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DNA for Defence Lawyers

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INTRODUCTION:

There are a number of unfair but true assumptions that can properly be made about criminal lawyers. First, not only do they not understand maths and statistics they fear them. Those who have conquered their fear have only done so in the one limited area needed to understand a Form Guide. Secondly, they all failed science.

DNA evidence involves science, maths and statistics. It will, if unchallenged, have persuasive appeal to juries and judges. It appears to offer a degree of certainty that is often missing from a criminal trial. It also has the cache of being the topic of the moment on popular television.

Recent study has shown that jurors believe DNA evidence to be "significantly persuasive". M Findlay & J Grix, *Challenging Forensic Evidence*, (2003) 14 Current Issues in Criminal Justice 269 at 273. Evidence of a DNA "match" between a crime scene and your client is very scary for those of us whose job it is to raise a reasonable doubt and prevent unjust and unwarranted convictions. Yet there appears to be a, "prevailing ignorance about the nature and potential of DNA evidence among lawyers and judges". Ibid at 272.

To conquer our fear and overcome our ignorance, if only temporarily, it is essential to know when to challenge DNA science and statistics and when to avoid battle and focus the jury's attention elsewhere. We also need to know when to advise surrender and secure the advantages of an early guilty plea.

Often the question is not, "Whose DNA is it?" but "How did the DNA get there?" This later question is the sort our legal skills best equip us to deal with.

This paper aims to address some of the issues that can arise when the prosecution seek to put DNA evidence before the court at trial. I cover four key areas:

· Science and Technology.
· Statistics.
· The law.
· Trial tactics.

Peter Zahra in his 2002 paper "DNA and Probability" Available on the Public Defenders Website www.lawlink.nsw.gov.au/pdonsf/pages/first sets out some of the basic science, which, apart from a few essentials, I will not repeat.

Deoxyribonucleic acid - DNA is found all cells, except red blood cells. That DNA is said by some to be unique to all but identical twins. However the fact, crucial for any understanding of DNA evidence, is – there is no scientific proof of such uniqueness.

Only a few cells, invisible to the naked eye, can be enough to obtain the DNA profile of an individual. DNA can be extracted from the sorts of things regularly left at crime scenes, such as traces of skin, blood, sweat, saliva or other bodily fluids.

Most testing in Australia focuses on the DNA found in the nucleus of a cell, although DNA can also be extracted from the mitochondria. This paper deals with DNA extracted from the nucleus of a cell. Peter Zahra's paper deals in more detail with mitochondrial DNA.

Legislation, in particular for NSW, the *Crimes (Forensic Procedure) Act* 2000 (NSW) and Part 1D *Crimes Act 1914* (Commonwealth), allows police to obtain a DNA sample from those suspected of involvement in a crime and from those convicted of serious offences See paper by Andrew Haesler on the Public Defenders Website- "*DNA - An Overview of Testing and the Crimes (Forensic Procedures) Act 2000.*". Each State and Territory now has a database of crime scene, suspect and convicted

offender samples that can be compared and matched with each other. Each State and Territory also provides samples, and has access to, the Federal DNA database, NCIDD National Criminal Intelligence DNA Database., managed by an organisation known as Crim Trac.

SCIENCE & TECHNOLOGY:

A crime scene sample is taken either by swab or by collecting an exhibit for sampling. Usual police crime scene or hospital sexual assault forensic exhibit procedures should be followed. The exhibits and/or swabs are then transferred to an Analytical Laboratory; in NSW it is the Department of Analytical Laboratories of the Institute of Clinical Pathology and Medical Research (DAL), where the swab is processed. A whole exhibit is examined visually and samples taken from areas where it is presumed DNA might be found. These samples and crime scene swabs are then tested to see if it is possible to determine the type of material found, blood, semen, skin (epithelial) cells or saliva, for example. It is not always possible to determine the type of material. Sometimes only a presumptive test can be done.

The item is then sent for processing. At this point the machines and technicians take over. In all Australian jurisdictions the processing of evidence for DNA follows a fairly standard procedure based on commercially available kits.

The DNA is first extracted.

It is then measured. Too much DNA can skew a sample. Too little can lead to a “no result”. Some products including cloth dyes or cleaning agents can inhibit DNA analysis. Ultra violet light, heat, humidity or bacterial action can destroy DNA. Ideally only a very small amount is needed. In NSW between 0.5 and 1 nanogram of DNA per 20 microlitres A micro litre (ul) is 1 millionth of a litre There are about 15 drops of water in a millilitre (1 thousandth of a litre). is used. A nanogram is one thousand millionth of a gram, which gives some indication of the sensitivity of DNA analysis!

The extracted DNA is then amplified. The process is akin to a photocopier, which not only turns out identical copies, but also does so exponentially. After a few repeats we get millions of copies. The amplification process used in Australia, known as PCR (Polymerase Chain Reaction), also enables multiple points/loci on a person’s DNA to be analysed at the one time (multiplexing).

Those copies are then placed in a machine and analysed. A process known as electrophoresis is applied and a series of graphs and readouts obtained. These are then interpreted.

The beauty of the science and technology of DNA testing is that the process results in visual charts and computer readouts that describe what cannot be seen.

What can’t be seen is this:

Every cell Except red blood cells which have no nucleus and sex cells (sperm and egg) which have only 23 chromosomes but combine to form 23 pairs. contains 23 pairs of chromosomes. Those chromosomes are made up of and act as a storage mechanism for our DNA. The DNA molecule or genome carries the entire genetic code of an individual. One half is inherited from our mother, the other from our father. Each chromosome is made up of genes, and spaces between them known as introns. Both in turn are made up of a series of bases Adenine, thymine, guanine and cytosine. Adenine always binds with thymine and guanine with cytosine. attached to a backbone of phosphate sugar. These bases occur in sequence Configured in the famous double helix. and are depicted by the letters A, G, T and C.

The sequence of bases follows regular patterns. It is the differing combinations of bases, which make each person’s DNA potentially unique, as at some points/loci the sequences vary markedly from person to person.

By locating a predetermined point on a gene (a locus) and measuring how many times a sequence of bases (say ACTG, ACTG, ACTG, and ACTG) occur, a DNA profile is obtained. Because they are less liable to deterioration the shorter sequences are used. These are known as Short Tandem Repeats (“STR’s”).

At each locus, or point analysed, we should get two readings for the number of Short Tandem Repeats of a particular sequence. These alternative sites on the chromosome are known as alleles. One allele comes from the person’s mother, the other from their father. If the number of STR’s is the same the

individual is said to be homozygous at that point/locus. If the number of STR's are different the individual is said to be heterozygous at that locus. We get two readings because each chromosome is made up of two linked strands, one from the father the other from the mother. If the parents share that number of STR's we may get a single result at that locus. For example, if Mum is 12 -14 and Dad 11- 14, the possible combinations are 14-14, 11-12, 11-14 & 12-14.

