CURRENT ISSUE

The need for caution in the use of DNA evidence to avoid convicting the innocent

By Michael Naughton and*
Senior Lecturer, School of Law and School of Sociology, Politics and International Studies (SPAIS), University of Bristol

*Gabe Tan***
Research Assistant, School of Law, University of Bristol

Keywords DNA evidence; Low Copy Number; Partial DNA profiles; Mixed DNA profiles

Deoxyribonucleic acid (DNA) profiles are obtained in forensic analyses by the identification of variations (known as alleles) within specific regions known as 'loci' (s.locus) within the human genome, which are then added to, or checked against profiles already on, the National DNA Database (NDNAD).[1] In the early years of the establishment of the NDNAD, a DNA profiling system known as Second Generation Multiplex (SGM) was used which measured six different Short Tandem Repeat (STR) loci to yield a DNA profile. This method of

* Email: M.Naughton@bristol.ac.uk.
** Email: Gabe.Tan@bristol.ac.uk. This article is an outgrowth of a paper that we presented at the Human Rights and Forensic Science Conference, co-hosted by the Irish Centre for Human Rights and the Centre for Anatomy and Human Identification, National University of Ireland, Galway, 24–25 April 2009. We are grateful for the feedback that we received at the session. We would also like to thank Allan Jamieson, Jenny McEwan and the anonymous reviewers for their helpful feedback too.

1 Human Genome Project Information 'DNA Forensics' (2009), available at <http://www.ornl.gov/sci/techresources/Human_Genome/elsi/forensics.shtml>, accessed 4 May 2011.

doi:10.1350/ijep.2011.15.3.380

DNA profiling was initially thought to be almost foolproof, with a claimed match probability (i.e. the odds of two individuals sharing the same SGM profile) of 1 in many millions.[2]

The belief in the reliability of SGM was short-lived, however, as a result of cases of coincidental/false matches such as Raymond Easton. In 1999, 48-year-old Easton from Swindon was arrested for a burglary in Bolton, 200 miles from his home, after an SGM profile yielded from DNA recovered from the scene of crime was found to match to his, which was placed on the NDNAD three years earlier following a domestic incident for which he received a caution.[3] Although Easton suffered from Parkinson's disease and could neither drive nor barely even dress himself, the police and prosecution were convinced of his guilt due to the apparent DNA 'match'. The charges against Easton were dropped, however, when his protestations of innocence, supported by strong alibi evidence, forced more rigorous DNA testing—a 10-point rather than a six-point test in which the four additional loci did not match Easton's profile, exonerating him of the crime.[4]

In the same year, the six-locus SGM profiling system was changed to a 10-locus profiling system known as SGM+ which is said to have discrimination potential beyond one in a billion, thus providing a surer statistical estimate.[5] However, not all DNA profiles recovered from crime scenes and loaded onto the NDNAD are full, SGM+ profiles from single sources. Frequently, DNA samples obtained from crime scenes are partial, degraded or mixed, and often in very minute quantities.[6] In response, new DNA testing methods have been developed in recent years to circumvent these limitations such as Low Copy Number (LCN) DNA testing which can yield profiles from smaller amounts of DNA than required for SGM or SGM+ testing, and the admissibility of partial and mixed DNA evidence in criminal courts.

2 W. Goodwin, A. Linacre and S. Hadi, *An Introduction to Forensic Genetics* (Wiley: Chichester, 2007) 99.

3 S. Jeffries, 'Suspect Nation', *Guardian*, 28 October 2006; N. Allen, 'George Orwell was Right: Spy cameras see Britons' every move', *Bloomberg*, 22 December 2007.

4 B. Schiffer and C. Champod, 'Judicial Error and Forensic Science: Pondering the Contribution of DNA Evidence' in R. Huff and M. Killias (eds), *Wrongful Conviction* (Temple University Press: Philadelphia, 2008) 43.

5 Crown Prosecution Service, 'Adventitious (Chance) DNA Matches' (2010), available at <http://www.cps.gov.uk/legal/s_to_u/scientific_evidence/adventitious_dna_matches/>, accessed 4 May 2011. But this does not mean that SGM+ is necessarily more reliable, see A. Jamieson, 'LCN DNA—Devil in the Detail', *The Journal Online: The Members' Magazine of the Law Society of Scotland*, 12 February 2007, 22.

