# Dealing with DNA Evidence in the Courtroom: A Plain English Review of Current Issues with Identification, Mixture and Activity Level Evidence

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*DNA has played a revolutionary role within criminal justice systems across the world. This paper, while honouring the role DNA evidence has played, nevertheless aims to set out (in plain English in order to make it readily accessible to lawyers dealing with this evidence) some on-going and new key aspects related to the use of DNA evidence in the courtroom. Areas canvassed relate to identification evidence, activity level evidence and DNA mixtures. Specific issues considered include the potential for misunderstanding of DNA statistics both generally and when 'partial' match profiles are involved; concerns in regard to underlying assumptions and interpretation of transfer and activity information to determine how and when the DNA was deposited; and a highlighting of a change to the way statistical calculations are made through new software being used across Australia and internationally, including 'black box' assumptions that go into those calculations that are particularly relevant to DNA mixtures. This article is Australian-based and some key Australian cases relevant to these issues are considered, however the issues and principles contained within the article are widely applicable within an international context.*



## I DNA in the Courtroom

DNA evidence has changed the face of the criminal justice system. It has played a revolutionary role in correcting the wrongful convictions of hundreds of factually innocent people in the United States.[1] Despite DNA exonerations only representing the tip of the wrongful

[1] See e.g., The Innocence Project, *DNA Exonerations in the United States*, online:

conviction ice-berg, the exposure has signaled the unanticipated magnitude of the wider problem. Internationally there is a growing awareness within the legal and broader community that the conviction of innocent people is real and on-going. Thanks to DNA testing, the fallibility of a range of other evidence routinely presented within the courtrooms (such as eyewitness identification, other less reliable forms of scientific evidence, confessions, informant evidence and more), is now known.[2] This in turn has demonstrated the need for new mechanisms for the uncovering and correcting of wrongful convictions more broadly.[3] The crucial part that DNA evidence has played and continues to play within criminal justice systems across the world is not disputed.

DNA evidence itself however is not infallible. Its use within the criminal justice system is vastly different and more complex than when it is used in the more pristine medical or clinical context.[4] Challenges particularly arise when utilizing DNA evidence for inculpatory (as opposed to exculpatory) purposes.[5] It has already led to the wrongful conviction of an innocent person in Australia. Farah Jama, a young man of 19 years old was wrongly convicted of the rape of a woman in the bathroom of a venue he had never visited, based solely on the (contaminated) DNA evidence presented in that case. It appears that the contamination occurred in the hospital where the rape kit was taken.[6] As reported by The Honourable Justice Vincent:

> It is almost incredible that, in consequence of a minute particle, so small that it was invisible to the naked eye, being released into the environment and then by some mechanisms settling on a swab, slide or trolley surface, a chain of events could be started that culminated in the conviction of an individual for a crime that had never been committed by him or anyone else, created immense personal distress for many people and exposed a number of deficiencies on our criminal justice system. But that, I believe is what happened.[7]

And as noted earlier in the Report:

> It became clear that the DNA evidence was perceived as so powerful by all involved in the case that none of the filters upon which our system of criminal justice depends to minimise the risk of a miscarriage of justice, operated effectively

<https://www.innocenceproject.org/dna-exonerations-in-the-united-states/>.

[2] Keith A Findley, "Learning from our Mistakes: A Criminal Justice Commission to Study Wrongful Convictions" (2002) 38:2 Cal WL Rev 333, online: <http://heinonline.org/HOL/Page?handle=hein.journals/cwlr38&div=15&g_sent=1&collection=journals> accessed 16 August 2017.

[3] See e.g., the range of DNA innocence testing regimes now in place throughout the United States.

[4] Erin E Murphy, *Inside the Cell: The Dark Side of Forensic DNA* (New York, Nation Books, 2015) at 5.

[5] See e.g., William C Thompson, "Forensic DNA Evidence: The Myth of Infallibility" in Sheldon Krimsky & Jeremy Gruber, eds, *Genetic Explanations: Sense and Nonsense* (Cambridge, Harvard University Press, 2013) at 230.

[6] The Honourable FHR Vincent, *Report: Inquiry into the circumstances that led to the conviction of Mr Farah Abdulkadir Jama* (Melbourne, Printing and Publishing Services Victoria, May 2010).

[7] *Ibid* at 48.

> at any stage until a matter of weeks, before Mr Jama's appeal was expected to be heard.[8]

It has been said that Jama got lucky and that the error was discovered because of the quality and diligence of the specific Crown Prosecutor whose desk this case came across. As stated by barrister Saul Holt QC at a DNA symposium held in Brisbane, Australia: 'the system didn't find the error, a person did. That is terrific at one level and should be celebrated, but it is quite terrifying at another.'[9]

While issues of potential contamination are not dealt with in this article, the Jama case highlights the need for those within the criminal justice system to be particularly diligent when dealing with this powerful evidence. Understanding the range of underlying complex scientific methodologies and assumptions related to DNA evidence, is far from an easy task for many lawyers and it can be both particularly relevant and problematic for lawyers when confronted with incriminating DNA evidence in their cases. Gary Edmond has previously noted that 'most lawyers confronted with incriminating DNA evidence encourage their clients to plead guilty and few challenge the evidence or go beyond the *low hanging fruit* of conflicts of interest, obvious chain of custody anomalies and the possibility of DNA mixes and mistakes.'[10]

