Assessing the use of DNA expert evidence, by justice system participants, in Ontario criminal courts.

by

Dawn Cohen

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Abstract and Keywords

What happens to forensic DNA opinion evidence when the expert witness is not present in the courtroom? Research addressing this issue has largely been focused on polling lawyers regarding their perceptions of DNA evidence, as well as studies of juror understanding of DNA expert evidence in real and mock court situations. This thesis attempted to address the question in a different way, by analyzing transcripts of expert DNA evidence, opening & closing addresses, and judges' instructions to juries, for cases that have passed through the Ontario criminal courts within the past fifteen years. This project is the first assessment of Canadian criminal court case transcripts, comparing expert DNA evidence with the (largely) non-scientist attorneys' and judges' inferred understanding and use of that evidence. Trial transcripts from cases involving DNA expert evidence were located by keyword searching Ontario Court of Appeal decisions via the Canadian Legal Information Institute (CanLii) public online database.

This research question was approached from a social science methodology, making use of both qualitative and quantitative analyses. Quantitative analysis was conceptualized first, as a survey that was developed to track topics of interest in Interval Ratio and Nominal variable form. Qualitative Data Analysis (QDA) Miner 4 Lite™ was used to code sections of these transcripts and complete the survey. Coded sections involved random match probabilities (RMPs), likelihood ratios (LR), mitochondrial & Y-STR lineage confidence intervals, as well as body fluid attribution statements by attorneys and judges. These transcript excerpts were compared to each case's respective DNA expert testimony. This enabled the application of qualitative analysis of question

and response exposition within the expert testimonies. The survey data were inputted into IBM Statistical Package for the Social Sciences (SPSS) Statistics 24 for pattern analysis and descriptive statistics.

For example, the sets of cases studied (N=32), contained 101 autosomal random match probability statements provided by DNA experts. Many times these RMPs did not enter into the crown summations (only 48.5%), defence summations (only 31.7%) or judges' instructions (only 57.4%). When attorneys and judges did discuss and review the DNA statistical evidence, mistakes and misstatements occurred in the majority of instances – these mistakes included statistical fallacies and numerical misstatements.

This research suggests a lacunae of knowledge with respect to the meaning of DNA evidence, and in particular, the correct understanding and communication of the RMP estimate of statistical weight of DNA profile comparison evidence. Further research is recommended, to address the use of transfer and persistence expert testimony, as well as testimony regarding complex mixture profile interpretations and comparisons.

Keywords: DNA, random match probability, likelihood ratio, statistical fallacy, expert testimony, transcripts, justice system

Dedication

For all the love with nowhere to go.

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List of Abbreviations

ASCLD-LAB	American Society of Crime Laboratory Directors – Laboratory Accreditation Board
CanLii	Canadian Legal Information Institute
DNA	Deoxyribonucleic Acid
LR	Likelihood Ratio
mtDNA	Mitochondrial Deoxyribonucleic Acid
OCR	Optical Character Recognition
QDA	Qualitative Data Analysis
RMP	Random Match Probability
SNP	Single Nucleotide Polymorphism
STR	Short Tandem Repeat
T&P	Transfer & Persistence
Y-STR	Y Chromosome Short Tandem Repeat

Introduction

1. Introduction

Expert scientific evidence plays a crucial role in the investigation, prosecution and defense of many criminal cases throughout Canada, as well as most other countries. However, relatively little is known about how well trial fact-finders, in particular juries and judges, and other justice system participants, primarily prosecutors and defense attorneys, actually understand and interpret what expert scientific witnesses communicate in a courtroom setting. The goal of this research project was to qualitatively and quantitatively assess the use of forensic biology evidence by lawyers and judges by addressing the following question: Do justice system participants accurately describe and apply what expert forensic biologists say in criminal court *viva voce* (oral) testimony?

Forensic biology and DNA evidence can present myriad challenges for non-scientists, including understanding and communicating the highly technical nature of the DNA profiling process as well as the complicated issues involving the transfer and persistence of DNA in various hypothetical scenarios. In addition, DNA mixture profile analysis, where there are two or more contributors to a DNA profile, can also present justice system participants with challenges in understanding and conveying highly technical issues of interpretation and validation (Gill, 2014). Another challenging area for non-scientists, and of primary interest to this thesis project, is the presentation of the statistical weight of DNA profile match evidence, including the mathematics and genetic principles behind these estimates.

Research in the general area addressed in this thesis project is usually accomplished in controlled experiments and polling, and tends to concentrate on juror,

rather than attorney or judicial, experiences. This research project has concentrated on specific topics within just one area of expert evidence: forensic biology and DNA analysis. It is the first time an assessment of actual criminal court case transcripts has been performed with the purpose of comparing expert DNA and body fluid identification testimonial evidence with the (largely) non-scientist attorneys' and judges' inferred understanding and use of such evidence.

2. Forensic biology evidence – Body fluid identification and DNA analysis

Introduction

The utility and relevance of body fluid and DNA evidence in criminal investigative casework is primarily due to the mobility, or transferability, of biological cells. This transferability is what allows for inferences of some evidential association between the source of the found biological material and the events surrounding the alleged crime under investigation. This is made possible by a finding of blood, semen, saliva, hairs, or any biological fluid or tissue at a crime scene or on or within the body of a party associated with the crime under investigation. Forensic biology evidence is therefore most useful in those crime types where body fluids and tissues are expelled, sloughed off, or otherwise transferred from one person or object to another. This is especially true for, for example, sexual assault, homicide, robbery, assault, and break & enter cases (National DNA Databank of Canada, 2006). During sexual assault and homicide crimes, to further explain, there is more person to person bodily contact. This type of physical contact is responsible for the increase in DNA and cell transfer from person to person.

Body Fluid Identification

Forensic DNA analysis is typically preceded by an examination of evidence items for the presence of body fluids and tissues that contain deoxyribonucleic acid (DNA). These tests are classified as either presumptive or confirmatory. The former tests are designed to be more sensitive than specific, while the latter tests are designed to be highly specific for the target body fluid component (Houck & Siegel, 2010; Johnston & Hageman, 1999). The following descriptions of forensic body fluid tests are taken primarily from the technical information sheet currently provided online to its clients and the public by the Centre of Forensic Sciences, Ministry of Community Safety and Correctional Services, Ontario (2015).

The presence of blood on an item (or at a crime scene) is determined through the use of one of a number of simple presumptive chemical colour tests targeting the hemoglobin component of blood. The Kastle-Meyer test used at the Centre of Forensic Sciences is not absolutely specific for blood, as it can sometimes indicate the presence of oxidants such as bleaches or fresh legumes (Peterson & Kovacs, 2013). However, the few potential false positives are not forensically relevant, and a positive result is considered "operationally specific" for the presence of blood.

The presence of semen is presumptively determined via the presence of acid phosphatase, a component of the liquid portion of the semen. Semen is conclusively determined microscopically by sperm cells (the male reproductive cells) or by the presence of a molecule, p30 (prostate specific antigen) produced by the males-specific prostate gland.

The Phadebas™ test for saliva targets amylase, a digestive enzyme produced in largest quantities in the mouth, but also in smaller amounts in other body fluids. This test is considered a presumptive test. While a presumptive test for saliva indicates the presence of amylase, this enzyme is not the source of DNA. The DNA containing cells (buccal, or cheek cells) are shed from the mouth tissues and mixed in with the saliva (and amylase enzyme). There is currently no confirmatory chemical test specifically for saliva, and there are currently no chemical tests, presumptive or confirmatory, for the presence of skin tissue.

DNA Analysis

Forensic body fluid identification tests answer the question of "which body fluid is it?", but addressing the question of "whose body fluid is it?" comprises a much greater part of the forensic biologist's work. Prior to the mid 1980's this question was answered with the application of techniques such as ABO blood group typing. However, ABO typing and related techniques were limited in their forensic usefulness, as they required a large amount of non-degraded body fluid evidence, and could not distinguish the identities of separate contributors of body fluid mixtures (Houck & Siegel, 2010). These limitations have largely been overcome by forensic DNA technology, in use in Canada since the late 1980s. The following is a short introduction to DNA and forensic DNA typing; it is not intended to be all encompassing, but only to provide the reader with the basics of the science.

What is DNA?

Humans, and indeed all living things, are composed of cells. Cells contain an internal structure called a nucleus which houses DNA within structures called chromosomes. Chromosomes are long molecular chains containing the genetic code to build and maintain a human being. This code is comprised of extremely long linear chains of combinations of just four genetic bases, the letters of the genetic alphabet – A (adenine), T (thymine), G (guanine) & C (cytosine). All cells in the body contain the same set of chromosomes, because all cells are copies of the original single fertilized egg, containing 23 chromosomes from the mother and 23 from the father. Twenty-two chromosome pairs are called autosomes, and the 23rd pair are the X & Y sex chromosomes. The forensic DNA profile from any one cell type will be the same as for any other cell type from a single individual. In other words, the same DNA profile will be found in a person's skin, blood, saliva, hair, and all other tissue samples.

Regarding the genetic code contained within a human being's 23 pairs of chromosomes, most of the DNA information is the same for all humans. Only a small portion of the human genetic code actually contains enough genetic variation to distinguish human beings from one another. These differences, called "alleles", can take the form of:

- Point differences – "Single nucleotide polymorphisms" (SNPs), are letter differences in the genetic code (Butler, 2015). For example, one person may have the genetic letter "A" at a defined position on a chromosome, where another would have a "T". These differences form the basis of many new forensic and medical tests, including genetic tests for ancestry and propensity for disease, such

as National Geographic's Genographic Project™ and various kits marketed to the public, such as 23andMe™.

- Length differences – The human genome is filled with areas where the same stretch of genetic code is repeated over and over again, in a tandem way. Humans display significant variation in the number of times particular stretches of code are repeated. For example, imagine the four-letter genetic sequence "AATG", repeated, end to end, a number of times. The more times it is repeated, the longer that particular stretch of DNA is. If a person inherits an allele size "5" (AATGAATGAATGAATGAATG) at a given genetic location ("locus") from one parent, and an allele size "6" (AATGAATGAATGAATGAATGAATG) at the same genetic location from the other parent, that person's type would simply be "5, 6". Most current forensic DNA tests target these types of genetic locations (Butler, 2015).

Mitochondria are cellular structures that exist outside of the nucleus, and therefore outside of the 23 pairs of nuclear chromosomes. These tiny structures, responsible for energy functions in the cell, contain their own small, circular mitochondrial chromosome ("mtDNA"). There can be small point differences (as explained above, letter differences), in some portions of this mitochondrial chromosome, and some forensic tests target these differences.

What is a forensic DNA profile?

Currently, forensic biologists target short tandem repeats (STRs), short stretches (usually 4 to 6 bases) of DNA that repeat themselves over and over, in tandem. These

STRs are scattered throughout the human genome. A person's forensic DNA profile is simply a picture of STR lengths (alleles) from various chromosome locations. Humans vary extensively in the number of times such short stretches of DNA are repeated, and this allows for extremely effective differentiation of biological samples.

Following the finding of biological evidence, a series of laboratory steps are performed to extract DNA from the sample and create a forensic DNA profile. DNA is first removed from the cell's nucleus and purified during the extraction step. Next, the amount of DNA in the sample is quantified. This step is crucial in ensuring there is enough and optimal DNA present in the sample to continue to the remaining steps. In the amplification step, the scientist zeroes in on STR locations of interest and makes copies of these DNA stretches. Finally, in the last step, the scientist separates the STRs on the basis of length (Butler, 2015). The final product is called an "electropherogram" – the example below is a typical result for a forensic analysis of a biological sample in a modern forensic biology laboratory (Figure 1).

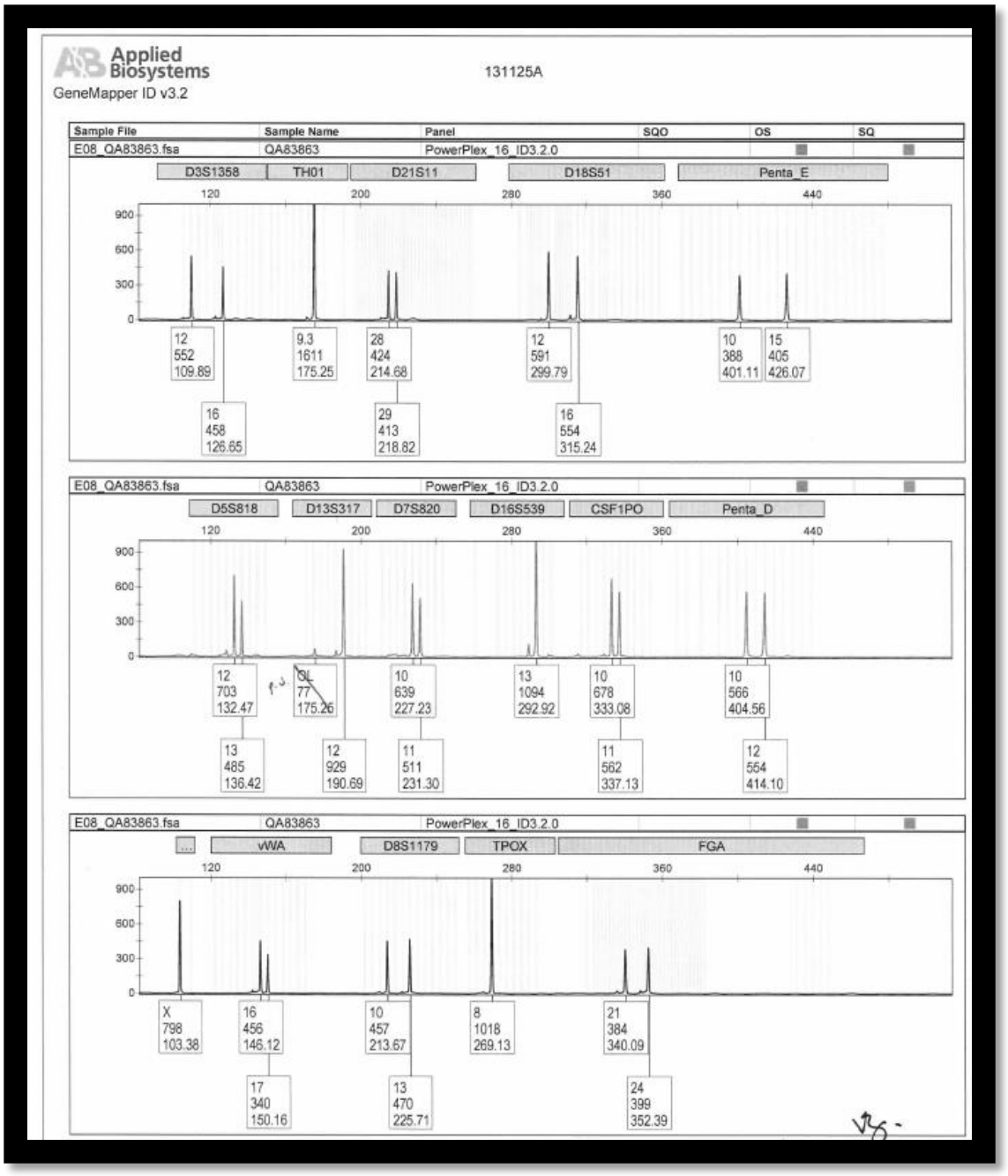


Figure 1 Electropherogram: PowerPlex® 16 Short Tandem Repeat Female 15 locus DNA profile; Courtesy of Wyndham Forensic Group (Wfg), Guelph, ON.

This is an STR profile, showing genetic differences at sixteen chromosomal locations ("loci"). It was developed using the PowerPlex® 16 kit (Promega, 2016); this kit is just one of a number of different STR kits, comprised of a series of replication

reagents, in use in forensic facilities. Others in general use in North America include Profiler Plus™ and Identifiler® Plus (Life Technologies, 2015).

Each peak in the electropherogram in Figure 1 represents a piece of DNA ("allele") of a particular STR length. The D3S1358 locus (Figure 2), a position on the 3rd pair of chromosomes, contains two pieces of genetic information:

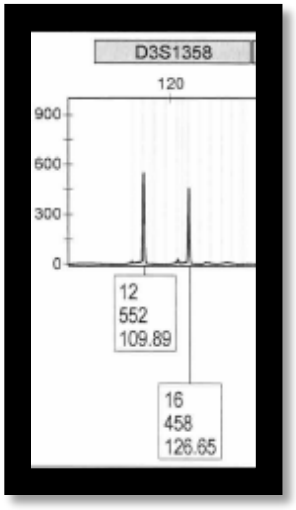


Figure 2 Magnification of Figure 1 Electropherogram, D3S1358 Chromosomal Location

- a peak labelled 12, representing 12 repeating STR units in tandem
- another peak of roughly the same height labelled 16 (16 repeating STR units in tandem).

This person's profile is, therefore, and simply, a "12, 16"; there are two STR results, reflecting each contribution of one allele per parent. Looking further down the electropherogram, this person is type "9.3, 9.3" at the THO1 location (Figure 3), because they inherited the same size allele from both parents.

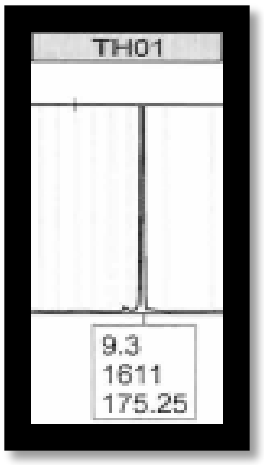


Figure 3 Magnification of Figure 1 Electropherogram, THO1 Chromosomal Location

This profile can be said to come from a female, due to the results at the bottom left of Figure 1. There is only one peak at the sex chromosome location ("amelogenin" (AM) peak), because the source is female (XX) (Figure 4). Male samples would show two different peaks (X and Y).

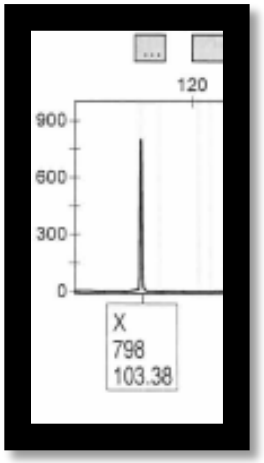


Figure 4 Magnification of Figure 1 Electropherogram, Amelogenin/Sex Chromosomes

Most forensic profiles contain genetic information from 9 to 15 STR locations, in addition to the amelogenin locus for determining sex. New kits are able to go even further, examining over 20 locations at once, such as GlobalFiler® Express (Life Technologies, 2016).

Once the full electropherogram is interpreted, a person's forensic DNA profile reduces to a simple set of (usually 15 or more) number pairs, each pair reflecting the STRs at each tested location ("locus"). The profile in Figure 1 is interpreted into its constituent alleles in Table 1.

Table 1 Resultant Genetic Profile from Figure 1 Electropherogram

Locus	TYPE	
D3S1358	12	16
THO1	9.3	9.3
D21S11	28	29
D18S51	12	16
PENTA E	10	15
D5S818	12	13
D13S317	12	12
D7S820	10	11
D16S539	13	13
CFS1PO	10	11
PENTA D	10	12
vWA	16	17
D8S1179	10	13
TPOX	8	8
FGA	21	24
AMELOGENIN	X	X

The electropherogram in Figure 1 details the result of an "autosomal" profile. This means that the STR locations studied are identical for both male and female samples, and are those found on the 22 pairs of chromosomes. This does not include the sex chromosomes as the amelogenin result only signifies source sex, and no further STR results.

There is another method of DNA analysis that only looks at the Y chromosome, containing male specific STR loci. Unlike the autosomal STR loci, each locus of a single source Y-STR profile only contains one peak, because a male can only have one father. The whole Y chromosome is inherited from the father, and there is no contribution from the mother.

Y-STR profiling would be attempted in cases of, for example, ancestry or mixture sources. Y-STR profiling is most commonly used in paternity and familial testing, to determine whether the full Y chromosome profile is identical in two paternally related males. The second purpose of Y-STR testing is to determine the number of potential contributors to a mixture profile. As there can only be one peak per male at most Y-STR loci, multiple peaks denote the number of males present within the biological sample.

There are documented instances of repeated information in a male profile that provides two peaks at a locus. This is due to a duplication of the locus, containing its own separate allele length. For a profile to contain more than one male's genetic information (under the assumption of a fully intact profile), multiple peaks would be observed at all studied loci. Figure 5 is an example of a single source Y-STR profile, and demonstrates the repetition of genetic information at a single locus (DYS385ab).

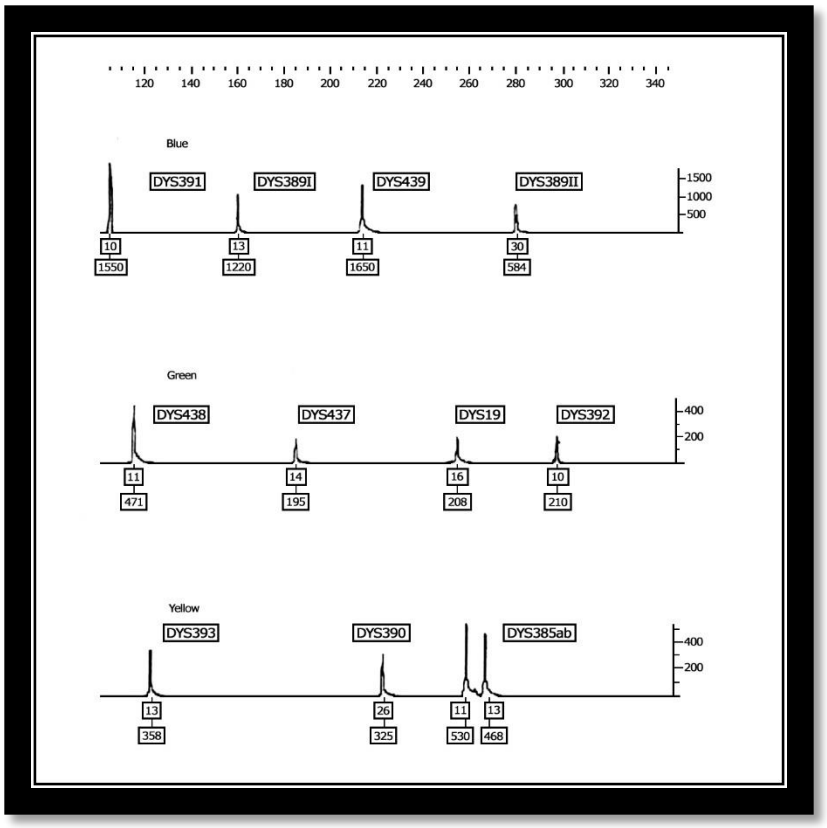


Figure 5 Electropherogram: Y-STR DNA profile (Hageman, Prevett & Murray, 2008)

Forensic DNA analysis is, at its heart, a comparison technique. Comparisons are performed between these number pair sets, from different evidence samples, to determine whether they are either the same ("match") or different ("exclusion") (Table 2).