6 National DNA Database (NDNAD), 'The National DNA Database Annual Report 2005–06' (2006), available at <www.homeoffice.gov.uk/documents/DNA-report2005-06.pdf>, accessed 4 May 2011.

Against this background, this commentary will show that such uses of DNA evidence and the NDNAD have the potential to yield erroneous and unreliable results that may cause factually innocent individuals to be wrongly convicted.

Low Copy Number DNA profiles

Low Copy Number (LCN) DNA, a specific form of Low Template analysis offered by the FSS since 1999,[7] is a much more sensitive variation of SGM+. Whereas conventional SGM+ analysis requires 50–100 cells for there to be sufficient DNA to yield a profile, LCN requires just 15–20 cells, allowing profiles to be yielded from miniscule amounts of biological material—such as skin cells or sweat residue from a single fingerprint on a variety of items which an offender may have touched[8] or come into contact with.[9]

The LCN DNA process 'facilitates the examination of a whole new range of evidence types that previously could not be analyzed because of the very low amounts of DNA recoverable from the sample'.[10] But this sensitivity is accompanied by a range of risks as it can mislead crime investigations and/or lead to possible wrongful convictions. First, the number of Polymerase Chain Reaction (PCR)[11] cycles has to be substantially increased to obtain LCN DNA profiles, which inevitably magnifies the risk of contamination and inaccurate results from 'stochastic effects', random statistical anomalies.[12] Secondly, even if a DNA profile is accurately yielded, there are difficulties associated with the propositions and interpretations that can be drawn from LCN DNA results. Since LCN DNA profile can stem from the cells of a single touch by an unconnected innocent individual prior to the crime, a phenomenon commonly termed 'adventitious transference'

7 Other forms of Low Template DNA analysis are offered by other forensic science providers such as Orchid Cellmark Ltd and LGC Forensics.

8 Low Copy Number DNA is therefore also often termed 'touch DNA'.

9 Crown Prosecution Service, 'Low Copy Number DNA Testing in the Criminal Justice System' (2010), available at <http://www.cps.gov.uk/publications/prosecution/lcn_testing.html>, accessed 4 May 2011; Forensic Science Service (FSS), 'DNA Low Copy Number' (2005), available at <http://www.forensic.gov.uk/pdf/company/foi/publication-scheme/communications/DNA_Low_Copy_Number_000.pdf>, accessed 4 May 2011.

10 J. Buckleton and P. Gill, 'Low Copy Number' in J. Buckleton, C. Triggs and S. Walsh (eds), *Forensic DNA Evidence Interpretation* (CRC Press: Florida, 2005) 276.

11 PCR is a technique in molecular biology to amplify a single or a few pieces of DNA, generating thousands to millions of copies of a particular DNA sequence.

12 In specific terms, Gill (2001) noted three key consequences of amplifying LCN DNA which can lead to different DNA profiles being observed: (a) allele drop-out may occur because one allele of a heterozygote locus can be preferentially amplified; (b) stutters may be preferentially analysed—these are sometimes known as false alleles; and (c) the method is prone to sporadic contamination—amplifying alleles that are not associated with the crime stain or sample. See P. Gill, 'Application of Low Copy Number DNA Profiling' (2001) 42(3) *Croatian Medical Journal* 230.

can occur.[13] Thirdly, low levels of DNA may also result from secondary transfer. For instance, if the perpetrator who is a poor DNA shedder had casual contact with an innocent individual who is a good DNA shedder prior to committing the crime, the perpetrator may leave behind DNA of the innocent individual whilst not shedding any of his or her own cells.[14]

The limitations of LCN DNA testing were revealed following the acquittal of Sean Hoey at the end of 2007 for the paramilitary car bomb attack allegedly carried out by the Real Irish Republican Army (RIRA) in Omagh, Northern Ireland, in the August of 1998 which led to 29 fatalities and 220 injured.[15] At the time of Hoey's arrest, more than eight years after the bombing, the Royal Ulster Constabulary (RUC) was under intense pressure from the public to bring someone to justice for the attack, as all of the 12 men arrested in September 1998 were released without charge. A further seven people were arrested the following year, of which only one of them, Colm Murphy, was convicted. However, in January 2005, Murphy's conviction was quashed due to irregularities in the evidence against him and a retrial was ordered.[16]