The structure and adversarial nature of the criminal justice system demands some level of DNA fluency within the courtroom context if lawyers are to effectively question on highly complex scientific evidence. For lawyers to ask the right questions, some understanding of how scientists reach their conclusions is necessary.[11] With validation processes for example, lawyers need to: (i) identify when assumptions are being used and how they impact on profile interpretation; (ii) understand what the statistical calculations mean and have the knowledge that the type of scientific question posed will result in different statistical conclusions reached; (iii) understand what the margin of error means in terms of the evidence presented; and more. If within a case it is accepted that the defendant's DNA profile is present on the crime sample but the question is *how* and *when* it got there (known as 'activity level' evidence), lawyers will need to understand and effectively question the scientist on: (i) how DNA is transferred (types of transfer); (ii) what affects transfer (surface, duration of contact, shedder status etc.); (iii) what assumptions, error and uncertainty relate to the expert opinion; (iv) how scientists convert 'ranking phrases' into appropriate weighting of the evidence; and (v) the difference and deciphering between expert opinion, scientific results and 'scientific' speculation.

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[8] *Ibid* at 11.

[9] DNA Symposium, *Lifting the Veil on DNA Evidence: What Do the Statistics Really Mean?* (Brisbane, 30 June 2017) [*DNA Symposium*].

[10] Gary Edmond, "The building blocks of forensic science and law: Recent work on DNA profiling (and photo comparison)" (2011) 41 Soc Stud Sci 127 at 145.

[11] For areas upon which lawyers should question scientific expert witnesses generally, see e.g., Gary Edmond, et al, "How to Cross Examine Forensic Scientists: A Guide For Lawyers" (2014) 39 Austl Bar Rev 174.

DNA methods and technology are not static. New technology has been rolled out across Australia and elsewhere in the world that not only increases the number of loci tested,[12] but also incorporates a new and different method of analyzing and calculating the results of that testing and the statistics presented in court.[13] It is therefore an appropriate time to devote renewed attention to the use of DNA evidence in the courtroom and to highlight potential areas for caution and concern in terms of its use.

This paper, while honoring the role DNA evidence has played in the criminal justice system,[14] nevertheless aims to set out some on-going and new key aspects of DNA evidence. It specifically aims to do so in plain English in order to make it readily accessible to lawyers dealing with this evidence. One of the many challenges for lawyers in properly understanding and evaluating DNA evidence, can be the application of scientific principles and use of scientific language that is not easily transferable outside the scientific paradigm. As such, this paper aims to present the issues it raises in a manner that enables understanding by a wide legal audience who may need to deal with this DNA evidence. Areas canvassed relate to identification evidence, activity level evidence and DNA mixtures. Specific issues considered include the potential for misunderstanding of DNA statistics both generally and when 'partial' match profiles are involved; concerns in regard to underlying assumptions and interpretation of transfer and activity information to determine how and when the DNA was deposited; and a highlighting of a change to the way statistical calculations are made through new software being used across Australia and internationally, including 'black box' assumptions that go into those calculations that are particularly relevant to DNA mixtures. While this article is Australian-based and some key Australian cases relevant to these issues are considered, the issues and principles contained within the article are widely applicable within an international context.

## II Identification Evidence

DNA testing is being rolled out across Australia, increasing the number of loci tested from 15 to 21.[15] Profiling with increased loci offers advantages including a greater ability to distinguish between related individuals, and decreasing the possibility of adventitious matches within criminal databases. Previously in Australia when the number of loci tested was nine, a DNA 'match' was said to occur when nine loci were matched from the biological sample at the crime scene to the

[12] National Institute of Forensic Science, *Introduction of New DNA Marker Sets in Australian Forensic Laboratories*, online: <http://www.anzpaa.org.au/forensic-science/our-work/products/scientific-papers-/introduction-of-new-dna-marker-sets-in-australian-forensic-laboratories>.

[13] Joanne Bright, et al, "Developmental Validation of STRmix™, Expert Software for the Interpretation of Forensic DNA Profiles" (2016) 23 Forensic Sci Int'l: Genetics 226; Mark Perlin, et al, "Validating TrueAllele® DNA Mixture Interpretation" (2011) 56:6 J Forensic Sci 1430 [*Bright*].

[14] See e.g., President's Council of Advisors on Science and Technology, [*PCAST*], *Report to the President - Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods* (September 2016), online: <https://obamawhitehouse.archives.gov/sites/default/files/microsites/ostp/PCAST/pcast_forensic_science_report_final.pdf>.

