Forensic Use of DNA

Michael J. Spence, Ph.D.

Demosthenes Lorandos, Ph.D., J.D.

INTRODUCTION

Litigators understand that prospective jurors gain information about forensic DNA evidence through the media and popular cultural sources.[1] Unfortunately, a majority of prospective jurors enter the courtroom with preconceived notions of the role DNA evidence plays in the criminal justice system.[2] Our prospective jurors are usually aware that the promoters of forensic DNA testing have claimed for decades that DNA evidence is virtually infallible.[3] This chapter is designed to assist litigators with comprehending the forensic use of DNA. This chapter should aid in the preparation for the *voir dire* of prospective jurors and the direct and cross-examination of forensic DNA scientists. There are many books about forensic uses of DNA, some less boring than others[4]. Certainly, the competent litigator faced with forensic DNA issues will consult standard references. This chapter is designed to provide an overview and to address essential issues which must be covered in the direct and cross-examination of forensic DNA testimony.

The forensic use of DNA began "as a method of determining paternity."[5] Shelton (2011) informs us that the first use of DNA in a successful U.S. criminal

prosecution was in *Andrews v. State*.[6] This case involved matched DNA samples from semen to the defendant's known DNA standard in a rape case.[7] The early years of forensic DNA litigation in the United States were referred to as the "DNA Wars".[8] A notable early case in the United States, *People v Castro*[9], involved a double murder and the court noted the exclusionary use of DNA, but refused to accept any evidence of inclusion.[10] In the United Kingdom, forensic DNA technology was first used to identify the individual responsible for the sexual assault and murder of two young girls in the Leicestershire countryside in 1983 and 1986. This resulted in the conviction of Colin Pitchfork in 1988.[11] In Canada, the earliest cases involving forensic DNA relied heavily on jurisprudence from the United States and opinions about technique, matching and reliability.[12] Edmond and colleagues informed us that, since the mid-1990's, Australian courts have accepted forensic DNA techniques as admissible.[13]

Today, if there are no obvious errors in labeling, handling of samples or fraud, forensic DNA testimony is universally admitted in our courts.[14] Competent litigators for the people, and the forensic biologists they work with, are establishing that the forensic use of DNA can be essential in ascertaining the "who" of criminal circumstances. Prosecutors and litigators who advocate for the wrongfully convicted, describe forensic DNA as the gold standard, a "truth machine".[15] The United States Supreme Court recently considered the question of whether there is a

federal constitutional right to post-conviction DNA evaluation, a matter that is especially important in jurisdictions that have not enacted statutes or rules regulating post-conviction DNA testing.[16] Since the mid-1990's, competent litigators have turned to well-credentialed molecular biologists who have been able to teach them about forensic DNA and about sloppy laboratory practices, improper validation processes, failure to adhere to proper protocols, and biased interpretations of data.[17] In this vein, Thompson and colleagues have argued that:

> "Promoters of forensic DNA testing have done a good job selling the public, and even many criminal defense lawyers, on the idea that DNA tests provide a unique and infallible identification. The problem with this assumption is that it ignores case-to-case variations in the nature and quality of DNA evidence. . . . Even when the reliability and admissibility of the underlying test is well established, there is no guarantee that a test will produce reliable results every time it is used."[18]

Clearly, our criminal justice system is establishing that the forensic use of DNA is not infallible;[19] it is subject to human error and false positives;[20] as well as contamination and mistakes of interpretation.[21] This is "the good", "the bad" and "the ugly" of forensic DNA evidence and that's what we aim to establish for the reader in this chapter.

OVERVIEW: FROM THE CRIME SCENE TO THE CRIME LAB

What is DNA?

DNA is an acronym for deoxyribonucleic acid. In humans, DNA is a long, double-helical, corkscrew-shaped molecule. The molecule is organized into structures called chromosomes. Chromosomes are contained within the nuclei of a broad range of cell types. When a person receives one X chromosome from mom and a second X chromosome from dad, that individual develops into a female. When a person receives an X chromosome from mom and a Y chromosome from dad, that individual develops into a male. Each human being receives twenty-two additional pairs of chromosomes, called autosomes. One set of twenty-two autosomes comes from the egg, provided by the mother. The second set of twenty-two autosomes comes from the sperm cell, provided by the father. The DNA contained within the two sex-chromosomes and the forty-four autosomes includes 6.4 billion nucleotides. Nucleotides are the building blocks of DNA.

With rare exceptions, these vast stretches of DNA code within each nucleated cell from a specific individual are identical, regardless of the area of the body from which that cell has originated. In other words, the DNA in your skin cells is the same as the DNA in your liver cells, or the DNA from the white blood cells traveling through your circulatory system. Siblings typically have very similar DNA, whereas identical twins have the same DNA profile.

How is DNA used to investigate crimes?

Within each crime scene, the investigators need to scrutinize any witnesses, video camera footage, blood spatter patterns, latent prints, footprints, tire tracks, vehicles, computers, cell phones, tool marks, firearms, bullets, shell casings, documents, animals, insects, food, drugs, alcohol, as well as a variety of potentially important trace materials. Within this chapter, the focus is upon the investigative quest to locate and collect crime scene sources of nucleated cells and DNA.

Decades ago, human genome scientists began recognizing regions within vast stretches of human DNA that are distinctly different from individual to individual. Over the years, methodologies were explored to capitalize on these detectable differences, for the purpose of developing a DNA-based human identification system from crime scene evidence. As these methods were optimized, an enormous degree of emphasis was placed upon astounding improvements in the sensitivity of DNA detection. In recent years, DNA technology has reached such a profound degree of sensitivity, tiny deposits of nucleated cells are all that is necessary to identify the individual DNA contributors. This enhanced sensitivity can be applied to a speck of blood that can scarcely be visualized with the naked eye. It can be applied to trace amounts of saliva from an old cigarette, or even from a single cough or a sneeze near a specific surface. Even without any detectable sperm cells, a rapist might be identified by a very small quantity of cells deposited onto the victim. Upon

briefly handled items, such as a towel, an article of clothing, a steering wheel, a door knob, or perhaps a murder weapon, skin cells might be successfully recovered and typed for DNA.

What sources of DNA evidence are typically collected from crime scenes?

The types of evidence collected from each crime scene depends on the nature of the incident and the objectives of the examination. The collected items, which may serve as useful DNA sources, can include almost anything. This includes, but is certainly not limited to the following examples: hats, bandanas, shirts, pants, shoes, socks, undergarments, bras, towels, sheets, bedding, bindings used to restrain a victim, fingernail samples or swabs from sexual assault examination kits, drink containers, cigarette butts, chewing gum, the contents found in trash cans, swabs, scrapings, or cuttings from furniture, walls, doors, windows, vehicles, knives, firearms, and other weapons. Therefore, the list of potential sources of biological material is seemingly endless.

Investigators placed in charge of crime scenes typically target the richest sources of DNA. These sources include three major biological fluids; blood, saliva, and semen. It is useful to note that crime scene investigators and laboratory forensic biologists are typically armed with presumptive and/or confirmatory tests for detection of these biological fluids. It is also important to keep in mind that these three body fluids are enormously rich sources of human cells and DNA. Within a

single drop of human blood, there are approximately 400,000 DNA-containing white blood cells. Within a drop of saliva, there are approximately 500,000 salivary epithelial cells. Within a drop of semen, there are an estimated 3,000,000 spermatozoa. A crime lab analyst needs fewer than 200 human cells from any of these sources, in order to extract a single nanogram (ng) of DNA. Approximately 0.5 ng of DNA is the optimal quantity for generating a full genetic profile from any evidence sample. Crime lab analysts can attest to the fact that 500 to 10,000 ng of DNA are routinely recovered from a single oral swab.

Sometimes, a crime scene investigator might suspect that there are no readily identifiable sources of blood, saliva, or semen available from a victim, a suspect, or a specific crime scene location. With this in mind, the extreme sensitivity of DNA typing can allow the detection of 'handling DNA', from casually deposited skin cells that might be present on a variety of potential surfaces at the crime scene.

DNA evidence typically collected by sexual assault nurse examiners.

Many criminal case investigations are prompted by allegations of sexual assaults. These allegations might originate from males, females, adults, or children. The early stages of the investigation often include a **s**exual **a**ssault **n**urse **e**xamination (S.A.N.E). From a SANE kit, a collection process might include, but is not necessarily limited to the following: swabs from the vagina, the cervix, the external genital area, the anal area, the breast area, or the penis.

The competent litigator should be wary of certain aspects of the medical records—stemming from these examinations. It is useful to keep in mind that—periodically—the **International Association of Forensic Nurses** releases **"Sexual Assault Nurse Examiner (SANE) Education Guidelines"**, with the most recent guidelines released on September 4, 2018.[22]

For case-to-case SANE processes, it is important to clarify the precise time frame between the alleged criminal sexual incident(s), and the beginning of the examination. It is fundamentally more favorable for evidence to be collected sooner, rather than later. Keeping this intuitive statement in mind, the factors affecting the importance of timing are highly variable and often complex. For more on this, refer to a 2010 NIJ Journal article with the title: **"Extending the time to collect DNA in sexual assault cases."**[23]**,** as well as a 2011 study published by Canadian researchers, with the title: **"Providing Evidence Based Opinions On Time Since Intercourse (TSI) Based On Body Fluid Testing Results Of Internal Samples."**[24]

Within the majority of SANE medical reports, one should find a list of what are referred to as ***'post-hygienic activities'***. These routine events may or may not have an impact on the case-to-case probability of recovering useful evidence. Activities often listed might include the following: washing, douching, brushing teeth, eating, drinking, or changing clothes. The competent litigator will work with forensic DNA experts to explore the potential impact of these activities.