Hoey was charged in 2005 on the basis of an apparent LCN DNA link between him and a number of exhibits recovered from crime scenes.[17] This evidence was subsequently discredited by defence experts Professors Allan Jamieson and Dan Krane on the grounds that LCN DNA testing could yield distorted results and was highly susceptible to contamination.[18]

The fallout of the acquittal of Sean Hoey led to the appointment of the Caddy Commission by the Forensic Science Regulator which issued a report saying

13 Gill, above n. 12 at 231.

14 A. Lowe, C. Murray, P. I. Richardson, R. Wivell, P. Gill, G. Tully and J. Whitaker, 'Use of Low Copy Number DNA in Forensic Inference' (2003) 1239 *International Congress Series* 799; A. Lowe, C. Murray, J. Whitaker, G. Tully and P. Gill, 'The Propensity of Individuals to Deposit DNA and Secondary Transfer of Low Level DNA from Individuals to Inert Surfaces' (2002) 129(1) *Forensic Science International* 25–34.

15 BBC News, 'Bomb atrocity rocks Northern Ireland', 16 August 1998.

16 'Timeline: Omagh bombing', *Guardian*, 8 June 2009. At the time of writing, Colm Murphy's retrial has just commenced in Dublin and a verdict has yet to be reached. See BBC News, 'Omagh bomb conspiracy retrial of Colm Murphy begins', 12 January 2010.

17 *R* v *Hoey* [2007] NICC 49.

18 K. Lotter, 'Setback for LCN DNA: Omagh Bombing Trial Outcome—LCN DNA Is Not Reliable as Evidence', 22 December 2007, available at <http://dna-trace-analysis.suite101.com/article.cfm/setback_for_lcn_dna>, accessed 4 May 2011. The manner in which exhibits were recorded and stored was described by Justice Weir as 'thoroughly disorganised', with numerous exhibits either unlabelled or mislabelled, coupled with a lack of a uniform system of logging exhibits recovered from the crime scene(s) (*R* v *Hoey* [2007] NICC 49 at [51]).

LCN techniques are 'fit for purpose' although 'best practice standards' were lacking.[19] Hoey's acquittal also caused a temporary suspension in the use of LCN DNA evidence by the British police amid concerns about its reliability.[20] It was revealed at the time that British police had used the LCN DNA technique approximately 21,000 times in criminal investigations, although the Crown Prosecution Service (CPS) did not disclose how many of these police investigations actually led to a prosecution and/or a conviction.[21]

In response, the CPS conducted what it termed a 'precautionary internal review' of current cases involving the FSS use of LCN analysis between 21 December 2007 and 14 January 2008. A statement issued by the CPS following the review said that it has 'not seen anything to suggest that any current problems exist with LCN' and the use of LCN in police investigations was reinstated.[22] However, the review left crucial questions unanswered such as:

- Why was the review internal rather than a transparent and more comprehensive review of the 20,000 plus times in which LCN DNA featured in police investigations?
- Why did the CPS conduct its review over a Christmas and New Year period when very few cases would be likely to be included?
- How many cases were actually included in the review?

Arguably, the approach adopted by the CPS reveals a commitment to retaining criminal convictions at the expense of attempting to unearth possible wrongful convictions and put in place protocols for preventing them from occurring in the future.

More recently, an opinion on how the courts should deal with LCN DNA analysis was expressed in the combined appeals of David and Terence Reed and Neil Garmson amid continuing concerns about its reliability. Overall, the judgment concluded that:

19 B. Caddy, G. R. Taylor and A. M. T. Linacre, 'A Review of the Science of Low Template DNA Analysis' (2008), available at <http://police.homeoffice.gov.uk/publications/operationalpolicing/Review_of_Low_Template_DNA_1.pdf>, accessed 4 May 2011. For a reaction to the Caddy Commission, see, e.g., J. Gilder, R. Koppl, I. Kornfield, D. Krane, L. Mueller and W. Thompson, 'Comment on the Review of Low Copy Number Testing' (2008) *International Journal of Legal Medicine*, available at <http:// www.bioforensics.com/articles/Krane_LCN_Comments.pdf>, accessed 4 May 2011.