[15] Linzi Wilson Wilde, "Introduction of New DNA Marker Sets in Australian Forensic Laboratories" (2012) 3:6 J Forensic Res, online: <http://dx.doi.org/10.4172/2157-7145.1000e109>.

suspect's biological sample. The scientific community in Australia, generally no longer use the term 'match', in part because consistency between an individual's DNA profile and that taken from a crime scene does not offer a definitive identification as only a portion of the whole DNA (genome) is being analyzed with the forensic markers, and even if those markers match, it doesn't mean that the entire genome matches. Statistics are offered to relay to the jury how rare a particular DNA profile is, by estimating the probability of a randomly selected person having the same DNA profile as that retrieved from the crime scene. This statistical expression is known as 'random match probability' (RMP). But statistics presented in the courtroom may not be easily understood by non-scientists.

Statistical calculations presented to the jury for a nine-locus match between a crime scene sample and a suspect could, for example, estimate that the RMP is one in billions. This indicates that the profile is 'rare' and may well provide compelling evidence of guilt. For those not familiar with statistics, however, the results of occasional studies where criminal databases have been searched for matching profiles from unrelated individuals (adventitious matches) may be surprising. For example, in an examination of an Arizona database of 65, 493 people, there were:

- 122 unrelated people who matched at nine loci; and
- 20 unrelated people who matched at 10 loci.[16]

Although these were in fact 'partial matches' in that the Arizona database used 13 loci and the additional testing showed other loci that mis-matched between the individuals, a lay person may be surprised at the number of potential 'matches'. To a statistician, however, these results are unsurprising. It is simply a matter of which question they are answering. The RMP and the Arizona database example, highlight two very different questions, using two different statistical formulas. This is why there are two very different answers. The RMP estimates the chance of picking one unrelated person at random who has the same DNA profile as that found on the evidence. In other words, if you were standing on a busy street with many thousands of people walking past you, and you can only randomly pick one person, what is the chance the one person you picked had the same DNA profile as the evidence? Intuitively, the chance of this occurring is extremely small. Evaluating the rarity of a DNA profile when posed in this manner generally leads to small probabilities when presented to courts.

On the other hand, estimating the number of DNA profiles in a criminal database that could match at 9 loci means that instead of having one chance to pick a person with one specific DNA profile (the same as the evidence), you have as many chances as there are profiles in the database for them to match any other profile in the database. This is a very different question to that being addressed by the RMP, and an entirely different probabilistic calculation is used.

In terms of understanding how the two different calculations can represent the chance of seeing 'two DNA profiles that are the same', think of standing on the footpath of a busy city street. As the crowd of people walks by, you can randomly select only one person. The chance that one person you randomly selected has the same DNA profile as the DNA from the crime scene is like

[16] Edward Ungvarsky, "What Does One in a Trillion Mean?" (2007) 20:1 Gene Watch 10, online: <http://wispd.org/attachments/article/244/What%20does%20One%20in%20a%20Trillion%20Mean.pdf>.

the RMP example (except the randomly selected person is the suspect). Continuing on from the 'people in the city' example, if you were in a city of 1 million people, the chance that anyone's DNA profile in that city will match anyone else's is like the Arizona Database example. Given you can match 1 million people against 1 million people, the chance of getting two people with the same DNA profile is much greater than if you only had one matching chance (the RMP).

The likelihood ratio (LR) calculation is yet another way that expresses the chance of seeing two matching profiles. The LR compares the probabilities that two opposing hypotheses might explain the evidence (the matching profiles), typically the prosecution's hypothesis (the DNA found on the evidence came from the defendant, or where relevant the victim) and the defence's hypothesis (the DNA found on the evidence came from an unrelated person randomly chosen from the population, that is, an adventitious match). The probability associated with the defence's hypothesis is calculated by using the RMP (the denominator in the LR equation), and for the prosecution's hypothesis is always a certainty at 100% (or 1, the numerator in the LR equation).

$$\text{Likelihood ratio} = \frac{\text{Prosecutor's hypothesis}}{\text{Defence's hypothesis}} = \frac{1}{\text{RMP}}$$

If the LR is greater than one, the prosecutor's hypothesis is supported. If the LR is less than 1, the defence's hypothesis is supported. An LR of 1 is neutral, the evidence has no probative value. This form of statistical evidence arguably requires the jury to understand the RMP, then understand the LR which evaluates a 'hypothetical theory', then requires the jury to convert the weighting of that 'theory' back to 'how rare is that DNA profile' and a further step of using this to appropriately weight the DNA evidence within the context of the factual scenario involved in the case.

The key to understanding the statistical evidence, is to understand what question it is actually addressing. The RMP and LR have been formulated by scientists for the intended purpose of assisting in answering questions of identity within the criminal justice context. Yet while statisticians may fully understand the different meanings of the statistics presented based on the question they are answering, very few untrained people have an intuitive sense of what the numerical value, provided by the RMP or LR, actually means when evaluating identification scenarios. The scientific community have therefore developed guidelines in an attempt to better convey to the courts how evidence should be weighted based on the statistical calculation, by creating LR thresholds linked to qualitative assessments of how strongly they support the prosecution's hypothesis, demonstrated in the table below.[17]

[17] John M Butler, *Fundamentals of Forensic DNA Typing* (Cambridge, Academic Press/Elsevier, 2010) at 253.

