☐	☐	☐
Quantity of DNA in sample	☐	☐	☐	☐	☐	☐
Percentage of successful analyses of trace samples, per sample type	☐	☐	☐	☐	☐	☐
Types of profiles recovered (eg full profile, partial, negative)	☐	☐	☐	☐	☐	☐
Turn-around times for trace DNA sample analysis (time from lab submission to receipt of results)	☐	☐	☐	☐	☐	☐
No. of database hits from trace samples	☐	☐	☐	☐	☐	☐
No. of cases in which the result was of relevance to the investigating officer and/or the courts	☐	☐	☐	☐	☐	☐

2.4 If you are the person, or work unit, collecting the trace DNA samples from exhibits or scenes (and you are not a reporting officer), are you informed on the quality and/or amount and/or success of the DNA obtained from the sample you collected?
☐ Yes regularly ☐ Yes in response to my request ☐ Yes, irregularly or rarely
☐ No, never

2.5 If you are the person, or work unit, extracting DNA, generating profiles and/or analysing profiles from collected trace DNA samples, is the quality and/or amount and/or success of the DNA obtained from the sample disseminated to the person that collected the sample?
A) If the person collecting the sample was a crime scene officer (external to the lab) who submitted the sample:
☐ Yes regularly ☐ Yes in response to a request ☐ Yes, irregularly or rarely
☐ No, never

B) If the person collecting the sample was someone from within your lab:
☐ Yes regularly ☐ Yes in response to a request ☐ Yes, irregularly or rarely
☐ No, never

2.6 If you are the person, or work unit, extracting DNA, generating profiles and/or analysing profiles from collected trace DNA samples, is the quality and/or amount and/or success of the DNA obtained from the sample disseminated to the police investigators?
☐ Yes regularly ☐ Yes in response to a request ☐ Yes, irregularly or rarely
☐ No, never

2.7 In summary, are you able to easily access all the data that you would like (or feel would be useful) regarding trace samples? (To improve your knowledge, interpretation, assessment, service delivery, identification of improvement opportunities etc)
☐ Yes ☐ Partly (access to some but would like more) ☐ No (would like far better access to relevant data)

2.8 If results are being collated, are the data used for any of the following policy applications?
☐ The results collected are used to modify or introduce new methods
☐ The results collected are used to change sample acceptance criteria
☐ The results collected are used to direct training
☐ The results collected are used for another purpose
Detail:

3. TRAINING/EDUCATION:
These questions relate to prior education, internal training and proficiency tests conducted in trace DNA.

3.1 Has the level of education in the entry requirements for your position changed since 2004?
☐ Yes has increased ☐ Yes has decreased ☐ Unsure ☐ No has stayed the same

3.2 In which year did you receive authorisation to:
A) Collect trace DNA samples from casework:
B) Extract, amplify and/or type trace DNA samples:

3.3 Has the level of internal training regarding trace DNA (i.e. scope and/or depth of content, the competency test requirement etc) changed in your organisation since 2004?

A) In relation to sample collection (at the scene or in the lab):
☐ Yes has increased ☐ Yes has decreased ☐ Unsure ☐ No has stayed the same
B) In relation to sample amplification to typing:
☐ Yes has increased ☐ Yes has decreased ☐ Unsure ☐ No has stayed the same

3.4 Has the frequency of refresher training regarding trace DNA changed in your organisation since 2004?
A) In relation to trace DNA sample collection (at the scene or in the lab):
☐ Yes has increased ☐ Yes has decreased ☐ Unsure ☐ No has stayed the same
B) In relation to trace DNA sample amplification to typing:
☐ Yes has increased ☐ Yes has decreased ☐ Unsure ☐ No has stayed the same

3.5 What is the frequency of proficiency tests that specifically relate to trace DNA (Note, the standard CTS Biology tests are not considered to be such a test)?
A) In relation to trace DNA sample collection (at the scene or in the lab):
☐ More than once a year ☐ Once a year ☐ Once every two years
☐ Less than once every two years ☐ None since original training
B) In relation to trace DNA sample amplification to typing:
☐ More than once a year ☐ Once a year ☐ Once every two years
☐ Less than once every two years ☐ None since original training

3.6 Do you spend time conducting research activities and/or reading relevant literature in relation to trace DNA?

☐ Yes, I spend considerable time on these activities
☐ Yes, I spend limited time on these activities, but I am happy with this amount
☐ Yes, I spend limited time on these activities, but feel that I should do more
☐ No, I don't spend time on these activities

3.7 If you don't spend time on trace DNA research activities and/or reading relevant literature, what is the reason for this?

☐ Lack of time
☐ Lack of facilities and resources in your organisation
☐ Lack of interest
☐ I am not encouraged by my organisation to conduct these activities
☐ I am happy with my level of knowledge in this area
☐ Other reason

Detail:

4. OPINIONS:

4.1 In your opinion, how significant are trace DNA samples as items of evidence in *volume* crime?

☐ Highly significant, of great value
☐ Average significance, of average value
☐ Highly insignificant, of little value

4.2 In your opinion, how significant are trace DNA samples as items of evidence in *major* crime?

☐ Highly significant, of great value
☐ Average significance, of average value
☐ Highly insignificant, of little value

COMMENTS:

Appendix B: Methods Survey

Total Responses by Jurisdiction

CRIME SCENE EXAMINERS - TRAINING, EMPLOYMENT and EDUCATION

Opinion of the significance of trace DNA	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Insignificant					3			7		10
Average	8	11	1	6	2	1	1	10		40
Highly significant	3	4	3	3	2	6	5	6	1	33
Total	*11*	*15*	*4*	*9*	*7*	*7*	*6*	*23*	*1*	83
Education level	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
High School	0	1	2	2	4	2	2	6		19
Certificate/Diploma	4	4	2	3	1	4	2	13		33
Undergraduate degree	6	7		1	2	1	1	6		24
Honours degree	2	7					1	1		11
Postgraduate degree/diploma	1	0		3	1				1	6
Total	*13*	*19*	*4*	*9*	*8*	*7*	*6*	*26*	*1*	93
Time employed	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
3-6 months							1	5		6
6-12 months					2		1	1		4
1-2 years	1	2			2	1	1	4		11
2-5 years	5	7	2	1	1	1	1	9	1	28
>5 years	7	10	2	6	3	5	2	7		42
Total	*13*	*19*	*4*	*7*	*8*	*7*	*6*	*26*	*1*	91
Original training in trace DNA	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
One-on-one	2	2	2	3			3	3		15
Group tutorial	4	2	1	1	2			11		21
Lecture/practical exercises	5	8	1	3	4	5		6		32
Other	2	7			2	2	3	6	1	23
No original training				2						2
Total	*13*	*19*	*4*	*9*	*8*	*7*	*6*	*26*	*1*	93
Length of original training	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1-2hrs	5	8	2	3	2	4	2	9		35
Half-day		5	1	2	1	2	1	2		14
Full day	7	1	1	1	2	1	1	3		17
Week		2			2			5		9
> Week	1						2	4	1	8
No original training				2						2
Total	*13*	*16*	*4*	*8*	*7*	*7*	*6*	*23*	*1*	85
Assessment at end of training?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
None	3	5		6	1	5	3	5		28
Practical	6	7	1	1	2	2		14		33
Practical and written	3	2	1		3			1	1	11
Written	1	1		1			2			5
Other		1	2		1		1	3		8
Total	*13*	*16*	*4*	*8*	*7*	*7*	*6*	*23*	*1*	85
Refresher course regularity	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
None	9	15	4	5	3	4	2	14	1	57
6 months							1			1
Yearly	2	1		2	1	2		7		15
>Yearly	1				3	1	1	2		8
Total	*12*	*16*	*4*	*7*	*7*	*7*	*4*	*23*	*1*	81