Multiple points, preferably from different chromosomes, are tested. In Australia nine points/loci are tested as part of the Profiler Plus system generally in use. In addition, a test is done of a gene known as Amelogenin, which enables the sex of the sample's donor to be determined. Each of the ten points/loci (that is nine loci plus Amelogenin) used in Profiler Plus is given an internationally recognised identifier symbol - D3 S1358, VWA, FGA, Amelogenin, D8 S1179, D21 S11, D18 S51, D5 S818, D13 S317 and D7 S820. The **D** stands for **D**NA. The next number is the number of the chromosome. **S**tands for **S**ingle copy sequence and the following number notes the order in which the particular sequence was discovered.

A typical Worksheet from the Department of Analytical Laboratories notes: the date, operator and method of extraction: and the date, operator and result of amplification: and analysis. All these tasks are undertaken by technicians under the direction of a supervising biologist, who then undertakes the interpretation of the results.

Separate readout graphs and charts noting peak heights and areas are also produced. The next worksheet will show the summary of case results and the profile of the individual or sample taken from a crime scene. That profile has two numbers corresponding to each of the known locations e.g. D3 S1358 - 15 and 16, meaning at point S 12358 on the 3rd chromosome there were 15 and 16 repeats of a particular sequence of bases. Further readings are given for the other nine loci, and a reading for Amelogenin, which can only be either XX (female) or XY (male).

These numbers can be computer coded and placed on the DNA database. When the same series of numbers comes up on another part of the database e.g. with a crime scene, suspect or convicted offender, a "match" is called and the two results further interpreted to see if the provisional match is justified. In other words, in the system used, no differences between the two samples could be found.

If the numbers do not match a suspect is excluded.

If a suspect cannot be either matched or excluded the result will be reported as "not excluded".

An inconclusive reading can result in the expert going further and giving either a "not excluded as a contributor" or a "not excluded as a source" finding. "Not excluded as a contributor," means there was no match found, as there was simply insufficient material either to match or exclude the person. "Not excluded as a source," means that it is possible a match may be made but the DNA is too weak or too complex a mixture to reach a reliable conclusion. That a person is "not excluded" can have no real relevance as a proof, as almost anyone taken at random could fall into this category.

Problems with the science and technology involved in DNA analysis:

A lot of time and effort is wasted on testing and challenging the unchallengeable. The science backing DNA analysis is good and getting better all the time. The technology has been tested and cross-tested. There are protocols in place designed to ensure that results are validated and possible contamination of results, or errors in analysis, picked up. Mistakes have occurred but they are so rare as to be notorious. UK DNA Mismatch http://www.scoop.co.nz/stories and "Murder DNA tests botched" The New Zealand Herald 26/5/1999. The police excused the error as "procedural difficulties in investigative analysis." The incident led to the establishment of the Scott Eisbaum Inquiry, which although it failed to find the cause of the error stated the most probable explanation was accidental lab contamination. Deliberate corruption of results has been noted in the US, as has institutional bias. However, it is rare and there is no evidence anything like that happens here. Our analytical labs are justifiably jealous of their reputations.

That doesn't mean that you go the other way and surrender and advise a guilty plea immediately you receive a damning DNA expert report! As they presently stand, the DNA reports from the DAL are simply inadequate to enable any assessment to be made of their validity. In a mental illness case it would not be sufficient for a defence expert to say, "I have examined the accused and he is mad". Why the DPP expect a report saying, "I have examined the test results and there is a match" to be any more

compelling is beyond me.

In any contested DNA matter it is essential that the DAL file be examined, if only to check that all procedures and protocols were followed. "*The cogency of DNA makes it particularly important that the DNA testing is rigorously conducted so as to obviate the risk of error in the laboratory. The method of DNA analysis and the basis of subsequent statistical calculation should- so far as possible- be transparent to the defence. The true import of the resultant conclusion [should be] accurately and fairly explained to the jury*" **R v Doheny & Adams** (1997) 1 Cr App 369 and **R v Karger** (2002) 83 SASR 135. Most DNA reports do not comply with the DPP's duty of disclosure - http://www.odpp.nsw.gov.auPolicyGuidelines How clear were the results? What judgements were made? Were there any dubious matches? Was there any evidence of contamination?

In many cases it is not the technology or the science but the supervising biologist's subjective interpretation of the results that is the crucial factor in assessing whether a suspect sample and a crime scene sample "match". What she/he is doing is looking at the Profiler Plus readouts and coming to a conclusion. In some cases the read outs will be clear and conclusive, in some the readings will not be so clear and in others they will be far from clear at all. Where professional judgement and expertise are required to be exercised there is often fertile ground for cross-examination.

This is particularly so in the following areas, each of which will be discussed below:

· Where there is only a partial match.
· Where the reading is weak.
· Where the crime scene sample is a mixture of more than one person's DNA.
· Where there may be contamination.
· Where the DNA may not have been directly deposited - Secondary transfer.
· Where there is the possibility the results were skewed by mutation.

Partial Match: A partial match reduces the opportunity for the full application of the statistical equation used to calculate the likelihood of a "match", known as the "product rule". A partial match creates the chance that the missing portion may yield a result that would exclude the suspect. At a certain point the match probability figures become so low as to be meaningless as corroboration.

Weak readings: A weak reading has similar problems to that of the partial match. It is often impossible to tell the difference between a true reading at a locus and a glitch on the graph brought about by the testing process. As a result alleles may be wrongly counted or missed altogether. Most labs have a minimum peak height below which they will not hazard an assessment. On occasion, a match will be given despite a low peak height. Examination of low peaks can also disclose a potential extra contributor to a sample, raising the possibility that this person may be the true culprit, or the possibility of secondary transfer (see below).

There is also a phenomenon known as a stutter, where an artefact of testing appears as a peak, mimicking an allele's graph peak. Trained analysts claim to be able to ascertain the difference between an allele and a stutter. There are certain signals to look out for, but that being said, we all look for what we want to see. Stutters have been, and will continue to be, be interpreted as peaks with the consequence of a false match or false exclusion.

Similar problems can arise if only a single reading is found at one locus. A single reading can mean the alleles at that point are the same. It can also mean something has dropped out or not shown up on the graph (known as allelic drop-out or a null allele). A false positive or false negative reading can result.

