



24 August, 2001

The Crimes (Forensic Procedures) Act 2000

Justice Action's supplementary submission to the Standing Committee on Law and Justice Inquiry

This submission addresses specific questions asked by the Standing Committee on Law and Justice which were not fully addressed by the evidence given at the 7 August 2001 hearings. As the answers tend to be interrelated the order of the questions have been rearranged in the interest of clarity (e.g. it is hard to answer a question about admissibility without first covering the reliability of DNA evidence).

10) How likely are false matches? Does the risk increase for prisoners?

Using modern forensic DNA analysis to compare two samples taken under clinical conditions will rarely produce a false match if done competently. However even the tiniest chance of a false match is magnified many millionfold when profiles are databased and compared with a huge range of other profiles.

Complicating matters is the fact that DNA comparisons for forensic purposes are rarely between samples taken under clinical conditions. Crime stains are usually not of optimum size and contain inorganic matter which can interfere with testing. They can also be degraded due to age and microbial activity and mixed with DNA from other human and non-human sources.

In some cases a profile for matching is not gained from an organic sample at all, rather it is derived by reference to other profiles. Thus the parents of a missing person might give samples which allow an array of the 'virtual' profiles of all of their possible offspring to be produced for comparison with samples suspected to have come from their missing child. Obviously if either of the parents DNA profiling was in error, so too will be the profiles of the 'virtual offspring'.

A match between DNA profiles can be declared for one of three reasons. These are traditionally referred to as

- 1) Match by identity - The two DNA profiles originated from the same source. Normally this would mean the same individual or identical twins but in

mitochondrial DNA analysis it would indicate that they came from one or more people of the same maternal line of descent.

- 2) Match by chance - The two DNA profiles shown are the same due to the inherent limitations of the testing system being used but they don't originate from the same source. The statistical probability of such a match is ostensibly quantified in 'match odds' given in court cases, but these are increasingly given in a manner so deceptive and irrelevant to the real chance of such an event that they verge on perjury (discussion below). In cases where the match odds are so large as to be probative of very little it is not unusual for Australian prosecution experts to fail to give them at all when declaring a match (e.g. The 1998 Queensland case *R v Renton and Festa* in which forensic expert Kenneth Cox declared a match between the defendants and a mixed profile extracted from a balaclava used in an armed holdup. However he neglected to tell the court that any randomly selected Australian would have a greater than 90% chance of matching the balaclava stain according to the test he used.) The 'UK mismatch(es)' and the 10 matches ESR's Dr John Buckleton reports on his database of just over 10,000 personal profiles are 'matches by chance'.
- 3) Match by error - The profiles match because an error has occurred in typing at least one of them. This can be the result of contamination, mislabelling/mixup, mistaken interpretation of results, procedural error in testing/analysis or an error produced by the equipment being used (i.e. chemical, mechanical, electronic or software faults which result in erroneous profiles). The possibility of a match by error is almost never considered in a court case and laboratories rarely seek to have it quantified in spite of the fact that it would normally be many thousands of times more likely than those given as the 'match by chance'. The implication of a Christchurch man in two Wellington murders detailed in the *Report on DNA Anomalies* was a 'match by error'.

Match by chance

Forensic Mathematics

To gain some understanding of the meaning of a DNA 'match by chance' it is necessary to have a basic understanding of statistics and probability. However, contrary to popular belief, most principles of forensic mathematics are within the grasp of HSC level maths graduates.

Unfortunately there are ways of presenting the results of such calculations in a manner which is highly likely to mislead the vast majority of potential jurors. Expert forensic witnesses giving DNA evidence not only take advantage of this fact - it has become the

standard way in which DNA match evidence is presented in court in Australian, NZ, the UK and the US.

The best known 'rule' of forensic mathematics is the one which is used to generate match odds at ever increasing orders of magnitude as more genetic loci are tested - the product rule.

In simple form it states that if one allele occurs with frequency $f1$ in the target population while another occurs with frequency $f2$ the chances of finding *both* in a randomly selected member of that population is $f1 * f2$. (e.g. the frequency of FES allele 12 in the European population is 0.23 (23%) while the frequency of FES allele 13 is 0.05 (5%) - so the chance of a randomly selected European of having a 12/13 FES profile is $0.23*0.05 = 0.0115$ (1.15%) or 1 in 87).

As extra loci are added precision increases. So if someone was found to have a FES profile which occurs in 1.15% of the population and a DQ-Alpha profile which occurs in 3.5% of the population the probability of randomly selecting someone with matching FES & DQ-Alpha is $0.0115 * 0.035 = 0.0004025$ (0.04025%) or about 1 in 2500. Modern forensic testing usually involves checking between 6 and 13 loci.

However use of the product rule is based on two contradictory assumptions, both of which are known to be untrue.

The first is that no two people in the target population are related and the second that all opposite gender members of the population are equally likely to mate with each other and produce offspring. While the errors introduced by the divergence between fact and these assumptions is relatively small when only a few loci are multiplied together they become larger with more 'discriminatory' testing. In the case of nine loci STR testing - as with Profiler Plus - the errors introduced are several orders of magnitude larger than the match odds ultimately produced.

The shortcomings of the product rule are recognised to varying degrees in the forensic science community and methods for dealing with them are suggested in formulas contained in *The Future of Forensic Testing* and *The Evaluation of Forensic DNA Evidence* (NRC-II).

Unfortunately there has been a steady discounting and downplaying of the limits of the product rule since the early 1990s to the point where the FBI now seeks to claim that its 13 point CODIS system can provide *unique* identification of the DNA contributor - even though most high school graduates could correctly tell you that this is a scientific impossibility.

According to page 25 of *The Future of Forensic Testing*, "The FBI in 1997 announced a new policy that has been used several times in court cases by the FBI and others and has not been rejected. This assumes that if the match probability is substantially less than the reciprocal of the U. S. population, then it can be stated with "reasonable scientific certainty" that a particular individual is the source of the DNA sample. ... The FBI procedure has been criticized by Weir (1999) and supported by Budowle, Chakraborty, et al. (2000)".

Note that Dr Bruce Budowle is head of the FBI's forensic DNA program and SWGDAM as well as the developer of Profiler Plus and the match reporting policy he endorses above.

Population Genetics

Before applying the product rule you must know the likely frequency of the alleles of interest in the target population - which is where statistical databases come in. You also need to know whether the various alleles are distributed evenly within the population or whether they are inclined to 'bunch up' in specific geographical areas or subpopulations.

When alleles are evenly distributed (albeit at different frequencies for each one) the population is said to be in *Hardy-Weinberg equilibrium* - a state which presupposes that for many generations any of its members is equally likely to have mated with any other opposite gender member and produced offspring.

Of course no populations are really in H-W equilibrium, but for many there have been so many generations of pretty random intermarriage the assumption holds reasonably true. Obvious exceptions would include countries with an aristocratic class which doesn't marry down (or a pariah class which doesn't marry up), cultures with strong marriage laws such as caste Hindus and 'skin group' Aborigines or populations which have had a relatively recent influx of immigrants from a group with different allele distributions.

You must also be reasonably certain that the alleles being multiplied aren't inclined to appear together (such as blue eyes and blonde hair - if half the population has blue eyes and half has blonde hair it is likely that significantly more than a quarter have both blue eyes and blonde hair, as they tend to go together). Two alleles which are not particularly likely to appear in tandem are said to be in *linkage equilibrium*.

Loci used in forensic DNA testing are selected for their apparent linkage equilibrium - indeed they are usually on separate chromosomes so that there is little chance of two of them 'sticking together' during meiosis. However linkage disequilibrium can still occur in certain populations - such as when particular allelic variations at several loci are introduced by a single immigrant (or relatively small group). As the introduced alleles will only ever appear in direct descendants of those who brought them they are also more

likely to appear together - at least until the immigrants have completely 'blended' into the local population after generations of intermarriage.

Confidence Limits

Finally, the statistical databases referred to for allele frequencies must be big enough and selected randomly enough to be reasonably certain that they accurately reflect the distribution of the alleles in the population. Of course they can't be perfect unless *everyone* is tested for the statistical database. Forensic experts try to reflect the limitation of precision in the database by calculating *confidence intervals* around the figure produced with the product rule.

When imagining confidence intervals it is useful to visualise a bell curve with the centre bounded by two vertical lines and shaded. If the shaded area is 90% of the area under the curve the two vertical lines represent the upper and lower 90% confidence limits around the axis of the curve - the axis being the match odds produced with the product rule. The unshaded areas under the curve represent the 10% possibility that the real match odds are outside the range defined by the confidence limits - with a 5% chance they are lower and 5% chance they are higher.

A forensic expert may say, for example, that the 95% confidence interval of a particular match may be from 1 in 850 million to 1 in 125 million. This is the equivalent of saying that s/he is 95% certain that the 'real' match odds lie somewhere between 1:850m and 1:125m (and there is a 5% chance that it is not in this range at all). Or in other words there is perhaps one chance in 125 million of a randomly selected person matching the sample, but one chance in 40 that the real likelihood of a match is greater - maybe much greater.

Obviously estimates like these are meaningless unless the confidence level is at least as high as the match odds are low (so match odds of 1:1,000,000 would require a confidence level of more than 99.9999% to be meaningful, for the same reason that it is not valid to give a measurement like 0.14mm if it is taken with a ruler which is only accurate down to half a millimetre) but forensic scientists routinely ignore this consideration in court.