Table 2 Comparison of evidence DNA sample to two potential source profiles

Locus	Evidence Sample	Profile A "Match"	Profile B "Exclusion"
D3S1358	12, 16	12, 16	11,16
THO1	9.3, 9.3	9.3, 9.3	9.3,10
D21S11	28, 29	28, 29	28,29
D18S51	12, 16	12, 16	13,13
PENTA E	10, 15	10, 15	11,15
D5S818	12, 13	12, 13	12,12
D13S317	12, 12	12, 12	12,15
D7S820	10, 11	10, 11	8,9
D16S539	13, 13	13, 13	13,14
CFS1PO	10, 11	10, 11	12,12
PENTA D	10, 12	10, 12	11,12
vWA	16, 17	16, 17	16,16
D8S1179	10, 13	10, 13	11,12
TPOX	8, 8	8, 8	8,9
FGA	21, 21	21, 21	21,22
AMELOGENIN	X, X	X, X	X,X

An exclusion requires no calculation of statistical weight – the Profile B person is unequivocally not the source of the evidence profile. However, while the Profile A person cannot be excluded as the evidence source, she cannot absolutely be attributed as source, because STR profiles are not necessarily unique. This finding, therefore, requires an evaluation of the rarity of the matching profile in the population and the calculation of a relevant weight of match statistic.

3. Evaluating the strength of a match between two DNA profiles

The Random Match Probability

In a typical forensic criminal case situation, a reference ("known") DNA profile is compared to a profile from an evidence sample. When there are no qualitative differences between two STR profiles (meaning that they only have alleles in common, and none that distinguish one from the other), the profiles "match" (as seen in Table 2, for the evidence profile and reference A). There are two explanations for a DNA profile match result: either the reference sample donor is the source of the evidence sample, or s/he is not; for the latter case, the DNA profile match must be a coincidence.

The random match probability (RMP) deals with the second explanation - it is the estimate of the *coincidental* match probability, and this measurement of coincidence reduces to a very basic question:

What is the probability of going into the population-at-large and picking one person, at random, who has that target DNA profile?

It might seem logical to attack this problem in a straight-forward manner by simply going into a population, sampling many people, and counting how many times the target STR profile is seen. This approach is not scientifically valid, and is certainly not feasible, because STR profiles are extremely rare. If a hundred, or a thousand, or even hundreds of thousands of persons were tested, the STR profile in question in a case would not likely be observed, and an accurate frequency of occurrence could not be estimated in that fashion (National Research Council, 1996).

In 1996, after nearly a decade of public fights ("the DNA Wars") over the proper way to assess the probability of a coincidental match of forensic DNA profiles, the forensic community came to a consensus with the publication of the seminal document *The Evaluation of Forensic DNA Evidence*, known colloquially in the community as "NRC II". As detailed extensively in NRC II (1996), it is necessary to refer to population genetics and statistics to compute profile rarity estimates. Instead of assessing the rarity of full profiles, forensic biologists employ principles of heredity, human mating patterns, and the rarity of each of the *individual components* (i.e. alleles) of the STR profile. This allows for an estimation of the probability that a particular set of STR alleles, and then at all genetic locations tested, would come together *all at once*. This estimate is based on an understanding of genetics (the study of heredity) and in particular, population genetics and human mating habits. As far as humans choose their mates *randomly*, children will have, at each of the tested STR locations, *pairs of alleles* that come together *randomly*. For example, probability results at just the first two loci from the previously described profile match (Figure 1) is demonstrated in Table 3.

Table 3 Sample calculation of Random Match Probability for two loci from the electropherogram in Figure 1

Locus	Evidence Sample	Profile A "Match"	Allele frequencies	Probability of allele pairing:
D3S1358	12, 16	12, 16	Allele 12: 2% Allele 16: 10%	2 x 2% x 10% = 0.004
THO1	9.3, 9.3	9.3, 9.3	Allele 9.3: 20%	20% x 20% = 0.04

Databases allow the analyst to determine the frequency of occurrence of each STR allele in the geographic region of interest. These databases exist for regions throughout the world – for Canada, the Royal Canadian Mounted Police and the Centre

of Forensic Sciences have each compiled a number of different racial databases, accessible to the public via portals such as the Canadian Society of Forensic Science (2017). Small adjustments to the RMP calculations are made to account for slight deviations from random mating, and databases from different races are used to account for small genetic differences between races (National Research Council, 1996).

The chance of finding the *whole* genetic profile at all of the STR locations tested is simply an exercise of multiplying together the chances at each and every genetic address. For the example above, the probability of the results at just the two loci (Table 3) would be 0.004 times 0.04, or 0.0016 (or 1 in 6250). The final RMP, especially for profiles determined at nine or fifteen STR locations, is typically extremely small. With current STR kits, scientists typically work with random match probabilities in the order of one in trillions, or even rarer.

A random match probability statement in a report (and in an expert's court testimony) would take the following general form:

> Ms. X cannot be excluded, at 15 STR loci, as the source of the DNA profile on the evidence sample. The probability that a randomly selected individual, unrelated to Ms. X, would coincidentally share the observed 15 locus DNA profile is estimated to be 1 in x-million (or billion/trillion/quadrillion, etc.).

The RMP calculation and statement for Y profile matches is different, due to the nature of Y chromosome inheritance – this chromosome is inherited as a single, complete package from father to son. There are no pairs of alleles coming together randomly.

There is no contribution from the mother. Similarly, a (male or female) person's mitochondrial DNA ("mtDNA") profile is inherited as a single, complete package from his or her mother. Again, there are no pairs of alleles coming together. As the inheritance of a complete package of DNA is a similar process for both Y profiles and mtDNA profiles (sometimes called "lineage markers"), the mathematical interpretation of profile probabilities is the same, but different than that for the autosomal profile. The statistical question is the same - it still asks "what is the probability of finding the matching Y profile or mtDNA profile in the population?"

The answer comes from a simple "counting method" – determining how often that entire Y-STR or mtDNA profile is found in a particular database. For Y profiles, the United States Y-STR database (US Y-STR, 2017) (containing over 35 000 male profiles) may be queried, while for mtDNA profile matches, the Federal Bureau of Investigation provides an allelic database (Monson, Miller, Wilson, DiZinno & Budowle, 2002).

A random match probability for a lineage-type profile would take the following general form:

> Mr. X, and all of his paternal male relatives, cannot be excluded, at 12 Y-STR loci, as the source of the male DNA profile on the evidence sample. The probability that a randomly selected individual, unrelated to Mr. X, would coincidentally share the observed 12 locus DNA profile is estimated to be, at most, 1 in x-thousand.

The forensic random match probability is a "conditional" probability – it contains an "if" statement (National Research Council, 1996). Where there is a profile match in a case, the RMP is the probability of finding that DNA profile match, *given that*, or *if*, the known reference is not the actual source. The RMP is *not* the probability that the known reference is not the source, given the profile match result. This may seem at first a minor difference in wording, but it is a mathematical mistake to confuse the RMP by flipping, or transposing, this condition (the "given", or the "if" part, of the probability statement) (Evett, 1995). The condition of "given the reference is *not* the source" should not be flipped in such a way that it now becomes a probability of the reference actually being, or not being, the source. This, improperly, turns the RMP into a probability of guilt or innocence, and this incorrect approach is a statistical fallacy.

Given the minor differences in wording and the adversarial nature of criminal court cases, it is not unusual for a forensic biologist to be asked a question that incorporates some sort of statistical fallacy (Hicks, Buckleton, Bright & Taylor, 2016). The forensic biologist expert has the responsibility, when on the stand or counselling clients, to be on the lookout for these problems, and to craft responses that either correct the questioner or restate the question in some statistically proper fashion. However, and of particular interest to the present thesis, once a forensic biologist is off the witness stand, he or she cannot make such corrections.

Table 4 Preview Example of DNA evidence presented with Random Match Probability, and Transposed Conditional

Participant	Example	Result
Expert	I determined the random match probability, and the probability that a randomly selected individual, unrelated to [victim], could coincidentally share the observed DNA profile was estimated to be 1 in 3.3 trillion.	Correct
Lawyer	The DNA was a male/female mixture with the probability of another female being the donor, other than [victim], being one in 3.3 trillion…	Fallacy

The Likelihood Ratio

Until now, the statistical weight of forensic DNA match evidence in Ontario (at the Centre of Forensic Sciences) and throughout Canada (at the Royal Canadian Mounted Police Forensic Laboratory System) has taken the form of random match probabilities. However, changes are occurring. In particular, at the Biology Section of Ontario's Centre of Forensic Sciences, likelihood rates are gradually supplanting the RMP approach (Centre of Forensic Sciences, 2017).

A likelihood ratio (LR) evaluates evidence under two alternative propositions. In a typical DNA profile match case work situation, the LR is the probability of the observed DNA test results given one proposition ("P") divided by the probability of the same DNA test results given another proposition ("D") – in forensic work, these propositions are typically aligned with the prosecution (P) and the defence (D). The propositions are typically formulated as follows:

Prosecution (P) hypothesis (the numerator): Pr(E|S), the probability of the DNA results IF the stain originated from the suspect

Defence (D) hypothesis: (the denominator): Pr(E|U), the probability of the DNA results IF the stain originated from an unknown individual.

The LR would be: Pr(E|S) divided by Pr(E|U)

If the LR is 1, then the DNA results are equally likely under both propositions. A LR greater than one favours proposition ("P"), and less than one provides support for proposition ("D"). The LR in a DNA match result situation would take the following general form:

The probability of the DNA evidence is x-trillion times more likely if the stain came from Mr. X than if it came from an unknown and unrelated individual.

It would be improper, and a statistical fallacy, to say that, for example, "the probability that the stain came from Mr. X is x-trillion times more likely...". In many cases, where there is a simple match between a single source evidence profile and a reference profile, the LR calculation is just the reciprocal of the RMP estimate (National Research Council, 1996) – for example, a RMP of 1 in 10 trillion would be an LR of 10 trillion. In other words, the RMP and the LR contain the same numerical information. However, the move away from RMPs to LR is spurred by their usefulness in the evaluation of complex DNA mixture profiles (Centre of Forensic Sciences, 2017) and in the potential application of Bayesian statistical approaches in forensic contexts.

A description and analysis of Bayesian approaches in forensics are well beyond the scope of this introduction – reviews found in Biedermann & Taroni (2012) and Kaplan & Kaplan (2006) provide general introductions to this topic. However, in short, likelihood ratio calculations can be "slotted into" Bayes' theorem in the following way:

> If "prior odds" are the odds that two DNA samples came from the same person using non-DNA information, then, "posterior odds" are the prior odds multiplied by the LR.

As stated in NRC II (1996), "whatever are the odds that the two samples came from the same person in the absence of DNA evidence, the odds when the DNA evidence is included are LR times as great". What Bayes' theorem and LRs allow is the statistical integration of DNA evidence with other non-DNA evidence. Whether this approach takes hold in Canada and North America is still a matter of significant debate (Saini, 2011; Kaplan & Kaplan, 2006), with the biggest hurdle likely being the courts' unwillingness to ask jurors to assign prior odds based on non-DNA evidence (Rondinelli, 2002).

4. Interpretation of DNA profiles in the context of a case – a hierarchy of propositions

Forensic scientists do not work in case detail "vacuums" – items are typically submitted with case information. They first review case circumstances, such as police statements, witness statements and what evidence items have been found to better

understand the questions of interest to both investigators and lawyers. They follow the scientific method in determining working hypotheses to decide what types of scientific testing are necessary and appropriate to the relevant questions. A hypothesis is an allegation to be tested using scientific methods. The Forensic Science Service (UK) has provided the forensic community with a very useful and oft-cited "hierarchy of propositions" to help set questions and then define the proper scientific hypotheses and testing conditions (Cook, Evett, Jackson, Jones & Lambert, 1998; Butler, 2015).

The top proposition in Table 5 deals with deciding whether the suspect actually committed a criminal offence. This is the ultimate issue in a criminal trial, and the competing hypotheses of guilt and innocence are not scientific questions – a scientist cannot, and never should, address this issue. The remaining three proposition levels, however, detailed in the table below, deal with questions of activity ("what happened?"), body fluid deposition ("what and whose body fluid was deposited?") and DNA deposition ("who is the source of DNA from some indeterminate cell deposition?") (Cook et al., 1998; adapted by Hageman, 2017).

Table 5 Hierarchy of Propositions: Levels of DNA Evidence discussion

Proposition Level	Description	Competing hypotheses: examples
"Guilt or innocence"	Was the activity a crime?	The suspect committed the offence The suspect did not commit the offence
"Activity"	What kinds of activities led to the deposition of the DNA-containing biological evidence?	The suspect assaulted/struck the complainant Another person assaulted/struck the complainant
"Body fluid deposition"	Who is the source of a particular body fluid or tissue deposition?	The suspect is the source of the particular body fluid (eg blood, semen saliva) from the evidence item Another person is the source of the particular body fluid (eg. blood, semen, saliva) from the evidence item
"DNA deposition"	Who is the source of this DNA profile?	The suspect is the source of the DNA profile from the evidence item Another person is the source of the DNA profile from the evidence item

Depending on the evidence and the scientific testing results, the scientist may be able to challenge hypotheses at all, some selected, or none of these three propositional levels (Hageman 2017). Forensic DNA evidence mostly corresponds to the bottom (sometimes called "subsource") level, and with the next body fluid deposition level.

Linking DNA profiles to actual physical activities is not always possible – there is nothing about a DNA profile itself that discloses how it arrived on a particular piece of evidence. With every downward movement in propositional level, the scientist addresses a question further removed from the relevant legal question of what actually happened, and therefore leaves the lawyers, judges, and juries more and more responsible for the integration of the DNA evidence into the ultimate (highest) propositional level of guilt or

innocence (Hageman, 2017). This situation puts a greater responsibility on the shoulders of scientists to alert both investigators and courts regarding the current, and ever changing, scientific understanding of the transfer and persistence of skin and other body fluid cells (Meakin & Jamieson, 2013). This is especially true in "touch DNA" situations, transfers of small numbers of skin and other cells by direct and even indirect methods (Gill, 2014).

5. The criminal court system in Ontario

Criminal trials in Ontario take place in both the Ontario Court of Justice (OCJ) and the Superior Court of Justice (SCJ). Where a particular trial takes place depends on both the classification of the criminal allegation and, in many cases, on the defendant's right, under section 554 of the Criminal Code of Canada, to elect a jury or non-jury trial. The placement of the case depends on whether the offence is indictable or summary conviction, which supersedes the defendant's choice. The defendant does, however, have the ability to opt for a "speedy" trial in the OCJ, or to first have a preliminary inquiry in the OCJ and then a jury or non-jury trial in the SCJ.

Once at the preliminary inquiry or trial, the reporting forensic scientist's role as an expert witness is to respond to a subpoena and to attend court to answer questions in examination-in-chief, in cross-examination, and in reply. In Ontario, most forensic DNA expert testimony is provided by scientists employed at the ASCLD-LAB-accredited Centre of Forensic Sciences (CFS), a division of the Ministry of Community Safety and Correctional Services. The DNA expert is no different than any other witness, in that he or she is typically not present during opening statements, closing statements, judges'

decisions and judges' jury instructions. However, these trial events are all places where forensic evidence may be referenced, argued and summarized. There is no quality check procedure by which expert witnesses, judges, and attorneys ensure understanding of the expert forensic evidence.

The latest edition of the Manual of Criminal Jury Instructions (Watt, 2005), does not contain any model jury instructions specifically for DNA evidence. In addition, jurors in Canada cannot be polled – there is no way to assess the jurors' perspective of any of the evidence presented at trial. What jurors have heard and understood about forensic DNA evidence in actual criminal cases, in Canada, remains a scarcely studied area of inquiry.

6. Literature and Research Review/Gap Analysis

A forensic scientist completes his or her testimony, and is then formally excused by the judge. The rest of the trial proceeds without the scientist. That scientific evidence is now in the hands of others. Do those "others" understand the evidence and consider it in a fair, unbiased and clear manner? The title of a paper by McQuiston-Surrett & Saks (2009) summarizes the issue well: "The Testimony of Forensic Identification Science: What Expert Witnesses Say and What Factfinders Hear". Edmond *et al.* (2017) take this concern a bit further, suggesting "what experts say might not be what lay audiences hear". In particular, they point to the challenges of communicating expert evidence, especially in probabilistic terms. They suggest that words such as "certainty" "match" and "similarity" may mean different things to experts and juries, and also that jurors may

fail to consider alternate explanations for events unless such hypotheses are made explicit to them.

Research in the field of juror, judge, and lawyer understanding of expert forensic evidence has focused primarily on the experience of the jury. There is a wealth of detailed information spanning several aspects of juror understanding of expert testimony. In the context of forensic biology, specifically, there have been varying opinions about where responsibility of clarity of presentation falls. This has led to investigations into the most effective methods of presenting such information to these judicial system players.

While the following sections detail the state of the field, it must be stressed that none of the currently available research attempts to study actual case transcripts, nor investigate the variables laid out in this current research project.

A. Responsibility for communication of scientific evidence to the finders of fact

The jury hears scientific evidence from the scientist, the lawyers, and the judge. It is of highest importance that a jury be provided, from all of these participants, the clearest, fairest, and most reliable presentation of scientific facts. There is a paucity of research in Canada regarding this courtroom process. Are jury members being presented the most consistent, clear, and accurate set of facts by scientists, lawyers, and judges? Further to that point, are all players in this system discussing forensic biological evidence in the most accurate of ways?

The initial consideration of much of the research is where the responsibility of clarity falls. Scientists, via their codes of ethical standards (Canadian Society of Forensic Science, 2017), have a continuing responsibility for communicating results and

conclusions in a clear, accurate and unbiased manner. The conclusion of a variety of researchers has been that legal professionals also bear a responsibility for maintaining the clear presentation of the scientific evidence. Among those published on the topic are Cashman & Henning (2012) and Findlay (2008). Through careful study of miscarriages of justice in Australia, as well as interviewing lawyers, Cashman & Henning (2012) highlighted the significant role that lawyers and legal professionals play in "ensuring that triers of the facts in criminal cases do not misapply or misinterpret DNA evidence". However, they noted that there exists confusion in the legal community, especially regarding probability, likelihood ratios, and scientific language. In a research paper published in 2008, dealing with juror comprehension issues, Findlay mirrors similar concerns.

It is of the utmost importance that information is presented to jurors with clarity, in so far as it enables the jury to render a verdict using expert forensic evidence correctly. To further this point, a review of jury instructions from the United States outlines that the American Bar Association encourages judges and lawyers to make use of more detailed instructions for juries (DesPortes, n.d.).

While most of the research mentioned here relates to the juror experience, there are often criminal cases in the Ontario Superior Court of Justice that do not involve a jury. In these cases it is solely the judge that is the trier of fact. It must be considered that even in cases where a jury is absent, the legal professionals maintain accuracy when presenting forensic evidence; but it is not only the lawyers' responsibility here. Taroni, Biedermann, Vuille & Morling (2013) assert that it is the expert witnesses themselves who are responsible for ensuring clarity of their evidence. They also suggest that expert

witnesses should be altering the way *they* testify to cater more to the types of answers the judicial system seeks.

To present their evidence as accurately to scientific principles as possible, an expert is not always able to answer "…'how did this DNA get here? rather than 'whose DNA is this?'". The concept of the hierarchy of propositions (Table 5) comes in strong to bridge this gap, when presented properly. While maintaining the correct level of proposition is certainly expected of an expert witness, it cannot be feasible for the responsibility to fall on no one else.

The argument put forth with this research project is as follows: the expert does not have the ability to maintain control over the communication or use of the scientific evidence, nor are they necessarily even aware of what happens, *while they are absent from the court room*.

Hageman (2016) advances the suggestion that the lawyers involved in questioning experts on the stand can exercise a larger responsibility to be acutely aware of, and maintain, the correct level of proposition. Therefore it is the joint responsibility of the legal professionals and experts involved in court cases to maintain the integrity of expert evidence to the best of their ability, whether presenting to a jury or a judge. Hageman (2016) has proposed some improvements in this regard, providing a series of suggested questions that legal professionals can use to guide their examinations, to ensure the most consistent and accurate presentation of the expert testimony.

There has been a demonstrated need for such questions. In research by Wheate (2010), respondents indicated a clear need for further investigation into aspects of the

expert testimony to aid in a higher understanding of the evidence and its limitations.

B. What aids in juror comprehension?

Unlike the legal standard in Canada, there are jurisdictions that allow for post-verdict questioning and surveying of jury members. This brings about two dominant categories of research: studies done with real jurors, and studies done with mock jurors. In-depth research into jury comprehension of DNA evidence, such as that completed by Findlay (2008), Wheate (2010), and Nance & Morris (2005) has afforded a look into which procedures most facilitate the understanding of DNA evidence.

Real juries, real cases

The research completed by both Findlay (2008) and Wheate (2010) made great use of jurisdictional allowances for contact with jurors of real cases. Findlay (2008) concludes his research paper with the final thought that "If the evidence is presented clearly, the expert testimony is consistent and largely not impugned... jurors seem to manage the science and weigh it significantly". Wheate (2010) developed interesting results with her look into how important DNA evidence is to juries. By interviewing two sets of 12 jurors, Wheate (2010) discovered that jurors consider DNA evidence to be of incredibly high importance. They even consider the presence of DNA evidence so important that when it is lacking, they turn to speculation about the significance of that void. This 24-juror consensus provides a strong indication that a consistent and accurate presentation of facts is not only what jurors need, but it is also what they *want*, to render a verdict. As mentioned above, Wheate (2010) concluded with the suggestion that a series

of questions directed at investigating why DNA results or the number of samples could be limited, and why scientific conclusions could be limited but scientifically sound, would increase juror comprehension of DNA evidence. Findlay (2008) concurred with providing a thorough explanation to the court room, with the further note that when lawyers become confrontational in an adversarial system, it tends to prevent a clear explanation being delivered to the jury.

Mock juries, hypothetical cases

Goos, Silverman, Rose & Newman (2002) compared the responses of mock jurors to different ways of communicating a DNA match, and found that there were no statistically significant differences when occurrence frequency, random match probability, and source attribution statements were used. Based on results from surveys, polls, and a videotaped mock jury deliberation, Holmgren (2005) suggested that jurors could benefit from special assistance in deliberating DNA evidence, including note taking, allowing discussion of the evidence during trial, allowing jurors to ask questions, and providing jurors with written instructions.

Nance & Morris (2005) conducted research into the most effective method of presenting the random match probability (RMP) to juries. The paper begins on the note that there has been controversy over the use of RMP, and concludes that Bayesian mathematical models were better for jury comprehension. The Bayesian model allows for the presentation of the statistical values as a likelihood ratio, rather than the simple probability of the RMP. Jurors tended to better understand that "Action A was 5300 times more likely to be true under this hypothesis" than "The chance of randomly

selecting an individual that would display the same DNA profile was one in 3.3 trillion". One conclusion made in this study, regardless of the method of presentation, however, was that the more complete the explanation of the results, the higher the rate of juror comprehension. It should be noted that Canadian and American criminal courts have had little to no exposure to Bayesian approaches, and this is not expected to change in the foreseeable future (Houck & Siegel, 2010).

Another point of investigation for Nance & Morris (2005) was the occurrence of statistical fallacies. The phrasing of the commonly used RMP is incredibly prone to transposition. As described above, the RMP is not directly linked to the guilt or innocence of the defendant. Where Nance & Morris viewed this as an issue, is when the fallacies of inference can cause undue favour for the prosecution or the defense. They concluded that providing more assistance to the juries for understanding DNA evidence, regardless of the statistical method, alleviates undervaluation of DNA evidence by juries.