Mixtures:

Three or more alleles at a locus indicate the presence of more than one contributor. It is often difficult to tell whether the sample originated from 2, 3 or 4 people. Statistical models can help analysts work out the probabilities of more than two contributors however a number of possible combinations could be consistent with the findings. Despite this unless more than five alleles are found at a locus, the DAL assume that only two people contributed to a mixture. This presumption has been proved correct in most cases. However, if this assumption is false it can lead to a part of a mixture being matched wrongly to a suspect.

An assumption is then made that the taller peaks are associated with the primary contributor and the shorter peaks the secondary. If all the alleles can be matched to the crime scene or victim sample, these are then taken out and the assumption made that the remainder match only the suspect. Peak heights

are often used in interpreting mixtures, but peak height imbalances occasionally occur. Peaks with the same height are presumed to be from the same person, but the reading of peak heights is far from an exact science. Even in a single person sample, peak heights may vary, so assumptions of regularity may be false.

In mixed samples alleles may simply be undetectable or indistinguishable from background 'noise'. Alternatively, as mentioned above, alleles can simply "drop out" and not appear on the graph or stutters can be confused with alleles from a minor contributor.

Contamination: Most matches are correct, but errors do occur. There may be innocent, accidental or malicious reasons for a false match or a false exclusion. No matter how good the lab procedures are, errors do occur. Protocols are in place to pick these up. It is rare, but not unusual to find a worksheet noted "possible contamination". This finding will result in the retesting of the sample. In every case I have seen a second clean result was obtained. For most cases of potential contamination in the lab the innocent explanation is just that. However, the lab will not know if handling errors in the course of collecting or delivering the exhibit to them have occurred. Nor will they know if the sample has been deliberately tampered with before it got to the lab. In **R v Lisoff** [1999] NSWCCA 364, the CCA ordered a re-trial. Lisoff was subsequently acquitted, presumably because the jury accepted defence evidence that the victim's blood found on L's trousers had been planted. It contained transfusion products and thus had arguably been taken from the victim after the assault and after he went to hospital.

Inadvertent or secondary transfer: Recent developments in DNA processing have enabled readable DNA to be obtained from tiny samples, unimaginable even a few years ago. DNA can now be recovered from a single cell and it is possible for as few as 30 cells to be processed in order to give a readable result. Similarly, DNA can now be recovered from objects where no bodily fluids are apparent, samples so small they can be obtained from a fingerprint impression and from items such as knife handles or spectacles. Van Oorschot & Others, Nature Vol: 387 (1997) page 787. These finding have however not always been reproducible, Ladd & Others, "*A systematic analysis of secondary transfer"* Journal of Forensic Science (1999) Vol: 44 page 1270-1272. See also, Raymond, Walsh, van Oorschot, Gunn & Roux, *Trace DNA: An underutilised resource or Pandora's box,* Journal of Forensic Identification. 56 (2004) 668-686. In some cases, enough DNA can be recovered for analysis by conventional techniques. Gill, "*Biological Evidence.*" Paper to 13th Interpol Forensic Science Symposium, Lyon, France Oct 2001, Van Renterghem & others, *"Use of latent fingerprints as source of DNA"*, Progress in Forensics Genetics Vol: 8 501-503.

Given we shed 40,000 skin cells a day, a lot of our DNA can be left lying around. It appears that some of us are "good shedders," and some not. Experimental studies on Low Copy Number DNA have shown that a simple series of handshakes can transfer DNA from the original source to a third party.

Some experts are reluctant (if not dismissive) of any suggestions that the DNA found by their tests got there by way of secondary transfer. They will say the secondary transfer tests involved smaller samples than are regularly tested for. They will say that transfer generally requires more than mere skin to skin contact. Although some studies support this conclusion others do not. At the same time they will triumph in their ability to get a sample from the smallest trace of material left at a scene.

The bottom line is that DNA is highly mobile and secondary transfer does occur. Every time we speak and release spittle we have transferred our DNA. If, while still moist, this spittle comes in contact with another object, transfer of a few cells can occur. And only a few cells are enough to get a profile. After all, the taking of a swab from a crime scene is but an example of secondary transfer. We are dealing in such small quantities of material and such new areas of science that assumptions, which presume against secondary transfer, must be put aside.

The trial of Barnes (Wollongong Supreme Court, February 2004) provides an example. A young woman was found dead in a park in Dapto, her discarded clothing covering her naked body. The accused's DNA was recovered from her bra. Evidence established that about an hour before her death the two had met outside a club. Both were drunk, and the accused in particular was in a jolly mood shaking hands with a number of complete strangers. The problem posed for the defence was, how did his DNA come to be on the bra strap of a women who when they met was wearing a vinyl coat and a singlet over her bra? The DAL analyst was dismissive of suggestions that spittle or DNA from Barnes's hand had got onto either the victim or her jacket and then been transferred to the bra. The jury as evidenced by their not guilty verdict were more accepting of the possibility of secondary transfer!

Be careful! Do not accept DAL reports at face value if they conflict with your instructions. A report giving a conclusion there is a match and a high figure for a match probability does nothing to distinguish

unassailably powerful DNA evidence from weak misleading DNA evidence. It does not provide any insight into the circumstances under which the sample was deposited. However, if the report checks out it may be time to ask your client to revisit his instructions.

Mutation: This can and does occur, although in most cases it will lead to a false exclusion rather than a false match. Interestingly, in **R v Bropho** [2004] WADC 182, the victim's DNA excluded her as the mother of the child she clearly bore. The explanation for the discrepancy in profiles was "mutation".

In paternity cases it has been shown that some of the loci regularly tested have such a high mutation rate that they should not be used in such testing. **R v Bropho** [2004] WADC 182. Mitochondrial DNA testing has revealed what is called somatic mutation within individuals, especially in hairs. Different DNA results can on rare but well documented occasions be obtained from the same individual, causing a problem with matching and risking false exclusions. Gill, "*Biological Evidence.*" Paper to 13th Interpol Forensic Science Symposium, Lyon, France Oct 2001.

STATISTICS:

A match between a crime scene sample and an offender is reported if the same series of allele numbers appears in the results for both samples. This is generally expressed in terms of a match probability, "*The suspect has the same profile (in the Profiler Plus system) as the DNA recovered from point A at the crime scene. This profile is expected to occur in fewer than 1 in 10 billion individuals in the general population*". Some courts allow the statistics to be expressed as a likelihood ratio, "*It is about 10 billion times more likely the suspect left the sample than if a random person left the sample"*. **R v Karger** (2001) 83 SASR 133 at 140.

There are only 6 billion people on earth. How do they get such an extraordinary figure and what does it mean? It doesn't mean that because there are only 6 billion people on earth there cannot be another match.