There is also reason to believe that statistical databases made up largely of the profiles of convicted offenders would not be a random sample of the Australian population at all - given that Australia's prisoners are drawn disproportionately from certain ethnicities, towns/suburbs and families.

There is controversy and dispute over some details of population genetics and forensic mathematics which impact on match odds - as almost every forensic scientist will concede. Those promoting DNA for prosecution purposes will always follow such a concession with claims that 'it doesn't really matter if the match odds are one in a billion or one in a hundred billion - its still almost certainly a real match'. This is nonsense.

Leaving aside the fact that match odds of hundreds of billions to one bear no relationship to the real possibility of a match by chance (see below for discussion) - when the intention is to create a database of profiles for mass comparisons in search of suspectless 'cold hits' there is a very big difference between match odds of one billion to one and 100 billion to one.

When DNA profiling with an 'error-free' method which gives '100 billion to one' discrimination between individuals it can be expected that one in 5000 Australians will have an *unrelated* 'DNA profile twin' (i.e. someone with the same DNA profile) somewhere else in the country (i.e. $20m / 100b = 1/5000 = 0.02\%$ [*]). When the odds are actually 1 billion to one, around one in fifty Australians will have such a 'twin'.

If the level of discrimination is one in 37 million - as was said to be the case in the 'UK mismatch' - for more than two in five Australians there will be an unrelated person somewhere in the country with an identical profile (i.e. $1 - ((37m - 1)/37m)^{20m} = 0.4176 = 41.76\%$). As the UK population is around 60 million, over 80% of UK citizens will have unrelated 'DNA profile twins' - assuming across the board match odds of 1 in 37 million.

By applying high school level statistical analysis to Britain's mass testing, databasing and crossmatching program it becomes obvious how irresponsible the use of the database to 'solve' suspectless crime really is.

Following at least two false matches on the UK database - one coming to light when a more accurate test revealed the error, the other when it was appreciated that two individuals on the database matched the crime scene profile - the Forensic Science Service has upgraded its testing and database from 6 to 10 loci.

[*] Actually the correct calculation is $1 - ((100b - 1)/100b)^{20m}$ which gives about 0.019998% but the method used above is sufficiently accurate for the two examples given and easier to understand.

Suspectless database searches

There are almost 20 million people in Australia, and looking for cold hits in the absence of other evidence is equivalent to making all of them suspects whether on the database or not. It can easily be seen that even with match odds of the order of hundreds of millions to one there is a significant chance that the wrong Australian will be matched to the sample.

This very real chance is often discounted with the claim that as it will mostly be convicted criminals on the database there is a high likelihood that a potential recidivist will be the subject of the match - therefore you are more likely to have got the right match.

This argument is particularly popular in the US where most jurisdictions only allow suspectless matching on the offenders index (e.g. "Clearly, because of recidivism, a person on the database has a greater probability of being the source than a random member of the population", *The Future of Forensic Testing*, NIJ 2000, p26).

While this view sits easily with popular prejudice it is far from clear what the connection between imprisonment and recidivism rates in offences which might be solved with DNA evidence might actually be.

The Crimes (Forensic Procedures) Act 2000 allows for the testing of all NSW prisoners whose offence may have theoretically carried five or more years in prison - regardless of the nature of the crime or the actual sentence handed down. This includes murderers (murder has a very low recidivism rate), marijuana growers, fraudsters, drunk drivers who caused serious accidents, spouse abusers, heroin dealers and those who have been wrongfully convicted. Very little research has been done on the recidivism rate of any of these categories of offenders (except murderers) and it does not seem likely that DNA would assist in solving many of these sorts of crimes.

Even sex offenders will not usually be recidivists who might be matched to unsolved crimes with DNA evidence. Different categories of sex offender have very different estimated recidivism rates, with none much higher than 50% and several below 10%. Most sex offence charges are not contested on whether intercourse took place but rather whether it was consensual or how old the participants were at the time - making DNA identification evidence moot anyway.

But if it were really possible to match crime stain DNA to individuals with, say, 100 billion to one accuracy, there would be good grounds for believing that a database search would *usually* produce the right match - and hopefully the occasional false matches might be sorted out with careful police work. Unfortunately, contrary to the impression given by forensic experts in court, forensic DNA analysis does not have anything like this kind of accuracy and is not likely to achieve it in the foreseeable future.

When DNA match odds are given in court they are almost always in terms of the likelihood of the profile matching a randomly selected Australian who is *unrelated* to the suspect. The reason the hypothetical Australian is never a relative is because extended family members are at a much greater chance of matching. And it will be obvious to anyone who bothers to think about it that the chances of a randomly selected Australian being related to the suspect are much greater than one in several billion.

Around one in 150 Australians is one of a pair of identical twins (i.e. one in 254 live births produces identical twins), so the chance that an unidentified DNA profile came from one of a pair of identical twins is about one in 150. Therefore the chance that any two randomly selected DNA profiles came from each of a pair of identical twins is the

chance that one sample came from such a twin divided by the population of Australia (i.e. the chance that the person who left the other sample is the other twin). This gives $1/150 * 1/20m = 1/3b = 1$ in 3 billion.

Thus anyone who claims that they can distinguish between the DNA of two different Australians with more than 3 billion to one accuracy without knowing the family background of the sample donors is clearly and demonstrably lying - no matter how accurate the testing method used.

If identical twins were the only problem we could perhaps solve it by insisting that anyone subject to DNA testing say whether they have such a twin and providing contact details if necessary - although this would not help those like Pat Forsythe MLC, who spent much of her life not realising that she may have an identical twin. But similar problems also arise when considering siblings, half-siblings, cousins etc.

When a nine-point testing system like Profiler Plus is used to try to distinguish between close relatives the possibility of a match by chance is much greater than one in billions. The possibility of a chance match between two same sex siblings using Profiler Plus is between one in 262,144 and one in 512, depending on the degree of homozygosity in the profiles of the parents. For most Australian sib-pairs there would be around one in 6,000 odds that their profiles would match by chance. Of course this accumulates for each same sex sibling - so a man with three brothers would be at three times the risk of a chance match to at least one of them - about 1 in 2000.

The odds of a chance match between half-siblings or cousins are somewhat lower - of the order of one in hundreds of thousands or millions - but of course most people have far more same sex cousins than they have siblings. When ESR in New Zealand falsely matched several murder scene samples with an assault victim - claiming one chance in 930 million of a chance match with an unrelated New Zealander - they at first tried to suggest that an unknown half brother of the victim was involved, as it would be far more likely than 'one chance in 930 million' that such a person may have a profile matching the assault victim.

The big impact that this often ignored limitation of DNA profiling has on correctly matching crime stains to suspects is due to the fact that members of the same family - whether they know they're related or not - often live in or frequent the same geographical areas, thereby increasing the chance that someone related to the suspect may have been present at the crime scene. This is especially so in the large proportion of serious crime which is carried out 'within the family'.

As with family members, those in the same ethnic group (or *subpopulation*) are at greater risk of matches by chance than conventional match odds would indicate. While many jurisdictions maintain separate statistical data for different ethnic groups (e.g. Caucasian

Americans, African Americans, Asian Americans, Eastern Hispanic Americans, Western Hispanic Americans and several different Native American groups on the FBI's CODIS database) there are severe limitations with this method in cases where the suspect pool includes populations which are highly *substructured* (i.e. containing groups with significantly lower levels of genetic variation than exists in the population as a whole).

Native Americans are thought to have around three times as much population substructuring as exists within the other main divisions on the CODIS database. In Australia, groups which could be expected to show distinct population substructuring would include Aborigines, caste Hindus (who traditionally observe strict intermarriage laws) and occupants of towns or suburbs created as the result of large scale migration from one or two Mediterranean villages.

So the possibility of a match by chance between DNA profiles from different people is much higher than is suggested by the odds bandied about by forensic scientists (often while under oath). The possibility of a match by chance to a family member or a member of the same sub-population is much higher than one in billions - for most people it would be more like one in a few tens of thousands, hundreds of thousands or, at most, millions.

If 'match by chance' was the only source of false matches in forensic DNA analysis it would still be accurate enough to deal with criminal cases where a handful of suspects are matched against a dozen or so samples taken from a crime scene - providing that all of the crime scene samples are of adequate quality and quantity.

But when carrying out 'suspectless' mass searches of a DNA database in an attempt to gain cold hits even match odds of billions to one means that false matches will occur from time to time (e.g. a database match between 100,000 crime scene profiles and 100,000 personal profiles represents 10 billion attempted matches - so if the true match odds were one in one billion you could expect about 10 false matches, but if they were closer to one in a million you would get many thousands of false matches).

Aggravating the problem is that false matches are likely to occur in prejudicial situations (e.g. the suspect is an ex-prisoner, the real offender is from the same family or ethnic group so the suspect matches eye-witness descriptions or lives in the same area).

There is no doubt whatsoever that allowing mass database searches for suspectless cold hits will result in false matches and it would be very naive to imagine that some of these will not result in wrongful convictions. As long as those protesting innocence are largely ex-prisoners it seems unlikely that this problem will be widely recognised and DNA convictions of prior offenders will just serve to strengthen the argument of those who insist that ex-prisoners are very likely to reoffend - even when the type of crime and modus operandi seem unconnected.