FINGERPRINT (FP) EXAMINATION

Most common FP method used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Standard powders (black & white)	11	13			7	6	5	17	1	60
Std powders and cyanoacrylate	1			1						2
Std and magnetic powders								2		2
Other powders				1						1
Magnetic powders				1						1
Most common applicator used in FP examinations	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Feather brush & magnetic wand				2						2
Fibreglass brush		1					2			3
Fibreglass brush & magnetic wand									1	1
Magnetic wand				2						2
Squirrel hair brush	9	12			6	6	4	19		56
Squirrel & fibreglass brushes					1			1		2
Paintbrush	1									1
All	1									1
Time applicator is kept in use	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1 month								1		1
1-6mths		2								2
6 months	4	5		2			1	1		13
>6mths	9	6		2	7	6	4	18	1	53
Other							1			1
Regularity of applicator cleaning	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Never	9	8		2	3		3	2	1	28
Occasionally	4	5		2	4	6	2	14		37
Monthly								1		1
Weekly							1	2		3

TRACE DNA SAMPLING

Methods of trace DNA sampling used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Whole exhibit collected	8	6		5	4	3	5	6	1	38
Section of sample cut out	2	1		3	3	1	1	1	1	13
Tapelift	9	1		3	2			2		17
Single swab	3				5		6	16		30
Wet & Dry swabs	9	15	1	9	1	1		3	1	40
Other						6		1		7
Type of swab used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Cotton swabs	11	15		7	6		6	22	1	68
Cotton and branded swabs								1		1
Cotton and foam swabs						1				1
Foam swabs			4			5				9
Branded swabs	3			1	1					5
Type of solution used in swabbing	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Sterile water	12	15		9	5		6	23	1	71
Water & Ethanol			3		2	1				6
Ethanol			1			5				6
Type of action used during swabbing	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Continual rotation	1	3	1	7	4	4	3	20	1	44
Maintain swab in set orientation, one side	10	6	2	1	3		2	1		25
Rotate swab at set times during swabbing	1	5		1		2		2		11
Other action			1				1			2

Times swab passed over substrate	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1-5x	6	4	1	4	3	3	1	9		31
5-10x	3	7	1	4	4	2	4	9		34
10-20x	2	2	1	2		1		5	1	14
More than 20x		1					1			2
Areas of vehicle swabbed	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Steering wheel	7	13	3	7	4	5	4	13	1	57
Part of steering wheel	2	2	1	1	1		3	3		13
Automatic gearstick	6	12	2	7	2	5	3	14	1	52
Manual gearstick	7	15	3	7	4	6	3	15	1	61
Doorhandles		5		2	1			3	1	12
Handbrake	1	6			1			1	1	10
Seatbelts	1	2	3	1	2			8	1	18
Ignition area	1		1	2	1	2	1	2	1	11
Rearview mirror	1							1		2
Other	1	1	1		1	1	1	5	1	12

TAPELIFTING

Tapelift action	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Pressed once on surface	3			1	1			1		6
Pressed a set number of times	1		1	1	1					4
Pressed multiple times on surface	6	1	2	1	1			1		12
Other	1			1						2
Pressure used during tapelifting	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Using fingers firmly pressing once	8		3	1				1		13
Using fingers firmly pressing 2-5x	1	1		2	2			1		7
Using fingers firmly pressing 5-10x				1						1
Tape just contacted to surface	2									2
Pressed firmly with palm and rubbed					1					1
How tapelifts are submitted	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
On an acetate sheet	3	1		3	2					9
Lifts in an envelope								1		1
In a petri dish	6									6
On transparent film					1					1
Tape whole in tube	2		3	1				1		7
How swabs are submitted	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Swab container with an opening, in a paper bag	8	13			2		4	8		35
Swab container with an opening	2			2	1		1	4		10
Swab container with an opening, in an envelope	1			6	3			9		19
Swab container closed			4			1		1	1	7
Paper bag	1	2					1	1		5
In a kit provided with swab						6				6
Box	1									1
Envelope/2 envelopes				2	1					3
How other trace exhibits are submitted	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Paper bag	4	7	1	4	3	2	2	6		29
Paper bag or box			2	1				1		4
Paper bag or plastic container		3								3
Paper bag, plastic container, box					1					1
Varies	5	3	1	1	2	4	3	9	1	29

CONTAMINATION PREVENTION

Gloves worn during FP exam?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always	12	13	1	1	6	5	5	18	1	62
For specific situations only	1			3	1	1		1		7
Frequency of glove change during FP	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
>once per scene	9	2		2	2	1	5	5	1	27
Per scene		6	1	1	2	4		14		28
Daily	1	2								3
Weekly	2	3			1					6
>weekly	1				2	1				4
Gloves worn during DNA exam?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always	13	15	4	8	7	7	5	23	1	83
For specific situations only				1						1
Frequency of glove change during DNA exam	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
>once per exhibit		2	2	3			1	1	1	10
Per exhibit	12	11	2	5	6	6	4	13		59
Per scene	1	2		1	1	1		7		13
Type of gloves worn during DNA exam	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Cotton								1		1
1pr cotton, 1pr latex	3	1						3		7
1pr cotton, 2pr latex									1	1
2pr latex	1	9	2	3	1	1	1	2		20
Latex	8	3	1	5	4	6	3	15		45
Nitrex/Nitrile	1	2		1	2		1	2		9
PVC			1							1
Facemask worn during FP exam?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always	1	8	1		1		2	2		15
Specific cases only	9	4		4	3	1	3	9	1	34
Never	3	1	1		3	5		8		21
Frequency of mask change	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Per exhibit							1			1
>once per scene	7	1	1	2	1		1	2	1	16
Per scene	2	2		2		1	3	5		15
Daily		2						1		3
Weekly		5			2			3		10
>monthly		2					1	1		4
Facemask worn during DNA exam?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always	3	11	1	3		7	6	20	1	52
Specific cases only	7	2	2	3	1			2		17
Never	3	2	1	3	6			1		16
Frequency of mask change	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Per exhibit	1		1	3		1	1			7
>once per scene	7	2		2	1	3	2	3	1	21
Per scene	2	2	1			3	2	17		27
Daily				1						1
Weekly		5					1	3		9
>monthly		2								2

Other protection worn?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No	2	11	1	1	2	4	2	13		36
Overalls only	4	2	2	2	4		4	8		26
Labcoat	3							1		4
Overalls+labcoat	1			3				1		5
Fullbody		1			1	2			1	5
Hairnet+fullbody				3						3
Other	3		1							4
Frequency of other protection change	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
>once per scene	3	1	1	4			3		1	13
Per scene	3	1	1	5	1	2		6		19
Daily	2	1	1		4		1	1		10
Weekly		1					1	3		5
Monthly								1		1
>monthly		2								2

TIME AND STORAGE

How trace exhibits are stored prior to lab submission	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
In fridge	11	6			1			4		22
In freezer									1	1
At room temperature	2	9	4	9	5	7	6	19		61
Varies					1					1
Time stored until lab submission	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1 day	6		2	1				1		10
1-3 days	5	4	2	3	1			6		21
3-5 days		4		1	1	2	4	3		15
1 week		1		3	2	1	2	7	1	17
2 weeks		2			1	1		1		5
> 2 weeks		2			2	3		5		12