| If the likelihood ratio is… | Then the evidence provides… |
|---|---|
| 1 to 10 | limited support… |
| 10 to 100 | moderate support… |
| 100 to 1,000 | moderately strong support… |
| 1,000 to 10,000 | strong support… |
| 10,000 or greater | very strong support… |

According to these guidelines, used by many laboratories around the world, a jury would hear that any LR over 1,000 provides *strong support* that the defendant was the donor of the evidentiary sample, and *very strong support* for any LR over 10,000. Yet it can be argued that these thresholds are only arbitrary and may in fact misrepresent to the jury the appropriate weighting that should be given to the DNA evidence. There have been suggestions that (i) this table should be scrapped and (ii) due to the risks involved of an adventitious match with any LR of less than 1 million, a measure of the probability of an adventitious match for the DNA profiles present in a mixture using appropriate population data should be reported.[18]

A partial profile may easily generate a LR of 1,000 - which raises the concern about using partial profile evidence. The threshold values used in the guidelines[39] permit partial profile evidence to be considered by the courts, which places responsibility on the scientist to disclose when partial profiles are used as evidence. Should only 'complete profiles' be used to generate a LR? The definition of a 'complete profile' will constantly change as loci expand. Nine loci would be considered a 'complete profile' using a nine-locus kit, however, it would be considered a partial profile if generated by the newer 21 loci kits. Gill states that:

> Provided that the (likelihood ratio) calculations are correct there is no reason to discount a low number as 'insufficient evidence' so long as the model used to interpret is reasonable.[19]

This reasoning is consistent with the approach used by forensic biology laboratories. Only the courts can decide the ultimate question of 'identity'. The scientists provide probabilities, not definitive conclusions, to assist the courts to make their decision when DNA evidence is relevant to the case. But if the statistics are not properly understood or the 'assisting' qualitative table is being received by jurors in a manner that over-represents the probative value of the evidence, then the courts may be misled, not assisted.

Any missing loci from DNA evidence may be exculpatory - and when a criminal database is searched, a partial profile may coincidently match one or more previous offenders. The RMP calculation does not provide the courts with an understanding of the chance of this occurring. While the 21 locus tests being introduced will see the number of loci tested rise, partial profiles

[18] Dr Brian McDonald, DNA Symposium, *supra* note 9.

[19] Peter Gill, *Misleading DNA Evidence: Reasons for Miscarriages of Justice* (Cambridge, Academic Press/Elsevier, 2014) at 92.

with any number of matching loci can still be used as evidence against the defendant. Even small numbers of matching loci can result in extremely low RMPs – i.e. one in millions.

Effective communication of DNA evidence is more than just exchange of information – it is ensuring that the receivers fully understand the meaning of the information. There should be a focus on elements of the information that are both complex and key to the receiver's needs. Statistics in general, may be poorly understood and poorly explained to the court, in part due to the non-concordant understanding of DNA evidence previously described. Recent research by Cronin found that how a statistical phrase was presented to 124 potential jury members, significantly affected their ability to correctly understand what the statistic actually meant.[20] DNA evidence presented using RMPs was correctly interpreted nearly twice as often as the same DNA evidence presented as LRs (83% versus 42%). This could be expected given the numerous steps required by the jury to convert the LR back to information they needed to weight the DNA evidence. Of note is the low percentage of correct interpretations when DNA evidence was expressed as a LR. Given that incorrectly interpreting the evidence when using LRs occurred 58% of the time in Cronin's study, a prejudicial effect could be occurring with this kind of DNA evidence in courts. Further research like this is needed to indicate how well statistical evidence is understood when presented in different formats. If misunderstanding the statistics is prevalent among key players within a criminal justice trial, then potential options for presenting this evidence in a way that is more easily and fully understood must be considered.

For example, forensic biologists working in the Thai Tsunami Victim Identification Centre reported their DNA evidence as posterior probabilities.[21] This was reported as a percentage, to more easily relate the statistical evidence to police investigators evaluating the DNA statements in the Reconciliation Team and to non-scientific experts on the Identification Board. The statement would read "the posterior probability is 99.9% certain that the remains belong to (person X)". The statements were presented in this way with the goal of more clearly addressing the question being asked of the evidence, providing a quantitative weighting of the evidence that is familiar to lay persons, and providing a margin of error that is also familiar to lay persons. It is possible for DNA evidence in criminal cases to be converted into a posterior probability and this is one option the authors submit should be considered. More broadly, extensive research has been undertaken in regard to the problematic issue of jury understanding of DNA evidence. It is submitted that the legal and academic fraternity are now best placed to act as the drivers for a fundamental re-think as to how DNA statistics are presented in the courtroom. In doing so, engaging with forensic biologists and statistical experts to evaluate alternative reporting methods and phrases that address their questions and relay the weighting of the evidence will be essential.

[20] Alanah Cronin, *Determination of Suitable Wording for Interpretation of Statistical Methods for Reporting DNA Evidence to The Various Audiences in Court* (Honours Thesis, Griffith University, 2017).