Accurate chain of custody records.

Crime scene evidence items are collected, packaged, sealed, marked for identification, and delivered to the analytical facility. Chain of custody[25] records must be carefully documented for each item. These records establish the precise time frames within which items are collected, delivered to the crime lab, and checked out of storage by the assigned forensic biologist. The documents must reflect the exact location from which each item was collected, as well as any temporary or long-term storage locations. Any gap in the chain of custody represents an ominous breach of procedure.

The Evidence: Prioritization, storage, and processing.

Law enforcement laboratory scientists rarely have the time and resources to examine every single evidence item that has been delivered to their facility. Attentive communication between case investigators and crime lab forensic biologists is necessary to assign a level of priority for the examination of each specific evidence item. It benefits the prosecution team, as well as the defense team, to embrace the fundamentals of logical crime scene analysis. It pays to scrutinize the mechanisms by which evidence items have been initially evaluated, collected, handled, prioritized, and examined within the crime lab.

Once the crime scene evidence items are delivered to a law enforcement

laboratory facility, they are typically checked into a secure area by an evidence clerk. An analyst is subsequently assigned to the case. When the crime lab analyst becomes available to begin conducting the work, items of interest are checked out of the storage area by the clerk, and into the possession of the analyst.

Evidence examination: Illumination, photography, and microscopy.

The scientific analysis begins with a few fundamental observations.[26] Keeping in mind the locations and circumstances under which the evidence items were collected, the analyst will typically lay out each item and use ambient light to create a photographic record of the evidence from various surfaces. After an initial round of scrutiny, items are often examined by the forensic biologist with an alternate light source (ALS).[27] These sophisticated instruments assist biological examinations by utilizing a multitude of light wavelengths. Whether using ambient light, or ALS, or both, it is essential for analysts to gather photographic records from each vital evidence item. It is also necessary to provide notations within those records, establishing the precise locations on each item—being subjected to tests for biological fluids and DNA.

Available to crime lab analysts are a number of presumptive and confirmatory tests for blood, semen, and saliva. Those tests are frequently used, provided that they offer valuable information toward the objectives of the investigation. The ultimate goal is to find sources of DNA. The analyst will often use microscopy in order to

examine the types of cells present on various evidence items. Microscopy is particularly useful for confirming the presence of spermatozoa. The microscopes in all modern forensic biology labs can be readily equipped with photographic equipment and computerized imaging software. The use of such fundamental technology can assist analysts with gathering photographic records—confirming the presence of specific cell types—such as sperm cells.

It is alarming that law enforcement lab analysts often do not bother with collecting a photographic record of 'alleged' sperm cells—during the investigation of sexual assault cases. An example of the importance of such records emerged during the course of a 2017 sexual assault trial. (Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). This specific investigation centered on one isolated area of clothing. From a small cutting of fabric, the analyst released an official October 2014 crime lab report, claiming: **"…a possible presence of semen"**. However, the report also clearly stated that: **"...due to the fact that no sperm cells were observed under the microscope, *...semen could not be confirmed*."** Despite three subsequent crime lab reports from the same analyst, there were no references to visualization of any sperm cells. In contradiction to these four reports, trial testimony from the analyst in August 2017, was as follows: "I ***did*** see 10 sperm cells per field of vision, under the microscope. This observation was indicated, where you see the ***'10'*** notation on one worksheet—

within my bench notes." Confronted with this mystifying contradiction, counsel for the defense asked: “Couldn’t you have collected a photograph of these alleged sperm cells?” Defying logic, the analyst responded: “Yes. When our microscopes are used to search for sperm cells, our field of vision is displayed on a computer screen—right in front of us. I could have pressed a button, and a photo would have been preserved.” The defense asked: “So, all you had to do was reach over, …and press a button, …and the jury could be looking at that photo right now?” The analyst acknowledged this fact.

Since this analyst testified over the course of two days, counsel for the prosecution asked the analyst to go back and further reanalyze that same fabric. With the trial still in progress, the prosecution proposed to allow the analyst to release a ***fifth*** lab report—in between days on the witness stand. When the defense objected, the Court promptly ruled against the accused. The analyst was allowed to testify that additional material was washed out of the fabric and placed under the microscope. This time, photos were collected—for presentation during the 2nd day of testimony from the crime lab analyst. Defying all conventional sensibilities, this ‘hail Mary’ took place 2 years, and 10 months after the October 2014 report clearly stated: ***“no sperm cells”***—with zero photos collected—from the exact same swatch of fabric. All of this occurred in spite of the fact that a DNA expert for the defense was present at the trial venue—but was never notified of any opportunities to witness the material

from which these sperm cells were allegedly removed. It is notable that no DNA typing was ever conducted from this ***'11th hour'*** analysis.

Processing evidence: Prior to the production of DNA typing data.

Once each potential source of biological material has been characterized, the forensic biologist will proceed to extracting and purifying any DNA from the appropriate surfaces on the evidence items. Extraction of DNA can be accomplished by a variety of methodologies. In today's crime labs, DNA extractions might be performed with assistance from robotic systems.

Litigators should explore various details of how human cells can be subjected to a process that is known as 'lysis'. In a forensic lab, lysis is a process by which cells are ruptured, in order to access the DNA within the nucleus of each cell. DNA from the ruptured cells is purified away from other components, such as proteins and lipids. There are numerous scientific procedures for accomplishing the purification of DNA. Relevant to criminal cases, it is important to know that there are two fundamental approaches to collecting and purifying DNA from cells that are presumed to be on evidence items. Suppose that a cotton swab is collected from a violent crime scene, and there is cause to believe that blood is present on the swab. The crime lab forensic biologist would typically subject a cutting from that swab to what is known as a **'straight extraction'**. This means that all of the cells on the cutting are 'lysed', and the DNA is extracted and purified for human identification.

Alternatively, suppose that a cotton swab is collected from the genital area of a female who has reported a sexual assault. In the event that the crime lab analyst has cause to suspect the presence of sperm cells, it is customary for the analyst to collect a cutting from the swab, in order to conduct what is referred to as a **'differential extraction'**. The differential extraction process attempts to separate a 'sperm fraction' DNA sample from a 'non-sperm' or 'epithelial' fraction DNA sample. This process begins by subjecting the genital swab cutting to a gentle lysis step. It is useful to visualize sperm cells as being much more like walnuts, whereas epithelial cells (such as skin cells) behave more like tiny water balloons. The gentle lysis step will readily rupture the vast majority of those much more flimsy epithelial cells. After this primary lysis step, the liquid sample is subjected to centrifugation. Ideally, a large percentage of sperm cells—behaving like walnuts—will have survived that initial lysis step, and are collected at the bottom of the sample tube, during centrifugation. A portion of the upper liquid layer within the tube is carefully transferred to a clean, new sample tube, which is set aside, and labeled "non-sperm fraction" or "E-fraction". Meanwhile, the sperm cell 'pellet' is repeatedly washed by adding more of the gentle chemicals. The primary lysis step, coupled with the subsequent rounds of washing, centrifugation; more washing, and more centrifugation, will cause the unwanted rupture of some sperm cells, and loss of DNA. In some instances, these losses can be quite substantial. However, if hundreds,

thousands, or perhaps millions of sperm cells are present within the original cutting, the final sperm cell pellet is likely to be sufficient for human identification.

To complete the differential extraction, the analyst will add a much more harsh chemical mixture. Similar to cracking open walnuts with a hammer, the harsh chemical lysis step ruptures the remaining cells present in the centrifugation pellet. Ideally, an adequate quantity of 'sperm faction' DNA will be recovered. While everyone should be aware that females do not produce sperm cells, it is not uncommon for some female DNA to be detectable within sperm fractions that are produced by these differential DNA extraction processes. This is especially true when the starting ratio of female-to-male DNA is excessively high. Thus, these extractions should not be considered a definitive method for a perfect, 100% separation of the non-sperm cells from the sperm cells, into the desired fractions.

In addition to the imprecise isolation of sperm cells, away from the typically less important non-sperm cells, the discerning litigator should be mindful of another improper assumption associated with differential extractions. Suppose that an analyst observes only a weak presumptive positive test for semen from an intimate female swab. Under the microscope, suppose that this same analyst reports the absence of any visible sperm cells. Regardless of that, the analyst decides to conduct a differential extraction, with the hope that very small numbers of sperm cells are actually present on the remainder of the swab. Regardless of the fact that not so much

as a single spermatozoa was ever visualized, crime labs customarily endorse the release of analytical reports, referring to **"sperm fractions"** and **"non-sperm fractions"**. Herein lies a potentially disastrous misconception. Jurors must be informed that the mere pursuit of these differential fractions does not authenticate that any sperm cells were ever actually confirmed by any of the reporting scientists. Indeed, if a crime lab analyst were to conduct the differential extraction process on an avocado, the report would contain references to the "sperm fraction" and the "non-sperm fraction"—despite the detection of zero human DNA from both.