The two cases of false matches in the UK which have come to light so far only became public knowledge after a long delay and largely due to chance. Both were dismissed as extreme examples of bad luck although an examination of the mathematics involved suggests that they are actually routine events. Whether a large number of such matches have been recognised by UK authorities and covered up or whether they have resulted in wrongful convictions is difficult to say - but it can be said with a fair degree of mathematical certainty that hundreds or even thousands have occurred to date.

It will probably take a publicised false match against a prominent and respectable person before the unreliability of database trawling for suspectless 'cold hits' becomes widely recognised. Until this happens it seems certain that innocent people will continue to be linked to crime scenes via false matches on DNA databases.

Match by error

Proficiency testing and estimating error rates

The claims by proponents of mass forensic DNA testing that 'it doesn't matter whether match odds are really one in one billion or one in 100 billion' are true in one sense. That kind of distinction is meaningless when it is realised that the chance of a match being declared due to errors in the laboratory or faults in the testing equipment is much, much higher - probably of the order of one in hundreds or thousands.

Although no field of human endeavour is entirely free of mistakes the evidence regularly given by forensic experts implies that forensic DNA testing has achieved exactly that. When a forensic scientist says that there is 'one chance in a billion that a randomly selected unknown Australian would match the profile obtained from the crime scene' s/he is implicitly also saying that there is significantly less than one chance in a billion that the lab made a mistake during testing.

Errors can be introduced into forensic DNA testing via contamination of samples, inadequate lab procedures (or a breakdown in adequate ones), misinterpretation of results, faults in the primers used in the test kit, glitches in the device used to detect the presence of alleles (usually due to poor maintenance) or bugs in the expert system software used to sort signal from noise and label the 'peaks' which represent alleles.

In the late eighties and early nineties the American Society of Crime Laboratory Directors (ASCLD) conducted regular proficiency testing upon labs conducting forensic DNA testing as part of their accreditation regime - making the error rates found available to courts.

Although the tests were notified (i.e. the technicians knew they were being tested) published results up until 1995 showed lab error rates of between one in 1000 and one in

44, with most accredited labs having an error rate of around 1%. The majority of these errors were false matches.

Although most lab accreditation regimes in the US, UK, NZ and Australia still call for such proficiency testing (which is blind in the UK - the lab doesn't know its a test) results have not been publicly available since the mid 1990s due to 'commercial in confidence' provisions and increasing hostility from the forensic science community towards anything which might provide a quantitative estimate of the chance that a test has been messed up.

The reason for this is because there are widely accepted mathematical methods (e.g. Bayes Theorem) for combining the estimate of a 'match by chance' obtained from a statistical database with the estimate of a 'match by error' obtained from the results of proficiency testing the lab or technician which did the testing. Doing so would produce match odds far less impressive than those routinely thrown around courtrooms and used to sell forensic DNA testing to the public.

Forensic scientists have countered by saying whenever an error is detected it results in changes to procedures which vastly reduce the chances of recurrence. Facts do not seem to bear this out though with numerous examples of forensic laboratories failing to respond to known errors and many cases - such as the ESR 'DNA anomalies' - where the cause of the error was never determined.

Senior forensic scientists have also told this writer that they always check important tests by having a colleague repeat them - if possible. This displays amazing mathematical ignorance. If the chance of a test being in error is one in a thousand and it is repeated - the lowest possible chance of them both being in error is still one in a million. This is several orders of magnitude higher than the 'billions to one' match odds routinely quoted.

But as all Australian forensic DNA labs use the same equipment and very similar procedures it is fairly likely that an error made once will be made again when the test is repeated - especially if the error is an artifact of problems in the test kit, analyser or expert system software. In the case of the second series of errors at ESR in NZ the samples were apparently contaminated very early in the process - extracts sent to other laboratories which used different equipment and protocols returned the same erroneous results.

But even were it true that detection of errors will result in better procedures there are still good reasons for ongoing monitoring of forensic lab errors and publication of the results. If they really do show an improvement over time it should be possible to incorporate this fact into a calculation which can be used to estimate the chance of an error on a given date.

But there can be no doubt that error rates in forensic DNA laboratories are much, much higher than the 'one in ten million' or 'one in one billion' which are routinely given as the

chance of a random match. This means that the unsaid part of the statement that "there is one chance in one billion of a randomly selected individual matching this profile" is "but probably more than one chance in a thousand that we messed up the test".

Profiler Plus, ABI 310/370, Genescan and Genotyper

All Australian forensic laboratories use the Perkin Elmer AMPFISTR Profiler Plus primer kit for DNA analysis. Although some still have the capability to perform tests with earlier RFLP and Quadruplex systems these are in the process of being phased out - the databases being set up are designed to be use with loci tested by Profiler Plus. Profiler Plus isolates and amplifies nine DNA areas - plus amelogenin, which is used to sex the source of the DNA - tagging the alleles of interest with fluorescent dyes of different colours.

All labs also use the ABI Prism 370 Genetic Analyser (or its earlier stablemate, the 310) which directs a laser onto the alleles amplified and tagged by Profiler Plus. The different dyes which bond to different alleles fluoresce in different colours - with a prism used to split the colours from the reflected laser, with each directed to an appropriate light detector which digitises the signal according to intensity.

Genescan and Genotyper software take the digitised signals arriving from the detectors and attempt to imitate an expert forensic scientist in checking for signals which may indicate an error in the process and filtering them out - labelling the remainder with locus designations and allele numbers. The expertise once required by individual technicians in interpreting these results is now almost a thing of the past - with the actual signal produced and the methods used to convert it into a DNA profile now in a 'black box' out of sight of the 'analyst'.

Profiler Plus has attracted a fair amount of recent attention in US and Australian courts as it became the most ubiquitous test kit in these countries without being subjected to proper peer review and evaluation by independent scientists - in contravention of long standing TWGDAM guidelines for forensic DNA test kits. This is because Perkin Elmer, unlike its competitor Promega, refuses to release the chemical composition of its primers or the records of in house validation testing (by PE and the FBI) - citing commercial confidentiality. One possible reason for this was recently revealed when another biotech company, Nycomed Amersham PLC, initiated a suit against Perkin Elmer for allegedly stealing the formulas for the fluorescent dyes used in Profiler Plus.

What has attracted less attention outside forensic science publications is the number of bugs which have come to light in the Genescan and/or Genotyper software macros used to interpret Profiler Plus/ABI Prism output.

The software appears to presume a maximum variation between peak height ratios which is sometimes exceeded in actual casework - especially when mixed or degraded samples are analysed. This can result in the misinterpretation of peak signals from saturated detectors (i.e. those receiving more laser light than they can register) and the erroneous labelling of peaks produced by *pull-up* (see below). These false 'bleed-through peaks' can be wrongly included in the profile obtained from the sample, especially if they occur at what are really homozygous loci. It is unclear at the time of writing whether a patch is available to fix this.

In July 2000 another bug in Genotyper's *Kazam* peak labelling macro was discovered which can result in true peaks not being labelled when typing mixed samples. It seems to have been the result of a straightforward programming error whereby loci with high stutter thresholds analysed late in a sequence resulted in inappropriate thresholds being applied to smaller amplicons earlier in the analysis sequence - often erasing the label on a valid earlier peak. The Oregon forensic scientist who discovered this 'stutter-filter back talk' attributed his tardiness in recognising the error to the fact that he had previously been analysing clinical quality samples and had only recently moved on to the mixed crime scene samples which trigger the bug. Australian forensic scientists had been using this software for at least two years on mixed samples without noticing the problem and it seems that some remained oblivious at least until April this year - although the recommended bugfix had been posted on the FBI website for over 8 months.

Although its primer sequences are not publically available it has become increasingly evident that Profiler Plus is more subject to allelic dropout than are comparable multiplexor kits. The FBI has published data showing one dropout in 600 tests at the *vWA* locus and three dropouts in 7,220 tests at the *x-specific amelogenin* marker.

Dropouts can occur for a number of reasons in crime scene testing, including contamination from artificial polymers which are common in clothing and following bacterial degradation of the sample. But the above dropouts were found in clinical samples, which indicates that there are problems with the primers - probably due to high mutation rates in the supposedly non-polymorphic sequences to which they bind in order to isolate the polymorphic ones of interest.

The dropouts documented so far indicate that we can expect between one in 450 and one in 500 Profiler Plus tests on clinical samples to produce dropout. No matter how many new samples are taken and retested using Profiler Plus the dropout will still occur. Doubtless further tendencies towards allelic dropout in Profiler Plus will come to light after the primer sequences are published and proper independent validation gets underway.

The Melbourne male forensic scientist who (according to Linzi Wilson-Wilde's evidence to the committee) has two X chromosomes almost certainly does not. He probably has a

mutation at the binding site used by the Profiler Plus *Y-specific amelogenin* marker - meaning that his Y chromosome marker drops out and he is incorrectly typed as having two X chromosomes instead.

Although some members of the forensic scientist community are painfully aware of the high dropout rate for Profiler Plus there are many who seem blissfully ignorant of it - at least if their evidence under oath is to be believed.