[21] Posterior probabilities are a revised probability which takes into consideration existing information (prior probability), such as the number of people killed in a disaster. Posterior probability = prior probability x LR.

## III Activity Level Evidence

The concepts of primary, secondary and tertiary DNA transfer have been widely reported in scientific journals and revealed in cases of wrongful conviction.[22] The issue of how and when DNA was deposited on an item found at a crime scene is becoming increasingly prevalent in the courts. Was it innocent transfer, or an activity that relates to the criminal offence? The newer DNA tests are more sensitive, so even smaller amounts of 'trace' DNA can be profiled from an item, which previously would not have been detected.[23]

As a result, the scope of DNA evidence has dramatically expanded, with transfer or 'activity level' information developing into an issue as critical to the courts as the question of identity. Different scenarios of how the DNA could have been transferred to an item are being offered to the scientist to evaluate. The scientist uses a range of factors to provide a response (including duration and nature of contact, type of surface, time since deposition, fluid type, 'shedder status', and environmental conditions).[24] Each factor considered by the scientist includes assumptions, uncertainties, errors, and results in a qualitative, rather than statistical, approach to the interpretation of the evidence, which is also at risk of 'contextual bias' (a subconscious conclusion about evidence based on external influences).[25] This may occur, for example, when police provide the scientist with a version of events prior to their analysis and interpretation of the evidence. Unlike DNA identification evidence where a scenario can be definitively excluded (i.e. the DNA does not match the suspect), exclusion of DNA transfer scenarios may not be possible and rather, the scientist may only be able to provide a ranking of 'most likely' scenarios. Activity level evidence is therefore, more prone to be inaccurate than identity or 'source level' evidence. Validation of scientific techniques is a key component in regard to the integrity and admissibility of scientific evidence within the courtrooms.[26] It is submitted that the ranking of DNA transfer scenarios currently lacks robust scientific validation. If the central question of a case is 'how did the DNA get there', then courts need to be cautious.

In 2014, the High Court of Australia (which is the highest court in the country) quashed the murder conviction of Daniel Glenn Fitzgerald after they found DNA transfer evidence was not sufficient to establish his presence or participation in a murder.[27] A DNA mixture was obtained

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[22] Mariya Goray, et al, "Investigation of secondary DNA transfer of skin cells under controlled test conditions" (2010) 12:3 Legal Medicine 117; Mariya Goray, et al, "Secondary DNA transfer of biological substances under varying test conditions" (2010) 4:2 Forensic Sci Int'l: Genetics 62.

[23] Ane Fonnelop, et al, "Secondary and subsequent DNA transfer during criminal investigation" (2015) 17 Forensic Sci Int'l: Genetics 155.

[24] Goergina Meakin & Allan Jamieson, "DNA Transfer: Review and implications for casework", (2013) 7:4 Forensic Sci Int'l: Genetics 434.

[25] Nikkita Venville, *A Review of Contextual Bias in Forensic Science and its potential Legal Implications* (Melbourne, Australia and New Zealand Policing Advisory Agency, National Institute of Forensic Science, 2010). Also see Itiel E Dror and Greg Hampikian, "Subjectivity and Bias in Forensic DNA Mixture Interpretation" (2011) 51 Sci & Just 204. For more on contextual bias in terms of forensic science generally, including DNA evidence, see also Gary Edmond, et al, "Contextual bias and cross-contamination in the forensic sciences: The corrosive implications for investigations, plea bargains, trials and appeals" (2014) 13 Law Prob & Risk 1.

[26] See e.g., *Tuite v The Queen* [2015] VSCA 148; 49 VR 196 at paras 101-104 [*Tuite*]; PCAST, *supra* note 14.

[27] *Fitzgerald v The Queen* [2014] HCA 28 [*Fitzgerald*]

from a didgeridoo found near the deceased, and the major component of the mixture was consistent with Fitzgerald's DNA. During the trial it was not disputed that the DNA was Fitzgerald's, rather, the case hinged on how and when the DNA was deposited on the didgeridoo. As stated by the High Court, an essential link in the prosecution's circumstantial case was that it be shown beyond reasonable doubt, that Fitzgerald's DNA was transferred by him to the didgeridoo during the attack.[28]

Defence counsel proposed that Fitzgerald's DNA was transferred to the item by a co-accused, after the pair shook hands hours before the murder (secondary transfer). Prosecution argued that the DNA was deposited on the item directly by Fitzgerald during the attack (primary transfer). The scientist was unable to exclude either scenario, however, indicated that primary transfer was the most likely scenario. The High Court decided three key points in terms of the DNA evidence, being: (i) that whether the DNA sample came from blood or another source could not be established beyond reasonable doubt; (ii) that how the DNA was deposited could not be established beyond reasonable doubt; and (iii) that the time and circumstances as to when and how Fitzgerald's DNA came to be on the didgeridoo, could not be determined. Therefore, it could not be accepted that the evidence relied on by the prosecution was sufficient to establish beyond reasonable doubt that the appellant was present at and participated in the attack, and a reasonable hypotheses consistent with innocence could not be excluded by the jury.