C. What is the Research Gap?

For future work, Nance & Morris (2005) suggested an investigation into just how often the statistical transposition fallacies occur. Until this study, this had not yet been attempted in the Canadian legal system. Aside from providing the legal system with a better understanding of how forensic DNA evidence is currently being used, a portrait of the fallacies may assist in preparing effective stock juror instructions.

DesPortes (n.d.) has discussed the concept of pattern jury instructions, which are meant to increase juror understanding of expert testimony; however such instructions "may not address the specific issues of an individual case", and may be insufficient at the

end of a long trial. While the point on general pattern instructions is valid, DesPortes (n.d.) discussed American jurisdictions. In Canada, judges refer to Watt's Manual of Criminal Jury Instructions (Watt, 2005), as it is the summation of all aspects of instructions meant for use in the Canadian criminal system. On the topic of expert testimony, the manual merely has general instructions available, not at all forensic DNA-specific, which may not aid jury understanding of DNA expert testimony.

In cases where a jury is not present, the legal professionals are crafting an understanding of the evidence for themselves. Taroni et al. (2013) have pointed out the questions that lawyers are often looking to have answered are not the types of questions that scientific expert witnesses are able to answer. They may function on different levels of proposition. What the valuable research done by Cashman & Henning (2012) can tell us is that lawyers can feel unprepared and untrained to attempt bridging that gap. Essentially, what all of these researchers have yet to investigate is whether (and the extent to which) the actual presentation of DNA evidence in court is as accurate and consistent as those used in mock interviews, or even real cases.

7. Goals of This Thesis

The goals of this research project were to determine how the Ontario criminal legal system construes and represents DNA evidence & expert testimony, and to produce statistically significant data relevant to criminal counsel, judges, and forensic scientists. Court transcripts from criminal trials were analyzed to determine what DNA experts *say*, and what counsel and judges *say about*, the expert testimony when the expert is *not* present.

The following areas of transcript were read in addition to the expert testimony:

- lawyers' opening statements
- closing statements
- submissions
- judges' rulings
- judges' instructions to juries.

The two sets of transcripts (the "say" and the "say about") were compared and contrasted in terms of scientific conclusions, inferences, assumptions, and in particular, statistical and probability statements.

It was *not* the intention of this project to reassess the final decisions of guilt or innocence in the chosen cases. Transcripts from all other witnesses were neither obtained nor analyzed, so that the expert testimony was considered without the influence of other experts, police, or eye witness statements. In addition to this step, the expert witness testimony was read after all other pieces of a case. The ultimate goals were to assess, qualitatively and quantitatively, the use of forensic DNA evidence by non-scientist judicial system participants in order to detect possible trends of strengths and weaknesses in the system, and propose solutions (including common jury instructions).

Methods

1. Case selection and transcript acquisition

Cases were targeted and requisitioned solely through the Ontario Court of Appeal, via the Records Office at Osgoode Hall in downtown Toronto. This approach was taken because all witness testimonies in the original criminal trials had already been fully transcribed by court reporters for the purpose of appeal court filings (which must include all original trial transcripts). This project's approach of only using criminal cases in, or in the process of, appeal eliminated the inclusion of testimony from most criminal trials in Ontario. However, trial court testimony that has not already been transcribed can only be obtained at a prohibitive cost of $8 per page (O. Reg 94/14, 2014), which is well beyond the cost scope of this, and most, projects.

Cases that included forensic biology *viva voce* expert evidence were targeted using Boolean searches (eg. "DNA AND Random AND Match") in the public legal databases Canadian Legal Information Institute (n.d.) (CanLii). This database was searched for relevant cases active in appeals within approximately the past ten years. This parameter was put in place in order to restrict the cases to those where the forensic biology testimony was based on current short tandem repeat technology.

Below in Figure 6 is an example of the CanLii database, having used the search parameters described here.

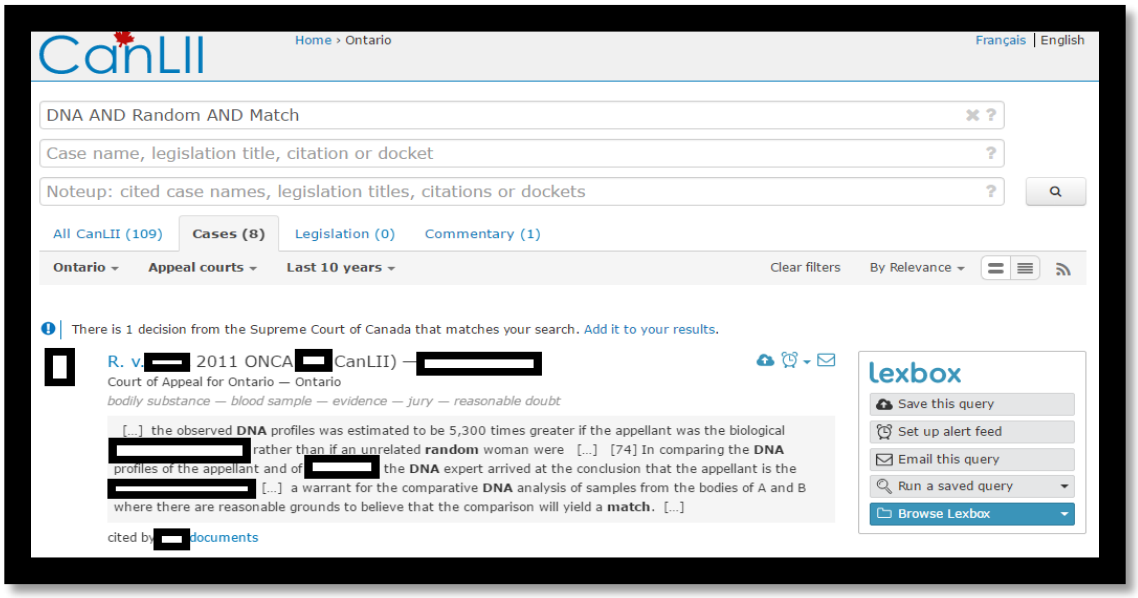


Figure 6 CanLii Database Search for cases using DNA, within Ontario Appeals, last 10 years.

Below (Figure 7), is an example of screening a case found with a CanLii database search. This image shows an excerpt from the appeal judge's review of the case evidence. This section of the database results was examined to determine the context in which the search terms were met, and to eliminate from consideration cases that only discussed DNA warrants and orders.

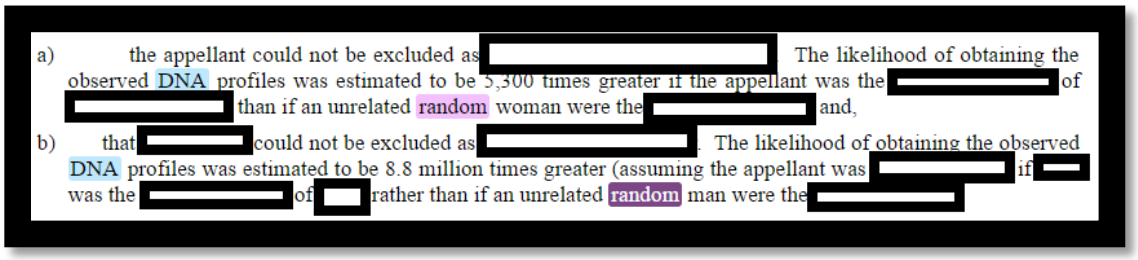


Figure 7 CanLii case page excerpt, previewed to determine context of key word search terms

For each case file obtained from the Records Office, the following paper-based transcripts were inspected for excerpts discussing the expert evidence and testimony:

- Opening and closing statements by crown and defense lawyers
- Expert testimony
- For jury trials: judge's instructions to the jury, including responses to jury instructions
- For non-jury trials: judge's decision and/or reasoning
- Other materials, as available: expert reports

Once the case materials had been screened, the desired sections were photocopied on location.

2. Transcript analysis: Optical character recognition (OCR) conversion, Coding and QDA software

Transcripts were qualitatively analyzed using Qualitative Data Analysis Miner 4 Lite software (Provalis Research, 2011). Each case was given its own file, and each section for review was uploaded together (Figure 8**)**.

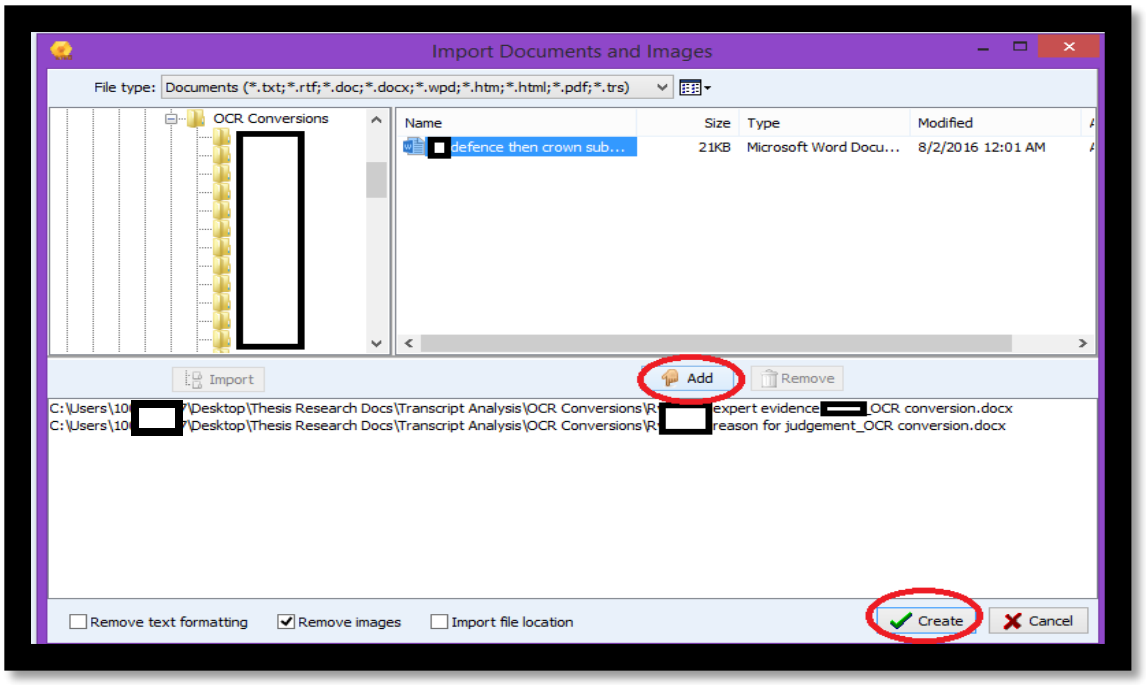


Figure 8 Creating a 'Project' in QDA Miner 4 Lite, from Word Documents

Once the files were imported into QDA, the coding tree (Figure 9**)** was created within the software, and the sections of text were ready for analysis.

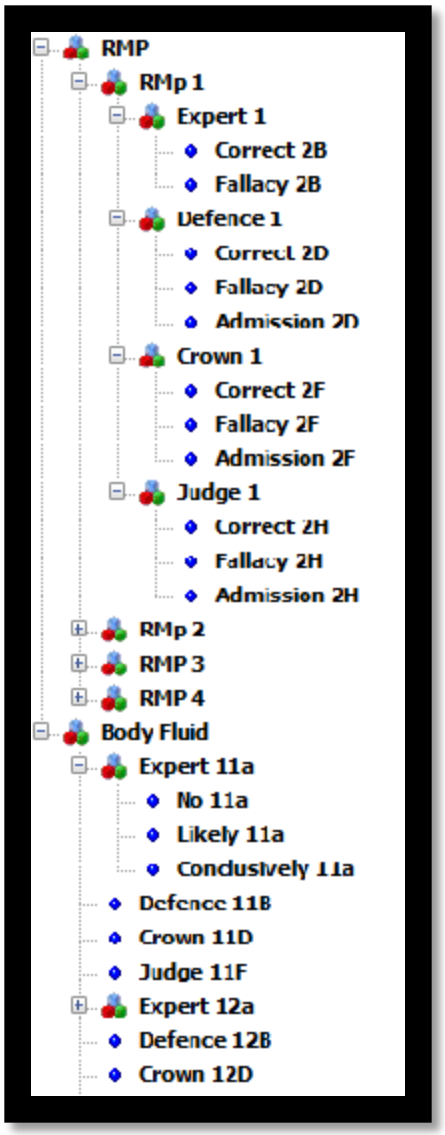


Figure 9 QDA transcript coding tree

In order to use QDA for the transcript analysis, the portable document format (pdf) copies of transcripts were first converted to Word documents through the use of Optical Character Recognition (OCRConvert, n.d.). This free digital software converts scanned images (pdf) into files with selectable text. This process took approximately 30-60 seconds per file, and could not convert files larger than 5 MB. As a result, the files were often saved into multiple pdfs before conversion, and the textfile output was recombined as Word documents.

As this conversion software included a digital image scan, resulting Word documents required editing for accuracy. The most common issue the converter had with the pdfs was that some of the original pages from the court house had printer ink stains, pen marks, comments, and smudges. The digital converter was unable to recognize all marks as English text, and regularly inserted the nearest facsimile character. The most common errors were incorrectly estimating dashes (-) were tildes (~), zeros (0) were the letter O (O, o), and the number one (1) was lower case L (l). Midway through the OCR conversion time period of May to December 2016 of this project, the service received an upgrade. This resulted in an even better rate of accuracy from the converter (approximately 95%).

3. Qualitative coding system and quantitative survey

The following coding system and survey (Appendix A) were developed, *de novo*, for transcript analysis:

The final version of the survey contained three sections: Autosomal Random Match Probability (RMP), Lineage RMP, and Body Fluid Identification. Questions 1

through 5 tracked up to four instances of Autosomal RMPs, questions 6 through 10 tracked up to four instances of Lineage RMPs (Y-STR and mtDNA), and section three tracked up to two instances of body fluid discussion within each case. The final question, 13, tracked whether the case was jury or non-jury.

In order to have a record of which section of transcript answered each question on a survey, the transcript was coded within the QDA software (Figure 10).

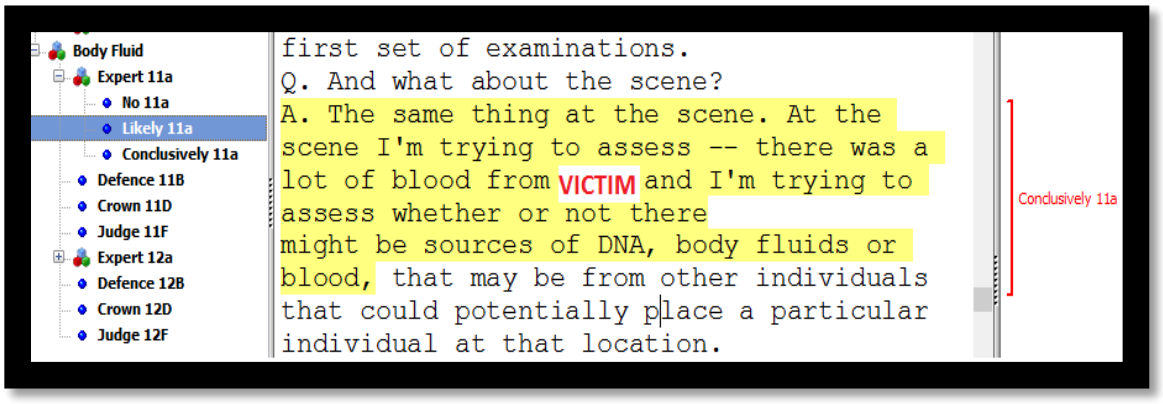


Figure 10 Example of coding a section of text in QDA. Here, the Expert was discussing the source of a body fluid conclusively.

- Q1. How many RMPs were presented by the expert?

This question was a Ratio variable designed to track how many autosomal RMPs were presented by the expert during their testimony. The decision to use an upper limit of four instances of RMP was made for the sake of efficiency, as the number of RMPs discussed in some cases was too numerous for the scope of this project.

- Q2A. Was an RMP presented by the expert?

This question was created to track the introduction of RMP #1 by the expert. If an autosomal RMP was not discussed by the expert, but was discussed by someone other

than the expert, the answer to this question was “No”. If an autosomal RMP was discussed by the expert, the answer to this question was “Yes”. If autosomal RMPs were not discussed by anyone in the case, this question was answered “n/a”.

- Q2B. If yes, was that RMP presentation by the expert correct or fallacy?

Here the options were “Correct”, “Statistical Fallacy”, “Admission of Source”, or “n/a”. In order for a section of text to be labelled “Correct”, the presentation of RMP had to be completely accurate. “Statistical Fallacy” was used as a catch-all term for any type of error. Refer to Q2D for a further explanation of “Statistical Fallacy” decisions. Sections of text were labelled “Admission of Source” only when it appeared that there was already an agreement regarding the identity of the profile source (meaning that an RMP was not necessary) – for example, if a defence lawyer conceded that his or her client’s DNA was, indeed, at the crime scene, such an admission of source would negate any further need for an RMP in a trial.

- Q2C. Was that RMP presented by a defence lawyer?

If an RMP was discussed by a defence lawyer, the section of text was labelled “Yes”. To decide between “No” and “n/a”, there were two factors. If the section of transcript was available, and it could be confirmed the lawyer did not discuss that section of evidence, the answer to this question was “No”. If the autosomal RMPs were not done in the case, or if that section of text was not available to confirm what a defence lawyer said, the answer to this question was “n/a”.

- Q2D. If yes, was that RMP presentation by a defence lawyer correct or statistical fallacy?

If the answer to question 2C was "No", there was no section of transcript to label for this question, and the answer was "n/a". If the answer to question 2C was "Yes", the section of transcript that corresponded to this question was labelled (in QDA) in one of the following three ways: "Correct", "Statistical Fallacy", or "Admission of Source". For the section to be labelled as "Correct", a defence lawyer had to correctly discuss that RMP. If a lawyer did not discuss the RMP completely and correctly the section of transcript would be labelled "Statistical Fallacy". This covered the typical fallacy errors such as transposing the conditional, as well as occurrences of justice system participants misquoting the expert.

If the lawyer stated the DNA profile belonged to someone without the relevant probability statement, when the expert had provided such, there were two options for labelling that section of text. If there was an "Agreed Statement of Facts" for the case, in which all parties agreed a particular profile belonged to someone, the section of text was labelled "Admission of Source".

There were two methods used to decide whether a statement of fact had been agreed upon in any given case. The first method was the most tangible; an agreed statement of facts was found within the boxes in the Appeals Records Office, or a list had been read by a justice system participant within the transcript. The second method required taking note of the way each lawyer spoke of the evidence. If both a defence lawyer and a crown lawyer spoke the same way of the evidence (often using the terms "we agreed" or "we conceded"), then both parties did not take issue with declaring the identity of the profile donor. It was assumed an agreed statement of facts existed within the trial level case, or as an agreed fact outside the doors of the courtroom.

If it appeared as though a crown lawyer was the only person speaking of identity with regards to the profiles, and a defence lawyer had only spoken of the RMP evidence, it was decided there was not an agreement or concession of source. If no such agreement existed, the decision to identify a profile without the statistical weight was considered incorrect, and was labelled "Statistical Fallacy".

- Q2E. Was that RMP presented by a crown lawyer?

The answer to this question was decided by the same principles as Q2C.

- Q2F. If yes, was that RMP presentation by a crown lawyer correct or statistical fallacy?

The answer to this question was decided by the same principles as Q2D.

- Q2G. Was that RMP presented by a judge?

The answer to this question was decided by the same principles as Q2C.

- Q2H. If yes, was the RMP presentation by the judge correct or statistical fallacy?

The answer to this question was decided by the same principles as Q2D.

- Questions 3B through 3H, 4B through 4H, and 5B through 5H all have the same response attributes as Questions 2B through 2H, to track up to 4 instances of RMP per case.
- Question 6 tracked up to four instances of lineage RMP used within a case.

This section combined Y-STR (male lineage profiles) with Mitochondrial DNA (maternal lineage profiles) as the method of statistical weighting is the same.

- The answers to survey Questions 7B to 10H were answered by the same decisions as Questions 2B to 2H.
- Q11A. Did the expert link a DNA profile/probability to a body fluid deposition?

This question targeted instances in which an expert stated the RMP or profile was sourced from blood, semen, saliva, or another tissue source. If an expert said that they could not state the body fluid source of the profile they were working with, the section of transcript was labelled "Said: no, cannot state it was _x_ fluid". This response attribute included both of the following situations:

- an expert did not have any information as to the type of cell or fluid the profile came from

- an expert stated that it could have come from a number of different sources and had no conclusive proof one way or the other.

If an expert had performed a presumptive test in addition to creating the DNA profile, but was not able to conclude with certainty the type of fluid the profile was sourced from, the transcript section was labelled "Said: Likely _x_ fluid" in QDA. This response attribute was created with the presumptive test for saliva amylase in mind.
If an expert was able to state that the profile came directly from a known fluid source, the section of transcript was labelled "Said: Conclusively _x_ fluid" in QDA. This response attribute was created for situations of positive Kastle-Meyer tests with confirmatory follow up, and the appearance of sperm on smear slides viewed with a microscope.

These two body fluid tests are highly specific and are able to assign body fluid results with certainty. If the expert did not discuss a body fluid, the answer to this question was "n/a".

- Q11B. Was the DNA profile linked to a body fluid by a defence lawyer?

This question was created to track instances of a defence lawyer stating that a particular profile was from a body fluid source. If a defence lawyer did not state that a profile was blood, or semen, or saliva etc., the answer to this question was "No".

If a defence lawyer stated that a profile was from blood, semen, saliva etc., the answer to this question was "Yes".

If the situation of a body fluid was not addressed in the case, the answer to this question was "n/a".

- Q11C. Was that linkage or non-linkage by a defence lawyer consistent with the expert testimony?

Once Q11B identified that a defence lawyer had or had not linked a profile to a body fluid source, the section of transcript was compared to the expert testimony. If what a defence lawyer stated of the body fluid was the same way the expert addressed the body fluid, the answer to this question was "Consistent with expert testimony".

If, for example, a defence lawyer did say a profile was from saliva when the expert stated it was likely saliva, the answer to this question was "Inconsistent with expert testimony".

If a defence lawyer discussed a body fluid as it related to a DNA profile, and an expert had not done so, the section was labelled "Not addressed by expert". Similarly to

Q11A, if a body fluid was not discussed within the case, the answer to this question was "n/a".

- Q11D through Q11G were answered by the same principles as Q11B and Q11C.
- Q12A through Q12G were coding a second instance of a body fluid attribution, and were answered by the same principles as Q11A through Q11G.
- Q13. Is this case Non-jury or Jury?

If the case was a non-jury case, the answer to this question was "Non-jury". If the case involved a jury, the answer to this question was "Jury". The option "n/a" was present as a safe guard in case that information was not available for any reason.

4. Statistical analyses

This project was the first glimpse into how DNA expert evidence was being used in the Ontario criminal court trials by lawyers and judges. As such, the survey was created with the intention of running descriptive frequencies in SPSS 24 (IBM, 2016) rather than inferential statistics. A combination of descriptive frequencies, a t-test, and first order cross-tabulations were run from the accumulated data set.