GENERAL PRACTICES

Is trace DNA collected if a suitable fingerprint is located?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Never	1	1		2	1			1		6
Often	6	6	4	6	4	5	6	13	1	51
Specific cases only	4	8		1	2	2		8		25
Is trace DNA collected if a suitable blood, saliva, or semen sample is located?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Never		5		1	1			6		13
Often	4	3	4	2	4	3	3	7		30
Specific cases only	7	7		6	2	4	3	10	1	40
Is trace DNA collected at volume crimes?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Never				4	1			2		7
More serious volume crimes only	5	9		1	3			9		27
Often	7	5	4	6	2	5	6	11		46
No. of trace samples collected per week	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
0-1	1	4		3	4		1	11		24
1-2	4	6		3	1			5		19
2-5	2	3	2	3		4		6		20
5-10	4	1	1		1	2	3			12
10-20	1		1		1		1	1		5
>20		1				1	1		1	4

No. of trace DNA samples collected from volume crimes	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
>once per day				1			4			5
Daily	3		2	1		2	1	2		11
1 per week	2	3	2	1	1	2		3		14
2-5 per week	2					1				3
Monthly	3	4		1	2		1	3		14
Rarely	2	4		1	2			9	1	19
Never				1	1	2				4

LABORATORY STAFF - TRAINING, EMPLOYMENT and EDUCATION

Opinion of the significance of trace DNA	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Insignificant					1					*1*
Average		1		6	1	2		2		*12*
Highly significant		1	4	2	2			4	2	*15*
Depends on the case circumstances		2						2		*1*
Education Level	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
High School								1		*1*
Certificate/Diploma	1					3				*4*
Undergraduate Degree	1	3	2	2		2	3	3	5	*21*
Honours degree		1	2	1		2	4	6	1	*17*
Masters		1	1	8	4		1			*15*
Postgraduate Diploma				3						*3*
PhD							8	3		*11*
Time since training	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<6 months						1			2	*3*
6-12 months			1	3	1	1		1	1	*8*
18 monthrs		1	1		1	1		2		*6*
2 years			2	2		1		2	1	*8*
>2 years	1	2	1	9	2	3	1	5	2	*26*
n/a								1		*1*
No formal training						1		2		*3*
Length of training	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1-2 hours		1	1		1	3		3	2	*11*
Half-day				6		1		3		*10*
Full day			2	3	1			2		*8*
Week				2		1		2		*5*
Ad hoc				1				1		*2*
Continual		1								*1*
> Week		1	2	1	2	2	16		4	*28*
Refresher courses	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
None	1	2	5	11	4	5	16	8	5	*57*
Yearly				1				1		*2*
>Yearly						1			1	*2*
Continual		1								*1*
Experience	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<3 months							1		1	*2*
3-6 months							1		1	*2*
6-12 months			1	2		1	4			*8*
1-2 years		1	3	3	1	2	4	4	1	*19*
2-5 years	1	1	1	6	1	1	4	4	3	*22*
>5 years		1		2	2	3	2	5		*15*
Format of training	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
One on one		2	5	10	4	6		6	4	*37*
1 on 1, with lecture/prac/or written	1			2		1				*4*
Group tutorial								2		*2*
Lecture and Practical				1				1		*2*
Practical		1		1			16	1	2	*21*

Assessment of training	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
None	1	2	1	4	3	5		7	5	*28*
Oral exam			1			1				*2*
Practical exam		1		8			16	1	1	*27*
Prac & Oral			3			1				*4*
Prac & written exam				1						*1*
Prac, Written and oral				1				1		*2*
Written & Oral					1			1		*2*

SAMPLING

Sampling methods used	**ACT n=1**	**NSW n=3**	**NT n=4**	**NZ n=13**	**QLD n=4**	**SA n=6**	**TAS n=1**	**VIC n=11**	**WA n=6**	***Total***
Whole exhibit used	1	1	3	6	1	5	1	4	5	*27*
Substrate cut up	1	3	1	7	2	2	1	9	5	*31*
Tapelift	1	3	4	11	4	6	1	11	6	*47*
Single swab			2	2	4	1	1	4	6	*20*
Wet & Dry swabs	1	3	3	3		4	1	9	1	*25*
Other method			1	1	2	5		4	1	*14*
Solution	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Water	3	1		13	1		1	10	4	*33*
%ethanol			4			3				*7*
%eth+H2O			1		3				1	*5*
Other						3				*3*
Swab	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Cotton	1	3		11	4			11	2	*32*
Branded swab				1					3	*4*
Foam			1			3				*4*
Foam/Cotton			3			2				*5*
Branded/Foam							1			*1*
Other			1							*1*
Swabbing motion	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Continual rotation throughout	1	2	2	8	1	5	1	7	3	*30*
Rotation at set times during swabbing		1		5		1		4	1	*12*
Maintain swab in set position, concentrating on one side			2		3				2	*7*
Other			1							*1*
No of times swab passed over surface	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1-2x				1	1	1				*3*
3-5x	1	1	1	3	1	2	8			*17*
5-10x		2	2	4	1	1		2	2	*14*
10-20x			2	5		2	1	1	4	*15*
>20x					1					*1*

TAPELIFTING

Tape brand	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
3M,Scotch, or Magic		2		6	1		1	8	4	*22*
Sellotape			1	4	1	6				*12*
Post-it			2							*2*
General, u/k brand			1	1						*2*

Tape action	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Pressed once on surface						4		1	2	*7*
Pressed 2-3x	1		2	4	1	2	1	7		*18*
Pressed 5x		2		2				1	1	*6*
Pressed 10-20x			2	3	1					*6*
Pressed multiple times		1		3	2				3	*9*
Other			1					1		*2*
How tape preventing from sticking to tube?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Pressed in bottom of tube	3		1						1	*5*
Cut up								1		*1*
Pressed until no sticky left		3	4	5	1	4	1	5	1	*24*
" +cutup					2			1		*3*
" +stretched								1		*1*
" +rolled up				1						*1*
Rolled up				2					1	*3*
" +s/side out					1	1			2	*4*
" +in buffer				1						*1*
" +pipette				1						*1*
Scrunched				1						*1*
Washing				1						*1*
Often can't								2	1	*3*
How tape is submitted for analysis	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Cut into a few strips		1			1					*2*
Cut into several small pieces	1	2	5		2		1	9		*20*
Placed in a petri dish									6	*6*
Rolled in tube						3				*3*
Scrunched and placed in a tube				6				1		*7*
Left whole and placed in a tube				6	1	3				*10*

CONTAMINATION PREVENTION: SAMPLING

Type of gloves worn during sampling	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
2 pairs latex			1	1				2		*4*
Latex	1	4	4	13	3	6	1	9	6	*47*
2 pairs vinyl								1		*1*
Frequency of glove change during sampling	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
> Once per exhibit	1	2	4	8	1	4	1	5	5	*31*
Per exhibit		2	1	5	2	2		7	1	*20*
Per case				1						*1*
Facemask worn during sampling?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always		3		14		6	1	11	6	*41*
Specific cases only	1	1	5		3					*10*
Frequency of facemask change during sampling	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Per exhibit			1	1	1	3			2	*8*
> Once per case	1	1	1	1	1	1				*6*
Per case				1		2			2	*5*
Daily		3	1	11			1	6	2	*24*
Weekly								4		*4*
Monthly								2		*2*
>Monthly			1							*1*

Other protection worn during sampling?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Hairnet/full body				1						*1*
Hairnet/lab coat		3		12					1	*16*
Labcoat	1	1	5	1	3	6	1	12	5	*35*