20 S. O'Neill, 'Police halt use of low-copy DNA evidence after Omagh judgment', *The Times*, 22 December 2007.

21 C. Hope, 'Omagh bomb verdict sparks DNA review', *Telegraph*, 22 December 2007.

22 BBC News, 'Police resume use of DNA method', 14 January 2008.

> ... a challenge to the validity of the method of analysing Low Template DNA by the LCN process should no longer be permitted at trials where the quantity of DNA analysed is above the stochastic threshold of 100–200 picograms [with a picogram being one trillionth of a gram] in the absence of new scientific evidence.[23]

The decision thus sets a minimum standard for when LCN DNA evidence can be deemed to be reliable by the courts in future trials. At the same time, the judgment potentially opens the door to challenges to criminal convictions based on LCN DNA if it can be proven that the evidence was obtained on samples below the 100–200 picogram range.

However, the cases of *R* v *Reed and Reed*; *R* v *Garmson* seem inappropriate ones to address the issue of how courts should deal with LCN DNA evidence. Criminal appeals usually deal with grounds of appeal that are actually brought by appellants in their challenges against their criminal convictions. In *R* v *Reed and Reed*; *R* v *Garmson*, although LCN DNA evidence featured in both cases at trial, the argument that the LCN DNA evidence might be unreliable was abandoned by all three appellants either days before the appeal (Reed and Reed) or at the outset of the appeal (Garmson).[24] The FSS had used LCN DNA testing when in fact there was a sufficient quantity of DNA to undertake SGM+ testing. SGM+ testing was then conducted on available remaining DNA samples and confirmed the reliability of the results obtained by the LCN DNA process that featured in evidence presented at the trial of David and Terence Reed.[25] The reliability of LCN DNA was therefore not in question in their appeal. Similarly, the issues in *Garmson* relate more to the presentation and possible misrepresentation of partial and mixed DNA evidence at trial and the methodologies used to interpret and convey the evidence, rather than the LCN DNA process by which much (but not all) of the DNA evidence was obtained.[26]

In this light, the intentions of the appeals in *R* v *Reed and Reed*; *R* v *Garmson* are questionable. It seems that this judgment can be read more as a general retaliation against what the court saw as the 'attack' on the reliability of the LCN DNA in the case of *R* v *Hoey*.[27] This might explain why the evidence of Dr Bruce Budowle and Professor Allan Jamieson (the latter whose evidence on the limitations of LCN

23 *R* v *Reed and Reed; R* v *Garmson* [2009] EWCA Crim 2698 at [74], *per* Thomas LJ; see also B. Woffinden, 'Bob Woffinden writes ...', *Inside Time: The National Newspaper for Prisoners*, February 2010, 24–5.

24 *R* v *Reed and Reed; R* v *Garmson* [2009] EWCA Crim 2698 at [68]–[71].

25 Ibid. at [62]–[70].

26 Ibid. at [178]–[191].

27 Ibid. at [106].

DNA had been instrumental in the acquittal of Sean Hoey for the Omagh Bombing) was accepted by the Court of Appeal *de bene esse*, meaning 'conditionally' or 'in anticipation of future need'. As such, the court took the opportunity to deal with the issue of challenges to the reliability of LCN DNA regardless of the apparent lack of relevance of LCN DNA in the final grounds for the appeals of Reed and Reed and Garmson. Yet it did not have to take account of any bearing that the evidence accepted *de bene esse* may have on the safety of the convictions of the appellants.

It is interesting to note, also, that the appeals of Reed and Reed and Garmson were summarily dismissed of all of the non-DNA-related matters. However, the court found that the evidence of Jamieson and Budowle did have some validity in terms of questioning the possible safety of the convictions, but declared the evidence inadmissible to the proceedings under the terms of s. 23 of the Criminal Appeal Act 1968. This requires evidence adduced in appeals to be new evidence that was not available or could not have been made available at the time of the original trial unless there are exceptional circumstances for why it was not or could not be adduced. The court declared further that:

> It is not therefore in the interests of justice now to admit evidence of Dr Budowle and Professor Jamieson simply on the basis that, had it been called, it might have affected the decision of the jury.[28]

This seems to forward a notion of justice at odds with public opinion. Rather than a genuine attempt to assess the reliability of LCN DNA to avoid future wrongful convictions, the judgment can be conceived as an explicit attempt to draw a judicial line under the ongoing challenges to the use of LCN DNA in criminal trials post-*Hoey*. This further legitimates its continuing use in police investigations and by the CPS despite its inherent limitations.