However, when the matter was earlier before the Court of Criminal Appeal in South Australia, their Honours' (Gray and Sulan JJ; Blue J agreeing) had determined that in light of the scientific evidence presented, secondary transfer was 'extremely unlikely'.[29] The High Court noted that in reaching this conclusion, the Court of Appeal did not refer to some of the evidence that had been presented by the scientist in regard to secondary transfer and 'dating' of DNA.[30] While the authors agree with the High Court's decision, this case nevertheless highlights a question for criminal justice systems more broadly as to whether DNA transfer evidence is properly understood and evaluated, whether there is an appreciation of the limitations and potential error involved in this kind of evidence, and whether there is an awareness of the underlying assumptions used by scientists to rank the DNA transfer scenarios. To help address this issue, it is suggested that forensic biologists need to more clearly articulate the assumptions, limitations and sources of error associated with activity level DNA evidence - or alternatively, not provide an expert opinion of this form of evidence.

Van Oorschot, et al, highlight another important consideration for providing evidence on DNA transfer, persistence, prevalence and recovery.[31] They encourage forensic biology laboratories to provide dedicated training, competency assessment, authorizations, and ongoing proficiency testing for experts providing DNA transfer evidence. Mock cases analyzed by scientists demonstrated a lack of appropriate training and standards, causing differences in activity level reporting within and between laboratories, and limitations in the ability of scientists to identify key factors that could impact on their conclusions.

[28] *Ibid* at 28.

[29] *R v Sumner, R v Fitzgerald* [2013] 117 SASR 271 at para 106.

[30] *Fitzgerald, supra* note 27 at para 26.

[31] Roland van Oorschot, et al, "Need for dedicated training, competency assessment, authorisations and ongoing proficiency testing for those addressing DNA transfer issues" (2017) Supp Series, 6 Forensic Sci Int'l: Genetics e32.

> In numerous instances, key factors known to influence the likelihood of (DNA) transfer were not considered, or assumed irrelevant, when assessing the profiles resulting in either an incorrect answer or the correct answer but with incorrect strength of likelihood. Of the 18 responses per participant, the per cent of correct responses by any participant ranged from 11 to 67% (average 42%).[32]

This raises concerns in regard to the accuracy and integrity of this evidence in the courtroom. If on average, a scientist evaluating and reporting on activity level evidence is doing so incorrectly 58% of the time, it must be questioned whether this evidence is of sufficient reliability to be admitted into the courtroom. Training, competency testing, and method validation based on agreed international standards are mandatory requirements for all other tasks performed by forensic biologists, including screening and recovering biological evidence, generating DNA profiles, DNA interpretation, statistical analysis and court reporting (at the identity level). It is submitted that the introduction of activity level DNA evidence into the courts has occurred prior to experts being properly prepared for such questioning, and without formal authorizations or validation. The courts should consider the weighting of DNA transfer evidence with great caution, and beware of 'evidence creep'. Activity level DNA evidence is not at the same level of scientific maturity as identity level evidence.

## IV DNA Mixtures and New DNA Methodology

DNA mixtures have long been a source of complexity in the interpretation and understanding of DNA evidence. The increased sensitivity of the new DNA tests has considerably affected how often DNA mixtures are obtained from items.[33] Items that would have produced single contributor profiles using the 9 locus test, are now producing mixtures of increasing complexity due to detection of previously latent trace DNA. Disentangling the contributors of complex mixtures may not be possible with standard methods, prohibiting a definitive statement of exclusion to the courts.[34] These complexities were recognized in the 2016 report by the United States President's Council of Advisors on Science and Technology (PCAST), 'Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods'. The report highlighted that the traditional method of interpreting complex mixtures is subjective and may be prone to bias, and that inconsistency of approaches exists between scientists.[35]

The scientific community have responded to the challenges of interpreting complex mixtures, applying an alternative method of statistically evaluating such profiles, which is broadly termed as probabilistic genotyping. Software such as STRmix™ and TrueAllele® provide statistical probabilities for complex mixtures that previously would not have been possible.[36] The

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[32] *Ibid* at e33.

[33] Promega Corp, *Two years later: a reflection on the implementation of STRMIX in a high throughput DNA laboratory*, online: <https://www.promega.com/-/media/files/products-and-services/genetic-identity/ishi-26-oral-abstracts/6-kerr.pdf>.

[34] Na Hu, et al, "Current developments in forensic interpretation of mixed DNA samples (Review)" (2014) 2:3 Biomed Rep 309.

[35] PCAST, *supra* note 14.

[36] Bright, *supra* note 13; Kathryn Kadash, et al, "Validation study of the True Allele® automated data review system" (2004) 49:4 J Forensic Sci 1.

introduction of evidence generated by STRmix™ into Australian courts is the most significant change to DNA evidence since the introduction of short tandem repeat (STR) profiling in the late 1990's. The software approaches the interpretation of the profile and calculation of probabilities in a very different manner to the established methods.