The first step in calculating the probability of a match is to find out what the chances are that another person chosen a random will have the same alleles at a certain locus. If there's a match at a point the search can be further narrowed by testing another locus, and then another until all nine are examined. (In reality, multiplexing allows all loci to be tested at once.) As matches are found at progressive loci, the more the argument becomes more convincing that the match is not by chance, and that the two samples come from the same source. Of course, if at any point the figures do not match, the suspect can be excluded.

How is this assessment turned into a calculation of probability? What is done bears some similarities to an opinion poll. Samples of DNA from hundreds of people are taken and an estimate made of the percentage of people in the general population who have a certain allele at a specific point/locus. Thus at locus D 13 S317, it may be found that 28% of people have allele 12 and 32 % have allele 11. The chances of a random match between a sample and a person from the general population at that locus can then be calculated. An expert in population genetics should prepare these estimates.

The statisticians then apply what is known as the Product Rule. They multiply the relative frequencies of each item matched. When the results of each allele and loci are combined with the chances of a random match at the remaining 8 loci, the combination of probabilities, or more correctly improbabilities, can become enormous.

> "*It is important to realise what a random match probability is not. It is not the chance that someone else is guilty or that someone else left the biological material at the crime scene. Likewise it is not the chance of the defendant being guilty or the chance that someone else in reality would have that same genotype. Rather, a random match probability is the estimated frequency at which a particular STR profile would be expected to occur in the population.* ***This random match probability may also be thought of as the theoretical chance that if you sample one person at random from the population they will have the particular profile in question***." JM Butler, *Forensic DNA Typing 2nd Ed*. Elsevier (USA) 2005 at page 500.

In some jurisdictions, the US for example, three different population databases are used for Caucasians, Hispanics, and African-Americans. In NSW, a single population database is used. In other Australian jurisdictions, Asian, and Indigenous databases are sometimes used.

The DAL uses a relatively large population database of 739 samples. No differentiation is made for racial variations. An Aboriginal database is presently being compiled.

In NSW, the DAL biologists do not usually calculate their own match probabilities. They use an EXCEL spreadsheet and a commercially available program. They simply add in the figures, including the theta value (see below) and up pops the match probability. It is generally so high for a 9 loci match that even allowing for an error range, figures well in excess of 1 billion are generated.

Problems with statistics:

Statistics determine the probability of an event occurring by looking at possible successes and dividing them by possible outcomes. Predictions can be made in a general sense, but no statistical analysis can say what the next outcome will be. What statistics can do is give a model of expected behaviour. Those models can be independently tested and validated for consistency and rates of error but they are tools and models - they are not real. They must, of necessity, be based on a number of assumptions, which in turn rely on statistical rules, and the developing science of population genetics.

Assumptions: The first step in calculating the probability of a match is to find out what the chances are that another person chosen a random will have the same allele at a certain locus. Before any match probability or likelihood ratio can be calculated the range of possible outcomes must be found. This involves an understanding of population genetics and the making of some basic assumptions in formulating the model or database against which a suspect sample can be compared.

The model used assumes that there is an infinitely large population in which no one selects a mate on racial or ethnic lines, a population in which there is no mutation, no migration and the biological process known, as natural selection does not apply. H Roberts, *Statistical evaluation in forensic DNA typing*, in Frecklton & Selby Expert Evidence, Chapter 80A.77 As none of these things are true, allowance must be made for error. There is no formula for what is an acceptable error rate. Some US laboratories pick an arbitrary figure of 10% but although it works in their models it is essentially a guesstimate.

In addition, it is assumed that:

· There is no genetic predisposition to crime, which might skew the results. To date none has been found.
· The samples used to compile the database are taken from a random selection of the population and contain no close relatives. Despite attempts to do so they are not truly random. However comparisons between databases in other jurisdictions show little variation and thus can be used to validate each other.
· The databases are as good as a whole population survey. They can't be, as we don't test everyone (yet!). The databases cannot be more than a model, but when they are crosschecked and validated they seem to work tolerably well. Realistically, they are much better checked and validated than most other forms of forensic comparison evidence, such as identification evidence, hair sample comparisons, bullet rifling or even fingerprints.
· The statistics take no account of other evidence. Such as, "I was in Vanuatu" or "I have six brothers all of whom live in the area" **R v Watters** CA UK, 19/10/2000.or "I have an evil twin". If there is a chance a close relative or same sex sibling has left the sample the probabilities of a match are again quite different. For example, there is a 1 in 10,000-match probability with a same sex sibling and a 1 in 100 million chance of a match with a first cousin Butler at page 511.
· Variations among populations are truly random. They are not. (See discussion on theta/FST below.)
· There is no link between the alleles tested. An example of linkage is the fact that blonde hair normally occurs in conjunction with blue eyes. Linkage can skew the product rule calculations. No linkage has been demonstrated in the Profiler Plus system (which analyses loci from different chromosomes, minimising the risk of linkage). As the complete absence of linkage has yet to be proved, a further assumption is made - that applying a theta/Fst value (see below) to the calculations will correct for any possible linkage.
· We can tolerate a degree of uncertainty. As defence lawyers, this is where our finely tuned doubt detection meters start to operate. How can there be uncertainty and not doubt? There can't, which is why we insist that DNA statistics be presented as a statistical model in terms of probabilities and not as evidence a direct match. Ignoring uncertainty about inbreeding, relatedness and failing to allow for difference between models may overstate the strength of the evidence.
While some assumptions are unlikely to be strictly true, it is thought that departures are mild Roberts, at 80A-202. and can be compensated for by giving conservative estimates of matches.

Is a 9-locus profile unique? A high match probability or likelihood ratio carries with it an implication

that no one else has the same profile and that another match cannot exist. But statistical probability cannot predict the next outcome. The circumstances that led to one person's genetic code may happen again by chance. We all have relatives who share similar genetic heritage. Checks of databases have shown random matches at four loci and some as high as seven. No check has, as yet, have demonstrated a random match at nine but we haven't tested enough people to rule the possibility out completely. The statistics are simply another tool, they are not a substitute for proving a case.

The Prosecutor's fallacy: What is the probability this animal has four legs given it's a cow? What is the probability that this animal is a cow given it has four legs? These two similar questions lead to quite different results. For those with a grammatical bent it is known as the problem of the transposed conditional. Similar errors of approach can be made in presenting DNA evidence.

Thus, while an expert may properly express a DNA match probability in these terms, "*the chance or likelihood of observing this profile in someone else other than the suspect is 1:1000*", a prosecutor may get things round the wrong way and express the opinion as if the suspect was the donor of the sample and say, "*The chance that the sample came from someone else is 1 in 1,000*" or even worse, "*There is a 99.9% chance the sample came from the accused"* or worse still, "*There is a 99% chance the suspect is guilty*". All are examples of fallacious reasoning: the match probability or likelihood ratio is not an expression of the probability that the accused is guilty!