The amount of DNA extracted from each sample is typically estimated using technology known as **'real-time PCR'** analysis.[28] Real-time PCR technology can estimate the recovery of remarkably tiny quantities of DNA. On any given item, a scientist might expect to recover trace amounts of DNA (guns, knives, tools, cotton swabs from door knobs, windows, steering wheels, etc.), or wearer DNA (clothing). Epithelial cells/skin cells have a tendency to slough off of human beings at a steady rate, and become attached to a variety of surfaces.

The Nobel Prize-winning work that facilitated forensic human identification.

In 1993, Kary B. Mullis was awarded the Nobel Prize in Chemistry,[29] for developing the polymerase chain reaction (PCR) process that eventually made modern-day forensic human identification possible.

Using the PCR technology developed by Dr. Mullis, a present-day crime lab analyst can start with, for example, a nearly invisible, isolated speck of blood from a crime scene. The analyst can extract the DNA, quantify the amount that has been recovered, and determine the typing results within several hours, or a few days. The scientist can subsequently collect known standard DNA typing data from a suspect, an alleged victim, or other known individuals, and comparatively determine the identity of the blood speck contributor. If this tiny quantity of crime scene blood provides typing results from all of the tested genetic locations (referred to as 'loci'), but there is no DNA match to a known standard, the results would be documented and reported as DNA from an "unknown male" or an "unknown female".

The goal of the 'molecular photocopier': Comparative DNA matches.

The Nobel Prize-winning accomplishments of Dr. Mullis was followed by an evolution of strategies that were developed for forensic DNA typing. Around the turn of the millennium, one of the most frequently used DNA typing systems in the U.S. was called Profiler® and COfiler®, manufactured at the time by Applied Biosystems. Also, available over the years has been the POWERPLEX® 16 Kit,[30] offered by the Promega Corporation. The Profiler/COfiler DNA typing systems were phased out, as AmpFlSTR® Identifiler®, and Identifiler® Plus Amplification Kits,[31] were eventually phased in. Until 2014 through 2016, crime lab analysis was targeting only 15 locations within the human genome (the singular term for these locations is

'locus', the plural term is 'loci'). In addition to these 15 loci, crime labs tested for gender determination at a 16th point in the human genome—the Amelogenin locus. Within the tested genetic locations, were the FBI's designated 13 core loci, for database processing.

Companies continuing to work in the human identification arena have recently released DNA typing systems that have been expanded to cover 24 loci in each kit. These kits include PowerPlex® Fusion, from Promega[32], GlobalFiler™, from Thermo Fisher Scientific[33], and Investigator® 24plex QS, from Qiagen[34]. In March 2015, the FBI published the expansion of their original 13 core genetic locations to an updated, Combined DNA Indexing System (CODIS) core of 20 loci. This expansion initiative came with an implementation date of January 2017 for U.S. laboratories.[35] For further information on DNA databases, refer to the section of this chapter bearing the title: **"The development of searchable DNA databases."**

Rather than scrutinize the detailed, sophisticated technology associated with each DNA profiling system, let us discuss how the results from these elegant forensic DNA processes might be visually represented to juries. Whether a crime lab analyst is conducting DNA typing on evidence items, or DNA reference standards from known individuals, the PCR process (provided by Dr. Mullis) functions like a 'molecular photocopier'.[36] If a juror tries to visualize the human genome as an enormously lengthy book, the PCR process targets 22 pages (or 22 loci) within that

'genomic book'. Countless copies are made of each of these carefully-chosen, pages for human identification—using a process that DNA experts refer to as ***'amplification'***. Amplification also includes molecular photocopying from a two additional pages—Y indel and Amelogenin—which allows gender determination from the evidence, or the known individual.

Each locus is a region of human DNA that is rich in what are referred to as ***'short tandem repeats'*** (STRs). Briefly, these are regions with repeating sequences of specific nucleotides. The cumulative information from the twenty-four loci demonstrates a genetic pattern of STRs that serves as a unique identifier, including gender, for each tested person (with the exception of identical twins). The competent litigator will be mindful that if the sample evidence is inadvertently or intentionally contaminated, prior to PCR amplification, the genuine identity of the donor may be masked by over-amplification of the false source.[37]

The actual DNA results observed by crime lab scientists resemble what some of us have seen on an EKG printout. While EKG stands for Elektrokardiogram (the Dutch/German version of the term), DNA data comes to crime lab analysts in the form of an electropherogram printout (in this chapter, referred to as ***'e-gram'***).[38] Each signal on an e-gram is visualized by the analyst as a 'heartbeat-like' peak, which rises above a low, jagged baseline of 'background noise'. The signal peak heights are measured by the crime labs in Relative Fluorescence Units (RFUs).[39]

RFU thresholds, analytical artifacts, and DNA data interpretations.

The competent litigator must be fundamentally aware that substantial RFU spikes can sometimes occur during collection of DNA data from evidence samples. These RFU spikes might be attributed to effects that include, but are not limited to: stutter peaks, nonspecific amplification products, pull-up peaks, dye blobs, electrophoretic spikes, or products of static/electrical interferences.[40] For additional information, regarding published interpretation guidelines for forensic DNA typing labs, it is extremely useful to research the specific Federal Bureau of Investigation (FBI) internet resources that have been dedicated to these challenging issues.[41]

To understand the differentiation between partial DNA profiles, or DNA data from a mixture of contributors—versus the occurrence of random noise, and other artifacts—one might explore information regarding Chaos Theory.[42] It is also useful to gain a full understanding of what is referred to as the ***'binary method'***[43] for forensic DNA data interpretation. This method employs ***'analytical thresholds'***,[44] and ***'stochastic thresholds'***.[45] It is useful to make the connection between the potential chaos associated with DNA interpretation, and the definition of the term, '**stochastic'**. According to the Oxford Dictionary, stochastic is defined as follows:

> "Having a random probability distribution or pattern that may be analysed statistically but may not be predicted precisely." [46]

In the context of e-gram interpretation, this translates into the realization of the following: When one allelic signal is observed ***below*** the stochastic threshold, the presence or absence of the second allele at that locus may be considered as a random probability. Thus, the observer cannot be guaranteed that the results from that locus are complete, or incomplete. Recently, many aspects of the methodologies associated with the stochastic effects and the binary threshold methodology have been carefully scrutinized via guidelines issued by the Scientific Working Group on DNA Analysis Methods (SWGDAM).[47]

Since the exploration of thresholds, background noise, and the myriad of possible artifacts have such a profound role in the assessment of DNA mixtures, these areas are covered in more detail in the sections of this chapter entitled: **"Reporting conclusions from LCN DNA, allelic dropout, and DNA Mixtures"** and **"The history of DNA mixture misinterpretations".**

DNA interpretation challenges, and the impact of various forms of bias.

When analyzing evidence items for DNA, the crime lab analyst often observes an extremely limited quantity of DNA—or perhaps DNA that is degraded, or otherwise compromised. When such limitations occur, the e-gram frequently provides an incomplete DNA profile. This might be due to the fact that various signal peaks occur at such low RFU values, they are not sufficiently distinguishable from the background noise and analytical artifacts. In some instances, a subset of DNA

signals might be entirely nonexistent. These limitations—taken together with the often-observed presence of multiple DNA contributors on the evidence—present considerable interpretation challenges for the scientists. At the heart of this challenge is the multitude of decisions that must be made, regarding exactly how prominent any given peak should be—in order to accurately designate the e-gram signal as a genuine allele.[48]

In some instances, tangible DNA data might be observed from the analysis. However, the genuine nature of the results could be inconsequential. The implications of inherently weak data might be overstated by the analysts, as they are summarized during discussions with the prosecution team. Through the preparation of reports, or during testimony, if an analyst describes results as stronger than they truly are, a great disservice to the criminal justice system could end up being the consequence. For example, prosecutors and defense attorneys should take careful notice when a crime lab DNA analyst offers conclusions resembling the following:

> "The observed DNA profile is incomplete, with possible added contributors. A number of the e-gram peaks fall well below our laboratory's RFU threshold. Those signals are of questionable reliability. Meanwhile, various DNA signals are clearly above that threshold. These are considered to be reliable alleles. However, quite a few of the signals fall within a gray area—somewhere in between unreliable and reliable. Let me ***first*** take a look at the DNA profile from the accused individual, and I will get back to you later—regarding which signals I believe we should call 'genuine alleles', and which ones we should ignore."

This hypothetical scenario illuminates the concept of observer bias.[49] Described more bluntly, this is one mechanism by which junk science surfaces in our courtrooms. Observer bias becomes an obstacle to the pursuit of truth when a scientist becomes excessively cognizant of an initial hypothesis that functions as the driving force behind the investigative effort. That hypothesis might be translated as: ***"The defendant did it."*** Observer bias can be further amplified when the assigned DNA scientist is allowed full awareness of the ***desired*** results from evidence items. As a logical consequence, this scientist will most likely become influenced during the course of the analytical efforts. In this fashion, efforts that should be adhering to strict standards of scientific methodology, unfortunately evolve into what is often affectionately referred to as the ***'Texas Sharpshooter Fallacy'.***[50] This fallacy is derived from an old tale describing a man who test fires several bullets at the outer wall of an old barn. A thought dawns upon the man. He grins widely, and rushes off to grab some red paint, as well as some white paint. A few hours later, the man leads an assembly of friends and neighbors out to the old barn. The group is genuinely amazed at all of the painted targets on the barn wall—with a bullet hole ***perfectly*** located in the center of each target. Our primary character savors the outpouring of admiration. His delight comes to an abrupt end when a savvy neighbor inspects the barn more closely—noticing that the paint is still sticky. The charade is completely exposed when the neighbor also realizes that some of the paint has been splashed

through the obviously ***pre-existing*** bullet holes, and is dripping down the inside of the barn wall.