Independent Samples T-Test

A t-test is a hypothesis test, used to determine whether there is a statistically significant mean difference between two groups. As this test was used for the purposes of determining whether there was a difference between two data groups, two-tailed tests

were employed. For a t-test, there are two hypotheses expressed: the research hypothesis and the null hypothesis. The research hypothesis describes the theory being tested, with a difference existing between two groups. The null hypothesis is the competing hypothesis, and states that there is no difference between the groups. For this study, the hypotheses were as follows:

> The Research Hypothesis: There is a statistically significant difference between the number of autosomal RMPs presented in a jury case and the number of RMPs presented in a non-jury case.
>
> The Null Hypothesis: There is not a statistically significant difference between the number of autosomal RMPs presented in a jury case and the number of RMPs presented in a non-jury case.

The independent variable used for this test was the nominal Q13 "Jury or Non-jury case". The dependent variable was the ratio Q1 "How many RMPs were presented by the expert?" The test was used to measure whether there was a statistically significant mean difference between the number of RMPs presented in a Jury case and the number of RMPs presented in a Non-jury case.

Cross-tabulations

Cross-tabulations are predominantly used to assess relationships and influences between independent and dependent variables. Inferences made with cross-tabulations require cells to have counts of more than five. As these data are sourced from a small

number of cases (N=32), the cells routinely contained too few responses for inferential statistics. Measures of association were not completed with this data set.

For the purposes of this project, cross-tabulations were used as a method of data display and organization. There were no relationship inferences made with the data presented, only observations. It was not the goal of this project to assess influences on lawyers' or judges' presentation of RMP evidence, but to observe what was occurring.

Zero order cross-tabulations are used to display two variables, one independent and one dependent. First order cross-tabulations are used to display these same two variables with the addition of a control (or layer) variable. This is an added layer of information under which the independent and dependent responses are split. With that in mind, cross-tabulations were created to display the array of answers coded for defence lawyers, crown lawyers, and judges, as broken down by the array of answers coded for expert testimony. An additional layer of information was put in place with question 13, Jury case or Non-jury case.

The answers to questions 2B, 3B, 4B and 5B (expert witness' answers regarding 4 instances of autosomal RMPs) were combined into a single, total independent (column) variable (Expert 2B to 5B). The answers to questions 2D, 3D, 4D, and 5D (Defence Lawyers' answers regarding four instances of autosomal RMPs) were combined into a single total dependent (row) variable (Defence 2D to 5D). Following this, Crown Lawyers' answers were combined into a single dependent (row) variable (2F to 5F) and Judges' answers were combined into a single dependent (row) variable (2H to 5H). This process was completed again for the four instances of Lineage RMPs, as well as the two instances of Body Fluid source discussion.

Expert 2B to 5B was “crossed” with each of Defence 2D to 5D, Crown 2F to 5F, and Judge 2H to 5H, all with the control (or layer) variable of Jury of Non-jury. This resulted in three cross-tabulation charts.

Expert 7B to 10B was “crossed” with each of Defence 7D to 10D, Crown 7F to 10F, and Judge 7H to 10H, all with the control (or layer) variable of Jury or Non-jury. This resulted in 3 cross-tabulation charts.

Expert 11A to 12A was “crossed” with each of Defence 11C to 12C, Crown 11 E to 12E, and Judge 11G to 12G, all with the control (or layer) variable of Jury or Non-jury. This resulted in 3 cross-tabulation charts.

In total, there were nine cross-tabulations completed, as viewed in the results section (p.75).

Results

Transcript procurement initially began with the work of Nicole Crawford, an undergraduate student working with Dr. Hageman for the Spring/Summer 2015 semester. Upon commencement of the graduate research program (September 2015), responsibility of case procurement moved to this graduate student. Obtaining cases spanned approximately 19 months (June 2015-December 2016). During the ongoing case retrieval phase, previously procured cases were processed through the OCR converter and edited. This rotating schedule meant the additional team of four undergraduate volunteers constantly had an influx of sections of expert testimony to edit.

Table 6 details the sections of transcript obtained for each of the cases studied (randomly assigned a numerical value 1-33). There were 32 cases that dealt with DNA evidence using the Random Match Probability, and a single case that used the Likelihood Ratio. Throughout the entire search process, inappropriate (to the thesis) cases were eliminated. The search terms "DNA AND Match" returned cases that discussed DNA warrants (legal orders to require DNA testing) which did not suit the purposes of this project. Cases that did not have the testimony of a forensic biologist were also not copied. Often forensic identification officers would testify regarding the DNA evidence, but as these witnesses are not qualified as expert opinion witnesses these cases were not copied. Each of the 33 cases studied in this case contains an expert qualified by the presiding Judge to give their forensic biology testimony.

Table 6 Summary of transcript sections obtained per each of the 33 cases

Case	Expert	Charge to Jury	Reason for Judgement	Submissions	Crown Opening	Defence Opening	Crown Closing	Defence Closing	Estimate Number of Pages Copied
1	x	x		x			x	x	50
2	x	x		x			x	x	690
3	x	x			x	x	x	x	309
4	x						x	x	85
5	x			x					245
6	x	x		x	x		x	x	38
7	x	x			x		x	x	124
8	x	x					x	x	166
9	x				x		x	x	403
10	x	x					x	x	101
11	x	x			x		x	x	589
12	x	x					x	x	105
13	x	x					x	x	257
14	x	x					x	x	192
15	x	x	x	x	x		x	x	544
16	x	x					x	x	109
17	x			x					186
18	x		x	x					41
19	x	x					x	x	1439
20	x		x	x					155
21	x	x		x	x		x	x	63
22	x		x	x					50
23	x	x		x					300
24	x		x	x					40
25	x	x			x		x	x	208
26	x	x					x	x	14
27	x	x			x		x	x	355
28	x	x	x	x			x	x	386
29	x	x			x		x	x	387
30	x	x							249
31	x	x			x		x	x	129
32	x	x					x	x	373
33	x	x					x	x	218
								Total	8600

Question 1

Table 7 Number of Autosomal Random Match Probabilities Discussed Per Case

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	One	3	9.4	9.4	9.4
	Two	4	12.5	12.5	21.9
	Three	6	18.8	18.8	40.6
	Four or more	18	56.3	56.3	96.9
	n/a	1	3.1	3.1	100.0
	Total	32	100.0	100.0	

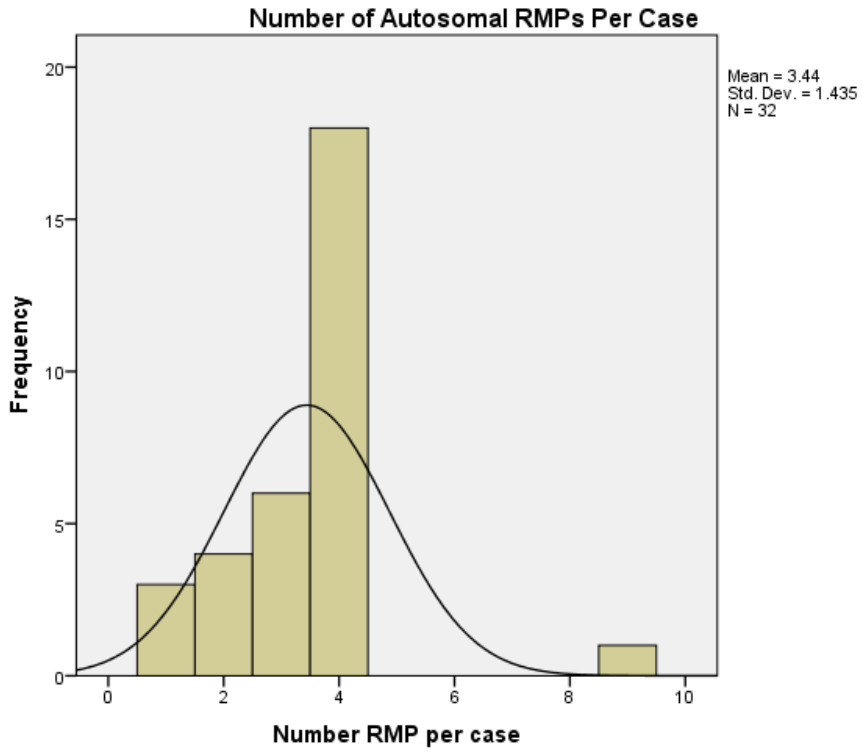


Figure 11 Visual representation of number of Autosomal RMPs discussed per case

The number of autosomal random match probabilities was recorded for each case. Three (9.4%) of the cases studied had one random match probability (RMP) presented by the Expert. Four (12.5%) of the cases studied had two RMPs presented, while six (18.8%) cases had three RMPs presented by the Expert. The largest number of cases (18,

56.3%) also had the largest number of RMPs presented, at four or more. A single case (3.1%) did not contain autosomal RMP evidence. The average number of random match probabilities presented by the Expert was 3.15 (101 total over 32 cases, excluding "n/a").

Questions 2 to 5

Summary of Expert discussion of Autosomal RMP:

Table 8 Coding of Expert Witness discussion of autosomal random match probability (Q. 2-5 B)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	87	68.0	68.0	68.0
	Statistical Fallacy	2	1.6	1.6	69.5
	Admission of Source	12	9.4	9.4	78.9
	n/a	27	21.1	21.1	100.0
	Total	128	100.0	100.0	

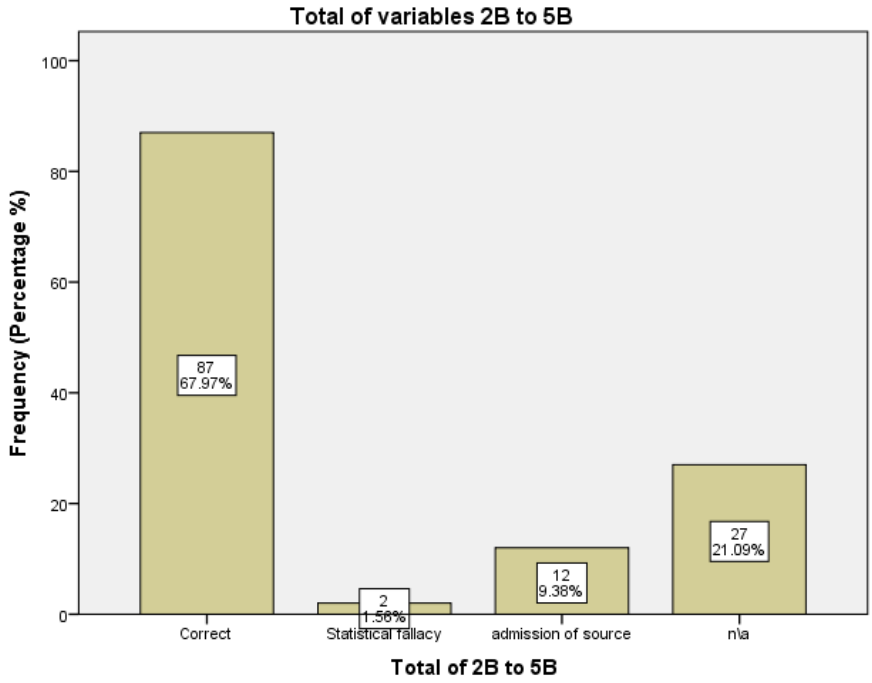


Figure 12 Visual representation of Expert Witness discussion of RMPs (Q.2-5)

This cumulative variable shows the results of all instances of RMPs from the cases studied. The question regarding presentation of an autosomal RMP was asked four times per survey. Table 8 shows the array of responses for the total of 128 possible responses (32 cases x 4 RMP instances per case), while Figure 12 demonstrates the information visually.

From the total of 128 possible instances of autosomal random match probability, 87 (68.0%) presented by the Expert were Correct. Only 2 (1.6%) were Statistical Fallacy, and 12 (9.4%) were Admission of Source. In 27 (21.2%) instances, the Expert did not present autosomal RMP evidence.

Without the instances that an Expert did not present an autosomal RMP (128-27=101), the total of 87 Correct responses make up 86.1% of the Expert responses. The Statistical Fallacy (2) then adjusted to 2.0% of responses, and Admission of Source (12) became 11.9%.

Summary of Defence lawyer discussion of Autosomal RMP:

Table 9 Coding of Defence lawyer discussion of autosomal random match probability (Q. 2-5 D)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	4	3.1	3.1	3.1
	Statistical Fallacy	19	14.8	14.8	18.0
	Admission of Source	9	7.0	7.0	25.0
	n/a	96	75.0	75.0	100.0
	Total	128	100.0	100.0	

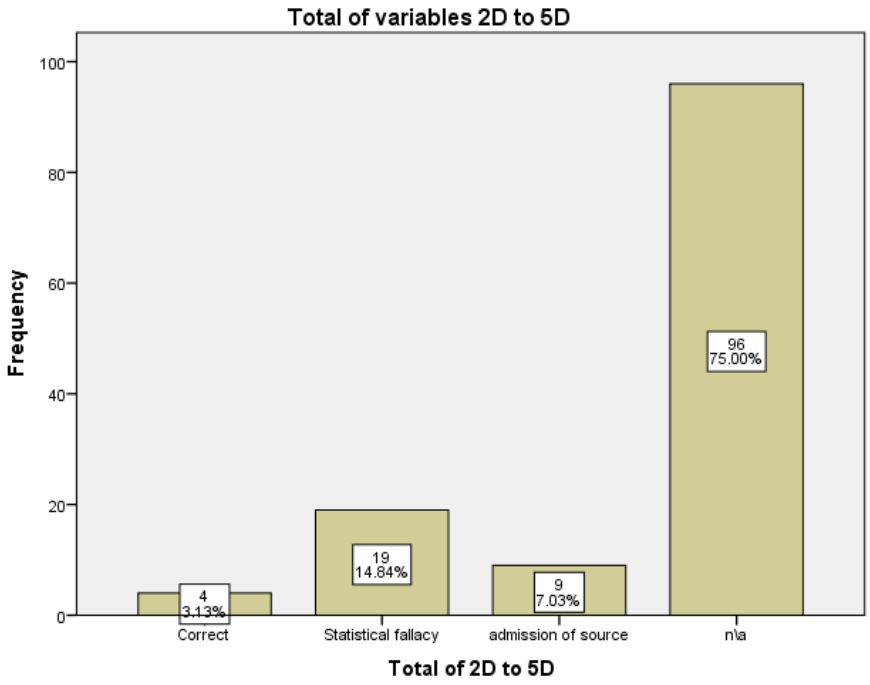


Figure 13 Visual representation of Defence lawyer discussion of RMPs (Q. 2-5 D)

Table 9 shows the array of answers of the possible 128 random match probability instances discussed in the cases studied. Only 4 (3.1%) responses were Correct. 19 (14.8%) of responses for a Defence lawyer were categorized as Statistical Fallacy, and 9 (7.0%) were Admission of Source.

The Defence lawyer responses show that 96 (75.0%) of a possible 128 instances do not discuss an autosomal RMP. Using the number of instances the Expert did not discuss RMP (27) as a correction factor, the Defence lawyer responses are as follows:

A Defence lawyer was Correct when speaking of an RMP 4 times (4/128-27=4.0%). A Defence lawyer created a Statistical Fallacy 19 times (18.8%), and admitted a source nine times (8.9%). Of the possible 101 instances that an Expert spoke of, a Defence lawyer discussed 32 (4+19+9/101=31.7%).

Summary of Crown lawyer discussion of Autosomal RMP:

Table 10 Coding of Crown lawyer discussion of autosomal random match probability (Q. 2-5 F)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	13	10.2	10.2	10.2
	Statistical Fallacy	27	21.1	21.1	31.3
	Admission of Source	9	7.0	7.0	38.3
	n/a	79	61.7	61.7	100.0
	Total	128	100.0	100.0	

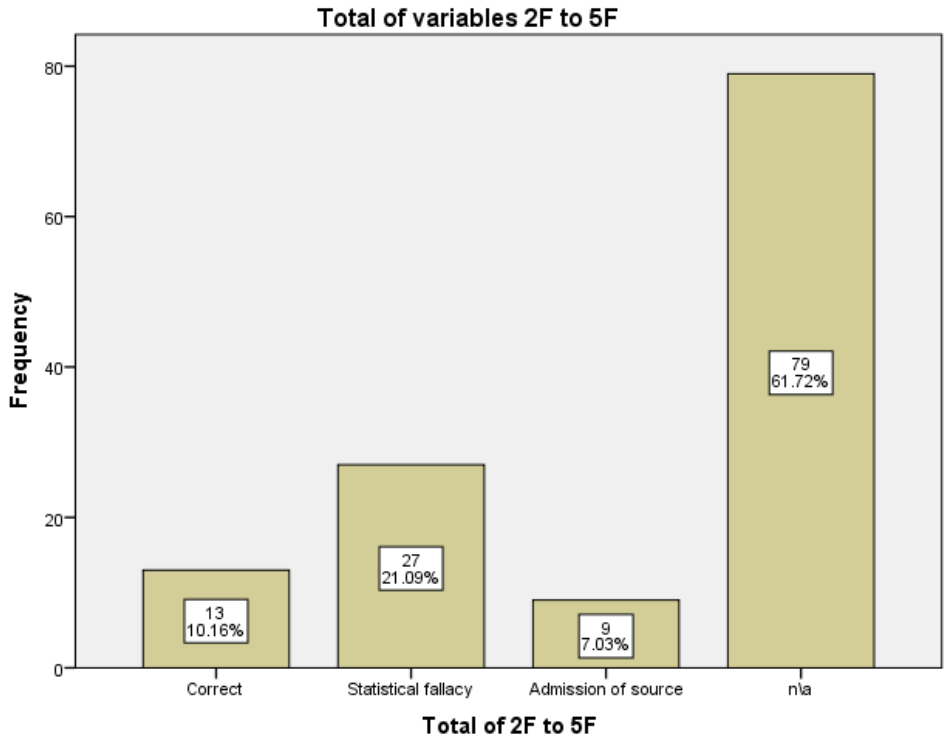


Figure 14 Visual representation of Crown lawyer discussion of RMPs (Q. 2-5 F)

Using the same correction factor (27), the Crown results are as follows:

A Crown lawyer was Correct when speaking of an RMP 13 times (13/101=12.9%). A Crown lawyer created a Statistical Fallacy 27 times (27/101=26.7%),

and Admitted a Source 9 times (8.9%). Of the possible 101 instances that an Expert discussed an RMP, a Crown lawyer discussed a total of 49 (49/101=48.5%).

Summary of Judge discussion of Autosomal RMP:

Table 11 Coding of Judge discussion of autosomal random match probability (Q. 2-5 H)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	29	22.7	22.7	22.7
	Statistical Fallacy	19	14.8	14.8	37.5
	Admission of Source	10	7.8	7.8	45.3
	n/a	70	54.7	54.7	100.0
	Total	128	100.0	100.0	

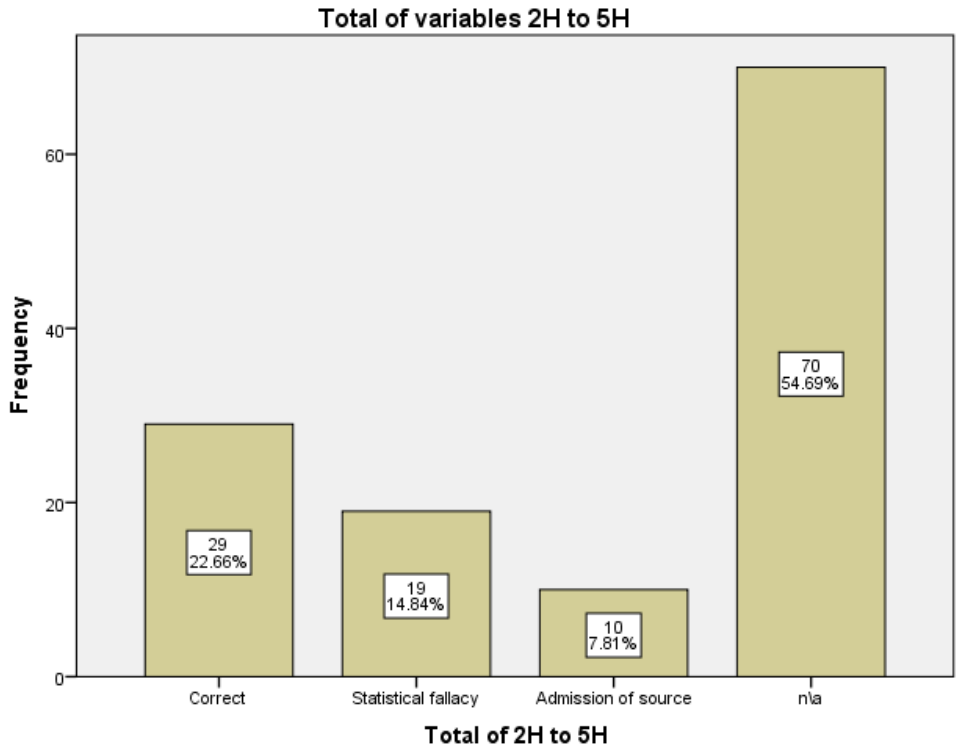


Figure 15 Visual representation of Judge discussion of RMPs (Q. 2-5 H)

Using the same correction factor (27), the Judge results are as follows:

A Judge was Correct when speaking of an RMP 29 times (29/101=28.7%). A Judge created a Statistical Fallacy 19 times (18.8%), and Admitted a Source 10 times (9.9%). Of the possible 101 instances that an Expert discussed an RMP, a Judge discussed a total of 58 (58/101=57.4%).

Question 6

Table 12 Number of Lineage Random Match Probabilities Discussed Per Case

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	One	4	12.5	12.5	12.5
	Two	1	3.1	3.1	15.6
	Four or more	1	3.1	3.1	18.8
	N/A	26	81.3	81.3	100.0
	Total	32	100.0	100.0	

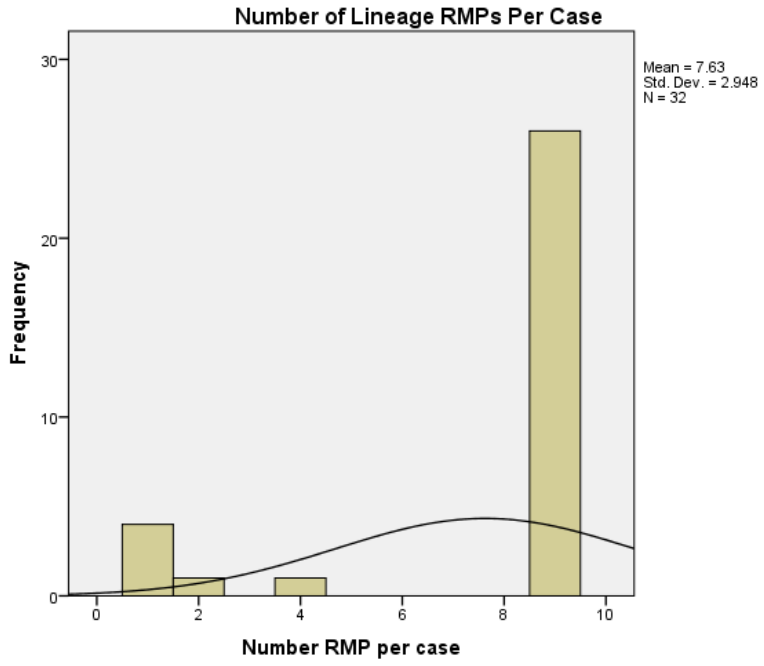


Figure 16 Visual representation of number of Lineage RMPs discussed per case

The number of lineage random match probabilities was recorded for each case. Four (12.5%) of the cases studied had one random match probability (RMP) presented by the Expert. One (3.1%) of the cases studied had two RMPs presented, while no cases (0.0%) had three RMPs presented by the Expert. One case (3.1%) had four or more lineage RMPs presented by the Expert. The largest number of responses for this question reflected that most cases (26, 81.3%) did not contain lineage RMP evidence.