The Prosecutor's other fallacy: If an expert concludes a suspect cannot be excluded, attempts may be made to get the expert to say to what extent that the suspect cannot be excluded.

Non-exclusion means no more than that. It really has no weight; it is a shorthand way of saying that the results are simply inadequate for a proper conclusion to be reached. It is an expression of the opinion that to call a match or exclude a suspect would be wrong, misleading, or both. The possibility of error is too great to reach any conclusions other than the suspect, along with all the other persons in the community who cannot be specifically excluded, is within the range of people about whom a "not excluded" conclusion can be made.

The so-called defence fallacy: There is a song by the Whitlams with the line, *"She was one in a million. So there's five more just in New South Wales."* *Up Against The Wall*, The Whitlams from their Album, *Eternal Nightcap*. Lets be realistic, if the singer was silly enough to let her go, it is most unlikely that there are 5 more available and interested women in NSW at all. The fallacy applies when the likelihood ratio is not at a ridiculously large level. It is to presume, wrongly, that you can say of a 1: X likelihood ratio, "*Well there are X more persons who it could be and they have not been eliminated. So there must be a doubt, as it has been statistically proved that the real offender could still be out there.*" The fallacy arises because this conclusion ignores all other factors personal to the accused, which make him a suspect above those other X persons; things like, opportunity, motive, proximity to crime scene, age, sex, and physical description.

If on the other hand there is simply no other evidence than the DNA "match" the reasoning is not fallacious at all.

Mixtures: The minimum number of contributors can generally be determined but the maximum cannot. There remains a possibility of a minor or partial contribution from another person or persons, or the possibility that alleles may have dropped out, been masked by other contributors, or that the contributors share alleles.

Generally the DAL give their calculations based on the minimum number of possible contributors to a mixture and the statistical likelihood of there being a mixture. The presumption that there are only two contributors, one of whom must be the victim, favours the prosecution. A proper and conservative assessment should assume that at least two more than the minimum number of contributors may be in a mixture. But DAL reports never include these additional calculations. These calculations can be done quite simply using the computer programmes available. Should the DAL withhold calculations favourable to the defence?

Random man not excluded: This method of calculating the likelihood ratio is generally more conservative than the product rule and is regularly used by some laboratories e.g. in Tasmania. It involves looking at the sample as a whole and not first separating out "known" components. It enables a comparison to be made between statistical outcomes. It can, however, be biased toward the prosecution in some specific instances. Roberts at 80A-603 & 604. That different methods of calculation give different match probabilities illustrates the hypothetical nature of any "match" conclusion.

Theta/Fst: We tend to mate with people of similar genetic backgrounds. In some societies there is a cultural tendency to inbreeding, such as first cousin marriages. Small or isolated population groups tend to have similar patterns of DNA. Allowance is made for this in calculations by allowing an error factor called theta or Fst. Although calculated differently theta and Fst have approximately the same effect.

Studies have shown that these values are generally very low - less than 1%. Databases even those among the general Australian community still use a conservative figure of 0.03 or 3%. This is incorporated into the standard programme for calculating match probability or likelihood ratios so that some allowance is made for both direct and underlying relatedness in the population. Although a theta value of 3% is generally allowed, it has been suggested that such is the level of long-term isolation and restricted breeding of some Aboriginal groups, that a theta value of 8% Roberts, 80A- 621, citing Cavalli-Sforza & Others, *The History and Geography of Human Genes*, Princeton Uni Press (1994) to 13% **R v Bropho** [2004] WADC 182. might be necessary **R v Bropho** [2004] WADC 182..

Like Aboriginal tribes or groups some other communities can be quite isolated in a geographic and genetic sense. Genetic variation is thus contained. For example, a variation or difference between those from Northern China and South China including Vietnam has been assessed as high as 6%. Roberts, 80A- 621, citing Cavalli-Sforza & Others.

Relatives: Where a close relative could be a suspect or where the suspect or suspects come from a genetically isolated population, many of the assumptions on which the mathematical calculation of a probable match do not apply. Close relatives are more likely to have the same profile as a suspect than the randomly selected person used as a basis of match probability calculations. If a brother cannot be excluded specifically and may have been involved then the match probability or likelihood ratios given by application of standard formulae must be very conservatively revised. If the brothers or cousins come from a small and genetically isolated group the figures must again be reduced.

The problems were graphically illustrated in the Western Australian case of **R v Bropho** [2004] WADC 182. This was a judge-alone trial of an old rape allegation. The complainant was not a reliable witness but a child had been born at the time of the alleged rape. DNA evidence of paternity pointing to the accused was crucial to the prosecution case. Initially the likelihood of the accused being the father compared to a random person using a theta/Fst value of 3% was assessed at 1:3,134. However, a theta of 13% reduced this to 1:358. Once problems with a number of the loci used and the fact that close relatives were also suspects were factored in, by the end of the day, the judge could not use the DNA evidence as "*reliable corroboration*". Mr Bropho was acquitted.

THE LAW:

What I hope to do here is to distil a number of important principles that have now been settled. Let me be blunt, the courts in Australia and internationally have bent over backwards to ensure that DNA evidence is admissible in criminal proceedings. Despite cautions, without careful analysis DNA evidence may appear more probative than it really is. **R v Pantoja (No. 2)** (unreported, NSW CCA, 5th November 1998) per Wood, CJ at CL at 37, **R v Pantoja (No. 1**) (1996) 88 A Crim R 555 at 561-562 and **R v Humphrey** (1999) 72 S.A.S.R. 558 at 567-568 The risk that jurors will commit the prosecutor's fallacy is high. In any event, they will tend to treat a match probability of 1: 10 billion as conclusive of proof the suspect left the sample and, if not carefully instructed, as proof of guilt.

The *Crimes (Forensic Procedures) Act* is not a code for the collection of DNA and other evidence. It does provide some limited protections from interference with personal liberty but more importantly, it operates as a facilitating mechanism for the collection of DNA and other forensic material.

· If they want your sample they will get it – (1): A Magistrate can order that a suspect provide a forensic sample (ss. 24 and 25 *Crimes (Forensic Procedures) Act 2000)*. To challenge a Magistrate's order as an error of law s.54 *Crimes (Local Courts Appeal & Review) Act & s.115A Crimes (Forensic Procedures) Act 2000.* you must do more than establish the decision is unsound and unreasonable. It must be shown, either that there was no evidence to support the conclusion, or there was a material misdirection of law.
Jawasansher v Johnson LCM [2004] NSWSC 872, per Barr J.