For an added understanding of the psychology of 'predisposed' scientific analysis and various associated fallacies, one might explore the concept of ***'confirmation bias'***.[51] Confirmation bias is the tendency to seek out and embrace any information that confirms our preconceptions. Falling into this analytical trap, the observer tends to ignore or neglect data that clashes with those preconceptions. An illuminating examination of how various forms of cognitive bias affect forensic investigations can be found within a 2012 **PBS Frontline broadcast**.[52]

Biased examination is epitomized by the forensic DNA analyst who decides to 'take a peek' at the suspect's DNA profile, prior to deciding on allele calls from a partial DNA profile or partial mixture DNA profile detected on a key evidence item. Note that a crime lab analyst might initially describe an e-gram signal as 'too weak', or 'inconclusive'. Weeks, months, or years later, that same analyst might notice that a newly-identified suspect possesses that same allele. Our criminal justice system must not allow a scientist to reverse their initial opinion—testifying that the signal should now be ***'miraculously'*** considered a genuine allele. Such forms of bias must be eradicated from all scientific processes, especially forensic DNA casework, which can lead to the wrongful imprisonment of innocent individuals.

The increasing power and prevalence of Y-STR typing technology.

Thus far, this chapter has covered conventional, forensic DNA-based analysis. This human identification process is accomplished by what scientists refer to as **'short tandem repeat'** (STR) typing. During the previous 10-15 years, Y-STR, or Y-chromosome-based DNA typing has played an increasingly substantial role in the investigation of certain types of criminal cases. Most pertinent to this scientific strategy is the fact that 80.1% of the arrests for violent crimes involve male suspects. Refer to the 2012 study directed by the Department of Justice and the FBI.[53]

The YFiler™ system (validated by the Life Technologies Corp. in 2006),[54] and other Y-STR technologies have proven to be extraordinarily effective diagnostic tools—particularly for sexual assault crimes. The reason for this effectiveness is the fact that, regardless of the load of DNA present from any female contributors—typically the alleged victim—Y-Chromosome-based Y-STR typing provides results only from any male DNA that is present on the evidence items.

The availability of Y-STR methods is particularly essential for the analysis of any 'intimate area' samples from an alleged female victim. Specifically, this includes oral, breast, anal, and vaginal swabs. In the event that a female victim manages to scratch her attacker, even if her efforts are only marginally successful, Y-STR testing holds the potential for the detection of a partial or full male profile

from the material under her fingernails.

Similarly, this technology can be useful in the analysis of intimate clothing items from an alleged female victim. Bras, underpants, and other intimate garments might contain trace quantities of male DNA, which would typically be swamped out by the overwhelming presence of skin cells/autosomal DNA from the female wearer.

Suppose that a female is murdered by a male perpetrator. Suppose that this crime takes place in close proximity to the victim's vehicle, and the perpetrator utilizes her vehicle to distance himself from the crime scene. If the female victim rarely loaned her car out to any male acquaintances, Y-STR testing could prove vital after gathering items from various surfaces on her vehicle. Among other locations, these surfaces could include the door handles, the steering wheel, and the gear shift. If a robbery is believed to have been part of the crime, tests can be conducted on samples from the vehicle's trunk, glove box, and center console—where valuables are often stored. If the female victim was—let us suppose—5 feet in height, and the perpetrator was well over 6 feet tall, the first surface he touched may have been the driver's side seat adjustment mechanism. Using a metaphorical description, Y-STR typing is exceptionally useful in searching for a male DNA needle, hidden within a female DNA haystack.

A drawback to excessive reliance on Y-STR based DNA typing is the fact that the technology does not possess anywhere near the discriminating power that is

achieved by using the conventional, STR-based typing system.[55] In the event that a specific Y-STR match is reported, that same match can be expected to occur among all paternally-related males within that ancestral line of individuals.

When a Y-STR based consistency is observed, the probability of such a consistency can be estimated by observing the rate at which the same genetic markers occur within a known population of male Y-STR profiles stored at a publicly accessible website.[56]

It is important to keep in mind that it is entirely plausible for two seemingly unrelated males to exhibit remarkably similar Y-STR profiles. First, note that two males, originating from the same biological father, will almost certainly share the exact same Y-STR profile. Taking that fact into account, let us take this a few steps further, with an example. Imagine that Male A has a son. We will refer to this son as Male A1—who perhaps is born shortly before World War II. Twenty years later, in the 1950s, suppose that Male A fathers another son—Male Aa—through a covert relationship with a female sexual partner. This female happens to be a long-time resident of the same city as Male A, and many of his family members. During the course of the decades that follow, Male A1 and Male Aa (half-brothers) become fathers, grandfathers, great-grandfathers, and so on. Once these related branches of the same paternal line reach the year 2020—in this hypothetical scenario—a substantial cast of male characters has accumulated. Furthermore, most of these

males may be residing in same geographic region where Male A and his sons built their lives and their paternal histories. Of course, some male individuals die young, with no male offspring. Others might become displaced to other, distant locations.

Keeping all of the above in mind, suppose that an investigation reveals no useful STR results from the scene of a crime. However, Y-STR typing efforts are successful in producing some unknown profiles. When the crime lab analyst compares an evidentiary Y-STR profile to one of Male A1's great-grandsons, perhaps matching genetic data are revealed. Consider that the true perpetrator could just as readily be the great-grandson of Male A1's long lost half-brother, Male Aa.

An investigation team might examine the biological brothers and paternally-related cousins of any accused man. However, when various males are found to be hundreds of miles away at the time that the crime in question was committed, and other males possess some other sort of ironclad alibi, the police naturally become convinced that the initially accused man ***must*** be the correct suspect. In the scenario summarized above, the investigative team would be entirely unaware of the existence of members of the Male Aa paternal family tree—perhaps residing only a few miles from the crime scene. Even when a random, mutational event alters one Y-STR allele, over the course a several generations, if the evidentiary Y-STR profile is not entirely complete, a clear allelic consistency could be the catalyst in tragic instance of mistaken identity.

When investigations inexplicably avoid additional DNA inquiries.

Regardless of whether an investigation utilizes STR typing, Y-STR typing, or both methods, litigators should be cognizant of an inexplicable cessation of an otherwise promising investigative effort. Often, there is a realization that—while some scientific results point to a ***'preferred suspect'***—additional utilization of the evidence items for genetic tests might implicate viable alternative suspects of the crime in question. Considering that too many DNA inquiries might compromise the chances of convicting the ***'preferred'*** target of the investigation**,** sometimes, there is a mysteriously abrupt halt to any further scientific initiatives. Litigators should recognize when such nonsense has occurred, and illuminate those facts for the jurors.

"THE GOOD" - DNA IN OUR CRIMINAL JUSTICE SYSTEM

Introduction: Scientific strategies of biological evidence/DNA examinations.

Television actors portraying Crime Scene Investigators (CSIs) or laboratory scientists often seem to possess an unrealistic knack for immediately identifying that single vital clue from a complex crime scene. In the real world of criminal investigations, such 'miracles' rarely play out. Real life CSIs and crime lab scientists do not possess superhuman or psychic powers. Effective criminal investigations can be attributed to hard work, careful documentation, minimizing the potential for errors, and diligent communications throughout the investigative process. In

addition to these considerations, skilled field investigators, lead detectives, scientists, and prosecutors are legally bound to share discovery with the defense team. This includes scientific information relevant to collection of evidence, case item examinations, body fluid identification, compilation of data, and genetic comparisons to DNA from known individuals.

Despite the extraordinary power of DNA technology, there is never a guarantee that useful DNA results will be found on any of the evidence items collected from a given crime scene. Any DNA profiles that are successfully recovered from an item are of little use until comparisons can be made to DNA reference standards from known individuals. Known individuals can include alleged victims, suspected criminal perpetrators, or innocent bystanders.

At the crime scene, and in the laboratory environment, the arch enemy of scientific success is contamination. Care must be taken to properly train crime scene investigators, SANE nurses, and forensic biologists to minimize the risk of contamination failures. Despite the astonishing utility of DNA technology, human negligence, occurring at a variety of levels, will sometimes nullify its effectiveness. Specific examples of human errors, scientific falsification scandals, and DNA evidence contamination catastrophes will be discussed in more detail, further into this chapter. Links to relevant articles are as follows:

- Baltimore City Police Crime Lab[57]
- Houston City Police Crime Lab[58]
- San Francisco City Police Crime Lab[59]
- New Jersey State Police Crime Lab[60]
- Michigan State Police Crime Lab[61]
- North Carolina State Bureau of Investigation[62]
- Chicago Tribune Article[63]
- Oklahoma City Police Crime Lab[64]
- Fred Zain[65]

The development of searchable DNA databases.

CODIS is an acronym for the Combined DNA Index System.[66] The CODIS system has been developed, provided, and maintained through efforts from the FBI. The system functions as network of criminal justice DNA databases as well as the software used to manage those databases. Frequently asked questions on CODIS can be found here.[67] In the United States, the DNA Identification Act of 1994[68] authorized the establishment of CODIS, our National DNA Index. This legislation specifies the categories of data that may be maintained within the database. These include: convicted offenders, arrestees, unknown DNA profiles from forensic DNA casework, unidentified human remains, missing persons, etc. DNA typing data may be collected and compiled onto local, state, and/or national DNA databases. In the United States, Federal law requires that laboratories submitting DNA data to the National DNA Indexing System (NDIS) are accredited by professional associations,

such as the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB)[69] and ISO/IEC 17025.[70]

DNA Databases, cold casework initiatives, reversal of wrongful convictions.