The average number of random match probabilities presented by the Expert was 7.63, a non-coded response attribute, which is a reflection of the larger number of cases not involving this type of evidence. Considering only the coded values, the average number of lineage RMPs was 0.31 (10/32).

Questions 7 to 10

Summary of Expert discussion of Lineage RMP:

Table 13 Coding of Expert Witness discussion of lineage random match probabilities (Q. 7-10 B)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	10	7.8	7.8	7.8
	n/a	118	92.2	92.2	100.0
	Total	128	100.0	100.0	

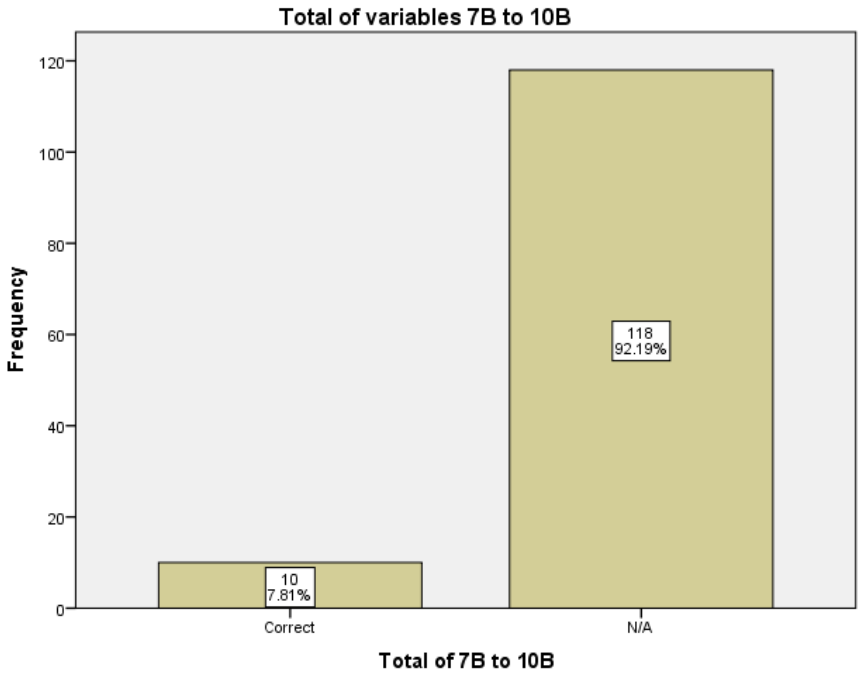


Figure 17 Visual representation of Expert Witness discussion of RMPs (Q. 7-10 B)

In 128 possible instances (32 cases x 4 instances per), Lineage RMP evidence only appeared 10 times (7.8%). All of the 10 instances of lineage RMP evidence presented by the Expert were Correct.

Summary of Defence lawyer discussion of Lineage RMP:

Table 14 Coding of Defence lawyer discussion of lineage random match probability (Q. 7-10 D)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	2	1.6	1.6	1.6
	Statistical Fallacy	3	2.3	2.3	3.9
	n/a	123	96.1	96.1	100.0
	Total	128	100.0	100.0	

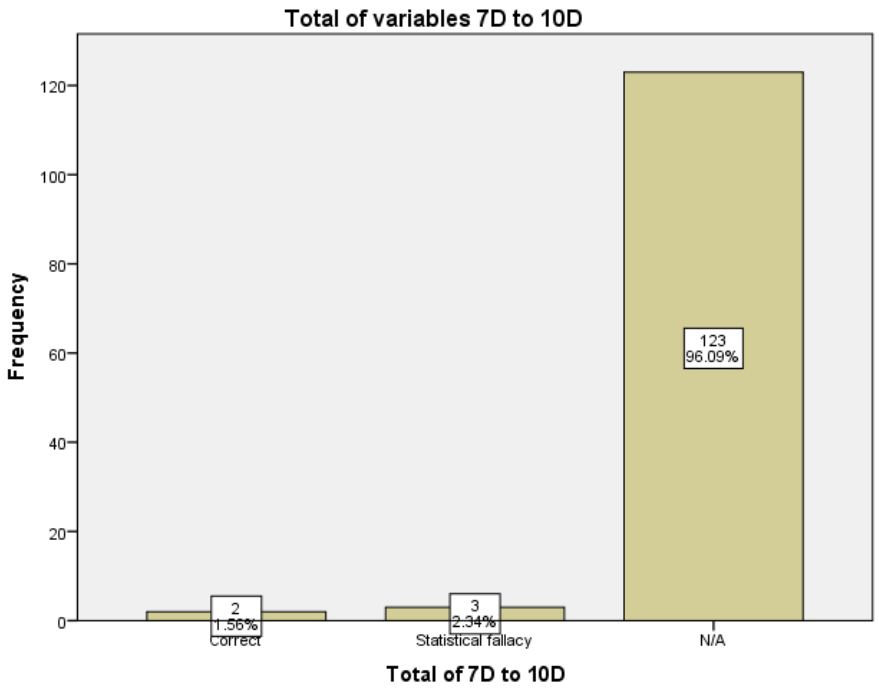


Figure 18 Visual representation of Defence lawyer discussion of RMPs (Q. 7-10 D)

As described in the autosomal RMP section, the numbers of Expert Lineage RMPs discussed were used as a correction factor for the percentages of Defence lawyer responses. Of 10 lineage RMPs to discuss, a Defence lawyer only discussed five (50.0%). Of those five, two were Correct (20.0%). The remaining 3 (30.0%) were Statistical Fallacy.

Summary of Crown lawyer discussion of Lineage RMP:

Table 15 Coding of Crown lawyer discussion of lineage random match probability (Q. 7-10 F)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	2	1.6	1.6	1.6
	Statistical Fallacy	4	3.1	3.1	4.7
	n/a	122	95.3	95.3	100.0
	Total	128	100.0	100.0	

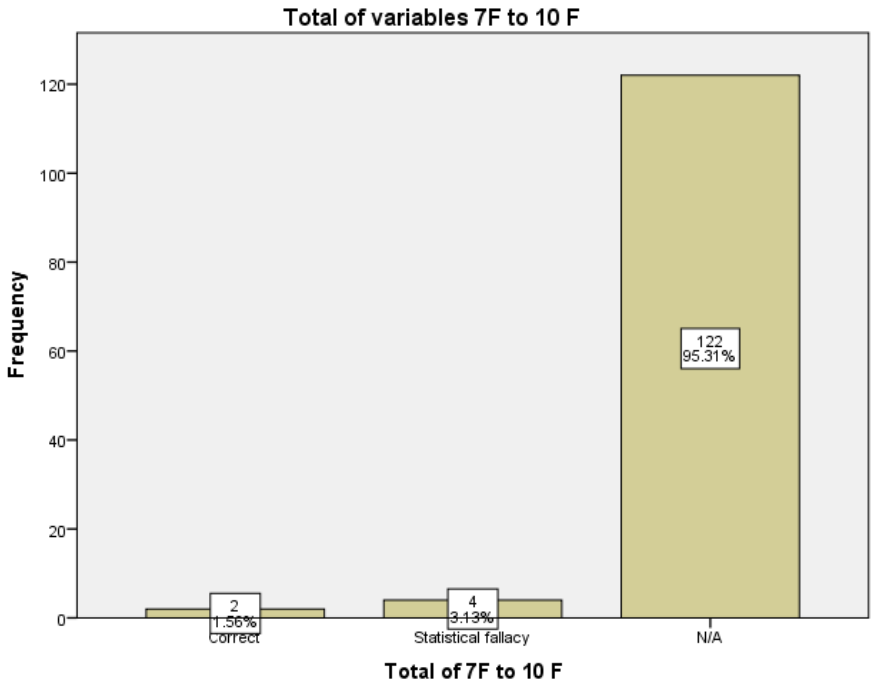


Figure 19 Visual representation of Crown lawyer discussion of RMPs (Q. 7-10 F)

Using the same correction factor of 10 possible Lineage RMPs, the Crown lawyer responses are as follows:

Of a possible 10 RMPs, a Crown lawyer discussed 6 (60.0%). Of those 6, Two (20.0%) were Correct. The remaining 4 (40.0%) were Statistical Fallacy.

Summary of Judge discussion of Lineage RMP:

Table 16 Coding of Judge discussion of lineage random match probability (Q. 7-10 H)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Correct	7	5.5	5.5	5.5
	n/a	121	94.5	94.5	100.0
	Total	128	100.0	100.0	

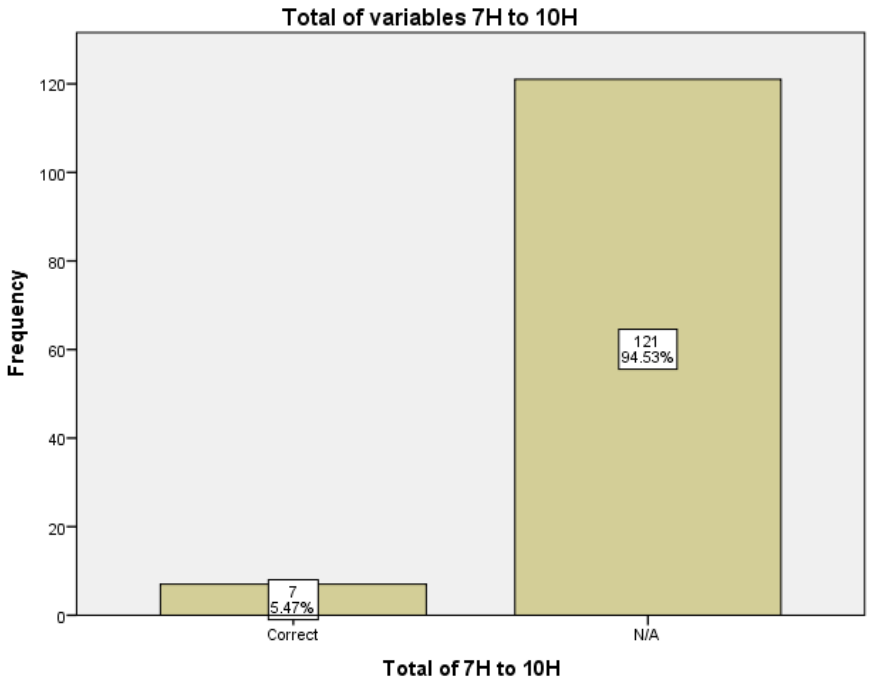


Figure 20 Visual representation of Judge discussion of RMPs (Q. 7-10 H)

Using the same correction factor of ten possible Lineage RMPs, the Judge responses are as follows:

Of a possible ten RMPs, a Judge discussed seven (70.0%). All of those responses were correct (70.0%). A Judge did not make a Statistical Fallacy with Lineage RMPs in the cases studied.

Questions 11 to 13

Summary of Expert Witness Discussion of Body Fluid

Table 17 Coding of Expert Witness discussion of body fluid source (Q. 11-12 A)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	No to source	15	23.4	23.4	23.4
	Likely source	5	7.8	7.8	31.3
	Conclusively source	32	50.0	50.0	81.3
	n/a	12	18.8	18.8	100.0
	Total	64	100.0	100.0	

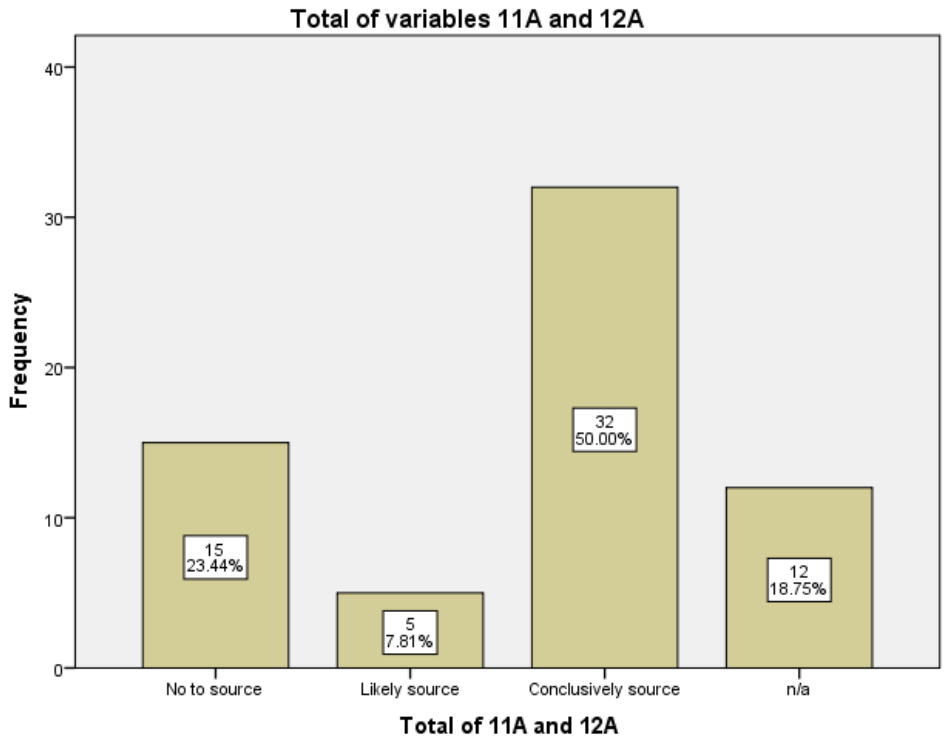


Figure 21 Visual representation of Expert Witness discussion of body fluid source (Q. 11-12 A)

In 64 possible instances (32 cases x 2 instances per), discussion of body fluid source appeared 52 times (81.3%). Of those 52 instances, an Expert stated they could not identify the body fluid source of a profile 15 times (15/52=28.9%). An Expert stated that

a particular body fluid was the likely source of a profile 5 times (5/52=9.6%), and stated that a particular body fluid was conclusively the source of a profile 32 times (32/52=61.5%).

The following three variables (11 & 12 C, E, and G) take measure of how often Defence lawyers, Crown lawyers, and Judges spoke consistently with the Expert witness about body fluid source.

Summary of Defence lawyer discussion of Body Fluid

Table 18 Coding of Defence lawyer discussion of body fluid source (Q. 11-12 C)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Consistent with expert	25	39.1	39.1	39.1
	Inconsistent with expert	15	23.4	23.4	62.5
	n/a	24	37.5	37.5	100.0
	Total	64	100.0	100.0	

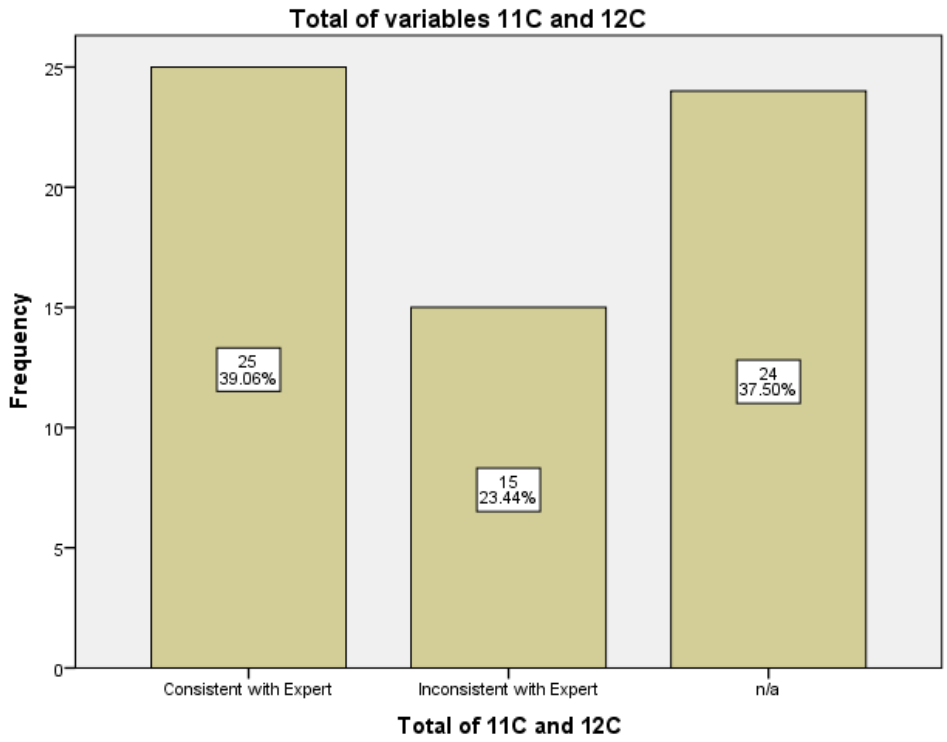


Figure 22 Visual representation of Defence lawyer discussion of body fluid source (Q. 11-12 C)

Using the number of body fluid source instances spoken of by an Expert (52) as the total, the Defence lawyer responses are as follows:

Of 52 possible instances to discuss body fluid source of a profile, a Defence lawyer discussed 40 (40/52=76.9%). Of those 40 instances, a Defence lawyer was consistent with the Expert 25 times (25/52=48.1%). The remaining 15 (15/52=28.8%) instances were inconsistent with the Expert.

Summary of Crown lawyer discussion of Body Fluid

Table 19 Coding of Crown lawyer discussion of body fluid source (Q. 11-12 E)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Consistent with expert	29	45.3	45.3	45.3
	Inconsistent with expert	12	18.8	18.8	64.1
	n/a	23	35.9	35.9	100.0
	Total	64	100.0	100.0	

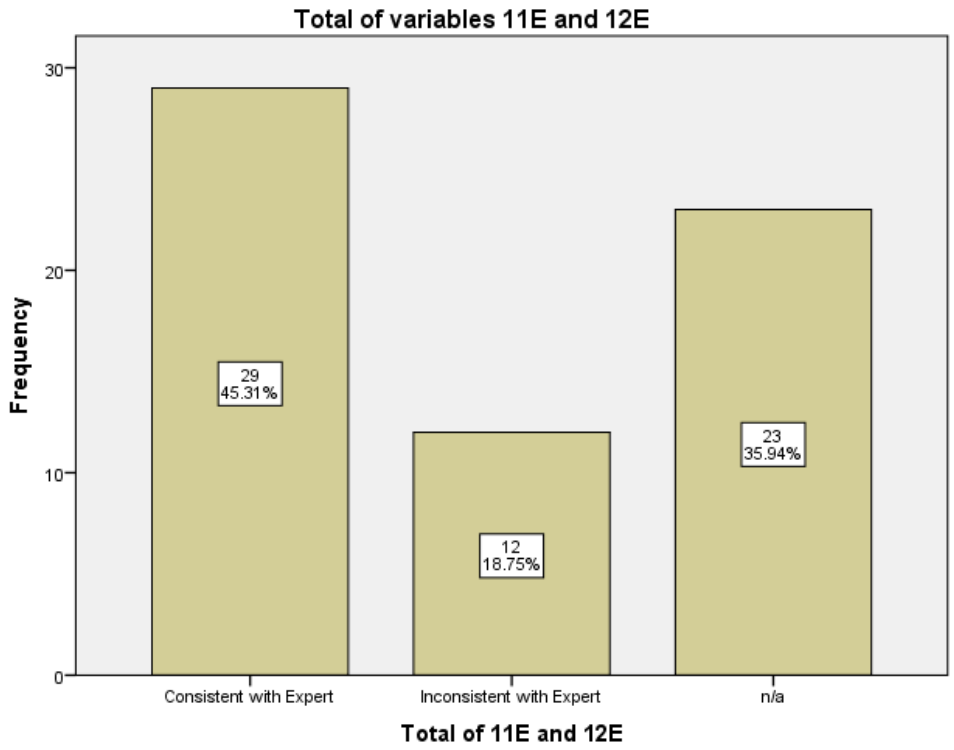


Figure 23 Visual representation of Crown lawyer discussion of body fluid source (Q. 11-12E)

Using the same correction factor of 52 possible instances of body fluid source, the Crown lawyer responses are as follows:

Of 52 possible instances to discuss body fluid source of a profile, a Crown lawyer discussed 41 (41/52=78.8%). Of those 41 instances, a Crown lawyer was consistent

with the Expert 29 times (29/52=55.8%). The remaining 12 (23.1%) instances were inconsistent with the Expert.

Summary of Judge discussion of Body Fluid

Table 20 Coding of Judge discussion of body fluid source (Q. 11-12 G)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Consistent with expert	32	50.0	50.0	50.0
	Inconsistent with expert	5	7.8	7.8	57.8
	n/a	27	42.2	42.2	100.0
	Total	64	100.0	100.0	

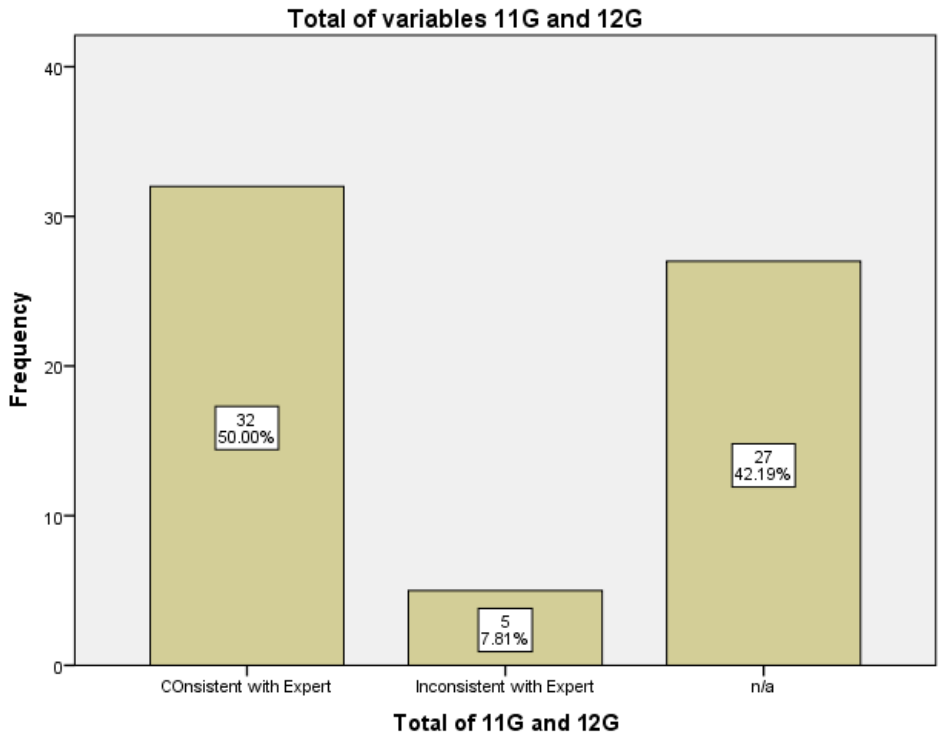


Figure 24 Visual representation of Judge discussion of body fluid source (Q. 11-12 G)

Using the same correction factor of 52 possible instances of body fluid source, the Judge responses are as follows:

Of 52 possible instances to discuss body fluid source of a profile, a Judge discussed 37 (37/52=71.2%). Of those 37 instances, a Judge was consistent with the Expert 32 times (32/52=61.5%). The remaining 5 (5/52=9.6%) instances of a Judge speaking of a body fluid source were inconsistent with the Expert.