Partial DNA profiles

Partial DNA profiles can also be questionable in criminal investigations,[29] although this is yet to be officially acknowledged in the form of acquittals in criminal trials or convictions overturned.

28 *R* v *Reed and Reed; R* v *Garmson* [2009] EWCA Crim 2698 at [143].

29 House of Lords Constitution Committee, 'Examination of Witnesses (Questions 154–159)', 30 January 2008, available at <http://www.publications.parliament.uk/pa/ld/ldconst.htm>, accessed 4 May 2011; R. Woods and D. Foggo, 'Should Britain have a compulsory DNA database?', *The Times*, 24 February 2008; Human Genetics Commission, 'A Citizens' Inquiry into the Forensic Use of DNA and the DNA Database: Contractor's Report', July 2008, available at <http://www.hgc.gov.uk>, accessed 4 May 2011.

It is fairly common that the amount of DNA in a biological stain recovered from the crime scene may be of such minute quantities and/or so degraded that neither SGM+ nor LCN DNA analyses is able to yield a full DNA profile. Rather, an incomplete or partial profile may be obtained, which, akin to SGM profiles described above, does not have the full 10 loci of a complete SGM+ profile.[30] Indeed, the CPS reported that some 50 per cent of DNA profiles yielded from samples recovered from scenes of crime are partial profiles.[31]

Under the present criteria of the NDNAD, DNA profiles yielded from the crime scene must contain a minimum of eight of the STR markers to be loaded onto the NDNAD.[32] However, partial DNA profiles that contain too few alleles to meet the requirement of the NDNAD can also be searched against (although not loaded onto) the NDNAD on a one-off basis.[33]

The use of partial DNA evidence to strengthen the case for criminal prosecution and even conviction of an *already identified* police suspect, particularly if there are other pre-existing forms of evidence to support his or her guilt, is in itself not problematic. What is, perhaps, more of a cause for concern is when such crime investigation methodology is reversed, i.e. rather than matching partial DNA profile found at the crime scene against an already identified suspect, the partial crime scene profile is speculatively screened against the NDNAD to 'trawl' for potential suspects.

From this perspective, the practice of constructing a matrix of criminal suspects from 'hits' on the NDNAD presents at least three key problems. First, and most obvious of all, without a complete crime scene DNA profile, there is no way of determining with any absolute certainty whether or not the crime scene profile and a suspect's DNA profile are indeed a match. Using the example of Raymond Easton discussed above, had the DNA profile obtained from the scene of the burglary been a partial profile that contained six or less STR markers (and assuming that LCN DNA testing could not produce a more complete or full profile), it would not have been possible to distinguish Easton's DNA profile from

30 A. Semikhodskii, *Dealing with DNA Evidence* (Routledge: Oxford, New York, 2007) 36–7; *Hansard*, HC, 'DNA: Databases', 17 June 2009, col. 312W, available at <http://www.publications.parliament.uk/pa/cm200809/cmhansrd/cm090617/text/90617w0008.htm>, accessed 4 May 2011.

31 Crown Prosecution Service, 'Summary of National DNA Database from the Prosecution Perspective' (2010), available at <http://cps.gov.uk/legal/s_to_u/scientific_evidence/summary_of_national_dna_database/>, accessed 4 May 2011.

32 National DNA Database, 'The National DNA Database Annual Report 2003–04' (2004) 19, available at <http://www.forensic.gov.uk/pdf/company/publications/annual-reports/annual-report-NDNAD.pdf>, accessed 4 May 2011.