EXTRACTION

% of swab used in extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Whole	2	3	2	12	1	3		7	6	*36*
Most		1	1					1		*3*
Half			2		2		1			*5*
Depends				2						*2*
Condition of swab prior to extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Wet						1				*1*
Moist		1	2	2	1					*6*
Dry	2	2	2	10	2	1		8	6	*33*
Moist or frozen							1			*1*
Moist or dry		1		1		1				*3*
All			1	1						*2*
How is the swab treated prior to extraction?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Cut into many small fragments		1	2		1	1			6	*11*
Cut up slightly		1	3	8	1	1		1		*15*
Cut or teased apart		1			1			2		*4*
Teased apart								4		*4*
None	2	1		6			1	1		*11*
What size of tube is used for extraction?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Std 1.5mL eppendorf	2	3	4	10	3	3		2	5	*32*
1.5mL or 10mL			1	1				6		*8*
1.5mL or other		1		2			1	1		*5*
Method of extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
5% chelex	2		3			3		3	4	*15*
Organic				14			1			*15*
5% chelex or organic			1					5	2	*8*
5% chelex or branded kit					1					*1*
5% or 20% chelex			1							*1*
20% chelex		3			2					*5*
Volume of chelex used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
50uL for 20% chelex		3								*3*
75uL						2				*2*
100uL						1				*1*
150uL					3					*3*
180uL			2							*2*
200uL	2		1					2	6	*11*
1mL								1		*1*
Sample dependent								4		*4*
Chelex incubation time at 56°C	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1 hour			5							*5*
20 minutes	2	2			3	3		8	6	*24*

Incubation method at 56°C	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Heatblock		3				3	1			*7*
Incubator				1				1		*2*
Shaking water bath			4					5		*9*
Shaking water bath/Incubator								1		*1*
Water bath	2		1		3				6	*12*
Water bath/Incubator								1		*1*
Incubation time at 100°C	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
8min	2	3	4		2	3		8	5	*27*
When is the sample vortexed?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Prior to 56°C incub, prior and post 100°C incub			4		2			6	4	*16*
Prior and post 100°C incubation	2	1				2				*5*
Prior 100°C incubation		2						1		*3*
Prior 56°C and 100°C incubation					1	1		1	1	*4*
Prior 56°C incubation			1						1	*2*
When is the sample centrifuged?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Post 100°C incub for 3 minutes	2	1	2			1		8	2	*16*
Post 100°C incub for 1 minute									1	*1*
Post 100°C incub for 5 minutes									2	*2*
Post 56°C and 100°C incubation		1				1				*2*
Between all steps for 3 minutes					1					*1*
Twice for 3 minutes			1							*1*
Between all steps			1		1	1				*3*
For 15 minutes				1						*1*
How is the extract isolated?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Remove extract and place in second tube	2	1	1	14	3	3		8	6	*38*
It is not isolated			2							*2*
Pierce tube and centrifuge							1			*1*
Using a spin basket		2								*2*
Variation in standard methods used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Use of spin basket						1				*1*
Addition of DTT for difficult samples			1							*1*
Chelex volumes								1		*1*
Longer incubation times					1					*1*
Organic method instead of chelex				2						*2*
Are cleanup methods used?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always	2			12		2				*16*
For certain samples		4	4	1	3	1	1	8	5	*27*
Cleanup method	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Brand kits									2	*2*
Centricon or QIAquick								8		*8*
Ethanol precipitation				10						*10*
Ethanol precipitation or Centricon				1						*1*
Ethanol precipitation or Microcon				1						*1*
Microcon	2	4	3				1			*10*
Microcon or Brand kits					3					*3*
Phenol/Chloroform				1						*1*
QIAquick						1			3	*4*
QIAquick or Microcon						2				*2*

Is variation to std methods permitted?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No		1		3	1	1		5	5	*16*
Yes	2	2	4	11	2	2	1	2	1	*27*

CONTAMINATION PREVENTION: EXTRACTION

Type of gloves worn during extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Latex	2	3	4	13	3	2	1	7	6	*41*
2 pairs latex			1	1						*2*
Frequency of glove change during extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Every half hour				2				1		*3*
Every 15minutes or at a specific step in protocol			1	1			1	1		*4*
Per extraction batch									1	*1*
When exiting the lab						1				*1*
After touching any tube		2	2			1			2	*7*
At a specific step in protocol	1		2	4	1	1		5	2	*16*
Other/varies	1	1		6	2				1	*11*
Facemask worn during extraction?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Always		3		1		3	1	7	6	*21*
Never	2		4	7	3					*16*
Only for specific situations/other			1	6						*7*
Frequency of facemask change during extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Per extraction series			1			2	1	2	3	*9*
When exiting the lab						1				*1*
Daily		3		3				3	3	*12*
Weekly									2	*2*
Specific situations/other				1						*1*
Other protection worn during extraction?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Full body covering				1						*1*
Labcoat	2	3	5	13	3	3	1	7	6	*43*
Frequency of this protection change	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
> Once per case							1			*1*
Per case					1					*1*
Daily		1		14						*15*
Weekly	2	2	5		2	3		5	4	*23*
> Weekly								2	2	*4*

QUANTITATION

Quantitation method	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
None for trace DNA samples			3	1		3				*7*
Quantiblot		3		11				6	6	*26*
Real-time PCR	1				3					*4*
Real-time PCR/Quantiblot								1		*1*
SYBR green							1			*1*
Volume of extract used for quantitation	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
10uL								6	6	*12*
20uL		3						1		*4*
5uL				11		1	1			*13*
2uL	1				3					*4*
Percentage of extract used for quantitation	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<5%	1				3				4	*8*
10-20%		2		11			1	7		*21*

Reporting estimates	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
A specific amount is reported				1	2	1	1			*5*
A specific concentration is reported	1	3		4	1			2		*11*
Reported as equal to one of the standards				1				4	6	*11*
Reported as equal to one of the standards, or an average								1		*1*
Both a specific amount and being equal to a standard				4						*4*
Are negative samples repeated if lowest std is not detectable?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No		3		10		1		1	6	*21*
Yes					2			5		*7*
Are you happy with your quantitation method?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No	1	2		2	1	1		5	6	*18*
Not really				5						*5*
Partly								2		*2*
Still developing					2					*2*
Yes		1		1			1	1		*4*

PCR

Multiplex used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Profiler Plus	2	3	2		2	3	1	8	2	*23*
Profiler Plus/Cofiler					1				3	*4*
Profiler Plus/Identifiler			3							*3*
SGM Plus				11						*11*
Reaction volume used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
50uL	2			11	3	2		8		*26*
25uL		3	2				1		4	*10*
25-50uL						1				*1*
20uL			2							*2*
10uL									1	*1*
Thermocycler	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
ABI 9600		2								*2*
ABI 9700	2	1	4	11	3	1	1		3	*26*
Both 9600 and 9700						2		5		*7*
Number of PCR cycles	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
28x	2	3	5	10	3	3	1	4	5	*36*
30x								2		*2*
28+34x				1						*1*
Is variation permitted to std methods?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No	2	1	3	7	3	2	1	7	4	*30*
Yes		1	2	1						*4*
Is the thermocycler in the same area where amplified product is used and stored?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Yes	2	3	4	11	3	3	1	7	4	*38*
No			1							*1*
Is the amplified product used and retained in a purpose committed area?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Yes	2	3	5	10	3	3	1	7	5	*39*
No			1							*1*

Are separate labcoats used in the PCR area, and how are they distinguished?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No					1					*1*
Yes - but not distinguishable									3	*3*
Yes - by colour		3	5	11			1	7		*27*
Yes - are disposable					1					*1*
Yes - have a label	2									*2*
Yes - by location only					1	3			2	*6*
Are shoecovers worn in the PCR area?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No	2	3	4	11	3	3	1	7	5	*39*
Yes			1							*1*
Have you tried, or are aware of Low Copy Number analysis?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No			1			1			3	*5*
Not tried, but aware of	1	3	1	5	3	2	1	5		*21*
Yes			2	1						*3*
Have tried and are aware of			1	5					1	*7*