Table 21 Summary of Defence, Crown, and Judge consistency with Expert while discussing body fluid source

	Consistent	Inconsistent	Missing
Defence	48.1%	28.8%	23.1%
Crown	55.8%	23.1%	21.1%
Judge	61.5%	9.6%	28.9%

Overall, the Judges were more consistent with the Experts when speaking about body fluid, while the Defence lawyers were the least consistent.

Jury or Non-jury?

Table 22 Summary of cases in Jury and Non-jury trials (Q. 13)

		Frequency	Percent	Valid Percent	Cumulative Percent
Valid	Non-jury	8	25.0	25.0	25.0
	Jury	24	75.0	75.0	100.0
	Total	32	100.0	100.0	

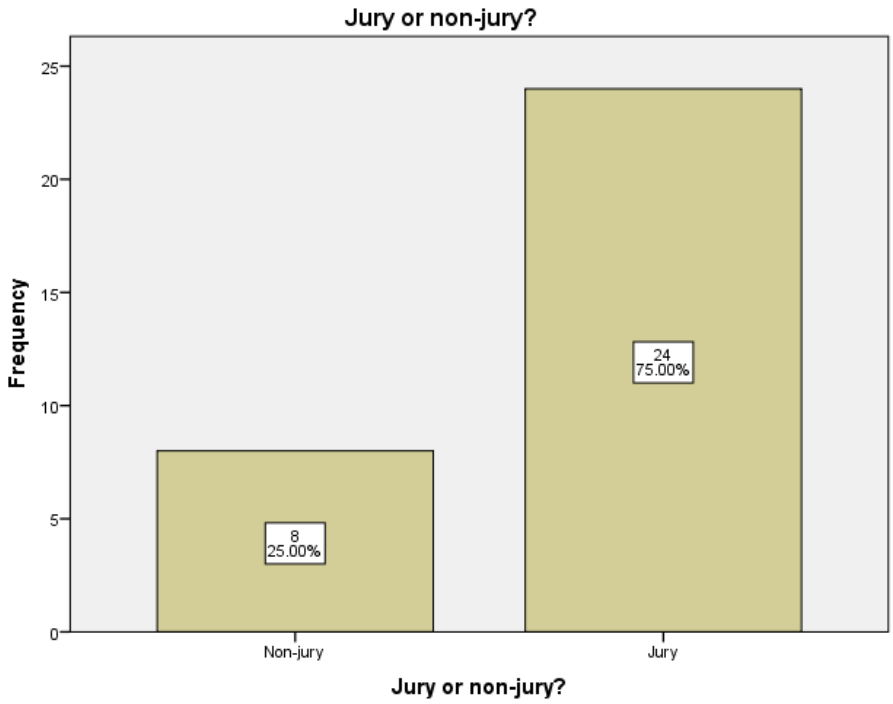


Figure 25 Visual representation of cases in Jury or Non-jury trials (Q. 13)

The total number of cases studied was 32. Of those, 8 (25.0%) were Non-jury cases, and 24 (75.0%) were Jury cases.

T-Test Comparing #Autosomal RMPs in Jury to Non-Jury Cases:

Table 23 Two-tailed t-test group statistics

Jury or Non-jury?		N	Mean	Std. Deviation	Std Error Mean
# RMP STR	Non-jury	8	2.13	1.126	.398
	Jury	24	3.88	1.262	.258

Table 24 Independent samples t-test

			# RMP STR	
			Equal variances assumed	Equal variances not assumed
Levene's Test for Equality of Variances	f		.544	
	Sig.		.466	
t-test for Equality of Means	t		-3.481	-3.691
	df		30	13.375
	Sig. (2-tailed)		.002	.003
	Mean Difference		-1.750	-1.750
	Std. Error Difference		.503	.474
	95% Confidence Interval of the Difference	Lower	-2.777	-2.771
		Upper	-.723	-.729

Hypothesis: There is a statistically significant difference between the number of autosomal RMPs presented in a Jury case and the number of RMPs presented in a non-Jury case.

Null: There is not a statistically significant difference between the number of autosomal RMPs presented in a Jury case and the number of RMPs presented in a non-Jury case.

Levene's test F statistic of 0.544 had a significance of 0.466 ($p>0.05$), and therefore equal variances were assumed. The t-value of -3.481 had a significance of 0.02

($p<0.05$), and therefore the null hypothesis was rejected. There is a statistically significant difference between the number of RMPs presented in a Jury case and the number of RMPs presented in a non-Jury case, with 1.750 more on average being presented to juries.

There were too few Lineage RMPs studied in this project to run a statistically significant t-test.

Cross-tabulations:

Comparing Autosomal RMP responses of Expert to Defence, to Crown, and to Judge, across Jury or Non-jury cases.

Autosomal RMP Defence cross Expert cross Jury or Non-jury

Table 25 Cross-tabulation of dependent variable Defence lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Autosomal RMP)

Jury or Non-jury			Expert				
			Correct	Statistical Fallacy	Admission of Source	n/a	Total
Non-jury Defence	Correct	Count	1	0	0	0	1
		% within total Expert	7.1%	0.0%	0.0%	0.0%	3.1%
		% of Total	3.1%	0.0%	0.0%	0.0%	3.1%
	Statistical Fallacy	Count	6	2	0	0	8
		% within total Expert	42.9%	100.0%	0.0%	0.0%	25.0%
		% of Total	18.8%	6.3%	0.0%	0.0%	25.0%
	n/a	Count	7	0	1	15	23
		% within total Expert	50.0%	0.0%	100.0%	100.0%	71.9%
		% of Total	21.9%	0.0%	3.1%	46.9%	71.9%
	Total	Count	14	2	1	15	32
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	43.8%	6.3%	3.1%	46.9%	100.0%
Jury Defence	Correct	Count	3		0	0	3
		% within total Expert	4.1%		0.0%	0.0%	3.1%
		% of Total	3.1%		0.0%	0.0%	3.1%
	Statistical Fallacy	Count	11		0	0	11
		% within total Expert	15.1%		0.0%	0.0%	11.5%
		% of Total	11.5%		0.0%	0.0%	11.5%
	Admission of source	Count	6		3	0	9
		% within total Expert	8.2%		27.3%	0.0%	9.4%
		% of Total	6.3%		3.1%	0.0%	9.4%
	n/a	Count	53		8	12	73
		% within total Expert	72.6%		72.7%	100.0%	76.0%
		% of Total	55.2%		8.3%	12.5%	76.0%
	Total	Count	73		11	12	96
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	76.0%		11.5%	12.5%	100.0%

3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by Defence, compared to 3.1% (3) in a Jury case. 18.8% (6) of responses by an Expert that were Correct, in a Non-jury case, were Statistical Fallacy by a Defence lawyer, compared to 11.5% (11) in a Jury case. 21.9% (7) of responses by an Expert that were Correct, in a Non-jury case, were not mentioned by a Defence lawyer, compared to 55.2% (53) in a Jury case. 3.1% (1) of responses by an Expert that were Admission of Source, in a Non-jury case, were not mentioned by a Defence lawyer, while 3.1% (3) of Admission of Source responses by an Expert in a Jury case were also Admission of Source by a Defence lawyer.

In a Jury case, 6 (6.3%) Correct responses by an Expert were Admission of Source by a Defence lawyer. The 2 (6.3%) Statistical Fallacies made by an Expert were in a Non-jury case, and were Statistical Fallacy by a Defence lawyer. All 15 (46.9%) of responses by an Expert in a Non-jury case that were Not Applicable, were also Not Applicable by a Defence lawyer, compared to 12 (12.5%) in a Jury case.

Table 26 Summary of Defence lawyer responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	4.1%	7.1%
Statistical Fallacy	15.1%	42..9%
Admission of Source	8.2%	0.0%
Not Applicable	72.6%	50.0%

Overall, a higher percentage of a Defence lawyer's responses were Correct, when an Expert was Correct, in a Non-jury case (7.1%) than a Jury case (4.1%). A higher percentage of a Defence lawyer's responses were Statistical Fallacy, when an Expert was Correct, in a Non-jury case (42.9%) than a Jury case (15.1%). A higher percentage of a

Defence lawyer's responses were Not Applicable, when an Expert was Correct, in a Jury case (72.6%) than a Non-jury case (50.0%). 6 (8.2%) of a Defence lawyer's responses, when an Expert was Correct, in a Jury case, were Admission of Source, compared to none in a Non-jury case.

Autosomal RMP Crown cross Expert cross Jury or Non-jury

Table 27 Cross-tabulation of dependent variable Crown lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Autosomal RMP)

Jury or Non-jury			Expert				
			Correct	Statistical Fallacy	Admission of Source	n/a	Total
Non-jury Crown	Correct	Count	1	0	0	0	1
		% within total Expert	7.1%	0.0%	0.0%	0.0%	3.1%
		% of Total	3.1%	0.0%	0.0%	0.0%	3.1%
	Statistical Fallacy	Count	7	0	0	0	7
		% within total Expert	50.0%	0.0%	0.0%	0.0%	21.9%
		% of Total	21.9%	0.0%	0.0%	0.0%	21.9%
	n/a	Count	6	2	1	15	24
		% within total Expert	42.9%	100.0%	100.0%	100.0%	75.0%
		% of Total	18.8%	6.3%	3.1%	46.9.%	75.0%
	Total	Count	14	2	1	15	32
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	43.8%	6.3%	3.1%	46.9%	100.0%
Jury Crown	Correct	Count	10		2	0	12
		% within total Expert	13.7%		18.2%	0.0%	12.5%
		% of Total	10.4%		2.1%	0.0%	12.5%
	Statistical Fallacy	Count	20		0	0	20
		% within total Expert	27.4%		0.0%	0.0%	20.8%
		% of Total	20.8%		0.0%	0.0%	20.8%
	Admission of source	Count	6		3	0	9
		% within total Expert	8.2%		27.3%	0.0%	9.4%
		% of Total	6.3%		3.1%	0.0%	9.4%
	n/a	Count	37		6	12	55
		% within total Expert	50.7%		54.5%	100.0%	57.3%
		% of Total	38.5%		6.3%	12.5%	57.3%
	Total	Count	73		11	12	96
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	76.0%		11.5%	12.5%	100.0%

3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by a Crown lawyer, compared to 10.4% (10) in a Jury case. 21.9% (7) of responses by an Expert that were Correct, in a Non-jury case, were Statistical Fallacy by a Crown lawyer, compared to 27.4% (20) in a Jury case. 18.8% (6) of responses by an Expert that were Correct, in a Non-jury case, were not mentioned by a Crown lawyer, compared to 38.5% (37) in a Jury case. 3.1% (1) of responses by an Expert that were Admission of Source, in a Non-jury case, were not mentioned by a Crown lawyer. In a Jury case, 2 (2.1%) Admission of Source responses by an Expert were Correct, 3 (3.1%) were Admission of Source, and 6 (6.3%) were not discussed, by a Crown lawyer, respectively.

The 2 (6.3%) Statistical Fallacies made by an Expert were in a Non-jury case, and were not mentioned by a Crown lawyer. All 15 (46.9%) of responses by an Expert in a Non-jury case that were Not Applicable, were also Not Applicable by a Crown lawyer, compared to 12 (12.5%) in a Jury case.

Table 28 Summary of Crown lawyer responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	13.7%	7.1%
Statistical Fallacy	27.4%	50.0%
Admission of Source	8.2%	0.0%
Not Applicable	50.7%	42.9%

Overall, a higher percentage of a Crown lawyer's responses were Correct, when an Expert was Correct, in a Jury case (13.7%) than in a Non-jury case (7.1%). A higher percentage of a Crown lawyer's responses were Statistical Fallacy, when an Expert was Correct, in a Non-jury case (50.0%) than a Jury case (27.4%). A higher percentage of a

Crown lawyer's responses were Not Applicable, when an Expert was Correct, in a Jury case (50.7%) than a Non-jury case (42.9%). 6 (8.2%) of a Crown lawyer's responses, when an Expert was Correct, in a Jury case, were Admission of Source, compared to none in a Non-jury case.

Autosomal RMP Judge cross Expert cross Jury or Non-jury

Table 29 Cross-tabulation of dependent variable Judge responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Autosomal RMP)

Jury or Non-jury			Expert				
			Correct	Statistical Fallacy	Admission of Source	n/a	Total
Non-jury Judge	Correct	Count	2	0	0	0	2
		% within total Expert	14.3%	0.0%	0.0%	0.0%	6.3%
		% of Total	6.3%	0.0%	0.0%	0.0%	6.3%
	Statistical Fallacy	Count	3	0	0	0	3
		% within total Expert	21.4%	0.0%	0.0%	0.0%	9.4%
		% of Total	9.4%	0.0%	0.0%	0.0%	9.4%
	Admission of source	Count	0	0	1	0	1
		% within total Expert	0.0%	0.0%	100.0%	0.0%	3.1%
		% of Total	0.0%	0.0%	3.1%	0.0%	3.1%
	n/a	Count	9	2	0	15	26
		% within total Expert	64.3%	100.0%	0.0%	100.0%	81.3%
		% of Total	28.1%	6.3%	0.0%	46.9.%	81.3%
	Total	Count	14	2	1	15	32
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	43.8%	6.3%	3.1%	46.9%	100.0%
Jury Judge	Correct	Count	24		3	0	27
		% within total Expert	32.9%		27.3%	0.0%	28.1%
		% of Total	25.0%		3.1%	0.0%	28.1%
	Statistical Fallacy	Count	16		0	0	16
		% within total Expert	21.9%		0.0%	0.0%	16.7%
		% of Total	16.7%		0.0%	0.0%	16.7%
	Admission of source	Count	5		4	0	9
		% within total Expert	6.8%		36.4%	0.0%	9.4%
		% of Total	5.2%		4.2%	0.0%	9.4%
	n/a	Count	28		4	12	44
		% within total Expert	38.4%		36.4%	100.0%	45.8%
		% of Total	29.2%		4.2%	12.5%	45.8%
	Total	Count	73		11	12	96
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	76.0%		11.5%	12.5%	100.0%

6.3% (2) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by a Judge, compared to 25.0% (24) in a Jury case. 9.4% (3) of responses by an Expert that were Correct, in a Non-jury case, were Statistical Fallacy by a Judge, compared to 16.7% (16) in a Jury case. 28.1% (9) of responses by an Expert that were Correct, in a Non-jury case, were not mentioned by a Judge, compared to 29.2% (28) in a Jury case. 5.2% (5) of responses by an Expert that were Correct, in a Jury case, were Admission of Source by a Judge, compared to none in a Non-jury case.

3.1% (1) of responses by an Expert that were Admission of Source, in a Non-jury case, was also Admission of Source by a Judge. In a Jury case, 3 (3.1%) Admission of Source responses by an Expert were Correct, 4 (4.2%) were Admission of Source, and 4 (4.2%) were not discussed, by a Judge, respectively. The 2 (6.3%) Statistical Fallacies made by an Expert were in a Non-jury case, and were not mentioned by a Judge. All 15 (46.9%) of responses by an Expert in a Non-jury case that were Not Applicable, were also Not Applicable by a Judge, compared to 12 (12.5%) in a Jury case.

Table 30 Summary of Judge responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	32.9%	14.3%
Statistical Fallacy	21.9%	21.4%
Admission of Source	6.8%	0.0%
Not Applicable	38.4%	64.3%

Overall, a higher percentage of a Judge's responses were Correct, when an Expert was Correct, in a Jury case (32.9%) than in a Non-jury case (14.3%). A higher percentage of a Judge's responses were Statistical Fallacy, when an Expert was Correct, in a Jury case (21.9%) than a Non-jury case (21.4%). A higher percentage of a Judge's

responses, when an Expert was Correct, were Admission of Source in a Jury case (6.8%) than a Non-jury case (0.0%). A higher percentage of a Judge's responses were Not Applicable, when an Expert was Correct, in a Non-jury case (64.3%) than a Jury case (38.4%).

Table 31 Summary of Defence, Crown, and Judge responses when Expert Witness discussion of Autosomal RMP is "Correct", across Jury and Non-jury trials

Response Attribute	Justice System Participant	Jury	Non-jury
Correct	Defence	4.1%	7.1%
	Crown	13.7%	7.1%
	Judge	32.9%	14.3%
Statistical Fallacy	Defence	15.1%	42.9%
	Crown	27.4%	50.0%
	Judge	21.9%	21.4%
Admission of Source	Defence	8.2%	0.0%
	Crown	8.2%	0.0%
	Judge	6.8%	0.0%
Not Applicable	Defence	72.6%	50.0%
	Crown	50.7%	42.9%
	Judge	38.4%	64.3%

Lineage RMP Defence cross Expert cross Jury or Non-jury

Table 32 Cross-tabulation of dependent variable Defence lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Lineage RMP)

Jury or Non-jury			Expert		
			Correct	n/a	Total
Non-jury Defence	Correct	Count	1	0	1
		% within total Expert	33.3%	0.0%	3.1%
		% of Total	3.1%	0.0%	3.1%
	Statistical Fallacy	Count	1	0	1
		% within total Expert	33.3%	0.0%	3.1%
		% of Total	3.1%	0.0%	3.1%
	n/a	Count	1	29	30
		% within total Expert	33.3%	100.0%	93.8%
		% of Total	3.1%	90.6%	93.8%
	Total	Count	3	29	32
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	9.4%	90.6%	100.0%
Jury Defence	Correct	Count	1	0	1
		% within total Expert	14.3%	0.0%	1.0%
		% of Total	1.0%	0.0%	1.0%
	Statistical Fallacy	Count	2	0	2
		% within total Expert	28.6%	0.0%	2.1%
		% of Total	2.1%	0.0%	2.1%
	n/a	Count	4	89	93
		% within total Expert	57.1%	100.0%	96.9%
		% of Total	4.2%	92.7%	96.9%
	Total	Count	7	89	96
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	7.3%	92.7%	100.0%

3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by a Defence lawyer, compared to 1.0% (1) in a Jury case. 3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were Statistical Fallacy by a Defence lawyer, compared to 2.1% (2) in a Jury case. 3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were not mentioned by a Defence lawyer, compared to 4.2% (4) in a Jury case. All 29 (90.6%) of responses by an Expert in a Non-

jury case that were Not Applicable, were also Not Applicable by a Defence lawyer, compared to 89 (92.7%) in a Jury case.

Table 33 Summary of Defence lawyer responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	1.0%	3.1%
Statistical Fallacy	2.1%	3.1%
Not Applicable	4.2%	3.1%

Overall, a higher percentage of a Defence lawyer's responses were Correct, when an Expert was Correct, in a Non-jury case (3.1%) than in a Jury case (1.0%). A higher percentage of a Defence lawyer's responses were Statistical Fallacy, when an Expert was Correct, in a Non-jury case (3.1%) than a Jury case (2.1%). A higher percentage of a Defence lawyer's responses were Not Applicable, when an Expert was Correct, in a Jury case (4.2%) than a Non-jury case (3.1%).

Lineage RMP Crown cross Expert cross Jury or Non-jury

Table 34 Cross-tabulation of dependent variable Crown lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Lineage RMP)

Jury or Non-jury			Expert		
			Correct	n/a	Total
Non-jury Crown	Correct	Count	1	0	1
		% within total Expert	33.3%	0.0%	3.1%
		% of Total	3.1%	0.0%	3.1%
	Statistical Fallacy	Count	2	0	2
		% within total Expert	66.7%	0.0%	6.3%
		% of Total	6.3%	0.0%	6.3%
	n/a	Count	0	29	29
		% within total Expert	0.0%	100.0%	90.6%
		% of Total	0.0%	90.6%	90.6%
	Total	Count	3	29	32
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	9.4%	90.6%	100.0%
Jury Crown	Correct	Count	1	0	1
		% within total Expert	14.3%	0.0%	1.0%
		% of Total	1.0%	0.0%	1.0%
	Statistical Fallacy	Count	2	0	2
		% within total Expert	28.6%	0.0%	2.1%
		% of Total	2.1%	0.0%	2.1%
	n/a	Count	4	89	93
		% within total Expert	57.1%	100.0%	96.9%
		% of Total	4.2%	92.7%	96.9%
	Total	Count	7	89	96
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	7.3%	92.7%	100.0%

3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by a Crown lawyer, compared to 1.0% (1) in a Jury case. 6.3% (2) of responses by an Expert that were Correct, in a Non-jury case, were Statistical Fallacy by a Crown lawyer, compared to 2.1% (2) in a Jury case. 4.2% (4) of responses by an Expert that were Correct, in a Jury case, were not mentioned by a Crown lawyer,

compared to none in a Non-jury case. All 29 (90.6%) of responses by an Expert in a Non-jury case that were Not Applicable, were also Not Applicable by a Crown lawyer, compared to 89 (92.7%) in a Jury case.

Table 35 Summary of Crown lawyer responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	1.0%	3.1%
Statistical Fallacy	2.1%	6.3%
Not Applicable	4.2%	0.0%

Overall, a higher percentage of a Crown lawyer's responses were Correct, when an Expert was Correct, in a Non-jury case (3.1%) than in a Jury case (1.0%). A higher percentage of a Crown lawyer's responses were Statistical Fallacy, when an Expert was Correct, in a Non-jury case (6.3%) than a Jury case (2.1%). A higher percentage of a Crown lawyer's responses were Not Applicable, when an Expert was Correct, in a Jury case (4.2%) compared to none in a Non-jury case.

Lineage RMP Judge cross Expert cross Jury or Non-jury

Table 36 Cross-tabulation of dependent variable Judge responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Lineage RMP)

Jury or Non-jury			Expert		
			Correct	n/a	Total
Non-jury Judge	Correct	Count	1	0	1
		% within total Expert	33.3%	0.0%	3.1%
		% of Total	3.1%	0.0%	3.1%
	n/a	Count	2	29	31
		% within total Expert	66.7%	100.0%	96.9%
		% of Total	6.3%	90.6%	96.9%
	Total	Count	3	29	32
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	9.4%	90.6%	100.0%
Jury Judge	Correct	Count	6	0	6
		% within total Expert	85.7%	0.0%	6.3%
		% of Total	6.3%	0.0%	6.3%
	n/a	Count	1	89	90
		% within total Expert	14.3%	100.0%	93.8%
		% of Total	1.0%	92.7%	93.8%
	Total	Count	7	89	96
		% within total Expert	100.0%	100.0%	100.0%
		% of Total	7.3%	92.7%	100.0%

3.1% (1) of responses by an Expert that were Correct, in a Non-jury case, were also Correct by a Judge, compared to 6.3% (6) in a Jury case. 6.3% (2) of responses by an Expert that were Correct, in a Non-jury case, were not mentioned by a Judge, compared to 1.0% (1) in a Jury case. All 29 (90.6%) of responses by an Expert in a Non-jury case that were Not Applicable, were also Not Applicable by a Judge, compared to 89 (92.7%) in a Jury case.