33 Crown Prosecution Service, above n. 31.

that found at the crime scene.[34] Secondly, as the match probability of a crime scene DNA profile is significantly increased when the profile is partial, speculative searches of partial crime scene profiles against the NDNAD very often produce multiple 'matches', a phenomenon which the Home Office recently acknowledged has occurred on over 50,000 occasions since 2001.[35] Finally, particularly where partial crime scene profiles are concerned, utilising the NDNAD or a subject's DNA profile in such random, speculative manner heightens the vulnerability of innocent individuals whose DNA profiles are on the NDNAD of being suspects of crime, of wrongful prosecution and, even, of wrongful conviction.[36]

It is acknowledged that the CPS will not instantly charge an individual simply on the basis of a match report from a speculative search on the NDNAD:

> ... a suspect should not be charged solely on the basis of a match between his DNA profile and a DNA profile found at the scene of the crime, unless there are compelling reasons to do so.[37]

However, such suspects are likely to be entered into the police matrix to be traced, interviewed and eliminated (TIE). If, upon being interviewed by the police, the suspect could not, for instance, produce a reliable alibi in his or her defence for a cold case that may have occurred years or even decades ago, or if the suspect has previous convictions for similar offences, he or she could be charged and even convicted of the crime. This is despite the fact that limitations of partial DNA profiles/matches inevitably mean that there is a real possibility that a suspect or individual convicted on such basis could be, in fact, innocent. At the same time, such a NDNAD guided investigative approach would also mean that the actual perpetrator would escape the police investigation completely if his or her DNA profile is yet to be loaded onto the NDNAD.

34 It is acknowledged that this problem is not unique to partial DNA profiles. One could make the same point about *any* DNA profile, hence this is not an inherent problem with partials. Moreover, the point carries little force so long as the laboratory correctly estimated the frequency of the profile that *did* match. The real problem with partial profiles, and with DNA mixtures, is that laboratories tend systematically to underestimate the likelihood of a coincidental match in such cases. See W. Thompson, 'Painting the Target around the Matching Profile: The Texas Sharpshooter Fallacy in Forensic DNA Interpretation' (2009) 8 *Law, Probability and Risk* 257. Hence, the likelihood of a coincidental match in such cases may be higher than laboratory experts, and police authorities, and jurors, realise.

35 R. Woods and D. Foggo, 'Should Britain have a compulsory DNA database?', *The Times*, 24 February 2008.

36 See, e.g., C. McCartney, 'The DNA Expansion Programme and Criminal Investigation' (2005) 46 *British Journal of Criminology* 175.

37 Crown Prosecution Service, above n. 31.

Mixed DNA profiles

DNA samples obtained from crime scenes do not always originate from single sources. Rather, many samples contain a mixture of DNA belonging to more than one person.[38] Despite this, there is yet to be a universal consensus on how mixed DNA profiles should be interpreted.[39]

The National Policing Improvement Agency (NPIA), which is the body responsible for overseeing the NDNAD,[40] provides the following description on its website on how mixed DNA profiles are processed:

> If two people leave their DNA together at a crime scene, and this DNA is recovered, a mixed DNA profile may be obtained. There are strict rules for placing a person's DNA profile on the NDNAD, when it has been obtained from a mixture of DNA ... If you know the DNA profile of the person who has contributed to a mixed DNA profile, it may be possible for this DNA profile to be taken away from the mixed one, leaving the DNA profile of the other person. This may be possible in cases where both a victim's DNA and that of an assailant are mixed together. An elimination DNA profile from a victim can be sufficient to identify the DNA profile of an assailant.[41]

This description is problematic as it oversimplifies the complexities involved in the interpretation of mixed DNA profiles. As mentioned previously, DNA profiling is done by comparing alleles within specific loci. Typically, in DNA from a single source, each marker/loci would contain two alleles, each inherited from one parent. A DNA mixture is identified when there are three or more alleles in a loci.[42] However, as several individuals may share many alleles, it is difficult to say with absolute certainty just how many contributors there are in a mixed DNA profile.[43]

38 Woods and Foggo, above n. 35.

39 P. Gill, C. Brenner, J. Buckleton, A. Carracedo, M. Krawczak, W. Mayr, N. Morling, M. Prinz, P. Schneider and B. Weir, 'DNA Commission of the International Society of Forensic Genetics: Recommendations on the Interpretation of Mixtures' (2006) 160 *Forensic Science International* 90.

40 National Policing Improvement Agency (NPIA), 'The National DNA Database' (2010), available at <http://www.npia.police.uk/en/8934.htm>, accessed 4 May 2011.