· If they want your sample they will get it – (2): A Magistrate considering an application under ss. 24 or 25 *Crimes (Forensic Procedures) Act 2000* can take into account hearsay material.

L v Lyons (2002) 56 NSWLR 600 per Sully J.

· If they want your sample they will get it – (3). What is contemplated by the notion of a forensic procedure, whether intimate or non-intimate, is that it is a procedure actually carried out on the person of some specific individual. The *Crimes (Forensic Procedures) Act 2000* does not apply to the chance circumstance that a person throws away say a cigarette butt which is then retrieved without any reference to, or interference with the person, even if that "chance circumstances" is manufactured by police desperate for a sample, which would not have been ordered by a Magistrate.

R v Kane (2004) 144 A Crim R 496, **R v White** [2005] NSWSC 60 per Studdert J.

· If they want your sample they will get it– (4): If a forensic procedure is undertaken illegally, a civil court will be very reluctant to intervene to prevent the results being analysed. Exclusion of such evidence should generally be left consideration by the court of trial.
Kerr v Commissioner of Police [2001] NSWSC 637 per Studdert J.

· Don't give up hope: If the strict requirements of ss.24 or 25 *Crimes (Forensic Procedures) Act 2000* are not met, error of law can be shown.

Orban v Bayliss [2004] NSWSC 428, per Simpson J, **Hardy v Pinazza**, unreported SC NSW, 18/4/2005, per Adams J., **Maguire v Beaton**, unreported SC NSW, 11/5/2005, per Latham J.

· DNA expert evidence is of such importance to the prosecution case that there can be substantial reasons, within the meaning of s.91 *Criminal Procedure Act*, for attendance of the expert to give evidence at committal, even if there is other evidence implicating the accused.
R v Micallef [2001] NSWSC 1172 per Hidden J.

· Generally, a court will rule that the desirability of admitting the evidence the subject of challenge outweighs the undesirability of admitting such evidence, even if it is clear that the evidence was obtained in contravention of the *Crimes (Forensic Procedures) Act 2000*.
R v White [2005] NSWSC 60 per Studdert J.

· A match probability simply shows that a sample, which could be the accused's sample, was left at the scene.

R v Doheny and Adams (1997) 1 Cr App R 369, **Pantoja (No. 1)** (1996) 88 A Crim R 555.

· A population database of a few hundred is sufficient, if properly validated by an expert in population genetics, to form the basis for a statistical analysis of DNA match probability.

R v Pantoja (No.1)(1996) 88 A Crim R 555, **R v Karger** (2002) 83 SASR 135, **R v Milat** (1996) 87 A Crim R 44, **R v McIntyre** [2001] NSWCSWC 311 per Bell J, **R v Gallagher** [2001] NSWSC 462 per Barr J.

· Reliable evidence can still be obtained, even if a database is used which does not precisely relate to the offender's race. Properly validated population databases are not unreliable per se, even if they are general and not specific to the suspect.
Pantoja (No.1) (1996) 88 A Crim R 555, **R v QVT** (2002) 131 A Crim R 264.

· The use of the Profiler Plus system has been sufficiently validated and yields consistent results. It is not unfair for the prosecution to rely on it.
R v Gallagher [2001] NSWSC 462, **R v Karger** (2002) 83 SASR 1.

· Statistical evidence can be undeniably strong evidence pointing to a conclusion that the accused was the source of the incriminating DNA, but is not direct evidence of that fact. And, as is obvious, the statistical evidence must be considered in the light of other evidence in the case.
R v Karger (2002) 83 SASR 135.

· The statistical evidence interpreting the significance of the DNA match is not evidence of the probability

that the appellant was the source of the incriminating DNA. To so regard it would be to make an error. However, the statistical evidence interpreting the DNA match is expert evidence that the jury could use in deciding whether it was satisfied beyond reasonable doubt that the appellant was the source of the incriminating DNA. It is necessary for the jury to appreciate these points if they are to make proper use of the statistical evidence.
R v Karger (2002) 83 SASR 135.

· If there is evidence before the jury which purports to exclude the accused, the jury will need to be satisfied that the accused has not been excluded to the higher standard required by Shepherd v The Queen (1990) 170 CLR 573 at 579.
Pantoja (No.1) (1996) 88 A Crim R 555 at 559.

· Unreliable DNA evidence and statistical evidence can be excluded if unfairly prejudicial.
R v Tran (1990) 50 A Crim R 233, **R v Lucas** (1991) 55 A Crim R 361.

· DNA evidence will not be excluded simply because it is complex.
R v Lisoff [1999] NSWCCA 364

· The fact that scientific evidence is complex does not mean that it would result in unfair prejudice (within the meaning of s137 of the *Evidence Act)* if admitted. Such evidence can be left to a jury. Conflict of scientific evidence is not enough to justify a conclusion that a jury could not decide whether or not the Crown had demonstrated beyond reasonable doubt that its evidence should be preferred.
R v Lisoff [1999] NSWCCA 364.

· Unless admitted, the chain of custody from collection of the sample to final analysis must be proved. To avoid any risk of unfairness, unless the defence do not require him or her, every person who handled and processed and analysed a sample should be called for cross-examination.
R v Sing (2002) 54 NSWLR 31 and **R v Ryan** [2002] VSCA 176.

· Where the only evidence is a match probability that is very low, this is simply not enough in itself for the jury to conclude with certainty the accused was responsible.
R v Watters CA UK 19 October 2000, **R v Bropho** [2004] WADC 182.

· If relevant DNA statistical evidence is tendered through a witness of due expertise then its probative weight cannot itself be a ground for withholding it from the jury.
R v GK [2001] NSWCCA 413.

· The total exclusion of “arithmetical figures” skews the experts’ evidence without contributing to the fairness of the trial. However it is inappropriate for a jury to be invited to determine guilt by the application of mathematical formulae suggesting how to aggregate the impact of different items of evidence.
R v GK [2001] NSWCCA 413.

· In every DNA case, the judge should warn the jury not to approach the question of guilt strictly on the basis of mathematical calculation.
R v Galli [2001] NSWCCA 504.

· DNA evidence, which does not advance the Crown case, because it cannot establish the suspect's presence at the scene, should not be admitted.
R v Ton (2002) 132 A Crim R 340.

· The judge’s use of the “prosecutor’s fallacy” can result in a miscarriage of justice and a re-trial.

R v Keir (2002) 127 A Crim R 198 at pp 202–203, **R v Wakefield** [2004] NSWCCA 288.

· DNA is but a part of the circumstantial case. A direction to the jury, which places the DNA evidence as part of the “strands in the rope” may be adequate.
R v Cohen [2002] NSWCCA 339.