Table 37 Summary of Judge responses when Expert Witness response "Correct"

Response attribute	Jury case	Non-jury case
Correct	6.3%	3.1%
Not Applicable	1.0%	6.3%

Overall, a higher percentage of a Judge's responses were Correct, when an Expert was Correct, in a Jury case (6.3%) than in a Non-jury case (3.1%). A higher percentage of a Judge's responses were Not Applicable, when an Expert was Correct, in a Non-jury case (6.3%) than a Jury case (1.0%). A Judge did not create a Statistical Fallacy or Admit a Source for Lineage RMPs in any of the cases studied.

Table 38 Summary of Defence, Crown, and Judge responses when Expert Witness discussion of Lineage RMP is "Correct", across Jury and Non-jury trials

Response Attribute	Justice System Participant	Jury	Non-jury
Correct	Defence	1.0%	3.1%
	Crown	1.0%	3.1%
	Judge	1.0%	3.1%
Statistical Fallacy	Defence	2.1%	3.1%
	Crown	2.1%	6.3%
	Judge	0.0%	0.0%
Not Applicable	Defence	4.2%	3.1%
	Crown	4.2%	0.0%
	Judge	4.2%	0.0%

Body Fluid Defence cross Expert cross Jury or Non-jury

Table 39 Cross-tabulation of dependent variable Defence lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Body Fluid Source)

Jury or Non-jury			Expert				
			No to source	Likely source	Conclusively source	n/a	Total
Non-jury Defence	Consistent with Expert	Count	3		4	0	7
		% within total Expert	50.0%		66.7%	0.0%	43.8%
		% of Total	18.8%		25.0%	0.0%	43.8%
	Inconsist. with Expert	Count	2		1	0	3
		% within total Expert	33.3%		16.7%	0.0%	18.8%
		% of Total	12.5%		6.3%	0.0%	18.8%
	n/a	Count	1		1	4	6
		% within total Expert	16.7%		16.7%	100.0%	37.5%
		% of Total	6.3%		6.3%	25.0%	37.5%
	Total	Count	6		6	4	16
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	37.5%		37.5%	25.0%	100.0%
Jury Defence	Consistent with Expert	Count	8	3	7	0	18
		% within total Expert	88.9%	60.0%	26.9%	0.0%	37.5%
		% of Total	16.7%	6.3%	14.6%	0.0%	37.5%
	Inconsist. with Expert	Count	0	1	11	0	12
		% within total Expert	0.0%	20.0%	42.3%	0.0%	25.0%
		% of Total	0.0%	2.1%	22.9%	0.0%	25.0%
	n/a	Count	1	1	8	8	18
		% within total Expert	11.1%	20.0%	30.8%	100.0%	37.5%
		% of Total	2.1%	2.1%	16.7%	16.7%	37.5%
	Total	Count	9	5	26	8	48
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	18.8%	10.4%	54.2%	16.7%	100.0%

18.8% (3) of responses by an Expert that were No to Source, in a Non-jury case, were Consistent with Expert by a Defence lawyer, compared to 16.7% (8) in a Jury case. 12.5% (2) of responses by an Expert that were No to Source, in a Non-jury case, were Inconsistent with Expert by a Defence lawyer, compared to none in a Jury case. 6.3% (1) of responses by an Expert that were No to Source, in a Non-jury case, were not mentioned by a Defence lawyer, compared to 2.1% (1) in a Jury case. 6.3% (3) of responses by an Expert that were Likely a Source, only in a Jury case, were Consistent with Expert by a Defence lawyer, while 2.1% (1) were Inconsistent with Expert by a Defence lawyer. 2.1% (1) was not mentioned by a Defence lawyer.

25.0% (4) of responses by Expert that were Conclusively a Source, in a Non-jury case, were Consistent with Expert by a Defence lawyer, compared to 14.6% (7) in a Jury case. 6.3% (1) of responses by an Expert that were Conclusively a Source, in a Non-jury case, were Inconsistent with Expert by a Defence lawyer, compared to 22.9% (11) in a Jury case. All 4 (25.0%) of Not Applicable responses by an Expert, in a Non-jury case, were also Not Applicable by a Defence lawyer, compared to 16.7% (8) in a Jury case.

Body Fluid Crown cross Expert cross Jury or Non-jury

Table 40 Cross-tabulation of dependent variable Crown lawyer responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Body Fluid Source)

Jury or Non-jury			Expert				
			No to source	Likely source	Conclusively source	n/a	Total
Non-jury Crown	Consistent with Expert	Count	5		2	0	7
		% within total Expert	83.3%		33.3%	0.0%	43.8%
		% of Total	31.3%		12.5%	0.0%	43.8%
	Inconsist. with Expert	Count	0		2	0	2
		% within total Expert	0.0%		33.3%	0.0%	12.5%
		% of Total	0.0%		12.5%	0.0%	12.5%
	n/a	Count	1		2	4	7
		% within total Expert	16.7%		33.3%	100.0%	43.8%
		% of Total	6.3%		12.5%	25.0%	43.8%
	Total	Count	6		6	4	16
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	37.5%		37.5%	25.0%	100.0%
Jury Crown	Consistent with Expert	Count	6	1	15	0	22
		% within total Expert	66.7%	20.0%	57.7%	0.0%	45.8%
		% of Total	12.5%	2.1%	31.3%	0.0%	45.8%
	Inconsist. with Expert	Count	2	4	4	0	10
		% within total Expert	22.2%	80.0%	15.4%	0.0%	20.8%
		% of Total	4.2%	8.3%	8.3%	0.0%	20.8%
	n/a	Count	1	0	7	8	16
		% within total Expert	11.1%	0.0%	26.9%	100.0%	33.3%
		% of Total	2.1%	0.0%	14.6%	16.7%	33.3%
	Total	Count	9	5	26	8	48
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	18.8%	10.4%	54.2%	16.7%	100.0%

31.3% (5) of responses by an Expert that were No to Source, in a Non-jury case, were Consistent with Expert by a Crown lawyer, compared to 12.5% (6) in a Jury case. 4.2% (2) of responses by an Expert that were No to Source, in a Jury case, were Inconsistent with Expert by a Crown lawyer, compared to none in a Non-jury case. 6.3% (1) of responses by an Expert that were No to Source, in a Non-jury case, were not mentioned by a Crown lawyer, compared to 2.1% (1) in a Jury case. 2.1% (1) of responses by an Expert that were Likely a Source, only in a Jury case, were Consistent with Expert by a Crown lawyer, while 8.3% (4) were Inconsistent with Expert by a Crown lawyer. None were not mentioned by a Crown lawyer.

12.5% (2) of responses by Expert that were Conclusively a Source, in a Non-jury case, were Consistent with Expert by a Crown lawyer, compared to 31.3% (15) in a Jury case. 12.5% (2) of responses by an Expert that were Conclusively a Source, in a Non-jury case, were Inconsistent with Expert by a Crown lawyer, compared to 8.3% (4) in a Jury case. All 4 (25.0%) of Not Applicable responses by an Expert, in a Non-jury case, were also Not Applicable by a Crown lawyer, compared to 16.7% (8) in a Jury case.

Body Fluid Judge cross Expert cross Jury or Non-jury

Table 41 Cross-tabulation of dependent variable Judge responses, independent variable Expert Witness responses, and layer/control variable Jury or Non-jury trial (Body Fluid Source)

Jury or Non-jury			Expert				
			No to source	Likely source	Conclusively source	n/a	Total
Non-jury Judge	Consistent with Expert	Count	5		2	0	6
		% within total Expert	83.3%		33.3%	0.0%	37.5%
		% of Total	31.3%		12.5%	0.0%	37.5%
	n/a	Count	2		4	4	10
		% within total Expert	33.3%		66.7%	100.0%	62.5%
		% of Total	12.5%		25.0%	25.0%	62.5%
	Total	Count	6		6	4	16
		% within total Expert	100.0%		100.0%	100.0%	100.0%
		% of Total	37.5%		37.5%	25.0%	100.0%
Jury Judge	Consistent with Expert	Count	6	1	19	0	26
		% within total Expert	66.7%	20.0%	73.1%	0.0%	54.2%
		% of Total	12.5%	2.1%	39.6%	0.0%	54.2%
	Inconsist. with Expert	Count	1	1	3	0	5
		% within total Expert	11.1%	20.0%	11.5%	0.0%	10.4%
		% of Total	2.1%	2.1%	6.3%	0.0%	10.4%
	n/a	Count	2	3	4	8	17
		% within total Expert	22.2%	60.0%	15.4%	100.0%	35.4%
		% of Total	4.2%	6.3%	8.3%	16.7%	35.4%
	Total	Count	9	5	26	8	48
		% within total Expert	100.0%	100.0%	100.0%	100.0%	100.0%
		% of Total	18.8%	10.4%	54.2%	16.7%	100.0%

25.0% (4) of responses by an Expert that were No to Source, in a Non-jury case, were Consistent with Expert by a Judge, compared to 12.5% (6) in a Jury case. 2.1% (1) of responses by an Expert that were No to Source, in a Jury case, were Inconsistent with Expert by a Judge, compared to none in a Non-jury case. 12.5% (2) of responses by an Expert that were No to Source, in a Non-jury case, were not mentioned by a Judge, compared to 4.2% (2) in a Jury case. 2.1% (1) of responses by an Expert that were Likely a Source, only in a Jury case, were Consistent with Expert by a Judge, while 2.1% (1) were Inconsistent with Expert by a Judge. 6.3% (3) were not mentioned by a Judge.

12.5% (2) of responses by Expert that were Conclusively a Source, in a Non-jury case, were Consistent with Expert by a Judge, compared to 39.6% (19) in a Jury case. 6.3% (3) of responses by an Expert that were Conclusively a Source, in a Jury case, were Inconsistent with Expert by a Judge, compared to none in a Non-jury case. All 4 (25.0%) of Not Applicable responses by an Expert, in a Non-jury case, were also Not Applicable by a Judge, compared to 16.7% (8) in a Jury case.

Discussion

Autosomal DNA Profiles

Of the 32 cases that included the random match probability in the presentation of DNA evidence, most (18) discussed "4 or more" such probabilities within a case (Table 7). The number of RMPs was limited to four in anticipation of the types of criminal cases that were analyzed. Due to the nature of homicides and sexual assaults, there can be upwards of dozens of samples per case, however, recording every instance was beyond the scope of this project.

The sum of all RMPs tracked was displayed as an array of the experts', defence lawyers', crown lawyers' and judges' answers. What the individual totals show, from the defence lawyers' (Table 9) and crown lawyers' (Table 10) individual responses, is that on the occasion an RMP was attempted, it was most often a Statistical Fallacy. The judges' responses (Table 11) demonstrated the only reversal of this trend, with most attempted discussions of RMPs being Correct.

The number of opportunities to discuss RMPs was significantly different when comparing Jury cases to Non-jury cases. The number of autosomal RMPs presented in a Jury case was 1.75 more, on average, than the number presented in Non-jury cases (Table 24). One consideration for this discrepancy could certainly be the type of cases that end up in Jury trials versus Non-jury trials. Often break and enter criminal cases contain fewer DNA samples than homicides or sexual assaults; however, charges for individual cases were not tracked in this project. This difference certainly impacted the number of opportunities for lawyers to discuss RMPs in a Non-jury case; however, the opportunities for a judge to speak of the evidence in a Non-jury case was skewed regardless. The

routine consequence of Non-jury trials is that judges do not have to give a review of the evidence in a charge to the Jury. Charges to the Jury are by far the largest source of discussion of DNA evidence for a judge, and as such, it is reasonable the results of this study show they speak of the evidence fewer times than lawyers, overall.

Therefore, the exploration into the breakdown of response attributes by category was necessary to fully explore how each of the three non-scientist justice system participants were discussing the expert's DNA evidence. Outside of this study, cross-tabulations are primarily used for inferential statistics and investigation into relationships between variables. However, as this project involved such a small data set, the number of responses per category were routinely below the suggested threshold for statistical significance.

What the cross-tabulations *were* able to organize was the array of answers for each non-scientist justice system participant, when considering the experts' discussion of an RMP in a Jury and/or Non-jury setting. While there were a few answers given by the experts other than Correct (Statistical Fallacy and Admission of Source), it is the array of answers given when the experts were Correct that are of most interest. The cross-tabulations provided data for all response attributes; however, the exploration of what is being done with Correct expert testimony was one goal of this research project.

When comparing data from the defence lawyers and crown lawyers, what is of significant interest, is that both sets of non-scientist justice system participants avoid more than half of the RMPs presented correctly by the expert in a Jury case (Table 31). While the numbers are fewer for Non-jury cases, they are still well above zero. At the inception of this project, it was anticipated there could be a difference between the

number of RMPs discussed by the experts and the non-scientist justice system participants, but these data were surprising; they suggested that much of the work done by expert witnesses to provide and explain RMPs and statistical results was of no apparent consequence in later parts of the trial.

Of the RMPs discussed by each defence and crown lawyer, the percentage of Statistical Fallacy responses are both larger than the percentage of answers for the Correct discussion of RMP. Going into this project, it was anticipated that there could be instances of Statistical Fallacy by lawyers, but in this project data these instances outweighed the Correct attempts at discussing DNA evidence.

Lineage DNA Profiles

There were very few lineage RMPs observed compared to autosomal RMPs. The most common use of these types of DNA tests is to assess familial relationships, and are generally reserved for kinship tests. While the assessment of maternal or paternal relatedness is not unusual in criminal cases, it is a much rarer approach than standard autosomal tests in homicide, robbery, or sexual assault cases. By nature of the circumstances of the samples studied, mtDNA lineage tests were not commonly performed, as these tests are usually reserved for hair shafts and degraded bone samples.

Testing of the Y chromosome is a more commonly seen DNA test, as the utility serves an additional purpose compared to mtDNA. Y-STR tests are routinely performed during mixture analyses to investigate the number of male contributors to a sample (Butler, 2015). Y-STR profiles only contain one allele peak per loci (Figure 5), so the number of potential donors in the sample are more easily defined. As DNA mixtures

were not studied for this project, it was correctly anticipated to not see many uses of Y-STR RMPs.

When viewing the limited number of Lineage data, what is of note is the trend for judges. When discussing Lineage RMPs (Table 16), judges were flawless (7 "Correct", 0 "Statistical Fallacy", 7:0), compared to their discussion of Autosomal RMPs (Table 11) (29:19).

Case examples of statistical fallacy

There are numerous ways to misrepresent the Random Match Probability. As mentioned in the Methods Section, the term "Statistical Fallacy" in this thesis carried a broader definition than the transposed conditional described by Evett (1995). Below (Table 42) are actual examples from the cases studied, demonstrating fallacies such as transposing the conditional when speakers (as described) discussed autosomal RMPs.

Table 42 Examples of "Statistical Fallacy", excerpts from real court transcripts

Case	Speaker	Example
24	Judge	The DNA Analysis concluded that the sample from the [item] matched the defendant's DNA profile and the chances that the sample came from someone else were approximately 1 in 32 billion. It is safe to conclude the defendant left the DNA on the [item].
14	Judge	[Expert] then talked about the way she expressed that in terms of possibilities and she said that if someone were selected at random, the odds of that person's DNA matching [victim]'s DNA were one in two hundred billion. So, my interpretation of that is that the probability that the [gender] DNA on [accused]'s [item] came from somebody other than [victim] is about one in two hundred billion.
17	Defence	So you had, not only is he within two percent of the population as a result of the first round of forensic testing now they couldn't, now he couldn't be excluded either. So it's not just one in two fifty, it's somebody who has the profile on one in two fifty but also who has already been discriminated to the point where it's only two, he's, he already fell within two percent of the population who could've done it.
19	Crown	She looks at the profile. She looks at the DNA alleles, the lengths at each site that are given by the mother and the father, compares it to a single profile of the nine locations and conducts her random match probability: 1 in 670 billion or a hundred times the population of the world. So I say to [Expert]: Why don't you just say it's [accused]? [Expert] says: Well, we assist the Court by testing items, going through the mathematical process and discussing associations, identifications. This is the intervention of fact finders in a criminal trial, that are the twelve of you jurors in the case, of [accused]. Nine locations, failure to exclude [accused's] blood sample, 1 in 670 billion. I've said it at the beginning of this trial, I'll continue it for the rest. This is [accused]'s [body fluid]. It is not a failure to exclude at 670 billion. That's the way [Expert] talks in her lab. It's not the talk of common sense of the use to be made in a criminal trial of this evidence. It's [accused]'s [body fluid] on the inside of [victim]'s [item]. That's the evidence of [Expert].
25	Crown	There was a major profile, a major DNA profile, found and tested on the [item] as well and it was compared to the known DNA sample from [accused] that was taken by police pursuant to the warrant and the results of that with respect to the major profile, DNA profile, on the [item] is the chances of that DNA being anybody other than [accused] is 1 in 9.2 billion.

The examples in the table above demonstrate a variety of the misstatements of the evidence found within the cases studied. The largest issue with deciding whether the excerpt was to be coded as correct of fallacy, was drawing the line between "spin" and misstatement. In the adversarial system it is commonplace for lawyers to discuss the evidence in a manner that puts their side of the aisle in the best light. Determining where to draw the line between speaking of the evidence in hypotheticals, and speaking of the evidence incorrectly, was the most involved qualitative step of the analysis.

While it is acceptable to ask a jury to consider many hypotheses that *could* explain the evidence, it is incorrect to state many of the hypotheses as fact. The line was drawn consistently across all cases, and very few decisions came down to gut instinct. The most careful consideration was given to situations in which a justice system participant attributed something to the expert witness. This occurred in a number of situations, and as the data prove, more often incorrectly than correctly. The largest red flag scenario was when a lawyer or judge stated that an expert stated a fact, when the expert did no such thing. This type of "fallacy" is a category of error on its own, as it is putting false information into the atmosphere of the courtroom. This is a separate issue from making a *mistake*, such as erring while repeating the numerical value of something.

What should be noted, is that none of the errors found of incorrectly speaking of the evidence, or the expert witness testimony, seemed to have been done maliciously. None of the justice system participants seemed to make an effort to deliberately incorrectly repeat the expert. The cases studied, and particularly the excerpts exhibited above, demonstrate a thin or nonexistent knowledge of how to discuss DNA evidence correctly as the source of errors (survey questions answered as "fallacy"), based on

context clues. The efforts of these professionals to re-word the evidence was not done to turn the evidence into something providing new "facts" for their side, it was all done to re-word the evidence into "layman's" terms. The errors were made in the translations.

As these errors do not seem to have been made with intent, the provision of educational seminars would make a significant impact on the accuracy with which justice system participants discuss DNA evidence.

Likelihood Ratio case and examples

Likelihood Ratios (LR) have been used, albeit sparingly, in the Ontario Criminal Court system. One case was studied for a small look into the efficacy of the likelihood ratio presentation of DNA evidence. While a statistically irrelevant sample size, this was done with the intent of qualitative comparison to the more abundantly used random match probability.

As the language of the LR presents the evidence in an inverse ratio, it becomes more accessible to the level of proposition that the legal system pushes to function in. This allows the non-scientist justice system participants to discuss the evidence as it relates to competing casework hypotheses. The examples in Table 43 are directly from one case studied. What is of considerable note is that the non-scientist justice system participants made no effort to re-word the evidence statement, unlike in the RMP cases. As it is presented in a more accessible format, there appears to be less need for their further interpretation for the "layperson", with not a single registration of "Statistical Fallacy" when assessing this case.

Table 43 Example of Likelihood Ratio presentation of DNA evidence, excerpts from real court transcripts

Participant	Use of Likelihood Ratio
Expert	…"The likelihood of obtaining the observed DNA profiles," so that's support for these findings...is estimated to be 5,000 time – 5,300 times greater under hypothesis one if [accused] was the [relation] of [co-accused] rather than if they're not related, which means that an unrelated random [gender] was the [relation] of [co-accused]
Defence	The likelihood of obtaining and observing DNA profiles is estimated to be 5,300 times greater if [accused] was the [relation] of [co-accused] rather than if an unrelated random [gender] was the [relation].
Crown	The likelihood of obtaining the observed DNA profile is estimated to be 5300 times greater if [accused] was the [relation] of [co-accused] rather than if an unrelated random [gender] was the [relation].
Judge	And what [Expert] said was: "It is consistent with [accused] being the [relation] of [co-accused] with the likelihood, considering there are no inconsistencies in the comparisons, to be 5300 times greater than if they are not related."

Based on this limited data, it can be reasoned that the shift of the Centre of Forensic Sciences from RMP to the LR is a good idea. The evidence is presented in a far more accessible manner, now evidenced by the success within this case. None of the non-scientist justice system participants demonstrated the need to re-word the evidence into a more accessible word format, because that is already the form in which it exists. This effectively removes the translation source of errors seen with the RMP evidence.

Body Fluid Evidence Trends

What was an encouraging result is that all three non-scientist justice system participants were more often consistent than inconsistent with the expert when discussing body fluids (Table 21). However, none of the participants were entirely consistent with the Expert. In concordance with previous studies, the desire for the experts and the justice system to function at two different levels of proposition appears to be at play.

Non-scientist justice system participants still had a tendency to present body fluid evidence at a different level of proposition than the level originally introduced by the expert (Table 44).

Table 44 Example of body fluid source discussion, excerpts from real court transcripts

Participant	**Example**	**Propositional Level**
Expert	I could not determine that it was blood that was present on the [item]…a whitish stain was present in a few areas, it gave a positive result with our blood tests, which suggests that it could be blood, but I can't conclusively say that it was from blood… [Victim] cannot be excluded at the nine STR loci as the source of the [gender] profile form the area with chemical indications of blood…	"DNA deposition" Who is the source of this DNA profile?
Non-scientist	The blood on the [item], his [item] was the blood of [victim]. That was from the DNA analysis.	"Body Fluid deposition" Who is the source of a particular body fluid?

In the above example, without being able to attribute the profile to a particular body fluid, the trier of fact would not be able to move further up the hierarchy, from "sub-source" to "body fluid source". A trier of fact would also be unable to determine whether the presence of the body fluid was caused by an activity, and further, whether that activity was a crime. The movement from lower propositional levels (Table 5) to higher is an important step for the judicial system to make, but cannot be accurately inferred beyond the scientific evidence presented by the experts.

Overall, qualitative assessments across autosomal RMPs, lineage RMPs, and body fluid identification were supported by quantitative analysis. The judges proved to be the most accurate when discussing experts' DNA evidence correctly of the three non-

scientist justice system participants studied. What may be inferred is that judges spend a great deal more time hearing this type of evidence. Judges appear to be the most prudent with their discussion of the facts, which can hypothetically be explained by the fact that judges are neither advocates nor adversaries - they are referees of the adversarial process. Another potential explanation is that judges must avoid causing any grounds for appeals based on misstated evidence. Anything a judge says can be reviewed for errors. Not only could this be cause for appeal, but any decision a judge voices can create case precedent. If a judge lists DNA evidence within their reasoning, this would create the ability for future cases to make an argument for the same decision or outcome. This is only problematic if there is an error in the usage of the evidence, as it would be grounds for the same error to be used again. For these reasons, it is logical that the studied words of these judges show the most careful consideration of this type of scientific evidence.