41 National Policing Improvement Agency (NPIA), 'The National DNA Database: Basic Facts—FAQs' (2010), available at <http://www.npia.police.uk/en/13340.htm>, accessed 4 May 2011.

42 J. Mortera, A. Dawid and S. Lauritzen, 'Probabilistic Expert Systems for DNA Mixture Profiling' (2003) 63(3) *Theoretical Population Biology* 191–2.

43 J. Buckleton, J. Curran and P. Gill, 'Towards Understanding the Effect of Uncertainty in the Number of Contributors to DNA Stains' (2007) 1(1) *Forensic Science International: Genetics* 20–8; W. Thompson, S. Ford, T. Doom, M. Raymer and D. Krane, 'Evaluating Forensic DNA Evidence: Essential Elements of a Competent Defense Review' (2003) 27(2) *The Champion* 16.

In addition, it is often difficult to attribute an identified suspect as one of the sources of the mixed DNA profile. Greg Hampikian provides a useful analogy in describing the problem with analysing mixed DNA samples. For Hampikian, alleles can be viewed as akin to the letters of your name and attempts to determine suspects from mixtures of DNA profiles can be conceived as trying to pinpoint a suspect based on whether his or her name can be derived, either fully or, thinking of the foregoing analysis of partial DNA profiles, partially, from the letters/alleles.[44] As this relates to us, our full names are, respectively, 'MICHAEL JOSEPH NAUGHTON' and 'GABE SI HAN TAN'. If our names/DNA alleles are mixed, the following full profiles can be obtained and these 'suspects' cannot be excluded: 'CAIN' and 'ABEL', 'JOSEPH STALIN', 'PLATO', 'TOM JONES' and/or 'JANE AUSTEN'. If partial profiles were searched for, the following 'suspects' cannot be excluded; 'TON(Y) BLAI(R)', 'AM(Y) (W)INEHOUSE' and/or 'MOTHE(R) THE(R)ESA'.

Similarly, Jamieson asserts that a mixed DNA profile of two individuals with the profiles AB and CD (notwithstanding that more than one person could share the same alleles) results in the mixed profile ABCD which could yield *at least* six different potential contributors: AB, CD, AC, BD, AD and BC.[45] Jamieson notes that across 10 loci, with two alleles per contributor, there are over one million ways to interpret a mixture of two contributors, that is, a mixture of DNA from two people could produce a million possible profiles.[46]

As with other forms of DNA evidence, the evidential significance of a purported link between an individual with a mixed DNA profile is commonly measured by what is termed the 'likelihood ratio', derived by comparing the prosecution's hypothesis that a known defendant is a contributor to a mixed DNA profile against one or more alternative hypotheses which exclude(s) the defendant.[47] However, Jamieson's analysis of DNA reports showed that forensic scientists often fail to take into account other possible explanations that exclude the defendant:

> It is frequently not obvious how a scientist derives the opinion that favours one of these options over any of the others. At the very least, the possibility of other interpretations should feature in reports but,

44 G. Hampikian, Presentation, Arundel House, London, 8 June 2009, available at <http://www.humanrightstv.com/innocence-inuk/hollis-whiteman/greg-hampikian>, accessed 4 May 2011.

45 A. Jamieson, 'Mixed results', *Guardian*, 28 February 2008.

46 A. Jamieson, 'The Philosophy of Forensic Scientific Identification' (2008) 59 *Hastings Law Journal* 1044–5.

47 See P. Gill, C. H. Brenner, J. Buckleton, A. Carracedo, M. Krawczak, W. Mayr, N. Morling, M. Prinz, P. Schneider and B. Weir, 'DNA Commission of the International Society of Forensic Genetics: Recommendations on the Interpretation of Mixtures' (2006) 2–3 *Forensic Science International* 90–101.