As well as problems specific to the kit, Profiler Plus suffers from all of the problems usually associated with PCR-based multiplex kits. These include :-

preferential amplification - For reasons which are not entirely clear - but are related to the length of amplicons - some alleles are replicated more readily by the cycles of PCR amplification than others. This results in different proportions of DNA in the final product of amplification than existed in the original sample. The interpretation of mixed samples becomes difficult but it can also result in the wrongful elimination of the smaller peaks of underamplified alleles in clinical samples. It also makes PCR analysis very sensitive to contamination.

stutter - Thought to be caused by 'slippage' of the polymerase during amplification. Results in a subset of the targeted sequence being amplified. Thus, for example, an allele containing 8 repeats can have a partial sequence containing 7 (or less) repeats amplified - giving a designation at that locus of 8/7 when the original sample was 8/8.

pull up - When the light produced by laser fluorescence is split in a prism it is often 'scattered' slightly to detectors near the one which is targeted. Normally this is easy to detect and filter but if the light signal was particularly strong it can saturate a detector and produce an off-scale reading which can confound the software designed to filter it and produce a false 'bleed-through peak'.

primer dimers - The mixture of primers used in multiplexor kits can sometimes bind to each other instead of the target DNA, producing the false peaks technicians call 'primer dimers'. Particularly likely if some of the primers have not been fully expended by binding to sites or being mopped up by 'null' reagents.

Almost a decade of commercial PCR analysis means that these problems are well recognised and various guidelines and protocols have been developed for detecting and correcting them. The bulk of these corrections are no longer a matter of judgement for a trained forensic scientist but a function of proprietary software supplied by the producer of the test kit. Errors are no longer so much a matter of lapses or incompetence by technicians but of bugs in software supplied by third parties - thus responsibility is placed outside the jurisdiction of the court evaluating the evidence.

Indeed, secrecy about primer sequences and some parts of the software makes it impossible for Australian forensic scientists to take full responsibility for their work. They must take it on faith from Perkin Elmer, just like the rest of us.

Errors in DNA typing are well known in the forensic science community, even if the statements of many give the impression they are unheard of.

In *R v Karger* Dr John Buckleton of ESR (who has had some hard experience in matches by error) gave evidence of corrections he and Dr Bruce Weir had made to the South Australian Forensic Science Centre's Profiler Plus database of Caucasian Australian profiles. In the first phase they had checked 377 records, finding mistypings, mistaken results and readings outside the guidelines - prompting a review of the whole database and retesting of several samples. In the second phase conducted on 414 records they removed two records which had been mistyped, three which weren't Caucasians and detected 19 errors in analysis which required changes to profiles on the dB.

What the error rate on the SA database might now be is anyone's guess, but before the Buckleton and Weir review it would have been between 5 and 10% at least.

CrimTrac policy seems to take testing error rates on board. According to a presentation given in April - since confirmed in personal correspondence - CrimTrac will declare a match when 16 of the 18 allele pairs in two profiles are the same - i.e. when 2 of 18 are different it is still 'a match'. This would seem to allow for an error rate of about 10% in the typing of alleles with the adjustment in favour of false matching (i.e. they don't assume that two alleles are in error when 18 out of 18 match).

If two alleles in 18 *don't* match there is no way the samples came from the same person unless there has been an error in testing. However there is a very strong chance that they came from two people who are closely related.

Mixed, partial and derived profiles

When DNA typing was developed for paternity testing it used sterile samples taken in clinical conditions. When a forensic sample is taken from a volunteer, suspect or prisoner it will normally be of similar clinical quality.

But crime scene samples are often degraded and mixed with organic and non-organic contaminants. When the mixture includes human DNA from two or more sources it is a *mixed sample*. Rape test kits are mixed samples as they contain the DNA of the victim and the offender - as well as possibly that of recent consensual sexual partners.

Other samples cannot be completely profiled - either because they are too small or contain contaminants which mask the readings of one or more alleles. This will result in a

partial profile which does not show readings for all loci tested. Dropout also results in partial profiles (see above) About 6% of the profiles on the SAFSC dB checked by Buckleton and Weir were partial profiles.

Derived profiles are the result of working out some or all of the DNA profile of an absent subject by referring to the profiles of near relatives. The Missing Persons Index will be used to produce such profiles.

When the profile of an absent child is derived from that of its parents what is produced is not a single profile of a missing child but an array of all possible profiles which can be produced from theirs. Thus if one parent has a profile of A/a at a given locus and the other parent has B/b , the possible profiles of the child are A/B , A/b , a/B or a/b . There are up to 262,144 possible nine loci 'virtual' profiles obtainable from two parents - though most would produce fewer due to homozygosity and shared alleles between the parents.

When the missing person is a parent a partial profile can be obtained by subtracting the profile of his/her partner from those of any children. Thus if a mother has a profile A/a at a particular locus and a child has a/B the profile of the father at this locus must be $B/?$. If another child has a profile of A/c then the father's full profile at that locus is B/c . If a third child has profile a/b there is good reason to doubt the parentage of at least one of the kids - the alleles B , b & c do not exist in the mother and no more than two of them could have come from one father.

These methods can be used in conjunction with birth records to build up partial or complete DNA profiles of most members of a community even though only a relatively small proportion of them have been actually tested. Needless to say they can also be used to uncover a lot of details about parentage & descent which may not be public knowledge within that community.

Partial, mixed and derived profiles complicate forensic matching and greatly complicate the calculation and explanation of match odds. A more complete description of these problems is given in the answer to question 4.

*An accurate tool - but not **that** accurate*

Given the possibility of match by chance plus the possibility of match by error it is obvious that false matches will arise with far greater frequency than would seem to be indicated by the match odds given by forensic scientists.

The real possibility of a pairwise match between profiles obtained from clinical samples is probably of the order of one in thousands or tens of thousands rather than the billions and hundreds of billions claimed. When one of the profiles comes from a mixed or

degraded sample the possibility is probably more like one in a few hundred but can even be so high as to render the evidence probative of almost nothing.

This kind of accuracy can still provide vital evidence implicating or exonerating a particular suspect in relation to a particular offence, but it becomes so useless as to be dangerous when the intent is to use massive database searches to try to crack suspectless cases.

Even if the fantasies of forensic scientists were true and it were possible to say that the possibility of a false match was as little as one in a billion, database searches would still throw up false matches from time to time. A more realistic - but still generous - estimate of one chance in a million of a false match would mean that most cold hits on a database randomly selected from the Australian population would be false matches.

Whether or not someone with prior convictions is really at increased chance of being correctly matched to a crime scene than a randomly selected Australian is moot - there is no doubt that database searches will result in many ex-prisoners being falsely matched to crime scenes as well. While their increased risk of recidivism is uncertain there can be no doubt that they will be at increased risk of being disbelieved when they deny the DNA is theirs - even by their own lawyers.

Whether these false matches go on to become wrongful convictions and false imprisonment will depend on the integrity & competence of investigating police and forensic experts as well as the defence resources available.

Ironically, prisoners who can really be shown to be recidivists are at less risk of being wrongfully convicted on DNA evidence than one-time offenders. As they spend much of their lives in prison they are more likely to have an airtight alibi for the offence in question.

12) How successful have overseas jurisdictions been in solving crimes and convicting offenders?

It is difficult to get exact and reliable figures as to how many convictions have been obtained with DNA evidence in different jurisdictions. In some cases the figures aren't collected and even when they are it is often in forms which does not allow cross-jurisdictional comparison. Adding to the difficulty is the hype and distortion which has surrounded the introduction of forensic DNA to many English speaking jurisdictions - for instance the figures given by UK police for database matches per month seem to be deliberately stated in a way which exaggerates their use in solving crime.

Professor Ian Shaw, who teaches forensic science at the University of Lancashire, says that the problem with forensic DNA testing "is we will never really know how many had

been locked in prison because of DNA matches who are innocent". The real success of DNA testing will only be known in the future, perhaps when new technology becomes available which can challenge DNA evidence in the same way that forensic DNA has exposed the frequent errors and abuses of earlier forensic techniques.

New Zealand

New Zealand is privileged to have produced two of the world's biggest names in forensic DNA.

Dr John Buckleton, principal scientist at Environmental Science & Research Ltd, is one of the world's foremost forensic serologists. Realising the potential of forensic DNA from the start he was one of its first major proponents, co-authoring the rebuttal to Eric Lander's seminal 1987 article in *Nature* which first seriously questioned the methods and claims of forensic DNA laboratories. Dr Buckleton is in worldwide demand as a forensic DNA expert at tribunals, committee hearings and at trials - where he usually appears for the prosecution.

Expatriate Bruce Weir is the 'William Neal Reynolds' Professor of Statistics and Genetics at the University of North Carolina and is probably the world's foremost expert on population genetics. While a supporter of forensic DNA use, Professor Weir is more reserved than Dr Buckleton in advocating its accuracy. His membership of the Research and Development Working Group of the National Commission of the Future of DNA Evidence provides valuable balance and attention to scientific fact as a counter to the gung-ho approach of some of his fellow members.

Though they disagreed over ESR match odds calculations during the Eichelbaum-Scott inquiry Dr Buckleton and Professor Weir often work together on forensic DNA projects, recently collaborating in detecting and correcting errors on South Australia's new Profiler Plus database.

In spite of the local talent the introduction of forensic DNA testing in New Zealand had a number of embarrassing teething problems (see *Legally Scientific?* under 'Errors at ESR'). The errors which resulted in the release of a rapist who went on to reoffend and the investigation of a Christchurch assault victim over two Wellington gang murders were probably due in part to overconfidence in the new technology caused by the international hyping of forensic DNA supplemented with the local marketing and lobbying efforts of ESR.