ANALYSIS

Analysis instrument	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
ABI 310	2		4							*6*
ABI 3100		3		11	3	3			1	*21*
Both 310 and 3100			1				1		5	*7*
ABI 377 and ABI 310								1		*1*
ABI 310, 3100 and 377								1		*1*
Volume of amped product added to loading mix	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1uL			1	7		3		2		*13*
1.5uL	2	3								*5*
2uL					3		1	2	4	*10*
4uL			2							*2*
6uL			1							*1*
1-3uL				3						*3*
10uL									1	*1*
Total volume of loading mix	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<10uL (varied responses)				9	3	3		3		*18*
10.1uL - 20uL (varied responses)	2						1	3		*6*
20.1uL - 28uL (varied responses)		3	5						5	*13*
Injection time for ABI 310/3100	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
5s	2		4					5	2	*13*
5s/10s									2	*2*
10s		1		1	2	3				*7*
22s					1					*1*
5-10s/2-15s							1			*1*
Run time for ABI 310/3100	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
20min						1				*1*
24min		1	1					2		*4*
25/30min							1			*1*
26min			1							*1*
28min	2		1							*3*
30min								3	2	*5*
4.5hr per plate					1					*1*
40min		2				1			1	*4*
45min				3	1					*4*

Internal standard used	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
400 GS		1				2	1	5	2	*11*
Rox500	2	2	1	8	3				1	*17*
Rox500/Liz500			3							*3*
Voltage used for ABI 310/3100	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
0.6kV					1					*1*
14.8kV			1							*1*
15kV	2	1	2			1	1	1	4	*12*
3kV						2				*2*
Criteria for calling an allele	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Genotyper used		1								*1*
Peak height		3	1	2	3			4	3	*16*
Peak height and morphology			1	4	1					*6*
Peak height, morphology and location							1			*1*
Peak height, morphology, allele designation, bp calculation						1				*1*
Peak height, morphology and presence of artefacts				1						*1*
Peak height, morphology and background				1				3		*4*
Peak height and ratio				1						*1*
Minimum limit for heterozygotes	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
50rfu			3	12				2	3	*20*
100rfu		4				2	1	1		*8*
150rfu					1					*1*
150rfu / 75 rfu					3					*3*
50rfu / 100rfu								4	1	*5*
Minimum limit for homozygotes	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
200rfu			3	11						*14*
250rfu								7	4	*11*
300rfu		4			1	2				*7*
400rfu							1			*1*
200rfu/100rfu				1						*1*
300rfu/150rfu					3					*3*
Do you ever use all of the sample?	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
No		1						1	3	*5*
Not routinely	1	2	2	5			1	3	1	*15*
Yes		1	1	7	4	2		2		*17*

TIME AND STORAGE

Time taken: Lab receipt to examination	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
1-6 days			3	10				2		*15*
1 week - 1 month			1	2		2				*5*
1-6 months		1			2		1	2	1	*7*
>6 months					1			2	2	*5*
Case dependent	1	1	1		1			2		*6*
Time taken: Examination to extraction	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<24 hours					1				1	*2*
1-2 days		3	2	8	1					*14*
2-6 days	1		3	4	1			1	2	*12*
1 week - 1 month				2	1	2	1	6		*12*
Time taken: Extraction to quantitation	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<24 hours		1					1			*2*
1-2 days		2		7	2	3		4	3	*21*
2-6 days	2			6	2			2	1	*13*

Time taken: Quantitation to amplification	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<24 hours						2	1			*3*
1-2 days		3	2	10	3	1		4	4	*27*
2-6 days	2		1	4	1	1		2		*11*
Time taken: Amplification to typing	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
<24 hours			2			1				*3*
1-2 days		3	2	2	3	1	1	1	2	*15*
2-6 days			1	10	1	2		4	2	*20*
1 week - 1 month	2			2				1		*5*
Storage of exhibit prior to sampling	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Fridge						1		2		*3*
Room temperature			3	10	1	1		5	2	*22*
Dependent on exhibit type	1	4	2	4	3	2	1	3	2	*22*
Storage of extracted DNA prior to amp.	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Fridge	2	3	3	14	1	4	1	8	4	*40*
-15°C Freezer			2		3					*5*
-80°C Freezer		1								*1*
Storage of extracted DNA after amp.	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Fridge		4	5	14		4		8	3	*38*
-15°C Freezer	2				4		1		1	*8*
Storage of amped product prior to typing	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Fridge		2	1	3		3		7	1	*17*
-15°C Freezer or Fridge		1				1				*2*
-15°C Freezer	1	1	4	9	3		1	1	3	*23*
-20°C Freezer				2						*2*
-70°C Freezer	1				1					*2*
Storage of amplified product after typing	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
Fridge		4	5			1			3	*13*
-15°C Freezer	2			12	4	3	1	7	1	*30*
-20°C Freezer				2						*2*

RESULTS

No of trace samples processed per week	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
0-5		2	1	2	3			6		*14*
5-10			1	1				1		*3*
10-20	1		1	4		1	1	1	3	*12*
20-50			1	3	1			2	1	*8*
>50		1				2				*3*
Varies		1					1			*2*
% of trace samples coming from volume crime scenes	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
0-5%		2	1		1			1	1	*6*
5-10%				1						*1*
10-25%				2				1		*3*
25-50%		1	1		1	1		1		*5*
50-75%			2	1	1	1			2	*7*
75%+			2	5			1	1	1	*10*
u/k		1						1		*2*
n/a								3		*3*
Estimate of overall success rate, trace	**ACT**	**NSW**	**NT**	**NZ**	**QLD**	**SA**	**TAS**	**VIC**	**WA**	***Total***
50-75%			1							*1*
25-50%		1		8	3			1	2	*15*
10-25%			2	4	1	1		5		*13*

The 'Average' Practitioner, circa 2004

The most common methods and practices for crime scene officers and laboratory scientists are summarised below, providing a snapshot of the 'average' 2004 practitioner. The majority percentage of responses is listed in brackets.

Crime Scene Officers

The crime scene officer does not hold a university degree (56%), and has been employed as a crime scene officer for more than 5 years (46%). It has been more than 2 years since their original training in trace DNA evidence (60%), in which they were practically assessed (39%). They have not received a refresher course in trace DNA evidence since their initial training (70%).

They use standard black and white fingerprint powders (92%) with squirrel or similar fibre brushes (84%) for fingerprint examination. The applicator is kept in use for longer 6 months or longer (95%) and is cleaned occasionally (54%).

Trace DNA is collected either by taking the whole item (52%) or sampled with wet and dry swabs (54%), using cotton swabs (82%) and sterile water (86%). The swab is continually rotated during sampling (54%) and passed over the target area 1-10 times (80%). The swab is then packaged in its container with an opening, in a paper bag (63%).

If officers are tapelifting (23%), they use Scotch or 3M brand tape (38%) pressed multiple times on the target area (50%) and then submitted on an acetate sheet (38%).

Officers wear one pair of latex gloves during scene examinations (54%). They change gloves during fingerprint examinations either more than once per scene or per scene (40 and 41% respectively). Gloves worn during trace DNA collection are changed per exhibit (72%). Officers 'sometimes' wear facemasks during fingerprint examination (49%) and always during trace DNA collection (61 %).

0-1 trace DNA samples are collected per week (29%). Trace DNA exhibits are kept at room temperature (68%) by scene officers, and submitted to the laboratory within 1-3 days of collection (30%).