> sadly, do not. In casework, we frequently come across DNA reports that all but ignore any other possible interpretation than the one that provides the best probative value against the accused. The most obvious explanation is that the scientist has been influenced by knowledge of the profiles of those involved, whether it is the complainer or the suspect.[48]

The likelihood ratio derived from this mode of statistical evaluation can, therefore, be overstated and has been known to cause wrongful convictions in the United States. In 1993, Timothy Durham was convicted and given a 3,000-year prison sentence for the rape of an 11-year-old girl in Oklahoma. Despite 11 alibi witnesses who placed him in a different state at the time that the rape occurred, Durham was found guilty on the basis of the victim's eyewitness identification, a hair found at the crime scene claimed to be similar to his, and most significantly, a claimed DNA match between Durham and the semen stain recovered from the crime. After serving four years of his sentence, Durham's conviction was quashed after further analysis found that the laboratory had misinterpreted the DNA results. The victim's alleles, when combined with those of the true perpetrator, produced a mixed DNA profile which was mistaken as a single source profile matching that of Durham's.[49]

Similarly, in 1998, Josiah Sutton was identified by a woman who was abducted at gunpoint and raped by two men in Houston, Texas.[50] Following Sutton's insistence on a DNA test to exonerate himself, semen samples recovered from the crime scene were tested. However, the tests yielded a DNA match between Sutton's profile and the mixed DNA profiles obtained from both the victim's vaginal samples and a semen stain found on the back seat of her car, which the Houston Police Department Crime Laboratory claimed had a probability of a chance match of 1 in 694,000. After serving four and a half years of the 25-year sentence he was given, Sutton's conviction was overturned when a further review of the DNA evidence against him not only showed the probability of a coincidental match to be in fact more than 1 in 8, but that the semen stain found on the back seat of her car did not belong to him at all.[51]

48 Jamieson, above n. 47.

49 W. Thompson, F. Taroni and C. Aitken, 'How the Probability of False Positive Affects the Value of DNA Evidence' (2003) 48(1) *Journal of Forensic Science* 2.

50 The best account of the case of Josiah Sutton is W. Thompson, 'Beyond Bad Apples: Analyzing the Role of Forensic Science in Wrongful Convictions' (2008) 37(4) *Southwestern Law Review* 1027.

51 W. Thompson, 'Houston Has a Problem: Bad DNA Evidence Sent the Wrong Man to Prison at Least Once. How Many More Are There and What Can Be Done About It?' (2003) 25(1) *Cornerstone* 17; The Innocence Project 'Josiah Sutton' (2010), available at <http://www.innocenceproject.org/Content/268.php>, accessed 4 May 2011.

Conclusion

DNA testing is not foolproof and there are limits to its application in crime investigations. As evidenced by scientific research and cases discussed in the foregoing, there are pitfalls associated with the NDNAD and the use of forms of DNA evidence, namely, LCN, partial and mixed DNA profiles, to convict suspects of crime. The use of such forms of evidence, therefore, has to be treated with caution to avoid the wrongful identification and conviction of innocent individuals.

Moreover, DNA, even when positively identified, is reliable evidence only of an association with a crime scene or a victim of a crime. It is not *prima facie* evidence of guilt for a criminal offence. There may well be an innocent explanation for why a person's DNA is found at a crime scene. Like all trace evidence, DNA is easily transferrable, it cannot be dated, it is susceptible to contamination[52] and can be misinterpreted. Despite these fallibilities, criminal investigators and the courts alike seem to have failed to take heed of the science and case law evidence on the inherent flaws in applications of DNA techniques.

The overall conclusion to be drawn from the foregoing analyses is that people who claim they are innocent despite forms of DNA evidence linking them to crimes for which they have been accused and/or convicted could well be telling the truth. DNA and the NDNAD are not the panacea of criminal identification that is popularly believed. The presumption of innocence that is claimed to lie at the heart of all criminal investigations and prosecutions dictates that this is more adequately recognised and acted upon by the criminal justice system to avoid causing wrongful convictions and to overturn those that have already occurred.

52 An example of cross-contamination of DNA samples is the case of Brian Kelly, who may well have been falsely incriminated by accidental 'carry-over' contamination in the DNA laboratory. In 2004, the Scottish Criminal Cases Review Commission referred the case to the High Court of Justiciary. The High Court reviewed scientific evidence about the danger of cross-contamination of DNA samples in circumstances like those in the Kelly case and found it to be 'evidence which is of such significance that the fact that it was not heard by the jury constituted a miscarriage of justice'. See High Court of Justiciary, 'Opinion in the Reference by the Scottish Criminal Cases Review Commission in the Case of Brian Kelly' (2004), available at <http://www.scotcourts.gov.uk/opinions/XC458.html>, accessed 4 May 2011.