New Zealand uses the same DNA technology as that of the UK's Forensic Science Services and, like the FSS, has spent the last few years updating its database from 6 loci to 10 loci - retesting old samples with the new kit where they are still available. It should be noted that the false matches examined by Eichelbaum and Scott were due to

contamination and would have occurred no matter how theoretically accurate the testing method used.

Since the Eichelbaum-Scott inquiry handed down its findings at the end of 1999 there have been no more publicised cases of similar mistakes at ESR's Mt Albert labs, which may be due to improved standards but may also reflect greater care in evaluating cold hits from the database and controlling the publicity they attract. Unlike the UK police, New Zealand law enforcers have been rather low key in claiming success for forensic DNA and database matching - although there are now regular NZ trials involving DNA evidence.

Recent court cases seem to indicate that New Zealand judicial officers and defence lawyers are none the wiser for the extensive evidence produced by the inquiries. While lawyers routinely raise the false matches when defending against DNA evidence there is little indication that they know what implications this might have when facing the unrealistic prosecution match odds which continue to be presented in NZ courts.

The United States

While the US was quick to leap onto the potential of forensic DNA it has suffered more problems than anyone else in its introduction.

The forensic DNA bandwagon has picked up many cowboys in the USA, both in private and police laboratories, with several cases coming to light of technicians systematically misinterpreting or misrepresenting DNA evidence in order to gain convictions. Although the FBI has been shown to be a major offender in this respect it continues to be the most powerful player in setting technical and legal standards for the use of the technology in the US.

While the CODIS database was established in 1994 it has been slow to realise the potential envisaged by its proponents, with only a handful of cold hits resulting in convictions nationwide by January 2001.

The main reason for this has been the ad hoc and hotchpotch way DNA testing was introduced in different jurisdictions and the lack of standards covering its collection, testing, databasing and use as evidence. This has led to delays in uploading state databases to CODIS and most significantly to a huge backlog of untested DNA samples and massive blowouts in laboratory budgets. In spite of hundreds of millions of dollars in funding in the last five years the US backlog now stands at over 1 million untested samples and is still growing.

The best publicised feature of the US experience with forensic DNA has been the number of people cleared of crimes for which they have served long sentences - or been executed - following testing of DNA evidence. Most of these cases have revealed serious

prosecution malpractice, often on the part of forensic scientists. While this has led many to hail DNA testing as a powerful weapon against unscrupulous investigators and prosecutors it has not resulted in measures which seek to prevent such people from using forensic DNA itself to gain wrongful convictions.

However this is not to suggest that the revelations of wrongful convictions in the US has not prompted any reforms. Illinois has suspended its death penalty in light of the number of death row inmates in that state who have been proven innocent with DNA evidence and a steadily growing list of states have introduced legislation to facilitate the reexamination of cases in which DNA evidence may cast doubt on the verdict. Several have also introduced measures to limit the amount of compensation payable to those shown to have suffered wrongful imprisonment.

Another unique feature of the US experience has been the emergence of a highly paid class of lawyer who specialises in challenging DNA evidence - with the best known example being OJ Simpson lawyer Barry Scheck. While most defendants in the US who face dubious prosecution DNA evidence still lack the resources to adequately challenge it there have been several well resourced cases which have served to highlight the weaknesses of forensic DNA evidence and the way in which it is collected and analysed.

But the US is also home to the companies and organisations which stand to gain the most from the rapid introduction of forensic DNA technology worldwide - turning admissibility standards into a high stakes battleground (see answer to question 4 below).

11) What can NSW learn from the UK experience of forensic use of DNA?

The United Kingdom

The UK has served as the 'best practice' model for forensic DNA investigation to law enforcers worldwide, although this has unfortunately been less a reflection of the sophistication of UK forensic science than of the police and government public relations campaign promoting it.

Although the Brits were the first to begin solving crime with Alec Jeffreys' 'DNA fingerprinting' it remained an under-resourced and marginal crime fighting tool for several years. That was to change in the early 1990s when PCR based testing increased the utility of forensic DNA while promising reduction in costs at the same time as revelations about the Birmingham Six were creating pressure for reform of forensic science in the UK.

In 1991 the UK Court of Criminal Appeal overturned the 1975 conviction of six innocent men imprisoned for the 1974 bombing of a Birmingham hotel which had killed 21 people and injured 162. Not only had the defendants been bashed by police and prison officers in order to extract bogus confessions, a forensic expert had testified that their hands had

been covered in nitroglycerine residue. In fact the test he used also reacts positively to residue from such mundane items as cigarettes, soap or playing cards - and five of the six had been arrested shortly after a game of cards. Naturally the court which convicted the Birmingham Six was not informed of this.

This had come hard on the heels of the 1989 breakup of the West Midlands Serious Crime Squad - the same people who had first approached Jeffreys in the Pitchfork case - following revelations of fabrication of evidence and bashing of suspects in at least 19 cases. The WMSCS had also played a major part in the conviction of the Birmingham Six.

The advent of DNA technology gave the government the opportunity to present the reform of forensic science in the UK as a progressive initiative rather than a belated reaction to a well documented history of malpractice.

The Forensic Science Service (FSS) was formed as a Home Office department separate to the police force and resourced sufficiently to allow for a huge expansion in DNA testing capability and databasing of profiles. By keeping the collection and analysis of samples separate to the investigation, potential for the corrupt collusion between police and technicians which has been a recurring theme of forensic science is kept to a minimum. Legal services also received increased funding to allow those tested access to quality legal advice as to their rights and obligations as well as legal aid lawyers competent to defend against DNA evidence.

FSS staff are also under strict instructions about speaking to outsiders. Although the author has received off the record research assistance from public servants, forensic scientists and prosecutors in New Zealand, Australia and the US all inquiries directed to the UK FSS have remained unanswered. Following revelations of the illegal retention of DNA profiles FSS staff told *The Sunday Observer* (June 11, 2000) that any comment would cost them their jobs.

The UK FSS is currently developing forensic testing of coding sections of DNA. They already claim to be able to test for the gene which results in red hair and expect to soon have tests which can reveal the build, complexion, race and even disease history of the contributor.

Figures of 800 hits per week on the DNA database need to be taken with a huge grain of salt - such as the fact that in the six months to February 2001 only 426 suspects were identified from DNA database searches and less than 300 arrests were made (*Sunday Observer*, 25 February 2001). The bulk of these hits were for 'volume crimes' such as burglary.

But even cold hits which go to trial in the UK do not always result in conviction. In two rape/murder cases last year suspects were set free when it was discovered that their DNA

profiles had been retained illegally by the FSS after the police 'neglected' to issue orders for their destruction as required by law. Home Secretary Jack Straw had been aware of the fact that thousands of samples and profiles were being retained illegally for some time, but seized on the publicity following the failure of these cases to push through retrospective laws allowing *all* DNA samples and profiles to be kept indefinitely, regardless of the legality of their initial collection or whether the DNA contributor was ever charged with anything.

As with admissibility standards in the US, rules governing the collection and retention of DNA samples in the UK have been neutralised via the simple expedient of ignoring them until authorities act to lower the bar.

Another interesting feature of the UK experience - which is has been paralleled thus far in NSW - is the failure of human rights groups such as 'Liberty' in their attempts to oppose the rapid recent expansion and function creep of the DNA testing program. However the 3 million UK pound project to test all serving UK police officers for DNA elimination purposes failed when the police union opposed it on the grounds that the profiles might be used in paternity suits. By September last year less than one third of UK police had complied with requests to provide samples.

The lesson from the UK experience which would be of particular interest to Australian legislators is how mass DNA testing can be introduced without the US experience of huge testing backlogs. The Brits have solved this problem by throwing vast amounts of money at it, with 252 million UK pounds allocated to upgrading testing and databasing facilities in the past year alone. Unfortunately the resources needed by police to properly carry out 70 odd DNA initiated investigations every month have not kept pace, meaning that checking of 'cold hits' is often cursory with guilt being assumed no matter how little supporting evidence is available.

Although the author is aware of at least three UK cases which collapsed when it was discovered that the 'cold hits' did not indicate guilt only one has received media attention and none have received anything like the coverage of the misleading claims made about matches on the database.

The best known case is that of Swindon Parkinsons sufferer Raymond Easton who was arrested and jailed for burglary in spite of a strong alibi and the sheer impossibility of him having committed the crime. He was exonerated several months later when a more discriminating DNA test eliminated him.

In a similar case the judge ordered acquittal of a defendant when evidence was produced which showed that *two* profiles on the FSS database matched the crime scene sample. The other profile was from someone living much closer to the scene of the crime and the police had no evidence beyond the match.

In a third case a man who had already spent several years in prison for safe cracking was freed following an appeal which revealed that although there was a reasonable chance that the DNA at the crime scenes also matched one of his brothers police had taken no action to eliminate them as suspects.

More significant than the cursory nature of UK police investigations of DNA cold hits is the way in which cases such as these rarely reach the public record. Following Raymond Easton's case the FSS received extensive funding to upgrade its testing from 6-loci to 10-loci, modify its database accordingly and retest old samples with the new system. Although forensic scientists in the UK, US and Australia were well aware of the error and subsequent upgrade it was almost a year before it was publicly acknowledged. Doubtless there are many similar cases which are yet to be covered by the media.