Laboratory Scientists

The lab scientist has at least an undergraduate degree (93%) in molecular biology/genetics (47%). They have been employed in their organisation for 1-5 years (60%), and it has been more than two years since their initial training in trace DNA analysis (59%). The scientist has never received a refresher course in trace DNA analysis (92%).

The scientist uses more than one method of sampling (100%), either tapelifting (47%), wet and dry swabbing (35%) or cutting (31%). 3M or Scotch is the brand of tape used (43%), pressed 2-3 times on the substrate (38%). Cotton swabs (67%) and sterile water (70%) are used for swabbing, with the swab continually rotated (60%) and passed 1-5 times (40%) over the substrate during the swabbing.

The whole swab is used during extraction (78%), and is dry when received for extraction (72%). Standard chelex and organic extractions are used equally (33% each), and the scientist is permitted to vary extraction methods to a degree (63%).

The scientist uses Quantiblot for quantitation of the extracts (70%), however is not happy with their particular quantitation method (80%). The scientist repeats samples with a negative quantitation result (65%). Profiler Plus reagents (51%) and a Perkin-Elmer 9700 thermocycler (74%) are used for amplification. 28 cycles of amplification are employed (92%). No variation is permitted in PCR methods (88%).

The scientist wears latex gloves during sampling (92%) and extraction (95%), and changes them more than once per exhibit (60%) during sampling. The scientist also wears a facemask during sampling (80%) and extraction (48%), changing it daily (48% and 46% respectively). The scientist does not wear a hairnet during sampling (67%).

An ABI 3100 analyser is used for analysis (68%). Alleles are called by peak height (52%), with the minimum height for heterozygotes being 50rfu (54%) and homozygotes 200rfu (38%).

Exhibits take 1-6 days to be examined after receipt (39%), are extracted 1-2 days after examination (35%), quantified 1-2 days after extraction (58%), and amplified another 1-2 days after quantification (66%). The samples are then typed 2-6 days after amplification (47%), giving a total time of 18 days from receipt to typing.

Exhibits are kept at room temperature on receipt (47%), with exceptions depending on the sample. Pre- and post-amplification extracts are kept in a refrigerator (87% and 82% respectively), and amplification and post-typing products kept in a freezer of -15°C or cooler (63% and 75% respectively).

The scientist will examine or analyse 0-5 trace DNA samples per week (33%). The scientist estimates a 25-50% success rate of trace DNA samples (50%).

Appendix C: Trace DNA Casework Data

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Country	Att. Burglary	1d	2	Window security screen	0	No Result
Country	Burglary	5hr50min	19	Plant pots	0	No Result
Country	Armed Robb.	23d	8	Replica pistol	0	No Result
Country	Burglary	1d	1	Screwdriver	0	No Result
Country	Burglary	3hr40min	1	Batteries	0	No Result
Country	Drugs	12d	1	Drug bags	0	No Result
Country	Burglary	17hr31min	66	FPs on window glass	0	No Result
Country	Burglary	1d	1	Nuts from motors	0	No Result
Country	Burglary	2d	13	FPs on front door POE	0	No Result
Country	Burglary	1d	219	FPs on window POE	0	No Result
Country	Burglary	3d	14	Partial FP on camera	0	No Result
Country	Burglary	3d	1	Plastic container in house	0	No Result
Sydney	Firearms	91d	1	Firearm	0	No Result
Country	SMV	4d	1	Scissors	0	Amel Only
Country	Burglary	1hr40min	225	FPs on window POE	0	No Result
Country	Burglary	11hr30min	1	Forehead marks on POE window	0	No Result
Country	Burglary	4hr25min	133	Cig lighter	0	No Result
Country	Burglary	6hr	1	Bolt cutters	0	No Result
Country	Malic.Damage	48d	1	Spray can	0	No Result
Country	Drugs	92d	1	Drug bags	0	No Result
Country	Drugs	92d	1	Drug bags	0	No Result
Country	Drugs	168d	20	Zip seal on drug bag	0	No Result
Country	SMV	2d	1	Smudge fps on rearview mirror	0	No Result
Country	SMV	2d	1	Smudge fps on sat nav screen	0	No Result
Country	Firearms	105d	9	Firearm	0	No Result
Country	Firearms	105d	9	Drug bag	0	No Result
Sydney	Armed Robb.	2hr23min	383	Security wire above counter	0	No Result
Sydney	Armed Robb.	2hr40min	9	Cash register, FPs	0	No Result
Sydney	Burglary	11hr40min	1	Screwdriver	0	No Result
Sydney	Burglary	4hr45min	20	Nuts on a clamp	0	No Result
Sydney	Burglary	19hr26min	14	Earprint on door	0	No Result
Sydney	Burglary	10h5min	173	FPs on windowsill	0	No Result
Sydney	Steal from Veh.	11d	1	Tool	0	No Result
Sydney	Burglary	9hr25min	31	Earprint on door	0	No Result
Sydney	Burglary	1d	1	Earprint ext front door POE	0	No Result
Sydney	Burglary	2hr45min	1	Earprint ext front door POE	0	No Result
Sydney	Burglary	1d	1	Earprint ext front door POE	0	No Result
Sydney	Burglary	1d	1	Ear/face mark, ext front door POE	0	No Result
Sydney	Burglary	21hr10min	226	Earprint on door	0	No Result
Sydney	Steal from Veh.	5hr15min	29	Area around reg plates	0	No Result
Sydney	Malic.Damage	3d	1	Telstra cable	0	No Result
Country	Burglary	1d	2	Smudge fps on window frame	0.04	No Result
Country	Drugs	8d	1	Drug bags	0.04	Partial <12

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Country	Drugs	8d	1	Drug bags	0.04	No Result
Country	Traffic/drugs	101d	152	Drug bag	0.04	No Result
Country	Traffic/drugs	101d	152	Drug bag	0.04	No Result
Country	SMV	20hr25min	131	Auto gearshift	0.04	No Result
Country	Burglary	14hr15min	1	Sledgehammer	0.04	No Result
Country	Burglary	1d	1	Bolt (Vending machine POE)	0.04	No Result
Sydney	Drugs	87d	134	Drug bag	0.04	No Result
Sydney	Malic.Damage	8hr30min	14	Golf club handles	0.04	No Result
Sydney	Malic.Damage	8hr30min	14	Golf club handles	0.04	No Result
Country	Burglary	10hr55min	1	Smudge fps on flyscreen	0.04	No Result
Country	SMV	4d	1	Screwdriver	0.04	No Result
Country	Burglary	7d	2	Rock	0.04	No Result
Sydney	Firearms	105d	9	Firearm	0.04	No Result
Sydney	Firearms	105d	9	Drug bag	0.04	No Result
Sydney	Armed Robb.	2hr30min	1	Cash register	0.04	No Result
Sydney	Steal from Veh.	3d	241	Arm mark on window	0.04	No Result
Sydney	Steal from Veh.	16hr	36	FPs on bumper	0.04	No Result
Sydney	Burglary	1d	1	Earprints on ext front door POE	0.04	No Result
Sydney	Steal from Veh.	5hr15min	29	Area around reg plates	0.04	No Result
Sydney	Burglary	1d	1	Crowbar	0.04	No Result
Country	Steal from Veh.	1d	1	Button of rear seat	0.08	Amel Only
Country	Burglary	1d	1	Smudge fps int doorframe	0.08	No Result
Country	Burglary	3hr55min	1	Metal bar	0.08	No Result
Country	Burglary	5hr40min	29	Computer harddrive	0.08	Partial <12
Country	Drugs	12d	1	Drug bags	0.08	Partial <12
Country	Burglary	10hr42min	24	Safe handle	0.08	No Result
Country	Burglary	2d	1	Screwdriver	0.08	No Result
Country	Firearms	1d	45	Firearm trigger	0.08	No Result
Sydney	Armed Robb.	1hr45min	39	Register note clips	0.08	Partial <12
Sydney	Armed Robb.	2hr40min	22	Arm mark on counter	0.08	Mixture
Sydney	Burglary	54d	1	Metal bar	0.08	No Result
Sydney	Arson	13hr18min	1	Fuel container handle	0.08	Mixture
Sydney	Burglary	19hr55min	12	Earprint on door	0.08	No Result
Sydney	SMV/Robb	9d	304	Handbag	0.08	No Result
Sydney	Burglary	1d	1	Earprints on ext front door POE	0.08	No Result
Country	Burglary	1d	1	Downpipe at POE	0.12	No Result
Country	Drugs	12d	1	Drug bags	0.12	No Result
Country	Traffic/drugs	101d	152	Drug bag	0.12	No Result
Country	Burglary	3hr40min	1	Spanner	0.12	No Result
Country	Firearms	63d	1	Firearm	0.12	No Result
Sydney	Arson	11hr35min	144	FPs on security camera	0.12	No Result
Sydney	Firearms	144d	1	Firearm	0.12	No Result
Sydney	Drugs	68d	83	Drug bag	0.12	Partial <12
Country	Burglary	10d	1	Forehead mark ext POE window	0.12	No Result
Country	Burglary	6hr	1	Bolt cutters	0.12	No Result
Sydney	Burglary	18hr20min	68	Replica pistol	0.12	Mixture