Traditionally, an allele would be included in comparisons against DNA profiles obtained from suspects if it met a certain analysis threshold (peak height). If the allele fell below the threshold, it was excluded as being a source of information. In scientific terms, this is known as 'the binary method'; the allele was either included in the calculations or not. Once the allele was included, statistical calculations would be carried out to assign a weighting to its presence in the DNA. No use was made of alleles which did not meet the required peak height. An alternative approach uses a 'continuous method' of interpreting the DNA profile, in which the actual peak height is included regardless of any threshold, and alleles with low peaks are considered as representing potential degradation or other profiling effects that can arise from trace DNA. Such effects are known as 'stochastic effects' and the probabilities of their occurrence are modelled using theoretical formulae and estimates based on experimental data and experience. To further complicate the matter, DNA techniques have improved to the point that the typical DNA profile is now a mixture of a number of contributors, requiring a far more complex interpretation than when a profile was simply from a single individual. To derive probabilities about who could be the donor of a mixture from such highly variable 'one off' information requires a method to evaluate the combined characteristics of the questioned DNA mixture.

The statistical methods used in the 'binary era' were part of the 'frequentist' paradigm where the belief is that there really is a true value of the allele's probability in the population of interest, and a sample of data (the database) will be used to estimate this true value. Consideration of the accuracy of the estimate given the size of the database used, was provided through a confidence interval (typically 95%) which gave a range which could be expected to cover the true value 95% of the time. Few assumptions were required for the implementation of the binary, frequentist method and no prior estimates were applied. With the advent of more refined DNA processes and the acknowledgement of stochastic effects and mixed profiles, a more complex statistical modelling approach is required. Probabilistic models are needed to predict the possibility of the different stochastic effects. These probabilistic models are regarded as prior information, and to fully define them for use in the forensic setting, research is needed to determine appropriate values to include in them, along with assumptions of the mathematical form they will take. The presence of a DNA mixture introduces the possibility of a large number of possible scenarios that could have produced the mixture, each of which needs to be considered and weighted against the others to identify the 'true' scenario.

The various probabilistic events are incorporated into the calculations by using decision trees or networks, which are constructed to represent all aspects of the process; the information used in these is regarded as *a priori* in that it is based on previous experimentation and/or assumed knowledge. At each point in the process, the *a priori* information required will be estimated from prior research or from expert knowledge, and will be either a single value (the frequentist approach) or some form of probabilistic distribution in which the value is used as part of an assumed mathematical formula (the Bayesian approach). Once estimates are available for each stage of the process, simulation will take place to select a random sample of values of what the

data is expected to look like coming from the decision process (or network). These samples will be summarised and used to form a final reported result. Various processes exist for selecting such random samples and the one in common use in the forensic community is known as the Markov Chain Monte Carlo (MCMC) Method.

Using this approach enables the range of possible probabilities from the questioned DNA mixture to be provided, along with a measure of how likely each of those probabilities is to be the truth. This methodology has been used for many decades in disciplines such as agriculture, engineering and medicine and while the forensic scientific community has largely welcomed this new approach, it is unclear whether the legal fraternity are fully aware that this is a significant change in the method for calculating probabilities in DNA casework. It should be noted that at each stage of the decision process (or network), assumptions are made which require knowledge from prior experience; if these assumptions are incorrect or the values used in them are poor 'guesstimates' the resulting conclusions may be in error.

At an interlocutory appeal in the 2015 Australian case, *Tuite v The Queen*,[37] the Victorian Court of Appeal (Maxwell ACJ, Redlich and Weinberg JJA) confirmed the decision of the pre-trial judge, allowing the admissibility of evidence generated by STRmix™.[38] The pre-trial hearing, which lasted twenty two days, involved consideration of STRmix™ calculations that included likelihood ratios in the billions and sextillions. For example, in regard to item 1 – 3 (trace from the ends of shoelace combined):

> The analysis showed a mixed DNA profile from three contributors. The complainant is an assumed contributor. Using STRmix™, it is estimated to be 2.7 sextillion times more likely that the DNA profile obtained from Item 1-3 would occur if the DNA originated from the accused, the complainant and one unknown person than if it originated from the complainant and two unknown people chosen at random from the Australian Caucasian population. This is reported using the default likelihood ratio for PP21 analyses of 100 billion.[39]

This case raised questions, among other things, about the reliability of the relatively new statistical methodology, now used by laboratories across Australia and adopted by a number of laboratories elsewhere in the world. It was argued that the methodology was largely untested and had not been generally accepted by the forensic science community, nor properly validated by the laboratory using the software. It was also disputed that the scientist did not have enough specialized knowledge about the statistical methodology used in STRmix™ to allow her to give the DNA evidence. In the pre-trial, Emerton J rejected the application to have the evidence excluded under either ss 79 or 137 of the *Evidence Act 2008,* Victoria. Relevant to the considerations at the preliminary hearing, was that although the scientist who presented the evidence (and another who testified on the validation of the software) were not mathematical experts, they were considered to

[37] *Tuite, supra* note 26.