Searchable DNA databases are proving to be enormously valuable for the investigation of unsolved 'cold cases'. Similarly, past criminal investigations, cases that were once presumed to be resolved, are often reinvestigated using new, expanded technology, and DNA databases. These initiatives are playing a substantial role in unexpected developments. The outcome of trials conducted years ago, in the 1990's, the 1980's, or in the much more distant past, can be turned upside down by new DNA results. According to the Innocence Project website[71], as of August 2020, in the United States alone, 375 wrongfully convicted individuals have been set free, as a consequence of DNA testing. This number steadily continues to climb.

A diligent litigator should be aware that not just anybody can upload DNA profiles onto the databases. Furthermore, many individuals working within the criminal justice system are unaware that crime lab analysts have more than one means of utilizing the databases. Suppose that—during the course of investigating a homicide—a partial, unknown DNA profile is found within the vehicle that was stolen from the victim. While this genetic information exhibits no consistencies with any known acquaintances of the victim, suppose that this partial DNA profile does not quite meet the criteria needed to qualify as a CODIS upload. When such a

scenario arises, the reporting crime lab analyst might take the initiative to conduct what is referred to as a ***'keyboard search'***—targeting various databases.

Initiating such a process will explore consistencies between the partial DNA profile from the vehicle, and similar genetic information housed within the database. While such discretionary keyboard searches can be extraordinarily useful toward a thorough investigation, the defense team for the accused has little or no influence/control—over whether or not such searches ever take place. As a consequence of this lack of access, a potentially sensational break in any case investigation might be locked away, on a seemingly unimportant evidence item. Unfortunately, genetic results from that item might remain unexplored for months, years, or decades.

Understanding the work conducted by Forensic Biologists.

As investigations near completion, the investigators and their crime lab are obligated to provide their findings to the prosecution—and eventually, the defense team. For most crime lab scientists, a case file includes evidence item lists, detailed bench notes, meticulously prepared worksheets, microscopic exam observations, body fluid test results, DNA data, statistical calculations, and records of all communications between the scientists, the investigators, and the prosecution team. The results of each case are typically summarized within one, or a few brief reports. Prosecutors often do not ask for any significant details beyond those few pages of

summary reports. Litigators must be mindful that these limited summaries do little to clarify or justify how any of the scientific conclusions were actually reached.

Counsel for the prosecution is routinely provided with a 'built in' forensic biologist—from the crime lab. In addition to the fact that this person is a trained DNA expert, this analyst has ample access to the actual case evidence items, as well as the DNA databases—throughout the course of the investigative processes.

In contrast, counsel for the defense has little more than a license to practice law. In many instances, the criminal justice system guarantees little or no access to a DNA expert—specifically assigned to the defense team. In this way, the criminal justice playing field can be quite slanted to the detriment of the accused. For this reason, the competent litigator must battle relentlessly for full disclosure of the underlying laboratory records. As Thompson points out:

> "A key aspect of discovery in DNA cases is the electronic data produced by the computer-controlled genetic analyzers that are currently used to 'type' DNA samples."[72]

DNA transfer events: "Every contact leaves a trace."

It is useful to keep in mind that trace quantities of DNA are ubiquitous, and readily detectable from a vast array of potential substrates or surfaces within any crime scene, or within any residence or workplace where no crime has occurred at all. Over a century ago in France, Professor Edmond Locard established the world's first forensic science lab for the Lyons Police Department.[73] This remarkable

scientist was the first individual to postulate the importance of transfer events in the investigation of crimes. Dr. Locard's ideas evolved into the time-tested Locard Exchange Principle[74] stating that ***"Every contact leaves a trace."*** Amazingly, Locard's principle became universally accepted about forty years before James Watson and Francis Crick described the first accurate model of the DNA double helix.[75] Locard's principle applies more appropriately to DNA than it does for any other form of trace material. This principle has been described as follows:

> "Wherever he steps, whatever he touches, whatever he leaves, even unconsciously, will serve as a silent witness against him. Not only his fingerprints or his footprints, but his hair, the fibers from his clothes, the glass he breaks, the tool marks he leaves, the paint he scratches, the blood or semen he deposits or collects. All of these and more, bear mute witness against him. This is evidence that does not forget. It is not confused by the excitement of the moment. It is not absent because human witnesses are. It is factual evidence. Physical evidence cannot perjure itself, it cannot be wholly absent. Only human failure to find it, study and understand it, can diminish its value."[76]

Beyond Locard's Principal: The reality of DNA transfer events.

Unlike the transfer of DNA from sweat and skin cells during human contact, the blood, semen, and saliva from human beings are enormously rich sources of cells and DNA. As thousands of human cells might be present in tiny skin cell deposits or body fluids that crime scene investigators are able to collect from evidence, without special equipment, it is impossible for humans to visualize the DNA within such deposits. Cells, and the DNA deposits contained within, are simply too small.

As the frosty weather begins to dominate each winter, litigators should devote some time for a few observations. Take a stroll through your local shopping mall. Visit the homes of some friends, family, or neighbors. Numerous nasal cavities are draining. Infected individuals are coughing and sneezing. Crumpled up facial tissues exist in abundance. Although we cannot see them, we know that common cold and influenza viruses are spread from hand-to-surface and hand-to-hand. Trillions of viral particles are spread by infected individuals to door handles, telephones, computer keyboards, car keys, steering wheels, stairway railings, currency, vending machines, TV remote controls, pens, pencils, clothing, and bedding. The list seems endless. If a person is not sufficiently cautious, it only takes a number of days for viruses to replicate themselves in the human respiratory system.

In the eyes of the average person, the structure and mobility of DNA differs marginally from the structure and mobility of viruses. Although our genetic molecules are not at all invasive and infective, DNA and viruses are quite similar in that they are both submicroscopic clumps of matter. Transfer events do indeed occur with both of these forms of matter in much the same way. Any person who argues against the prevalence of DNA transfer events in our homes, our workplaces, our vehicles, and within crime scenes, must also doubt that infectious agents are able to spread among human populations. Such an argument is intuitively frivolous.

In a 2009 article entitled, **"Transfer Theory in Forensic DNA Analysis"** published in ***Law Officer***[77] (a journal for law enforcement), forensic biologist Suzanna Ryan instructed as follows:

> "Obviously, the inadvertent transfer of DNA is an area that should be further studied. Since so many of the available journal articles present conflicting information, more work is needed to see how likely it is to both transfer and detect DNA in a secondary or even a tertiary fashion, especially considering the sensitivity of modern forensic DNA analysis."[78]

Scientific debates focusing on the mechanisms of incidental DNA transfer involving such miniscule amounts of DNA, are far from settled. In December 2010, van Oorschot, Ballantyne, and Mitchell, who are some of the world's most renowned authorities on forensic trace DNA, published a review[79] in ***Investigative Genetics.*** In the section on **"Transfer Issues"** the authors argued:

> "Greater effort needs to be made by police/crime investigators to investigate how a DNA sample arrived at the location where it was found, as well as by scientists to better understand the impact of activities on the relative amounts of DNA from particular sources at a crime scene. In some instances, it is possible to derive the chain of events that led to a trace DNA sample being present at a crime scene - for example, prior visits to the scene or the known use of an item. Awareness of these variables, and their impact on transfer events, will assist in weighting the likelihood of proposed alternative scenarios."[80]

Also in 2010, Allan Jamieson and Georgina Meakin of The Forensic Institute in Glasgow, UK, published an article in ***The Barrister Magazine*** entitled **"Experience is the Name That Everyone Gives to Their Mistakes"** [81] in which they cautioned:

> "The examination of evidence for handler DNA can reveal DNA of people who have, or have not, handled the item; the stronger profile may, or may not, be the person who last handled the item; an inference of direct contact between an individual and the item may or may not be supportable, depending on the circumstances of the case. In other words, we did not know enough to make any sensible scientific judgments as to how DNA came to be on an item."[82]

Later in their article, Jamieson and Meakin provide their viewpoint as follows:

> "Frequently, the underlying hypothesis is that touching, or direct contact, is a more likely scientific explanation for the finding of a DNA profile on an item than indirect contact. This to the extent that it may be described as providing 'extremely strong' support for direct versus indirect transfer. In our view, such an opinion on DNA transfer is not supportable based on case experience or on the available scientific research."[83]

In July 2013, Dr. Jamieson and Dr. Meakin published an updated review[84] on this vital area of forensic biology/DNA. In ***Forensic Science International: Genetics***, this article was entitled: **"DNA transfer: review and implications for casework"**.