What is apparent is that while expert witnesses carry the ongoing responsibility of ensuring their presentation of the evidence is correct, there is no check or balance when they are absent. Though judges, of the 3 participants, were the most often correct, and most often consistent with the expert witnesses, there is still a lot of room for improvement.

The conclusions of Cashman & Henning (2012), and Findlay (2008) suggested that justice system participants play a significant role in ensuring triers of fact do not misinterpret DNA evidence, and that a clear presentation of this evidence aids in juror comprehension. While Taroni et al. (2013) opine that experts have the responsibility of altering their testimony to rise up to the level of proposition the justice system needs to function in, it is not always possible. Experts are bound to the scientific facts, and cannot

hypothesize truthfully beyond what information is available. A more defined outline of an expert's responsibility was adjudicated in a recent decision from the Supreme Court of Canada. Precedent has been set, ensuring expert witnesses are to be objective and "impartial in the sense that it reflects an objective assessment of the questions as hand" (SCC 23, [2015] 2 S.C.R. 182).

While always tasked with remaining unbiased, experts cannot alone maintain the way evidence is discussed, as they are absent for the majority of trial proceedings. Non-scientist justice system participants cannot alone use the DNA evidence to answer the questions that function on a higher level of proposition (Table 5). What is clear from the examples in Table 42 is the need for a joint effort with regard to maintaining the integrity of the clear communication of DNA evidence.

The cumulative quantitative and qualitative results demonstrate a paucity of discussions of RMPs from defence and crown lawyers, and sporadic struggle when attempted. When considering the previously mentioned research of Cashman & Henning (2012), these results are not surprising.

> "The overwhelming majority of lawyers said they did not know enough. For these lawyers, the major challenge was in understanding and challenging random match probabilities and statistics used by experts in forensic reports or in court."

Cashman's & Henning's (2012) research detailed that lawyers did not feel prepared to deal with RMPs and there is now empirical evidence of this conclusion in the Ontario criminal court system.

Projected Impact

This project was unique in that it does not belong solely under the forensic science umbrella. Having a foothold in both forensic science and social sciences, as well as the legal field, means that the impacts this project can have span a wide gap. The gap between where the justice system needs DNA evidence to provide answers, and which answers the evidence actually *can* provide has been highlighted here.

The justice system currently relies on the ability of judges and lawyers to interpret and use this evidence without the aid of an expert for the many parts of trial proceedings. By discovering the frequency with which DNA evidence is spoken of incorrectly, this research project stands to influence not only future research, but the understanding of DNA evidence in the courtroom.

This project has demonstrated a need for educational programs that can expand the base understanding of DNA evidence for justice system participants. Quantifying the issue has opened the door to a much more in depth conversation between both sides of the adversarial system, and between the legal system and expert witnesses. As expert witnesses are not present in the courtroom for the majority of a trial's proceedings, lawyers and judges may need assistance from another source. This is a living example of the "teach a man to fish" proverb. Educating the non-scientist justice system participants is the way to equip the most number of people with the proper tools to handle this type of evidence correctly when the expert is not present.

In addition to that, forensic experts now have a glimpse into how their evidence is being repeated and used in their absences. This could also provide motivation for a change in the training of forensic experts. By both quantifying and qualifying the errors

that are occurring within the courtroom, expert witnesses, in addition to presenting their evidence correctly, can be vigilant when it comes to identifying these typical problem areas.

Professional development is key in succeeding in any field. This project, hopefully compounded by even further research, should provide enough justification for an adjustment in both forensic science and the legal system.

Reflections

Overall this project provided significant results and an exciting first look with the variables developed. It was a successful proof of concept that justifies an even further look into this topic.

As with any project, there are a number of things that could be done more efficaciously with the knowledge gained throughout the project process. Given infinite resources, the results from this project would have benefited from increasing the variable list to accommodate different types of fallacies. Separating the true "fallacies" from other types of errors in the future will certainly give a more detailed picture of the current use of RMP evidence. Developing an understanding of which type of fallacy (prosecutor's fallacy or defendant's fallacy, as examples) is most commonly made, or at the rate each are made, is the first step in crafting a solution to the issues successfully highlighted by this first assessment.

As an example, a commonly observed error was a non-scientist justice system participant trying to construct perspective of the RMP numerical value by comparing it to the population of the world. While this might give a perspective on just how large the

commonly used value of a quadrillion is, it unnecessarily creates an easement into regarding the autosomal RMP solely as a measure of the frequency of that profile within the existing population. This leaves out the concept of the true probability, which is the random assortment of all of the observed alleles coming together by chance to create the profile.

The coding of anything not Correct could also have been developed further with a Likert Scale (Stangor, 2007). Now having observed the array of answers from this project, an adjustment would only further describe the issue. A measurement of the severity of the fallacies or errors, set upon a scale from one to five instead of treating all errors in the same fashion is the ideal method for developing the next variable set.

While the current variable list was a good place to start, there is always room to grow. A number of components about the cases studied could also have been tracked. More information would have been garnered from the level of trial (Ontario Court of Justice or Superior Court of Justice) and the type of crime (homicide, assault, robbery).

Again, now that the concept has been proven, further variable lists are justified. These additions, paired with ensuring a better balance between jury and non-jury cases, and a better balance between autosomal STR, mtDNA and Y-STR DNA evidence, will provide a much larger insight in the future.

As this was the first look, there was no standard in place for the sections required of a case, beyond ensuring the expert witness was in fact an expert forensic biologist. Now it can be stated that uniformity will be improved greatly by balancing the numbers of Jury/Non-jury cases, the autosomal and lineage RMPs, as well as the selection of trial sections.

Ensuring each case studied contains the same combination of opening statements, submissions, charges to the jury or reasons for judgement, and closing statements will enable a much more proportionate representation of the variables.

Limitations

There was a large limitation inherent with this study purely by the nature of transcript procurement. Sourcing cases from the appeal level, while cost effective, significantly limited the number of cases available to study. While there are likely hundreds of cases that use forensic DNA evidence at the trial level each year, only a small subset reach the appeal level. However, the benefit to this is the added randomness of selection, as there appears to be no trend relating to the DNA evidence to the causes of a case moving to appeal. In addition, this project only considered Ontario cases; however, through the efforts of a UOIT undergraduate student, work has already begun to determine transcript procurement protocols for other common law jurisdictions across Canada, the United States, and Australia.

Yet another limiting factor was time. The length of time it took from the first step of selecting a case to completing the survey, impacted the number of cases that could be studied. With a structure now in place from which to model future studies, it is recommended that the number of cases be increased to fifty or more. The larger the number of cases studied, the more relevant the findings can potentially be.

The transcripts themselves presented a unique limitation. It cannot be known whether a seemingly odd combination of words was the error of the speaker, the court reporter, or the transcriber. In one example, the crown lawyer was credited with saying

the Random "Mass" Probability. While seemingly innocuous, there were other differences that caused more than a moment's pause, and required the best guess by the researcher. Somewhere along the transcription process, the term "AP", the short form for the acid-phosphatase test for amylase, was confused with the word "eighteen". There is a significantly large number of numerical values dealt with within DNA evidence cases, and it can only be assumed that what the researcher is reading is accurate.

With regard to the non-scientist justice system participants, individual progress was not captured. Whether a single individual appeared in several cases, making the same mistakes, or improving with time, was not information tracked with this study. As such, there could be one, or a few, individuals skewing the resulting trends.

Recommendations

To expand upon the conclusions made in the current study, future studies should explore different types of fallacies separately. Being able to differentiate between fallacies or errors will better develop an understanding of exactly where non-scientist justice system participants are struggling with DNA evidence the most.

DNA and body fluid transfer and persistence (T&P) questions and hypotheses frequented nearly every case studied in the current project. The information that this flourishing area of research can provide is constantly outpaced by the questions asked of it. As thresholds of DNA technology require less and less initial genetic material, the reasoning behind how a single cell reached a sampled location becomes paramount in prosecution of related activities (Butler, 2015). In the most recent decade, there has been

an increase in the amount of research dedicated to this area, the demand for which increases alongside the sensitivity of detection technology.

Szkuta, Ballantyne & van Oorschot (2017) performed one such study, finding that DNA acquired during a handshake was detectable both immediately, and 15 minutes later. What this study, and others like it, accomplished was bringing awareness to an entirely different set of hypotheses, proposition levels (Table 5), and questions surrounding DNA evidence. As research in this area progresses, it is no longer sufficient to ask "whose DNA is that?" without also considering "the likelihood of detecting a profile of an individual under various event hypotheses" (Szkuta et al., 2017).

DNA technology is constantly advancing. Ontario's Centre of Forensic Sciences began using STR technology in the mid-1990s, sampling only 4 to 6 genetic locations per profile. As the technology, and testing kits (such as the PowerPlex® 16 System), advanced to profile information at 9 and upwards of 15 loci, the analysis and presentation of that information evolved (C. Hageman, personal communication, November 4th 2015). At the time of writing, the recommendation for future studies of DNA in the court system is to restrict the date range of cases to within the most recent 15 years. This will ensure the technology and evidence being presented in the case is consistent, and up to date.

One of the more recent evolutions in the presentation of DNA evidence is on the Likelihood Ratio. Many jurisdictions (e.g. UK) function in the LR, and Canada's own Centre of Forensic Sciences has begun the process of shifting their DNA analysis method from RMP to LR, by employing STRmix™ (Centre of Forensic Sciences, 2017).

While only a single LR case example was studied, there was a hint of success with that method of presenting DNA evidence. One of the larger recommendations to be

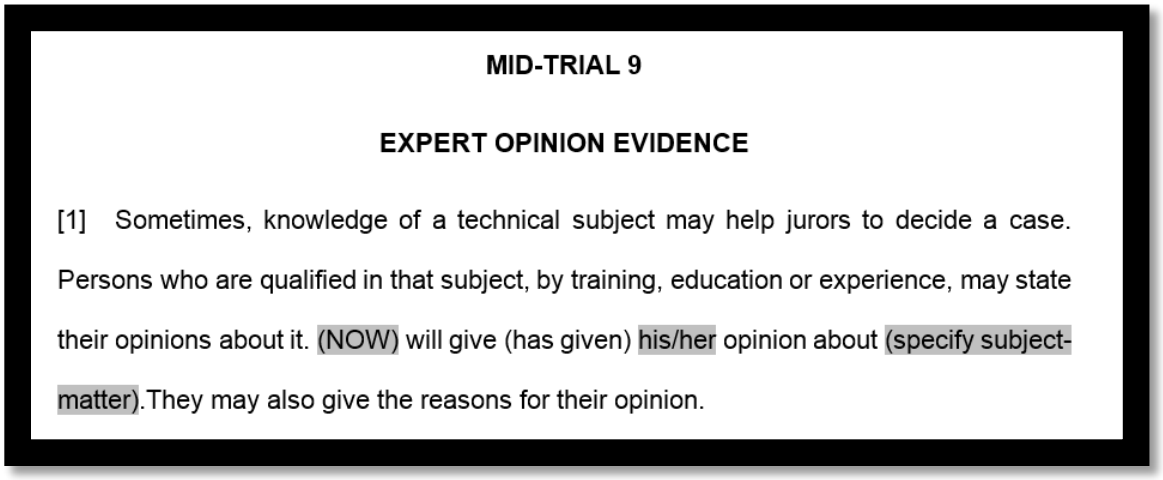
made is a similar study conducted in a jurisdiction that works predominantly with the LR. This would provide an in depth look into the success rates of the LR as a comparison to the RMP, and perhaps make a case itself for pushing more jurisdictions in the LR direction.

In conjunction with addressing the method of DNA presentation, a recommendation for educational programs is warranted. Without all justice system participants understanding DNA evidence, a decision regarding the method of DNA presentation is moot. What is being put forth here is the suggestion for training seminars for lawyers that aim to break down the concepts of DNA science and evidence into accessible information. Programs that can grow with the specific concerns lawyers have, such as those expressed in Cashman's and Henning's 2012 paper, are an ideal way to begin addressing the issues highlighted in this project.

What can be recommended as a starting point is a polling of willing lawyers and judges. Asking each of these justice system participants exactly where they need further explanation would be the best way to ensure actual concerns of these professionals are being addressed. Ensuring the proper baseline for the beginning of the explanation will help establish the foundational understanding of DNA evidence desired for our justice system.

The above recommendation would address both lawyers and judges, but an additional suggestion needs to be made for jury cases specifically. Under Canada's federal jurisdiction, criminal court judges have the option to utilize Watt's Manual of Criminal Jury Instructions (Watt, 2005). Recalling the recommendations of the American Bar Association (DesPortes, n.d.), more detailed jury instructions are required

to give jurors an improved comprehension of the evidence. At present, Watt's Manual barely touches on expert witnesses at all.



MID-TRIAL 9

EXPERT OPINION EVIDENCE

[1] Sometimes, knowledge of a technical subject may help jurors to decide a case. Persons who are qualified in that subject, by training, education or experience, may state their opinions about it. (NOW) will give (has given) his/her opinion about (specify subject-matter).They may also give the reasons for their opinion.

Figure 26 Watt's Manual of Criminal Jury Instructions: Expert Witness Testimony

Figure 26 shows exactly what is available for Canadian judges for pattern instructions to juries; one sentence, detailing the "Name of Witness" (NOW) has given their opinion on "Insert Topic Here". This one sentence is meant to give juries, in all types of cases, dealing with all types of experts, sufficient understanding of what to do with that evidence. While the wave of the future brings a shift into Likelihood Ratio, it will take several years for that transition to take place in full. Until then, the Random Match Probability will be ever present in the court system. What is recommended to address the current state of DNA evidence, as a result of this thesis study, is a more specific approach. The aim is to make the complexities of the RMP more accessible. If a judge included a final summary of what an RMP is, and what an RMP is not, juries would certainly have a better chance at understanding the evidence.

> "A Random Match Probability is an estimate of the coincidental match probability. It is an estimate of the chance of selecting an unrelated person, at random, from the population, and obtaining the same profile. A Random Match Probability is not the chance that the known reference is not the source, and does not equate to guilt or innocence."

This recommendation only addresses RMP situations. While more work needs to be done to assess the extent to which LR is successful in the justice system, it can be extrapolated that there will be errors made with the probabilities associated with this method of DNA presentation as well. Once a LR jurisdiction has been studied for the frequency of fallacies, recommendations for jury instructions to combat common errors associated with those probabilities can be made.

Conclusion

This study begins to uncover how wide the gap in current research is. This first assessment of the use of DNA evidence in court can serve as a potential guide for future studies, as it indeed highlights a discrepancy between expert presentation of DNA evidence and discussion of that evidence in the expert's absence.

Before solutions can be fully formulated and implemented, a more detailed understanding needs to be developed, and that process has begun here. There is a clear difference between how experts discuss DNA evidence, and how non-scientist justice system participants discuss DNA evidence.

Future research into more complex aspects of DNA evidence, such as mixtures and transfer & persistence, will help expand the current knowledge of what is being done with this evidence in the court room. As it is the joint responsibility of experts and non-scientist justice system participants to maintain the integrity of DNA evidence, implementation of training seminars and more detailed jury instructions may be of help in the final trial summary statements.

Appendix A

Respondent/Case Name:_____.
SECTION ONE Sub/Source level (Random Match Probability)
1. How many RMP's were presented by the expert?
    [0] None
    [1] One
    [2] Two
    [3] Three
    [4] Four or more
    [9] n/a

The following questions pertain to RMP #1
2a. Was an RMP presented by the expert?
    [0] No
    [1] Yes
    [9] n/a
2b. If yes, was that RMP presentation by the expert correct or fallacy?
    [0] Correct
    [1] Statistical Fallacy
    [2] Admission of Source
    [9] n/a
2c. Was that RMP presented by a defence lawyer?
    [0] No
    [1] Yes
    [9] n/a
2d. If yes, was that RMP presentation by a defence lawyer correct or fallacy?
    [0] Correct
    [1] Statistical Fallacy
    [2] Admission of Source
    [9] n/a

2e. Was that RMP presented by a crown lawyer?
    [0] No
    [1] Yes
    [9] n/a
2f. If yes, was that RMP presentation by a crown lawyer correct or fallacy?
    [0] Correct
    [1] Statistical Fallacy
    [2] Admission of Source
    [9] n/a
2g. Was that RMP presented by a judge?
    [0] No
    [1] Yes
    [9] n/a

2h. If yes, was the RMP presentation by the judge correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to RMP #2

3a. Was a second RMP presented by the expert?
[0] No
[1] Yes
[9] n/a

3b. If yes, was that RMP presentation by the expert correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

3c. Was that RMP presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a

3d. If yes, was that RMP presentation by a defence lawyer correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

3e. Was that RMP presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a

3f. If yes, was that RMP presentation by a crown lawyer correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

3g. Was that RMP presented by a judge?
[0] No
[1] Yes
[9] n/a

3h. If yes, was the RMP presentation by the judge correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to RMP #3

4a. Was a third RMP presented by the expert?

[0] No
[1] Yes
[9] n/a

4b. If yes, was that RMP presentation by the expert correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

4c. Was that RMP presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a

4d. If yes, was that RMP presentation by a defence lawyer correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

4e. Was that RMP presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a

4f. If yes, was that RMP presentation by a crown lawyer correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

4g. Was that RMP presented by a judge?
[0] No
[1] Yes
[9] n/a

4h. If yes, was the RMP presentation by the judge correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to RMP #4

5a. Was a fourth RMP presented by the expert?
[0] No
[1] Yes
[9] n/a

5b. If yes, was that RMP presentation by the expert correct or fallacy?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

5c. Was that RMP presented by a defence lawyer?

[0] No
[1] Yes
[9] n/a

5d. If yes, was that RMP presentation by a defence lawyer correct or fallacy?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

5e. Was that RMP presented by a crown lawyer?

[0] No
[1] Yes
[9] n/a

5f. If yes, was that RMP presentation by a crown lawyer correct or fallacy?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

5g. Was that RMP presented by a judge?

[0] No
[1] Yes
[9] n/a

5h. If yes, was the RMP presentation by the judge correct or fallacy?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

SECTION TWO Lineage Profile (Y-STR or mitochondrial profile)

6. How many Y-STR RMP/Confidence Intervals were presented by the expert?

[0] None
[1] One
[2] Two
[3] Three
[4] Four or more
[9] n/a

The following questions pertain to Y-STR/MITO RMP/C.I. #1

7a. Was an RMP/a Confidence interval presented by expert?

[0] No
[1] Yes
[9] n/a

7b. If yes, was the RMP/C.I. presented by the expert correct?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

7c. Was the RMP/C.I. presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a
7d. If yes, was the RMP/C.I. presentation by a defence lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a
7e. Was the RMP/C.I. presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a
7f. If yes, was the RMP/C.I. presentation by a crown lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a
7g. Was the RMP/C.I. presented by a judge?
[0] No
[1] Yes
[9] n/a
7h. If yes, was the RMP/C.I. presentation by a judge correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to Y-STR/MITO RMP/C.I. #2
8a. Was a second RMP/a Confidence interval presented by expert?
[0] No
[1] Yes
[9] n/a
8b. If yes, was that RMP/C.I. presented by the expert correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a
8c. Was that RMP/C.I. presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a
8d. If yes, was that RMP/C.I. presentation by a defence lawyer correct?
[0] Correct
[1] Statistical Fallacy

[2] Admission of Source
[9] n/a

8e. Was that RMP/C.I. presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a

8f. If yes, was that RMP/C.I. presentation by a crown lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

8g. Was that RMP/C.I. presented by a judge?
[0] No
[1] Yes
[9] n/a

8h. If yes, was that RMP/C.I. presentation by a judge correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to Y-STR/MITO RMP/C.I. #3

9a. Was a third RMP/a Confidence interval presented by expert?
[0] No
[1] Yes
[9] n/a

9b. If yes, was that RMP/C.I. presented by the expert correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

9c. Was that RMP/C.I. presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a

9d. If yes, was that RMP/C.I. presentation by a defence lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

9e. Was that RMP/C.I. presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a

9f. If yes, was that RMP/C.I. presentation by a crown lawyer correct?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

9g. Was that RMP/C.I. presented by a judge?
[0] No
[1] Yes
[9] n/a

9h. If yes, was that RMP/C.I. presentation by a judge correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

The following questions pertain to Y-STR/MITO RMP/C.I. #4

10a. Was a fourth RMP/a Confidence interval presented by expert?
[0] No
[1] Yes
[9] n/a

10b. If yes, was that RMP/C.I. presented by the expert correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

10c. Was that RMP/C.I. presented by a defence lawyer?
[0] No
[1] Yes
[9] n/a

10d. If yes, was that RMP/C.I. presentation by a defence lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

10e. Was that RMP/C.I. presented by a crown lawyer?
[0] No
[1] Yes
[9] n/a

10f. If yes, was that RMP/C.I. presentation by a crown lawyer correct?
[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

10g. Was that RMP/C.I. presented by a judge?
[0] No
[1] Yes
[9] n/a

10h. If yes, was that RMP/C.I. presentation by a judge correct?

[0] Correct
[1] Statistical Fallacy
[2] Admission of Source
[9] n/a

SECTION THREE Body Fluid Source Level

The following questions pertain to instance #1 of linkage to a body fluid

11a. Did the expert link a DNA profile/probability to a body fluid deposition?
[0] Said: No, cannot state it was _ x _ fluid
[1] Said: Likely __x__ fluid
[2] Said: Conclusively __x__ fluid
[9] n/a

11b. Was the DNA profile linked to a body fluid by a defence lawyer?
[0] No
[1] Yes
[9] n/a

11c. Was that linkage or non-linkage by a defence lawyer consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

11d. Was the DNA profile linked to a body fluid by a crown lawyer?
[0] No
[1] Yes
[9] n/a

11e. Was that linkage or non-linkage by a crown lawyer consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

11f. Was the DNA profile linked to a body fluid by a judge?
[0] No
[1] Yes
[9] n/a

11g. Was that linkage or non-linkage by a judge consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

The following questions pertain to instance #2 of linkage to a body fluid

12a. Did the expert link a DNA profile/probability to a body fluid deposition?
[0] Said: No, cannot state it was _ x _ fluid
[1] Said: Likely __x__ fluid

[2] Said: Conclusively __x__ fluid
[9] n/a

12b. Was the DNA profile linked to a body fluid by a defence lawyer?
[0] No
[1] Yes
[9] n/a

12c. Was that linkage or non-linkage by a defence lawyer consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

12d. Was the DNA profile linked to a body fluid by a crown lawyer?
[0] No
[1] Yes
[9] n/a

12e. Was that linkage or non-linkage by a crown lawyer consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

12f. Was the DNA profile linked to a body fluid by a judge?
[0] No
[1] Yes
[9] n/a

12g. Was that linkage or non-linkage by a judge consistent with the expert testimony?
[0] Consistent with expert testimony
[1] Inconsistent with expert testimony
[2] Not addressed by expert
[9] n/a

13. Is the case Non-jury or Jury?
[0] Non-jury
[1] Jury
[9] n/a

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