[38] *Ibid*. Their Honours noted that the standard of review to be applied at the interlocutory appeal (as opposed to a conviction appeal) was whether the decision of the pre-trial judge was "reasonably open", not whether it was correct: [8]. See also earlier decision at pre-trial: *Tuite v The Queen* [2014] VSC 662 (Emerton J). For later considerations in this matter, see also: *DPP v Tuite* (Ruling No 3) [2017] VSC 442 (11 August 2017) (Hollingworth J).

[39] *Tuite, supra* note 26 at para 19.

have sufficient expertise to understand and operate the system. The judge conceded that STRmix™ involved the application of 'black box' technology (in part because its software is not open source), however, evidence about the mathematical and statistical models underpinning the STRmix™ could be provided in this case, by one of the developers.[40]

In 2015 it was reported that the laboratory in Queensland, Australia, had been using STRmix™ for six months with a 'miscode', which led to errors in calculated probabilities in 60 cases.[41] The developers of the software highlighted that the laboratory had been given the software for free, but had not purchased an updated software manual, and speculated user error. This raises concerns over reporting evidence using a 'black box' method. Without a thorough knowledge of how the software works, the assumptions it relies upon, or appropriate training or expertise in the system, scientists will struggle to detect when errors are made. Lawyers, more so.

David Bentley QC in the Law Society Gazette (UK) commented on the new software models:

> To understand (and therefore critique) these models, you need the skills of an advanced statistician, a computer scientist and a molecular biologist. Little wonder therefore that there have been few challenges to such evidence when it has come before our courts.[42]

Moreover, the use of secret source-codes appears at odds with a legal system that includes the rights of an accused person to cross-examine evidence to expose potential problems. If it cannot be revealed as to how statistical conclusions are reached, then the use of proprietary 'black box' evidence in court remains a live issue.

The data models used in probabilistic genotyping rely on a number of assumptions. Some of these assumptions vary across the different software packages available. The main assumptions include (i) mixture ratio (how differences in DNA input by each donor will be reflected in peak heights across each locus in the mixture), (ii) noise peak height distribution (how non-DNA peaks and real DNA peaks will be distributed), (iii) forward stutter (if it is included or excluded from the model), (iv) the number of contributors in the DNA mixture. The assumption of number of contributors is made by the forensic biologist using the software. Not knowing the true number of contributors to the questioned DNA mixture, they must provide a best guess based on the number of peaks at each locus. Assuming the incorrect number of contributors may affect the accuracy of the model and the resulting probability. Swanminathan *et al.* found in all four probabilistic models tested, intra-model variability increased when the number of assumed contributors also increased.[43] PCAST considered probabilistic genotyping to have "foundational validity…under

[40] *Ibid* at paras 33-40.

[41] Courier Mail, *Queensland Authorities Confirm "Miscode" Affects DNA Evidence In Criminal Cases* (20 March 2015), online: <http://www.couriermail.com.au/news/queensland/queensland-authorities-confirm-miscode-affects-dna-evidence-in-criminal-cases/news-story/833c580d3f1c59039efd1a2ef55af92b>.

[42] David Bentley QC, "DNA and case preparation" *The Law Society Gazette* (12 January 2015), online: <https://www.lawgazette.co.uk/practice-points/dna-and-case-preparation/5045883.article>.

[43] Harish Swaminathan et al, "Four model variants within a continuous forensic DNA mixture interpretation framework: Effects on evidential inference and reporting" (2018) PLOS One 13 (11), Online:

limited circumstances (specifically, a three-person mixture in which the minor contributor constitutes at least 20 percent of the DNA in the mixture), but that substantially more evidence is needed to establish foundational validity across broader settings". Laboratories, however, are using probabilistic genotyping for three or more donors' mixtures with low level DNA contribution from some donors.

## V Conclusion

DNA has exonerated hundreds of individuals in the United States. It has highlighted to us more broadly, weaknesses within a range of different types of evidence accepted within our courtrooms. It is the gold standard of scientific evidence. DNA evidence has played and continues to play a crucial and welcome role within criminal justice systems across the world. There are however, areas where its use in the courtroom in regard to both identification and activity evidence as outlined in this article, would benefit from greater attention so as to ensure its accuracy and integrity. These include: (i) the potential over-representation of the value of the DNA statistics as used against the defendant where the (arguably outdated and potentially misrepresentative) qualitative table has been used; (ii) the use of low-level 'partial' match profiles that may offer high-level statistical calculations against an accused even though it may be an adventitious 'match'; (iii) activity level assumptions and misinterpretations that may lead to inaccurate evidence being presented; (iv) the use of insufficiently validated 'ranking' scenarios; and (v) the invisibility of scientific assumptions within the new black box statistical software currently used across Australia and internationally that includes in its calculations, alleles that are not present or would previously have been below the reportable threshold – and where miscoding by scientists has already been alleged to have occurred.

Methodology and scientific calculations upon which DNA evidence is presented is continuously evolving and progressing. If DNA 'identification' or 'activity' evidence is inaccurate, misinterpreted or misunderstood, then we are faced with the possibility of prejudice against the accused or an outright wrongful conviction. The challenge for the criminal justice system is how to maintain the use of highly probative DNA evidence, while also addressing the complexities associated with the use of this evidence in the courtroom.

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