In the article's abstract, the authors wrote:

> "DNA-bearing cellular material can come to be on a surface by either direct or indirect transfer. Direct transfer includes contact, but also includes activities within the vicinity of an item that may result in the transfer of DNA directly from an individual without any contact, such as speaking, coughing, and sneezing. Indirect transfer of DNA is when DNA from an individual comes to be on an item via an intermediary surface. It is important to consider indirect transfer in the evaluation of trace DNA in casework."[85]

In the section: **"Introduction to trace DNA"**, Jamieson and Meakin continue:

> "Several different terms have been coined to describe such DNA. For example, the term 'touch DNA' has been used, but this can be misleading in two ways: Firstly, such a term infers that the DNA recovered from a surface got there via that surface being touched, but this is usually not known, and secondly, there is a misconception that 'touch DNA' can only be detected by LT-DNA (low-template-DNA) techniques."[86]

The most recent, comprehensive review focusing on criminal casework and DNA transfer events bears the title: **"DNA transfer in forensic science: A review"**. At the beginning of the abstract within this peer-reviewed January 2019, article, van Oorschot, Szkuta, Meakin, Kokshoorn, and Goray stated as follows:

> "Understanding the variables impacting DNA transfer, persistence, prevalence and recovery (DNA-TPPR) has become increasingly relevant in investigations of criminal activities to provide opinion on how the DNA of a person of interest became present within the sample collected." [87]

Deeper into this review article, the authors emphasize the following facts:

> "The discovery that DNA can be detected from non-visible biological material left on a surface merely through touching it by hand, and the extrapolation of this observation to contact with skin in general, drastically broadened the types of items that could be targeted to obtain DNA profiles and the variety of situations in which DNA profiling could be applied. This discovery of the ability to generate profiles from touched objects was initially met with disbelief by many within the forensic community, but once verified, became a welcome tool for law enforcement agencies. Within several jurisdictions, samples collected from touched objects now represent more than half the total number of samples processed for DNA profiling."

Today's state-of-the-art DNA detection technology can produce a full DNA profile from less than a billionth of a gram of DNA. Recall that a scientist needs only 200 human cells in order to get that single nanogram (ng) of DNA. A jury of non-scientists might inquire: ***"Exactly how much is 1 ng?"***

Visualize the amount of material in a small packet of artificial sweetener. This is one gram of material. Imagine setting aside 1/1000th of this material and disposing of the remainder. The tiny pile of material set aside would weigh one milligram. Now imagine setting aside 1/1000th of this milligram and discarding the remainder.

We now have one microgram of material, which is 1 million times less than the contents of the original sweetener packet. This amount of material cannot be seen without the use of a microscope. By some means, we must now set aside 1/1000th of that microgram of artificial sweetener, and discard the remainder. This results in one ng of material, or one billion times less than the initial sweetener packet. It is important to keep in mind that the astonishing sensitivity of this technology does not diminish the fact that we are indeed working with remarkably tiny masses of DNA. Such small quantities of DNA can be casually transferred through a multitude of ordinary, incidental, everyday events.

Transfer events: Whose DNA is it?

If a case involves an earnest search for DNA, it is no surprise when at least some genetic material, from somebody, is indeed recovered. Regardless of how informative and powerful forensic DNA technology has become, DNA typing by itself cannot tell us ***how*** the DNA arrived where it was detected. The operative questions are: Whose DNA has been found? Precisely where has the DNA been found? Jurors, case investigators, prosecution teams, and the defense teams should be asking whether or not DNA from the defendant was present in any truly incriminating locations. Similarly, we should ask whether or not DNA from the victim has been found in a place that implicates any specific suspect. It is also important to carefully consider the quantity of recovered DNA.

A fundamental calculation illuminates the reality of human skin cell transfer.

A question often emerges during the course of criminal trials involving presumed transfer of DNA from a person to a surface: How many skin cells does the average-sized human shed—from head to toe—during the course of a single minute? Various medical resources suggest that the average adult human being sheds approximately 30,000-40,000 skin cells per minute. Interestingly, these resources are actually projecting a profound ***under-estimation*** of human skin cell shedding.

Refer to a 2013 article published in the journal, *Annals of Human Biology.*[88] This article, authored by Bianconi et al., is entitled: **"An estimation of the number of cells in the human body."** Organ by organ, the authors estimate the total number of cells in the body of an average-sized, adult human. This number was reported to be: 3.72×10^{13}, or **37.2 trillion**. It is interesting to note the medical community seems to have universally agreed that the largest organ in the human body is—indeed—the skin. Keeping that in mind, refer to the section of the Bianconi article bearing the title: **"Skin: Epidermal and dermal total cell number"**. The authors estimate that the total number of cells in both of those two layers adds up to 2.03×10^{12}, or **2.03 trillion skin cells**—covering an average-sized, adult individual. Utilizing the numbers compiled thus far, we can now estimate that the combined epidermal and dermal cell layers comprise about 5.5% of the total cells within a human body.

Bianconi et al. estimated that that epidermal contribution accounts for only

0.176 trillion of the total 2.03 trillion epidermal/dermal cellular material generically referred to as 'skin'. In the calculation being conducted here in this chapter, we will proceed ***only*** with the estimated 0.176 trillion ***epidermal*** cells found in the average human—to the exclusion of the remaining 1.854 trillion ***dermal layer cells***.

Refer to the 2002 published 4th edition of **"Molecular Biology of the Cell"**, authored by Bruce Alberts, et al.[89] In the section entitled: **"Epidermis and Its Renewal by Stem Cells"**, the authors provided the following:

> "The period from the time a cell is born in the basal layer of the human skin to the time it is shed from the surface, is of the order of a month, depending on the region of the body."

Rather than use Dr. Albert's 30-day estimation for skin cell turnover rate, let us work with a much more conservative 60-day estimation. The cause for this is the fact that the 30-day cellular turnover time frame—although accurate for younger individuals—can extend a few weeks longer—as human individuals age. Bringing all of the above together, we start with the extremely conservative estimate of **176,000,000,000** epidermal layer cells covering the body. Operating on—yet another conservative estimate—we will estimate that all of these cells would take a full **60-day** time frame to be released by shedding:

176,000,000,000 ÷ 60 days=2,933,333,333 cells per day.

Next, 2,933,333,333 cells per day ÷ 24 hours=122,222,222 cells per hour.

Next, 122,222,222 cells per hour ÷ 60 minutes=2,037,037 cells per minute.

Based upon these calculations, it is clear that the informally reported 30,000-40,000 skin cells per minute is excessively conservative. The genuine number of cells shed during the course of a minute is much closer to 2 million. The attentive litigator should grasp the implications of these calculations: It should be no surprise when trace quantities of skin cells/DNA are readily detectable from a vast array of potential substrates or surfaces within any crime scene, residence, workplace, or other location coming into direct or indirect contact with human individuals.

Lukis Anderson: Scientific proof of DNA transfer.

Despite the mountains of forensic research initiatives—establishing that DNA transfer can play a significant role in the landscape of any investigation—the detractors of this fact were not fully disproven until the latter part of 2012. Refer to the final section of this Chapter, entitled: **"Recent developments in the forensic use of DNA"**. The first case to be described is as follows: **"The Lukis Anderson case: A 'perfect storm' for incidental DNA transfer."** Without a doubt, a remarkable series of events must have triggered the enormously misleading/incriminating detection of a man's DNA at the scene of a homicide. Precisely what where those circumstances? Nobody is certain. However, it is now clear that—while DNA transfer has been clearly demonstrated through experimentation—a ***'perfect storm'*** of incidental events can become linked together, and point law enforcement investigators in an entirely faulty direction.

Important connections between transfer events and low copy number DNA.

If Dr. Locard was alive today, he might feel gratified with the application of his principle to the assessment of crime scene DNA. However, perhaps he would feel compelled to caution our criminal justice system—regarding the interpretation of case-by-case findings, generated from this remarkably sensitive technology.

Among our most highly recognized, modern-day contributors to forensic biology/DNA is Dr. Bruce Budowle. From 1983-2009, Dr. Budowle was a leading scientist—and the Lab Director, with the Federal Bureau of Investigation (FBI). He has published more than 530 articles, provided more than 630 presentations, and testified in well over 250 criminal cases. In 2009, Dr. Budowle became the Executive Director of the Institute of Applied Genetics and Professor in the Department of Forensic and Investigative Genetics at the University of North Texas Health Science Center, at Fort Worth, Texas. In line with the teachings of Dr. Locard, Dr. Budowle recently weighed in on the topic of transfer events and the questionable reliability of interpretations from **L**ow **C**opy **N**umber (LCN) DNA. LCN DNA can be simply described to non-scientists as: **'an extremely small amount of DNA'**.

The article authored by Dr. Bruce Budowle in 2010 bears the title: **"Low Copy Number Typing Still Lacks Robustness and Reliability."**[90] Dr. Budowle defines LCN as: ***"Typing of DNA samples at or below 100-200 pg of DNA…"*** Note that a single nanogram (ng) is equal to 1000 picograms (pg).

Dr. Budowle concludes this distinguished article, urging scientists as follows:

> "Forensic DNA typing has been labeled the gold standard of forensic science. The methodology has been demonstrated to be robust, reproducible and reliable. In contrast, LCN typing has not been well developed and applied appropriately. Moreover, the validation studies do not comport with protocols, assumptions for calculating the weight of the evidence are in question, and the scientific literature recommendations are not necessarily in concert with practices. It would be a shame to abandon the standards in place for forensic DNA typing just to push the envelope with LCN typing. Assisting in solving crime with DNA typing is our desire and our responsibility. However, we should pursue forensic analyses by employing robust and reliable technologies so that we can have the greatest confidence in the reliability of our results. Substantially more work is needed before the conditions are known under which LCN typing should be used for reliable identification purposes."