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Sydney	Traffic/Burg.	6hr45min	18	Screwdriver handle	0.12	No Result
Sydney	Burglary	2hr	1	Screwdriver	0.12	No Result
Sydney	SMV	1d	1	Screwdriver	0.12	No Result
Sydney	Burglary	1hr40min	33	Earprint on door	0.12	Partial <12
Sydney	Theft	5d	1	Pen	0.12	Mixture
Sydney	Burglary	4d	213	Spanner	0.12	No Result
Country	Drugs/firearms	22d	180	Bersa pistol	0.16	No Result
Country	Drugs/firearms	22d	180	Glucodin powder box	0.16	No Result
Country	SMV	4hr50min	1	Screwdriver	0.16	Mixture
Country	Armed Robb.	1hr15min	1	Ext driver's window (POE)	0.16	No Result
Country	Steal from Veh.	11d	142	Cheque book	0.16	Partial <12
Sydney	Burglary	1d	249	Screwdriver handle	0.16	Partial <12
Sydney	SMV	1d	1	Scissors	0.16	Partial <12
Sydney	Burglary	4hr	1	Bolt cutters	0.16	No Result
Sydney	Theft	4hr5min	4	Register keyring	0.16	Amel Only
Sydney	Burglary	2hr40min	9	Crow bar	0.16	No Result
Country	Drugs	12d	1	Drug bags	0.2	No Result
Country	Firearms	63d	1	Firearm	0.2	No Result
Country	Burglary	3d	1	Smudge fps on padlock	0.2	No Result
Sydney	Armed Robb.	4hr10min	1	Coin dividers in till tray	0.2	Amel Only
Sydney	Burglary	8hr37min	1	Screwdriver	0.2	No Result
Sydney	Burglary	15hr45min	14	Bike handle	0.2	No Result
Sydney	Burglary	1d	1	Screwdriver	0.2	Mixture
Sydney	Burglary	1d	1	Screwdriver	0.2	No Result
Sydney	SMV	6d	2	Pen	0.2	Mixture
Sydney	Malic.Damage	1d	1	Sledgehammer	0.2	No Result
Sydney	Robbery	123d	1	Firearm	0.24	Amel Only
Sydney	SMV	35min	146	Screwdriver handle	0.24	No Result
Sydney	Burglary	1d	1	Screwdriver	0.24	No Result
Sydney	Burglary	1d	1	Screwdriver	0.24	No Result
Country	Drugs/firearms	22d	180	Taser	0.28	No Result
Country	Drugs	10d	1	Pistol	0.28	Partial <12
Country	Burglary/Malic.Damage	11d	146	Screwdriver handle	0.28	Partial <12
Country	Burglary	1d	1	Smudge fps interior doorframe	0.28	No Result
Sydney	Firearms	75d	226	Firearm	0.28	Partial <12
Sydney	Firearms	68d	1	Firearm	0.28	Mixture
Sydney	Armed Robb.	3hr30min	230	Freezer door	0.28	Partial <12
Sydney	Burglary	16d	127	Dustpan brush handle	0.28	No Result
Sydney	Burglary	1d	1	Screwdriver	0.28	No Result
Sydney	Burglary	11d	1	Gilette razor packet & base	0.28	Mixture
Country	Fraud	9d	1	Debit card	0.32	No Result
Country	Drugs/licensing	55d	207	Baton handle	0.32	Amel Only
Sydney	Drugs	87d	134	Drug bag	0.32	Partial <12
Sydney	Firearms	91d	1	Firearm	0.32	No Result
Country	Drugs	86d	13	Small drug bag	0.32	No Result
Sydney	Firearms	68d	1	Firearm	0.32	Partial <12

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Sydney	Armed Robb.	2hr40min	22	Arm mark on counter	0.32	Full Profile
Sydney	SMV	6d	1	Pen	0.32	Partial <12
Country	SMV	21d	1	Cig lighter	0.36	No Result
Sydney	Drugs	43d	1	Drug bags	0.36	Partial <12
Country	Burglary	2d	9	Torch handle	0.36	Partial ≥ 12
Country	Drugs	92d	2	Drug bags	0.36	Full Profile
Sydney	Malic.Damage	5d	1	Rock	0.4	Partial <12
Sydney	Att. Burglary	1hr5min	1	Front flyscreen d/h	0.4	Partial <12
Sydney	Burglary	1d	1	Shovel	0.4	Amel Only
Country	Malic.Damage	88d	8	Knife handle	0.44	Partial <12
Country	Burglary	4hr20min	1	Chisel	0.44	No Result
Country	SMV	1d	1	Jemmy bar	0.44	Mixture
Sydney	Drugs	87d	134	Drug bag	0.44	No Result
Country	Burglary	3d	150	Jemmy bar	0.44	Partial <12
Country	Burglary	3d	1	Shears	0.44	Mixture
Sydney	Burglary	3hr	3	Screwdriver	0.44	No Result
Sydney	SMV	7hr55min	1	Knob from ignition	0.44	Mixture
Country	Burglary	9hr52min	1	Screwdriver	0.48	Amel Only
Country	Theft	2d	165	Wheelbarrow handles	0.48	Amel Only
Sydney	Burglary	2d	1	Stanley knife	0.48	Mixture
Sydney	Burglary	11d	1	Gilette razor packet & base	0.48	Mixture
Sydney	Drugs	43d	1	Drug bags	0.52	Mixture
Sydney	Steal from Veh.	20hr25min	146	Torch handle	0.52	Amel Only
Country	Burglary	2d	1	Cig lighter	0.56	Partial <12
Country	Drugs	26d	1	Drug bag	0.56	Amel Only
Sydney	Robbery	11hr35min	121	Glovebox handle	0.56	Mixture
Sydney	Burglary	5hr10min	1	Screwdriver	0.56	Amel Only
Country	Drugs	12d	1	Drug bags	0.6	Partial <12
Country	SMV	3d	1	Scissors	0.6	Mixture
Country	Burglary	12hr45min	29	Hose	0.6	Amel Only
Sydney	SMV	1hr5min	111	Motor bike handlebars	0.6	Partial <12
Country	Firearms	144d	1	Firearm	0.64	Partial ≥ 12
Sydney	Burglary	11hr40min	1	Blackberry case	0.64	Partial <12
Sydney	Theft	4hr4min	1	Interior office doorhandle	0.64	Partial <12
Sydney	Armed Robb.	1d	1	Interior doorhandle	0.64	Mixture
Sydney	Armed Robb.	2hr15min	11	Handmark on counter	0.68	Amel Only
Sydney	Burglary	3d	1	Handbag moved by POI	0.68	Partial <12
Sydney	Steal from Veh.	1d	1	Swiss army knife	0.68	Partial <12
Sydney	Burglary	1d	1	Screwdriver	0.68	Partial ≥ 12
Sydney	Armed Robb.	1d	1	Interior doorhandle	0.68	Mixture
Country	Att Armed Robb.	2d	1	Cash register key	0.72	Mixture
Country	SMV	5d	149	Screwdriver handle	0.72	No Result
Country	SMV	2d	1	Screwdriver	0.8	Amel Only
Country	SMV	9d	1	Scissors	0.8	Mixture
Country	Burglary	14hr25min	24	FPs on ext door POE	0.8	Partial ≥ 12
Sydney	Burglary	49d	1	Crowbar	0.8	Mixture
Sydney	Burglary	1d	1	Earprint ext front door POE	0.8	Partial ≥ 12