4) Your submission identifies the complexity of forensic DNA evidence as a problem for judicial officers. What measures could be taken to overcome this problem?

While the potential for DNA match by chance and match by error have been touched upon above the greatest risk of wrongful conviction on DNA evidence remains incomprehensible, misleading or just plain wrong evidence given by forensic scientists in court.

The author has long lost count of the number of transcripts of Australian and overseas cases involving DNA evidence he has read. In *every* case prosecution experts have exaggerated the strength of the DNA evidence. Rarely is the testimony of the expert witnesses competently challenged by the defence and even more rarely does the judge and/or jury reject even the most unsupportable claims made for forensic DNA.

While it is sometimes clear that the expert witness is deliberately lying more often it seems a matter of a laboratory technician with limited understanding of the mathematics behind match odds choosing the numbers which seem most likely to support a technology in which s/he has a strong personal investment. A well known NSW case will serve as an example.

DNA evidence in Milat

When calculating match odds for derived profiles it needs to be remembered that the comparison is not being done against the single profile obtained from the crime stain but against the entire array of 'virtual' profiles which could be arrived at by combining those of blood relatives. This seems to have been forgotten by DAL senior forensic scientist Robert Goetz in *Regina v Milat*.

The crown led evidence that the bloodstain on a rope allegedly found on the Milat property was consistent with that of a daughter of Mr & Mrs Clarke - whose daughter Caroline was one of the Belangalo victims too decomposed to be DNA tested. Goetz further stated that the chance of a randomly selected Caucasian having a DNA profile which matched the stain on the rope was between 1 in 54,000 and 1 in 229,000.

Leaving aside the dubious validity of Goetz using the product rule on frequencies obtained from several different databases and the unlikely tightness of the 95% confidence interval claimed, the fact is that the rarity of the DNA obtained from the rope is almost irrelevant in determining whether it came from Caroline Clarke.

What should have been calculated was the possibility that DNA from a randomly selected Caucasian could have matched any of the 256 to 65,536 different profiles which can be obtained by combining alleles from the tested DNA loci of each of the parents of the deceased. Without the parent's profiles and appropriate frequency tables it is impossible to do this calculation, but it is a safe bet that the real match odds are many orders of magnitude higher than those given by Mr Goetz - perhaps as high as 1 in 10 or more.

What Mr Goetz did was to assume from the start that the profile obtained from the rope *was* that of the deceased then go on to calculate the possibility of a random match to it. He failed to incorporate the possibility that the blood on the rope, while consistent with a child of Mr & Mrs Clarke, did not match the profile of Caroline Clarke at all.

Also interesting in *Milat* was the preparedness of CJ Hunt to accept that the size of the statistical databases were sufficient by reference to other cases and papers which accepted even smaller dBs. However none of the cases referred to by Hunt used different databases collected in different ways for different loci then combined them into one calculation using the product rule as did Goetz. Given the unreliability inherent in such a method it is doubtful whether even databases much larger than those examined by Hunt could give reliable results - and certainly not results with a 95% confidence interval as tight as that claimed by Goetz.

Nonetheless Hunt seemed satisfied that the databases were sufficient, especially as they were collected from Caucasians and "There is no suggestion in this case that the offender or offenders was or were other than Caucasian". What Hunt seems to have forgotten is that whether the DNA matched the 'offender' was not the question here, but whether it matched one of his victims. No evidence was led as to the race of Mr & Mrs Clarke but luckily for CJ Hunt they are probably Caucasian as well.

Common misrepresentations of DNA evidence

Building assumptions consistent with the guilt of the accused into calculations which are supposed to account for the possibility of his/her innocence is a cognitive problem which seems to afflict many forensic scientists.

Professor Barry Boettcher details several other examples of this in his upcoming book about forensic evidence in Australia, including another case where Robert Goetz calculated a likelihood ratio of a defendant being a contributor to a mixed sample on towel by starting from the assumption that the defendant's DNA *was* present on the towel. A discussion of this case will appear in the next issue of *The Australian Journal of Forensic Science* under the title 'Commentary on an approach by prosecution expert witnesses to determine the origin of a mixture of DNA in a bloodstain'.

Similar 'errors' by prosecution experts include matching a partial profile from a crime stain to the full profile of a suspect then giving random match odds against the suspect profile rather than the crime stain. Here the calculation is whether a randomly selected person is likely to match the defendant when it should be whether such a person would match the crime stain.

Absolutely routine are match odds given specifically in terms of the defendant and one profile found at a crime scene, when perhaps dozens of profiles were obtained from the scene. Obviously the possibility of a chance match increases the more profiles you compare but evidence of samples which *didn't* match is never given in Australian courtrooms.

Some inadequate measures

It may be possible to improve the quality of forensic evidence in NSW courts by providing education for the judiciary on forensic mathematics and techniques, but the fact is that even experts who spend their working lives in a particular speciality of forensic science seem to prone to frequent error when straying from that field. For instance very senior lab technicians often display amazing ineptitude when attempting statistical analysis.

It might also be possible to simplify DNA evidence by insisting on consistent formalised methods of giving evidence in situations which commonly apply to DNA evidence. However a consensus on what methods to use would not be arrived at quickly and would fail to deal with evidence which does not fall clearly within a predefined category. Nor would it help courts to evaluate new innovations in DNA evidence - which are certain to continue for some time to come.

The appendix of '*Legally Scientific?*' gives some indication of the struggle US courts have had in determining admissibility standards for new kinds of DNA evidence. The standard set in *Daubert v Merrill Dow Pharmaceuticals* was a high water mark which is now being

retreated from in the face of the expense of such a thorough evaluation and pressure from organisations such as the FBI and Perkin Elmer who have no desire to try their evidence against such a high standard.

Actually *Daubert* was not a DNA case at all. Rather it was an attempt to sue Merrill Dow on the claim that its morning sickness drug, Bendectin, causes birth defects. It is ironic that a standard set to accommodate the scientific stringency demanded by a biotech multinational before accepting that its products are faulty is being eroded by Perkin Elmer, another multinational biotech company which does not want to be forced to demonstrate that its products are not faulty. When giants collide it is perhaps inevitable that some pygmies will be crushed.

Given the many areas of scientific expertise which contribute to the production of DNA evidence, frequent innovations in technology and practice and the number of situations calling for different methods of calculating match odds it seems unreasonable to expect that Australian courts will ever be in a situation to scientifically test DNA evidence in even the most straightforward cases.

Regulating the Experts

In the face of the complexity of DNA evidence courts in Australia and the US seem to have given up on trying to weigh scientific testimony - rather they weigh the apparent qualifications and credibility of the witnesses who give it. While this method is offensive to those dedicated to scientific truth and objectivity it is the only option currently on offer which might be realistically employed in an Australian courtroom.

What is needed is some guidelines whereby the court can make a decision about the reliability of expert witnesses without having to seek wideranging expert opinion about the evidence in question or simply reducing it to a charisma contest.

The best method which comes to mind would be to create an independent expert body with responsibility for advising courts as to the degree of credence which should be given to accredited forensic experts in different areas of forensic expertise. This should be done via a combination of notified tests or examinations, blind proficiency testing and regular audits of evidence given. Such a body could also recommend counselling or retraining for experts whose evidence is not up to standard. Members should not be involved in legal cases themselves nor have any direct involvement in the forensic testing industry.

Regardless of what measures might be adopted to improve the quality of forensic evidence in NSW courts it is vital that sufficient resources be provided defendants to enable them to challenge DNA evidence. Given that prisoners are at greatest immediate risk of abuse and wrongful conviction resulting from the Crimes (Forensic Procedures) Act the budget of the Prisoners Legal Service should be increased substantially.

1) The submission from Justice Action contains a number of criticisms of the Crimes (Forensic Procedures) Act 2000, but does not suggest prohibiting forensic use of DNA entirely.

(a) Under what circumstances and with what safeguards would you consider DNA testing and forensic use of DNA appropriate?

(b) In particular, under what circumstances do you consider it appropriate for a forensic procedure to be ordered or requested on

_____ (i) a suspect

_____ (ii) a prisoner?

Circumstances

Justice Action believes that the compromise of someone's genetic privacy and bodily integrity is a very serious matter and should not be done lightly. It should not even be considered in circumstances where there is not good reason to believe it likely to produce important evidence in respect to a serious offence which could not be practicably obtained in a less physically and personally intrusive manner (such as asking whether the person was present at the crime scene or checking their alibi if they claim they weren't).

Taking DNA under current legislation will result in the contributor being placed under DNA surveillance for at least a year. More if s/he is convicted of something - regardless of whether DNA played a part in the conviction. The contributor will *permanently* lose control over the sample and the information taken from it, which can also reveal information about the contributor's family. Even though it can be 'deidentified' under some circumstances in NSW, other jurisdictions which receive copies are under no obligation to follow suit - Tasmania has already indicated that it will not.

Databasing and fishing for 'cold hits' adds considerably to the concerns raised by DNA testing by increasing the risk of personal information 'going astray' and - more importantly - by placing the contributor at real risk of being implicated in a crime s/he did not commit.

Databasing of unsourced crime scene profiles is less of a concern, but should the contributor of such a profile be identified they should have the same rights in regard to that sample and profile as they would have if it had been taken directly from their body - including the right to have it removed from the database.