Yet another facet of the LCN DNA transfer issue is the concern associated with our measure of confidence that a reporting scientist has detected ***any*** DNA at all. Earlier in this chapter, it was established that real-time polymerase chain reaction (RT-PCR) technology is currently used to estimate the recovery of remarkably tiny quantities of DNA. The RT-PCR technology being used for detection of picogram (pg) quantities of DNA is truly extraordinary. However, it is greatly misguided for individuals to embrace the whim that this technology offers a high degree of quantitative ***accuracy***—regardless of the infinitesimal amounts of DNA being estimated. Litigators must work closely with the scientists to understand the concepts of limit of detection (LOD), limit of quantification (LOQ), as well as the impact of background noise[91].

As a hypothetical, let us presume that a crime lab analyst estimates a total DNA yield of 0.03 nanograms (ng) of DNA—which is contained in perhaps one drop of a liquid DNA sample. This 0.03 ng is identical to 30 picograms (pg), originating from no more than an estimated ***five*** human cells. Refer to the 2010 article published by John Butler and Carolyn R. Hill, bearing the following title: **"Scientific Issues with Low Amounts of DNA."**[92] In part, the authors of this learned treatise advise forensic DNA scientists as follows:

> "Since the advent of quantitative PCR (qPCR) assays, DNA quantitation tests have become more sensitive—enabling quantities as small as a few genomic copies to be detected. Use of qPCR assays, such as Quantifiler®, or PlexorHY®, can enable detection of minute amounts of DNA. However, it is important to keep in mind that qPCR also is subject to stochastic variation, especially on the low end of DNA quantity measurement. Thus, numbers in the low pg range may not be reliable, and results with little or no 'detectable' DNA may still amplify with STR kits."

Note the authors use of the term, **"detected"**, as well as the phrase, **"detection of"**, rather than claiming that **"accurate measurements"** are possible at this **"low pg range"**. They are not. Although the RT-PCR system is indeed quite sensitive, the accuracy of the system—especially at pg levels—is wildly erratic. It is faulty science to report that **"DNA was detected"**, when the estimation is based upon an extremely meager number of cells.

It is useful to note that Dr. Butler is currently a fellow at the National Institute of Standards and Technology (NIST), and is serving as the NIST Vice-Chair on the

Commission of Forensic Science. Dr. Butler also serves on the Scientific Working Group on DNA Analysis Methods (SWGDAM). This highly regarded scientist has written several textbooks on forensic DNA typing, covering all aspects of the underlying molecular genetic methods, the application to forensic casework, and bio-statistical interpretation of results. Dr. Butler serves as the Forensic DNA Section Editor for the Encyclopedia of Forensic Sciences (2nd Edition). Among many other awards, in 2003, Dr. Butler received the distinguished Scientific Prize of the International Society for Forensic Genetics.

Within this article, and referring to LCN samples that are prone to severe stochastic effects, Dr. Butler and Dr. Hill describe **"…two schools of thought on how to handle these types of samples:…"** First, the authors describe: **"The Stop Testing Approach"**.

This approach addresses the fears experienced by crime lab management—that the template DNA is simply insufficient to obtain any reliable results—regardless of the methods utilized. In other words, perhaps it is most prudent to simply halt the analysis. I am in agreement that this **'Stop Testing'** approach is sometimes quite rational. However, it is morally corrupt for such an approach to be utilized as ***leverage*** against a defendant. A hypothetical centering on this strategy, might be outlined as follows: Suppose there are allegations from a young female, claiming that: **"He touched me inappropriately"**—referring to an adult male.

Suppose that the crime lab analyst extracts DNA from pertinent samples, and estimates the presence of male DNA. However, as ample nanogram quantities from the young female are clearly present, the estimated male DNA quantities translate into 15 male cells, or 5 male cells, or perhaps ***only one*** male cell. When this presumed detection points to DNA quantities all the way down in the **6 pg-to-90 pg** range, the quantitative results, and the DNA typing results, are of highly questionable reliability. The limit of detection, limit of quantification, and the background noise associated with such tiny estimated quantities of cells/DNA simply do not allow accurate scientific reporting of what has been observed. It is not uncommon for crime lab management to decide to utilize the **"Stop Testing Approach"**, as a mechanism of opening the door for prosecutors to persuade a panel of jurors: **"Male DNA is present. However, our detection limits do not allow us to identify *who* that male might be. But who else *could* it be?"** In such instances, the science is clearly being voiced in a disingenuous fashion. Diligent litigators should recognize that halting the analysis—within the context of a case that is parallel to this hypothetical—will only serve to prejudice the panel of jurors.

Second, Drs. Butler and Hill describe the **"Enhanced Interrogation Approach"**. This strategy entails **'pushing the envelope'**, by increasing the sensitivity of the DNA testing methods, and increasing the DNA testing replications. If more aggressive methodologies can provide enhanced results, and replicate testing

can demonstrate the reproducibility of the data, it might be possible to overcome the limitations of LCN DNA.

Reporting conclusions from LCN DNA, allelic dropout, and DNA mixtures.

Crime labs are compelled by universally accepted standards to conduct validation studies on their DNA profiling instruments/systems to determine an RFU threshold at which each signal on an e-gram can be trusted as a genuine DNA signal, as opposed to a potentially unreliable artifact.[93] As clarified earlier in this chapter, when the quantity of DNA recovered from a crime scene evidence item is profoundly limited, the apex of various e-gram peaks might be all the way down between the baseline of background noise, and the RFU threshold for reliable interpretation of a genuine allele. During circumstances within which allelic signals are expected, but no signal is detected at all, this phenomenon is referred to as: ***'allelic dropout'***.[94]

Under the various challenging interpretive scenarios—and keeping in mind the astonishing sensitivity of modern day forensic DNA detection systems—accurate, unbiased interpretations are of paramount importance toward achieving a fair criminal trial. Crime lab analysts must report the results of any DNA comparison in one of the following five ways:

1) Observation of a perfect, single-source ***match*** between a known DNA reference standard and the DNA from a specific evidence item;

2) The known individual can be ***excluded*** as a potential contributor of the alleles, or part of the mixture of alleles, observed on the evidence item;

3) The known individual ***cannot be excluded*** as a potential contributor to the alleles, or part of the mixture of alleles, observed on the evidence item;

4) Without the benefit of more testing and additional data, the DNA comparison is insufficient for any sensible, scientifically reliable conclusion;

5) The evidence item provided virtually no DNA data. Specifically, complete allelic dropout is observed at all of the tested genetic locations. In this instance, all human individuals can be unconditionally excluded.

When a crime lab forensic biologist chooses to report **Option 3**, ***cannot be excluded***, universally embraced quality assurance standards demand that the analyst must provide valid statistics, giving weight to this non-exclusion finding.

When a crime lab analyst reports **Option 4**—characterizing data comparisons as ***inconclusive***—this finding typically causes anxiety for litigators representing both the defense and the prosecution. The cause for such severe trepidation might be the fact that—within business/legal circles—there is a prevailing corporate revulsion when confronted with the response*: **"I don't know."***[95] Although scientists are aware

of this aversion to reality—sometimes—the negative results lead only to that clearly appropriate, three-word assessment. Perhaps it would be better for scientists to report that: **"Until significantly improved data can be collected, we simply have no answer here."** Regardless, defense teams insist upon arguing that ***'inconclusive'***, for example, proves the absence of DNA from the defendant. This is incorrect.

In contrast, prosecution teams typically argue that ***'inconclusive'*** establishes that the defendant's DNA ***"cannot be ruled out"***. This is incorrect—as ***that*** wording is fundamentally identical to **Option 3**—***cannot be excluded***. Recall that when a suspect cannot be excluded, stats are required to provide weight to this finding. When any analyst reports ***inconclusive,*** no weight can be attached to the response: ***"I don't know."***

There is a consensus among crime labs regarding the following fundamental policy: When results within any genetic locus include signals falling below the stochastic threshold, it is acceptable to disregard—for statistical purposes—any results from that locus. As an example, suppose that threshold is set at 100 RFUs. Thus, for statistical purposes, analysts will rely strictly on loci at which they are confident in assuming that all of the contributors' alleles are clearly detectable on the e-gram. In light of this concept, Thompson and colleagues have argued that:

> "Stochastic thresholds are not a perfect solution to the problem posed by unreliable DNA data because it means that the lab may ignore potentially exculpatory data."[96]

LCN, DNA mixtures, and the impact of cognitive bias on RFU thresholds.

In addition to the challenges of LCN DNA—as described by Dr. Budowle—which typically lead to low RFU, weak DNA profiles, the added challenge presented by multiple human DNA contributors can cause interpretations to become profoundly more daunting. Suppose that crime lab validation studies set the ***'analytical threshold'*** at 50 RFUs. During the investigation of a specific case, suppose that the reporting forensic biologist notes that the typical background noise ranges between 6 RFUs and 14 RFUs. Suppose that—from a crucial evidence item—the analyst observes a moderately complex DNA mixture.

Relying upon experience and professional discretion—this crime lab analyst decides that any signal on the e-gram, extending to or beyond four-fold above the average background noise level of approximately 10 RFUs, ***will*** be regarded as a potentially reliable allelic signal. In other words, a signal of 10 RFUs x four-fold=40 RFUs, will not be simply ignored, merely because 40 RFUs is below the arbitrary 50 RFU threshold. Clearly, such low RFU signals should not be factored into any statistical calculations for inclusion. However, the presence of such peaks on the e-gram might be worthy of noting to a panel of jurors.