· The proper approach to the issue of whether the incriminating DNA came from the appellant, and to the issue of guilt of the crime charged, is to treat the statistical evidence as evidence to be considered

and weighed along with the other circumstantial evidence. It should not be allowed to displace or to overwhelm the consideration of all material evidence, but at the same time it should be given such weight as the jury think proper.
R v Karger (2002) 83 SASR 135 at [21]

TACTICAL CONSIDERATIONS

A DNA "match" can be the centrepiece of the Crown case. Despite all the potential problems noted above, it will, more often than not, remain so. The legitimacy of DNA evidence has been enhanced by the relatively few cases where DNA has been used to exonerate an innocent. Butler at page 8, notes that in the US only about 150 exonerations of convicted felons have occurred. Most DNA analysis following "innocence projects" simply confirm the offender did it. Exclusions have resulted in no bills or the direction of police investigation along more fruitful lines.

No one could legitimately complain about DNA evidence that helps focus police investigations and secures justifiable convictions. I have argued elsewhere Andrew Haesler on the Public Defenders Website- "*DNA - An Overview of Testing and the Crimes (Forensic Procedures) Act 2000* that forensic evidence and DNA in particular, may reduce the present reliance on heavy penalties as a deterrent. DNA evidence enhances the police capacity to catch wrong doers; we may be able to rely on the certainty of being caught as a more credible deterrent. Jacobs J in **Griffith v R** (1977) 137 CLR 293 at 327, noted: "*The deterrent to an increased volume of serious crime is not so much heavier sentences as the impression in the minds of those who are persisting in a course of serious crime that detection is likely and punishment will be certain".* However, when confronted by expert evidence of a DNA "match" and firm *We all know there are instructions and instructions.* instructions consistent with innocence, defence lawyers have no choice but to confront the demon.

Challenging match probability: A lot of time and effort can be expended in confronting a DNA "match" to no avail - **R v Karger** is an example. Attacking the statistical basis of an expert's conclusion can be rewarding if there is no other evidence or the other evidence is weak - **R v Bropho** is an example. Reducing a match probability from 1: 10 billion to 1: 1 million can be a waste of time and effort unless the expert's opinion is in the process totally discredited. A 1: 1 million match is still impressively persuasive if combined with other evidence. There is certain futility in challenging large numbers, particularly where there is other evidence implicating the accused. However, where there is no other evidence it may be all you have.

Alibi: An alibi may defeat DNA. This occurred in the "Manchester mismatch" case the first known example of a false match, said to be a one in 37 million chance. Only retesting, after an unassailable alibi was put forward, led to the dropping of charges. UK DNA Mismatch http://www.scoop.co.nz/stories But realistically how many of us have ever had a case proceed to trial where the alibi evidence was watertight "*What do you want from Life? A fool-proof plan and a watertight alibi!"* The Tubes.?

In another notable UK case, the defence of alibi, "I was in gaol at the time," failed when it was revealed the guards were letting him out to paint their homes. The rapes and murder were committed on his way back to gaol!

Breaking the connection: While a connection between the accused and the crime scene, together with DNA, can be more than sufficient to convict, the absence of a such a nexus can be vital to defusing the impact of the DNA evidence. This is what occurred in **R v Cohen** [2002] NSWCCA 339, a gaol killing. There, the fact that the suspect's sock was found in the victim's cell simply showed that anyone that could have put it there. The extreme portability of DNA makes the possibility of planting a sample a fertile field for testing and cross-examination. Even a semen sample can be planted, although to date the only evidence I have of this is in fiction. See, Scott Trurrow, *Presumed Innocent*, and the Harrison Ford movie of the same name.

Who else's DNA is in the mixture? If it is possible, introduce another plausible explanation or interpretation of the crime to challenge the Crown's claim that the DNA completes the circumstantial puzzle.

The finding of multiple donors in a crime scene sample, in particular an unknown minor contributor, can cast doubt on the inferences the Crown wish the jury to draw. If the DNA can be made consistent with an alternative theory, the very power of the DNA evidence in the minds of the jury can lead to it being co-opted into the fabric of doubt.

What does a match mean? If there is an unknown contributor, could he be the culprit? In the Barnes trial for example, DNA from two men who could not be identified was found on the waistband of the deceased's jeans. The failure of the prosecution to exclude the donors of these samples seriously weakened their case against the accused.

In sex matters question whether, prior to extraction, attempts were made to separate sperm from other cells, which may have come from the victim. Were only sperm cells examined? "Where did the minor contributor's DNA come from, sperm or other cells?" In most cases the answer must be, " I can't be sure." If it is sperm, it may mean a second male suspect. If not, it may simply be from the complainant or contamination during the collection of the sample.

Why wasn't my client's DNA found? As DNA becomes more regularly used its absence too can be used. "We would expect the accused's DNA to be found given the power of technology and the actions he is accused of, "Why wasn't it?" Defence lawyers can and should celebrate the science and express disappointment when there is a negative -outcome.

If the Crown's knockout blow doesn't come from the DNA match its probative power can be deflected. As we know there are strong pre-existing prejudices in juries in favour of DNA as conclusive proof. The responsibility is on defence counsel to manage prejudice or turn it around towards their preferred conclusion.

Spread confusion? While often done inadvertently or because of incompetence, as a tactics spreading confusion has doubtful merit. Confusion between experts does not always favour the defence. It is a fallacy that confused juries acquit. M Findlay, *Managing Juries in NSW*, AIJA (1994). Most jurors approach the trial with high expectations for the significance of DNA evidence. They will see through attempts to side step its probative and prejudicial weight.

Challenging the probability calculations: As indicated above, the figures used to calculate probability can never prove that the two samples came from the same source. Statistics are a useful tool they are not proof. Questions can usefully be asked, "Why was one test used and not the other e.g. Random man not excluded?" "Why aren't relatives factored in?" "What theta value was used and why?" We have learned from **Bropho** such challenges are far from futile.

Evidence of a DNA match is just opinion evidence after all. The problem is it can be very good opinion evidence.

Challenges to the chain of custody: What have the police done with the DNA before it got to the Lab? **R v Lissoff** is a possible example of deliberate contamination. However contamination is just as likely to be accidental or innocuous, for example – was the correct exhibit sent to the lab? Has there been a mix up of offender and victim's samples? Check the Exhibit records, "was the exhibit signed out a week earlier?" "Does it refer to the same thing that was delivered to the DAL lab?" Sloppy record keeping can provide a fertile source of material for cross-examination.