To justify such a breach of personal rights the crime being investigated would have to be very serious - far more serious than many of those which can potentially attract a penalty of five years or more under NSW law. If a crime is judged serious enough to warrant a

DNA test the results should *only* be used in connection with that crime. To allow police to use the opportunity to try to 'solve' less serious crimes only invites them to be very creative in 'suspecting' people of serious offences when investigating relatively minor ones.

People should never be required to contribute DNA simply because it may tend to *disprove* that they committed an offence. This is the same as saying that they must do it to *prove* their innocence - an obvious reversal of a basic tenet of our justice system. However it may be acceptable for someone to be required to give a sample if it is believed that it may *prove* that they have falsely confessed, as with the original suspect in the Pitchfork case.

Prisoners should not be tested simply for being prisoners. They should be subject to the same criteria as everyone else (i.e. that the test is likely to provide evidence that the prisoner has committed an unsolved very serious offence which cannot be practicably obtained with other means).

There is probably a case to be made for testing prisoners judged to be at high risk of serious recidivism if the order is made as part of the sentencing procedure. It should probably be in the form of reduced non-parole period for those who agree to subject themselves to DNA surveillance for a specific period following release. Care would need to be taken in setting guidelines to ensure that this does not become a net widening measure which will only serve to increase the sentences of those who are not DNA tested.

'Consent' should play no part in DNA testing and police should never 'ask' someone to volunteer (although volunteers should not be prevented from giving samples of their own accord). If the circumstances justify an order for a DNA test such an order should be made - there should be no ambiguity regarding whether the suspect can be forcibly tested.

Safeguards

No DNA testing is acceptable under the pathetic safeguards currently provided by the Crimes (Forensic Procedures) Act.

The most serious omission of the Crimes (Forensic Procedures) Act is its failure to regulate DNA information which is not intended for the database. This has been covered at length in the main Justice Action submission.

Another safeguard which must be introduced is true expungement of DNA records - even when a conviction has been obtained. Beyond the unsupportable 'cold hit' fishing expeditions or indefinite DNA surveillance there is no reason consistent with criminal investigation which could justify even the cost of indefinite retention of samples and/or

profiles much less the invasion of privacy and compromise of civil rights. Even the most serious repeat offenders will eventually reach the stage where they are no longer a credible threat to society (if they live long enough) and should no longer be subject to surveillance.

Police and prison officers should play no part in collecting DNA samples nor seeking consent or making orders for testing. NSW should have a truly independent DNA collection agency as does the UK.

Orders for taking forensic samples from living people should be made only by magistrates, although provisions for rare circumstances in which this is not practicable might be made. While 'blanket' warrants for DNA testing a handful of suspects might be acceptable the criteria for permitting mass 'Wee Waa style' testing should be set high enough to reflect the cost, disruption and invasion of personal rights this entails - whether or not it is envisaged that the contributors will have the option of refusing to volunteer.

Personal profiles should only be kept on a DNA database in the tiny minority of cases in which there is real risk of serious reoffending in a way which is likely to produce DNA evidence.

As noted above, safeguards should extend to the way in which DNA evidence is likely to be used. This should include an oversight body to regulate expert forensic witnesses and appropriate legal funding for those arrested for crimes involving DNA evidence.

(2) What concerns, if any, does Justice Action have about the consent provisions for prisoners?

Many of the concerns Justice Action has about consent provisions for prisoners are covered in '*Consent by Coercion*' - often in the words of the prisoners themselves.

Under the Crimes (Forensic Procedures) Act prisoners can be DNA tested following consent, a police order or a court order. The test can be self-administered with consent, complied with without consent or made forcibly following alleged resistance. It can be by way of buccal swab, hair sample or blood test. Prisoners have the option to seek legal advice or decline to do so. Many can also choose whether or not to have an interview friend present during consent and/or testing.

Rather than see this as an admirable choice of options the Department of Corrective Services has seen a potential logistical nightmare and has brought considerable pressure to bear upon prisoners to 'mainstream' them into a standardised procedure (i.e. consensual self administered mouth swab, no legal advice, no interview friends). Their plans have not been helped by the faulty drafting section 87 which has led Justice Action and the Prisoner's Legal Service to advise prisoners *against* consenting to DNA testing.

Under these circumstances, 'consent' to DNA testing has become a shallow farce in NSW prisons, with prisoners continuing to suffer intimidation, sanctions and violence for resisting the 'preferred DCS model' of forensic testing.

Most NSW prisoners should not be subject to compulsory DNA testing at all. The tiny minority for which it is justified should not be asked for consent - which is a bit of a joke under the shadow of a compulsory test anyway. Nor should prisoners be encouraged to 'volunteer' DNA samples while in prison - they are going nowhere anyway and instructions for volunteering to a DNA test should be included as part of the kit they receive on release.

(3)What has been the nature of complaints received by Justice Action from prisoners who have been DNA tested?

The list of complaints received by Justice Action in relation to DNA testing includes

- Corrective Services misinformation about DNA technology and the Crimes (Forensic Procedures) Act
- Unavailability of copies of the Act in spite of commitments to the contrary by Corrective Services
- threats of sanctions and violence against prisoners who indicate that they may refuse consent
- an air of intimidation at the testing venue caused by the presence of four police and up to a dozen prison officers
- interference in communication within the prison about DNA testing
- interference in seeking advice from outside prison about DNA testing
- pain and a rash caused by the NSW police method of taking hair samples
- irregularities in testing and videotaping procedures
- discouragement of prisoners who may exercise their right to interview friends - including incitement of racial tension in Goulburn over interview friends provisions
- inability to gain any assistance in seeking DNA based appeals

But the most serious complaints have come from prisoners who have refused to consent to a test and apparently been used as 'examples' by the Department of Corrective Services to other prisoners who may be contemplating a similar decision - perhaps because they have been legally advised to refuse consent.

Selected prisoners have suffered loss of privileges, reclassification, loss of work release, violence and transfer to high security prisons following refusal of consent to forensic testing. Some of these prisoners have still not been DNA tested (and therefore aren't subject to videotaping or Ombudsman oversight) though they were asked for consent as long ago as January.

Of course the reason for such treatment is never given as 'refusal to consent to a DNA test'. If an old outstanding incident can't be dredged up to justify sudden penalties which 'just happen' to coincide with a refusal of consent a new incident will be manufactured - such as an undisclosed 'intelligence report' or a verballing to the effect that the prisoner has made threats or admitted to other offences.

In the most recent case to come to the attention of Justice Action, on August 22 a prisoner in the Malabar Special Programs Centre who refused DNA testing was bashed in his cell, forcibly tested then thrown into segregation. The case was brought to our attention by distressed fellow inmates and has since been confirmed by Corrective Services. However, contrary to prisoners claims, DCS maintains that the prisoner used a ruse to escape from the testing venue and return to his cell, whereupon he took up a defensive stance and threatened officers who issued 'three warnings' then employed 'reasonable force'. DCS claims that the prisoner was only segregated the next day when he continued to threaten prison officers (even though he had already been tested), but Justice Action had been told he was in seggro a day before the threats allegedly took place.

(6)What are your concerns about the retrospectivity of the provisions relating to prisoners?

The obvious concern with any legislation which seeks to impose further penalties upon prisoners who have already been dealt with by the court is that it is adding to the punishment which was originally handed down to deal with the specific case. This essentially means that parliamentarians with no specific knowledge of the circumstances of individual prisoners have taken it upon themselves to increase penalties with no recourse to the court.

Apart from the erosion of Westminster's separation of powers this represents it places prisoners in the invidious position of being subject to the whims of the political process rather than the rulings of the court which heard their case. The danger of prisoners being used as a convenient can to kick whenever a political diversion is needed would be clear, especially to anyone who has observed NSW politics in recent decades.

The prisoners serving on January 1, 2001 were not sentenced to having their bodies invaded, genetic privacy compromise, being subject to lifelong DNA surveillance and being placed at increased risk of wrongful conviction. It seems more than likely than many prisoners would have received reduced sentences if the judge had considered the extra penalties which would be imposed later, especially as DNA surveillance equates to a kind of lifetime parole period at the end of the sentence.

Compulsory DNA testing has created a new underclass of NSW citizens who are considered to have less right to privacy than the rest of us. In the case of prisoners this loss of rights is for life - even if their magistrate only saw fit to sentence them to three

months. By increasing their susceptibility to police harassment and wrongful conviction while forever banishing them from 'first class' citizenship ex-prisoners' stake in society is reduced and their chance of reoffending increased.

7) In your opinion, what potential problems arise from de-identifying rather than destroying forensic material and analysis?

Justice Action has been raising the risk of deidentified samples being diverted for other uses for over a year and our concerns are a matter of record. We are yet to hear a single reason justifying this bogus 'destruction' which is consistent with the criminal justice use of forensic DNA.

There is no reason why 'deidentified' profiles are necessary for a statistical database. Standard practice worldwide is to combine allele frequencies into a table which does not allow for the unpacking of individual profiles. Many examples of such tables are available on the internet (e.g. The excellent University of Dusseldorf tables at www.uni-duesseldorf.de/WWW/MedFak/Serology/database.html).

In fact fully 'deidentified' data is of less use when compiling statistical tables. Accepted practice in overseas and Australian courts is to use statistical databases made up of profiles from the same subpopulation as the offender (more usually the defendant in practice). If profiles are to be deidentified before inclusion on the database there is no way of knowing the subpopulation of the DNA contributor.