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Country	SMV	6hr	9	Straw/sledgehammer	0.84	Mixture
Sydney	Robbery	3hr5min	1	Ext doorhandle (POE)	0.88	Mixture
Sydney	Assault	5d	17	Passenger doorhandle	0.88	Full Profile
Sydney	Agg Burglary	1hr50min	2	Interior front doorhandle	0.88	Mixture
Country	Burglary	1d	1	Computer cords	0.92	Mixture
Country	Burglary	1d	1	Screwdriver	0.92	Mixture
Country	Burglary	2d	1	Chisel	0.96	Mixture
Country	Robbery	1d	1	Purse	0.96	Amel Only
Sydney	SMV	2d	13	Knife handle	0.96	Amel Only
Country	SMV	1d	1	Dipstick	1	Partial ≥ 12
Country	Drugs	86d	13	Large drug bag	1	No Result
Sydney	Armed Robb.	2hr23min	383	FP on inside POE door	1	Partial <12
Sydney	Armed Robb.	2hr19min	37	Service counter	1	Amel Only
Sydney	Armed Robb.	4hr10min	1	Note dividers in till tray	1	Mixture
Sydney	SMV	2d	134	Bike handle	1.04	Amel Only
Sydney	Firearms	144d	1	Firearm	1.08	Partial ≥ 12
Country	Burglary	19hr31min	35	FPs on window frame	1.12	Partial <12
Sydney	Burglary	2d	143	Screwdriver handle	1.12	Partial <12
Country	Burglary	1d	1	Ext POE sunroom window	1.16	Full Profile
Country	Drugs	3d	6	Gas bottle handle	1.28	Mixture
Country	Burglary	62d	8	FPs on laptop	1.28	Mixture
Sydney	Burglary	3hr50min	169	FPs on window sill	1.32	Mixture
Country	Drugs/firearms	22d	180	Black handled weapon	1.4	Partial <12
Country	Burglary	3hr40min	1	Screwdriver	1.44	Mixture
Sydney	Burglary	2hr	1	Claw hammer	1.48	Mixture
Country	Armed Robb.	1d	1	Smudge fps on cash register	1.52	Mixture
Sydney	Robbery	4d	1	Handbag	1.52	Mixture
Sydney	Drugs/firearms	22d	180	Black case	1.56	Partial <12
Sydney	Burglary	14d	225	Knife handle	1.6	Full Profile
Sydney	Burglary	2d	1	Powercord	1.68	Full Profile
Country	Drugs	92d	1	Drug bags	1.84	Full Profile
Sydney	Armed Robb.	3hr10min	13	Perspex partition	1.84	Mixture
Sydney	Burglary	3hr53min	1	Lip/chin print ext sliding door	1.84	Partial ≥ 12
Sydney	Steal from Veh.	1hr50min	1	Screwdriver	1.88	Partial ≥ 12
Country	SMV	2d	1	Hose	1.96	Mixture
Sydney	SMV	14hr16min	1	Glove box release button	1.96	Mixture
Sydney	Burglary	4hr55min	1	Crowbar	1.96	Mixture
Country	Drugs/firearms	22d	180	Mace	2	Partial <12
Country	Firearms	7d	1	Firearm	2	Mixture
Sydney	Firearms	43d	91	Firearm trigger	2.24	Partial ≥ 12
Sydney	Burglary	29d	13	Screwdriver handle	2.32	Full Profile
Sydney	Armed Robb.	3hr30min	230	Rear loading dock door	2.64	Mixture
Country	Burglary	1d	1	Chisel	2.76	Mixture
Sydney	Burglary	1d	3	Purse	2.8	Full Profile
Sydney	Burglary/SMV	1d	16	Wallet	2.96	Amel Only
Sydney	Armed Robb.	2hr30min	2	Light switch	3	Full Profile
Sydney	Att Burglary	12hr7min	10	Knife handle	3.04	Partial ≥ 12

Location	Offence	Offence & sample collection	Collection & lab submit. (days)	Sample	DNA quant. (ng)	Profile
Sydney	Burglary	1d	1	Screwdriver	3.16	Mixture
Sydney	Malic.Damage	1d	1	Spanner	3.36	Mixture
Sydney	Robbery	123d	1	Firearm	3.44	Mixture
Sydney	Burglary	1d	1	Hatchet	3.48	Full Profile
Sydney	Burglary	5d	1	Hammer	3.56	Mixture
Country	SMV	2d	13	Screwdriver handle	4	Mixture
Country	Burglary	9hr15min	151	Screwdriver handle	4.52	Mixture
Country	Burglary	13hr15min	2	Cig lighter	4.64	Partial ≥ 12
Country	Steal from Veh.	1d	2	Screwdriver	4.72	Partial ≥ 12
Country	Burglary	2d	1	Bolt cutters	4.76	Mixture
Country	SMV	4d	43	Mobile phone	4.88	Mixture
Sydney	Steal from Veh.	2d	11	Screwdriver handle	4.88	Partial ≥ 12
Sydney	Burglary	3hr	1	Hammer	5.28	Full Profile
Country	Theft	8d	1	Debit & other cards	6	Mixture
Sydney	Armed Robb.	3hr30min	230	Shopping basket	7.12	Mixture
Country	SMV	1d	1	Smudge fps on ext of veh	7.52	Full Profile
Country	Burglary	7hr55min	1	Smudge fps interior doorframe	10.32	Full Profile
Sydney	SMV	2d	134	Motor bike handlebars	12.76	Partial ≥ 12
Sydney	Steal from Veh.	50min	1	Screwdriver	16.32	Full Profile
Country	Drugs	92d	1	Drug bags	44	Full Profile
Country	Burglary	3d	1	Shovel	49.6	Full Profile
Sydney	Burglary	1d	1	Screwdriver	49.6	Full Profile
Sydney	Theft	2hr	1	Mobile	50.8	Full Profile

Abbreviations

SMV = stolen motor vehicle
Veh. = vehicle
Malic. Damage = Malicious Damage
Att. Burg = attempt burglary
Robb. = robbery
Agg. = aggravated

FPs = fingerprints
Ext. = exterior
Int. = interior
Amel. Only = Profile contains the Amelogenin locus only
Partial<12 = Profile contains less than 12 alleles
Partial≥12 = Partial contains 12 or more alleles

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