Despite what was argued in **R v Sing** and **R v Ryan** I have never seen anything useful come from calling for cross-examination the lab technicians, other than the person who first examined the potential DNA sites on the exhibit and the supervising biologist. The DAL Worksheet tells you all you generally need to know about what the technicians did. The person who initially tested the exhibit may be fruitfully examined about why some areas of an object were tested, and not others.

Contamination: As indicated above, most lab contamination is picked up by the protocols in place. The few examples of lab mix up have been thoroughly investigated. Lab contamination is more likely to lead to the exclusion of a suspect, because a contaminated sample cannot be accurately analysed, than falsely inculpate a suspect.

The presence of a weak, but unmatched or unmatchable, DNA sample may be used to say the accused is not excluded. However that weak DNA may come from people or things that the object came into contact with. It may have got there because of poor collection or storage procedures being used before the object got to the Lab. All the DAL staff have their profiles on file to allow for comparisons to be made to detect possible contamination. The Police Association have to date been successful in preventing a similar database of police-DNA being established for contamination elimination purposes.

The best advice I can give is focus on the police, not the lab. The OJ Simpson case is a textbook

example of how the police can be attacked either for sloppy or biased investigation. The OJ case is extensively referred to in both Butler and Buckleton, Triggs & Walsh, *Forensic DNA Evidence Interpretation*, CRC (USA) 2004. Carefully cross-examine the Crime Scene police: "Who was fiddling about the crime scene when they arrived?" "Was each piece of evidence picked up with clean tweezers?" "How often did you change your gloves?" "Were facial masks worn?" "How were the separate exhibits stored - at the crime scene, on the way to the station and at the station?"

The police continuity evidence will consist of a statement saying, "I collected the exhibit from point A and took it to point B". It may appear innocuous however, the author rarely adds in "Oh, and by the way the exhibit fell out of the bag as I picked it up" or "I forgot to use gloves".

The apparent cogency of DNA evidence brings the real risk that it will be tampered with by anyone interested in falsely implicating a suspect. But it may not be the police who contaminate a sample or exhibit. What better way to cast a doubt on a police investigation than to leave a rival criminal's DNA at your crime scene, for example by leaving his cigarette butt?

Bias in the Lab?
"*Forensic scientist may become partisan. The very fact that he police seek their assistance may create a relationship between the police and the forensic scientists. And the adversarial character of proceedings tend to promote this process. Forensic scientists employed by he government may come to see their functions as helping the police. They may lose their impartiality*". **R v Ward** (1993) 96 A Cr App R 1 at 51. An example in Australia can be found in **R v Button** [2001 QCA 133 where the forensic scientist looked only for evidence which would implicate the accused and missed because they did not do the relevant tests, vital evidence pointing to the real culprit. Justice Williams described the various failures in the case as resulting in "…*a black day in the history of the administration of justice in Queensland*." Deliberate failure to investigate is rare but we must be alert for them. The more likely cause of a failure to investigate alternatives is pressure of work and a focus on output rather than using the genuine forensic expertise of the analysts. The more procedures are automated the less the analyst has to do with analysing the samples themselves. See S J Walsh , *Is the double helix a double edged sword ,* UTS Speaks public Lecture , unpublished paper May 2005. The quest for volume can mean only one exhibit or part of an exhibit is analysed. Sometimes as **R v Button** shows this is simply not good enough. When cross-examining an expert or technician about what was tested it is sometimes prudent to find what was *not* analysed.

Secondary Transfer: In my experience most prosecution experts will try to avoid a concession that secondary transfer can occur (see discussion above) At the same time those same experts will acknowledge that the sensitivity of the "normal testing" equipment now available to the DAL is so good that they can now re-test old samples, that a few years failed to reveal DNA, and find it.

As Ms Freidman noted during the Barnes trial, much will depend on the quantity of DNA, deposited and subsequently recovered, and the nature of the original specimen. The smaller the sample and the more portable the specimen e.g. skin or saliva, the greater the possibility it has been innocently transferred.

Ms Friedman stressed that in her view secondary transfer was not, "a big issue in DNA analysis". The problem is that it can be a big issue for the defence. If DNA can be innocently transferred, as we know it can, then this transfer may explain the apparently inexplicable. A concession by an expert that secondary transfer can occur must undermine the certainty with which an opinion is given. If the DNA could have come from anywhere, a "match" has little if any relevance.

Concessions will not generally be made unless you work for them. To get them requires detailed and careful cross-examination and the putting of a possible alternative hypothesis that has common sense plausibility.

A line of cross-examination which may work for spittle for example may not be so successful if the defence are trying to explain the a "match' between the accused's DNA and semen found on a high vaginal swab. But if DNA can be picked up on a police swab, why can't another like object, if it is moist and/or absorbent pick up traces of DNA if rubbed on or put in contact with the original DNA bearing object? In the Barnes matter, the defence hypothesis was that after meeting Barnes and getting his DNA on her hand or clothing the victim used her hand to adjust her bra thus transferring Barnes' DNA to it. She was later murdered by a person unknown.

How long does DNA last? This often depends on whether the prosecution want to use the evidence or not. Experts have been known to give quite different answers, often to suit a preferred scenario. The studies simply haven't been done to say exactly how long DNA will last and there are too many

variables for any answer to be definitive.

Mitochondrial DNA samples have been obtained from very degraded objects - **R v Keir** is a good example. (In **Keir** mitochondrial DNA was extracted from a few bone fragments said the be the missing Mrs K. They had been found under the family home 10 years after she "disappeared".)

Examinations of "cold cases exhibits" have turned up nuclear DNA from exhibits over 10 years old – **R v Stone** [2004] NSWSC 224, where Stone pleaded guilty in 2004 to a 1990 murder, is an example.

DNA will degrade in sunlight, heat and humidity and can simply be eaten up by bacteria and other microorganisms. It can be washed and cleaned away. It is not particularly resistant to modern cleaning products. However if kept away from light and heat, in a cool, regulated environment, it can last a surprisingly long time. DNA is regularly extracted from under fingernails hours, and sometimes days, after an incident. (Perhaps if the new technology does not produce a more wary criminal it may lead to a cleaner one).

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As defence lawyers we will have to learn to live with DNA evidence. If we are to live with it, we have to understand it. If we are to challenge it, we need to understand it better than our opponents do. If we are to use DNA evidence, we must understand how juries view it. We need to work out strategies to use it, challenge it or reduce its significance. Alternatively we can accept the expert's conclusions and work our case around their findings, even if the only advantage is an early guilty plea. DNA can also exclude a suspect or point to an alternative culprit. We should not waste the courts or our time on futile challenges. Rather, we need to learn to use the evidence to our client's advantage.

Andrew Haesler
May 2005

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