There are many risks involved in keeping 'deidentified' data other than the possibility that authorities may later 'reidentify' it by reference to collection records or data-sharing jurisdictions which do not 'deidentify' the data. A list of deidentified profiles in the hands of a private investigator would allow him/her to determine with reasonable confidence whether the subject of their investigation had ever been suspected or convicted of a serious offence.

The greatest risk is the value that the deidentified data and, especially, samples to medical research companies. Not only does this create the spectre of a corrupt public servant or cash-strapped future government selling convenient job lots of stored samples or data to biotech companies it creates financial pressure to increase the scope of testing and the amount of contributor data kept with 'deidentified' samples/data in order to increase its potential value. At the same time it will lead to a steady increase in the cost of keeping data and samples securely, adding to the pressure to recover expenses by flogging the samples.

But the real cost will be the loss of public confidence in the testing program when it becomes more widely known that once the government gets its hands on your DNA it will *never* let it go.

(5) What are the implications of the Act for
(a) protections against self-incrimination
(b) privacy?

Many of the concerns Justice Action has about self-incrimination and loss of privacy from forensic DNA has already been covered in previous submissions and even more adequately in the evidence of other witnesses such as Jeremy Gans and Chris Puplick.

It is worth emphasising again that the intended use of the database will result in the incrimination of a large number of people in offences of which they are not even suspected - and in many cases of which they have no involvement whatsoever. As different categories of test subjects will suffer different degrees and duration of such risk of self-incrimination it represents a differentiation in the rights of NSW citizens - often for reasons as arbitrary as having been innocently present at a crime scene.

According to extensive criminological research more than half of all NSW citizens have committed an imprisonable offence at some time in their lives. Within a few years we can expect many of these offences to result in permanent profiles on the crime scene index - just waiting for the day that a personal DNA test throws up a match. Members of the committee might contemplate what course their political careers may have followed if they had been suddenly and unexpectedly implicated in a teenaged indiscretion of several decades ago. If half the citizens of NSW can be implicated in crime by virtue of a DNA test it becomes clear that 'criminalisation' of an individual becomes largely a matter of police discretion to order a test or follow up on the results of crossmatching. The potential for selective blackmail by people with access to such information also becomes clear.

Whether or not DNA serves to implicate someone in a crime, privacy concerns remain. If a crime scene is a brothel or abortion clinic for instance the potential for compromising the privacy of clients is obvious. Of greater concern is the potential DNA has to reveal details of family relationships.

In a recent Sydney case (SMH, 22-Aug-2001, p5) a man was arrested in a house containing the drowned bodies of his three children. He had been involved in a custody dispute with his ex-partner. Although there is no question that the father had been present at the crime scene - he lives there - nor that he will seek to deny that he is the killer, police took samples of his saliva, hair *and* blood, explaining that it was for "DNA comparison to the blood of the children". There would seem to be no valid reason why the true parentage of the children should be of interest to the police investigating the case. They have invaded the privacy of a bereaved family - most of all the mother - simply

because they can. This allows great potential for harmful intervention in the many incidents of domestic dispute attended by NSW police.

If there is a privacy issue which has not been sufficiently emphasised already it is the potential for forensic DNA information to compromise the privacy of not only the DNA contributor but also the members of his/her family. This will become worse as more members of a particular extended family are tested. For example, by testing 20% to 30% of a particular Aboriginal community and referring to birth records it becomes possible to derive profiles or partial profiles for most other members of that community.

(9) In your opinion, how would the proposed 'Innocence Panel' best be constituted and operated?

It is difficult to see what Bob Carr really intends to achieve with the 'Innocence Panel'.

Justice Action is of the opinion that it is nothing but a cynical public relations exercise intended to placate those concerned over the draconian provisions of the Crimes (Forensic Procedures) Act but is concerned that it may also be intended to be a 'gatekeeper' for forensic evidence which may overturn existing convictions. The proposed composition of the panel raises concern that it is meant to keep the gate firmly closed in most cases.

Justice Action feels that an acid test of the Innocence Panel will be whether it permits Ivan Milat to conduct tests upon the forensic samples taken from the Belangalo forest - including the hair found clutched in the hand of one of the victims.

If the real intent of the government is to expedite the overturning of wrongful convictions in cases where DNA testing might provide the needed evidence it could do so far more effectively by putting guaranteed access to such samples, testing facilities and legal resources in the legislation itself. By attempting to control it via a panel of government appointees it is inevitable that unsuccessful applicants will claim political interference in their case, probably with some justification. Legislation should also ensure that such samples will not be 'lost' or destroyed if they might overturn an existing conviction.

If the 'Innocence Panel' really starts doing its job properly there will be a temptation for any government faced with the embarrassment and expense of having wrongful convictions exposed to hobble or terminate it unless its existence and independence is guaranteed in legislation.

The second best option would be for the government to properly fund *independent* bodies which might identify possible cases of DNA exoneration and pursue them. Examples of such a bodies are the UTS Innocence Project or community law centres. A fund for compensating those found to have been wrongfully imprisoned should also be set aside.

But if the government is determined to involve itself directly in such cases any 'Innocence Panel' clearly needs to be more balanced than the one currently proposed. It should include legal defence representatives as well as those of prisoners and ex-prisoners (e.g. Law Society, Prisoner's Legal Service).

(13) The Police Service submission, a copy of which you would have received, seeks a number of amendments to the Act, including:

(a) to enable time out for a forensic procedure to be permitted at the beginning of an investigative period (s.6)

The danger of allowing 'time out' for the carrying out of a forensic procedure is that it constitutes a form of detention which might be used to place pressure on a suspect - to consent to a forensic procedure for instance.

Police should only be permitted to detain people against their will for the purposes of obtaining a forensic sample if there are clear grounds for ordering such a test with or without consent. Justice Action is of the opinion that this should only apply to those already under lawful arrest - as had already been provided for in S353A of the Crimes Act.

(b) to enable a suspect on remand to be treated as a suspect under arrest so that a forensic procedure may be carried out without a court order at any time (s.6)

It is not necessary for police to have the power to order a test on someone on remand. Such a person is already under court orders and application can easily be made for a magistrate ordered test. If the person was considered to be at risk of absconding in order to avoid serious charges the court would not have granted bail.

Given the incredibly low threshold the Crimes (Forensic Procedures) Act now allows for senior police to order a hair sample it is difficult to imagine a situation where a suspect could not be tested when under arrest but would qualify for testing when on bail. However it would certainly allow police to harass remandees by ordering unjustified tests.

Similar provisions should apply to prisoners who are appealing against conviction. If the appeal is unsuccessful there will be plenty of time to conduct the test. If it is successful there was no reason to carry it out in the first place.

(c) simplification of the information sheet for suspects and serious indictable offenders (s.13)

Justice Action has some sympathy for police who must try to navigate the complexities of the Crimes (Forensic Procedures) Act and attempt to explain them to test subjects. The confused planning and shoddy drafting of the Act advantages no one.

Explanations of matching and deletion rules can be dropped as they are ineffective in the Crimes (Forensic Procedures) Act anyway. Police can carry out any off-database matching they wish and the passing of information to other jurisdictions neutralises any safeguards in the NSW legislation. To give precise definitions of ineffectual safeguards is merely to mislead people about the use to which their samples may be put.

The best way of simplifying explanations of the Act would be to simplify the Act. This would be best carried out by rewriting it from scratch in the manner suggested in the last part of Justice Action's main submission to the inquiry - which would begin from the rights of the contributor of the DNA. This would result in more consistency and rationality in the way samples and information will be subsequently treated and make explanations much easier.

But under the current Act there is a strong case for *increasing* the amount of information which must be given to potential DNA contributors if consent to DNA testing is to be truly informed. This would include

- the potential for off database matching and transfer of information to other jurisdictions
- the fallibility of forensic DNA and the implications of that for mass database trawling
- family relationships which might be revealed by forensic DNA testing
- that the contributor will *never* regain control of his/her genetic information as the government will keep samples and profiles *forever*

(d) to enable police to exclude an interview friend where the police 'reasonably suspect' the interview friend will obstruct the process

There is already too much potential for police to deny access to interview friends. In the case of prisoners in particular many possible interview friends are automatically excluded because they cannot attend the testing venue - either because the prisoner cannot afford to bring them there at his/her expense or because Corrective Services will not admit them into the prison (parolees, for instance, are not allowed on prison grounds).

The police arguments that a co-accused interview friend could compromise the investigation would seem to lack merit. As questioning of suspects is forbidden during forensic procedures it is hard to imagine what information the interview friend might gain beyond the fact of the forensic test itself - and it is hard to see how this could compromise an investigation. In any case, if the co-accused does not 'obstruct the process'

the proposed amendment would still not allow police to exclude him/her, even if it could potentially compromise the investigation.

If an interview friend it to be excluded there should be much stronger guidelines than 'reasonable suspicion' that they will obstruct the process. Police should be made to justify any such exclusion by recording the grounds upon which it was carried out. If it is later determined that the exclusion of the interview friend was not justified the test should be considered unlawful and all samples and information obtained from it should be destroyed.

But police proposals for amendments to the Act should be largely academic. Police should play no part in the collection of DNA samples - it should be the responsibility of an independent body as is the case in the UK.

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