Indeed, there are precedents for the above-described scenario. Many crime labs have incorporated statements into their standard operating procedures and/or technical manuals, resembling the following: **"Limited data, including signals in**

these ranges, should not be used to determine inclusions or calculate statistics. However, such results may be utilized *for exclusionary purposes only*." Another means of expressing this has been as follows: **"Analysts may utilize alleles labeled between the analytical and stochastic threshold to determine an exclusion."**

The rationale justifying why some limited, marginally reliable results are considered worthy of reporting exclusions, but not for inclusionary purposes, is as follows: A set of allelic signals might exhibit consistency with a known individual. However, the observation of those alleles could be a coincidental result of the fact that one given individual will often share a subset of genetic markers with various other individuals within the human population. Meanwhile, when an interpretable allele is observed—and the individual under comparison simply does not possess that allele—that signal peak cannot be considered as anything but ***exclusionary***. DNA typing from an evidence item might resemble the example depicted below:

Loci	Alleles
Locus 1	17, 18
Locus 2	7, 7
Locus 3	29, 30.3
Locus 4	18, 18
Locus 5	11, 12
Locus 6	10, 13
Locus 7	9, 10
Locus 8	9, 9.3
Locus 9	10, 10

Locus 10	11, 14
Locus 11	12, 12
Locus 12	8, 11
Locus 13	24, 27
Gender Locus	X, Y

Note that this illustration is not derived from any actual person. This person, if real, would be a male (as indicated by the 'XY' at the gender locus), and the names of the loci are not Locus 1, Locus 2, etc. The actual human loci have designations such as **vWA**, **TPOX**, and **DS1358**, etc. If a DNA profile, resembling this example, did indeed come from a specific individual, this male would almost certainly be the only person on our planet (assuming the absence of an identical sibling), with this precise compilation of genetic markers (called "alleles").[97]

It is important to note that, with rare exceptions, each human has two DNA markers at each locus. These markers are often different from each other (example from above: the 17 and 18 at Locus 1). However, sometimes an individual receives two copies of the same DNA marker (example: the 7 and 7 at Locus 2), which would be indistinguishable from each other on an e-gram.

Hypothetically, let us suppose that an evidence swab from a stain on a knife blade establishes the presence of a murder victim's blood on that weapon. Suppose that, when a second swab is collected from the knife handle, a multitude of genetic markers are detected—with the victim excluded as a possible contributor. At a few

loci, two alleles are reported. However, at other loci—to the dismay of the investigative team—three, four, five, or as many as six alleles are observed. Recall that modern DNA typing is capable of detecting remarkably tiny quantities of genetic material. When DNA deposits are comprised of DNA mixtures from multiple individuals—interpretations can become quite challenging.

The scientist should not report that the mixture of alleles is from 'touch DNA', from multiple contributors. The forensic tests have most likely failed to identify any of the types of cells on the knife handle, nor have they confirmed ***how*** the cells/DNA came to be there. The scientist must not attempt to testify regarding ***when*** the various alleles arrived on the knife handle, since DNA typing technology is unable to answer that question. The presence of six DNA markers at one locus establishes that at least three individuals deposited the DNA mixture on the knife handle—at some unknown points in time. If seven DNA markers had been detected at one locus, the analyst should report the presence of at least four contributors within this DNA mixture.

Suppose that the investigation team assigned to this knifing homicide finds a new suspect. Upon obtaining a known DNA profile from that suspect, a comparison is made between that profile and the DNA mixture, previously reported from the knife handle. Suppose that some similarities between this new suspect and the knife handle DNA are notable. However, perhaps one or two, or more of the alleles from the suspect are simply absent from the DNA mixture. The analyst is faced with the

challenge of pondering an imperative question: How should one interpret these various genetic similarities—taken together with ***multiple*** allelic absences?

The crime lab forensic biologist might believe that missing genetic markers should be attributed to the previously described event—allelic dropout. Clearly, the absence of genetic information might be due to the fact that the suspected contributor left behind an insufficient amount of DNA to get a complete genetic profile—at all loci. This observation ***defines*** the essence of allelic dropout. Alternatively, it is quite plausible that DNA from this new suspect is genuinely altogether absent from the knife handle. ***This distinction is vital***. A properly trained forensic biologist will not simply 'forgive' one allelic dropout, plus another, then another—indefinitely. At some point, the scientist must consider the **'inconclusive'** interpretive option in reports, as well as when testifying at trial. As numerous additional allelic dropouts become apparent, the results must qualify as an outright **'exclusion'**.

The dilemma ultimately becomes: **"*Where should we draw the line?*"** This is a question that plagues every crime lab analyst who has ever been confronted with a complex DNA mixture—resulting in a challenging interpretation. As an analyst is faced with such a challenge—and possible dropout events—the clock keeps moving. Eventually, the crime lab scientist is compelled to articulate various conclusions into an official DNA report. Diligent litigators should explore whether or not crime lab managers have provided their forensic DNA analysts with scientifically sound

guidelines—regarding the appropriate steps toward resolving these challenges. Such guidelines might effectively summarize how comparisons can be made between the DNA standards collected from known individuals and an endless assortment of diversely configured DNA mixtures.

The history of DNA mixture misinterpretations.

Examination of evidence items can lead to the characterization of DNA mixtures with endless gradations of complexity and variability. From locus-to-locus, no two DNA mixture e-grams will exhibit the identical 'allelic landscape'. As STR typing initially became the basis of human identification, law enforcement labs were not provided with sufficient centralized standards for the appropriate interpretation of DNA mixtures. Forensic DNA lab managers and analysts were lacking direction. As this scientific obstacle became progressively realized, and efforts were made to implement various guidelines, controversies and legal debates ensued. For a few decades, a clear consensus for reliable DNA mixture interpretations has continued to elude forensic DNA labs. Within the DNA interpretation guidelines maintained by one accredited crime lab, the opening statement of the document touches upon these concerns as follows:

> "The interpretation of results in casework is a matter of professional judgement and expertise. Not every situation can or should be covered by a predetermined rule."[98]

It is useful to explore the evolution of efforts to address the misinterpretation of DNA mixtures. In 2005, forensic DNA scientists worked in concert with the National Institute of Standards and Technology (NIST), with the purpose of organizing a widespread inter-laboratory study of DNA mixture assessments. This initiative was referred to as the NIST MIX05 Study[99]. Sixty-nine forensic DNA laboratories were provided with the identical two-person mixture data. Alarmingly, forty of the reporting labs characterized the DNA mixtures as ***"inconclusive"***. Among the twenty-nine labs that provided a statistic—based upon non-exclusions—the random match calculations ranged from **1 in 31,000** to **1 in 213,000,000,000,000**.

In recognition of this astounding lack of consistency, in February, 2008, a DNA mixture interpretation workshop was held in Washington, D.C. This was one of a multitude of similar workshops—focusing in part, on the results of the MIX05 Study. Dr. John Butler—the acting chairman of this D.C. workshop—summarized the disturbing results with his presentation, entitled: **"A High Degree of Variability Currently Exists with Mixture Interpretation."**[100]

Part of Dr. Butler's presentation included a commentary from the highly recognized forensic scientist, Dr. Peter Gill—which was as follows: **"If you show 10 colleagues a mixture, you will probably end up with 10 different answers."** Among Butler's final thoughts from the presentation was the following conclusion:

> "…the behaviour of each mixed sample can be different and multifunctional and occasionally its interpretation turns out to be complicated—sometimes paralleling the importance of the evidence in the resolution of the case. In some casework mixtures our experience has proved that theoretical assumptions from studies with laboratory samples, albeit very useful, can turn out to be impracticable."

During the years following MIX05, many scientists expressed concerns regarding the use of a simple inclusion/exclusion threshold. This presented a high potential for failure—as it encouraged the ***'Texas Sharpshooter Fallacy'*** (previously described in this chapter) in forensic DNA interpretations[101], and that such rigid inclusions/exclusions make no sense[102]. As scientists continued to wrestle with the DNA mixture interpretation version of this fallacy, a chasm formed between many forensic biologists/mathematicians—on one side, and the FBI/SWGDAM—on the other side. While the NIST MIX05 studies were illuminating, and may have somehow succeeded in nudging rational DNA mixture guidelines forward, harsh inconsistencies persisted for years to come. Around 2009/2010, the FBI/SWGDAM initiated a movement toward resolving this mixture interpretation crisis by implementing a second, **'stochastic'** threshold. The use of this threshold was defined previously in this chapter—in the section entitled: **"RFU thresholds, analytical artifacts, and DNA data interpretations."**

Refer to a 2011 article in ***Science and Justice***, from the authors, Itiel Dror and Greg Hampikian[103]. This article was entitled: **"Subjectivity and bias in forensic DNA mixture interpretation"**. The authors wrote the following:

> "Because of the esteem of DNA evidence, it is important to study and assess the impact of subjectivity and bias on DNA mixture interpretation. The study reported here presents empirical data suggesting that DNA mixture interpretation is subjective. When 17 North American expert DNA examiners were asked for their interpretation of data from an adjudicated criminal case in that jurisdiction, they produced inconsistent interpretations."

Further into the article, the authors continued:

> "The great degree of variability in laboratory methods regarding DNA mixtures has been the subject of concern in the DNA community, and the Scientific Working Group on DNA Analysis Methods (SWGDAM)."

Further, the authors point out that SWGDAM guidelines have established that:

> "The laboratory must perform statistical analysis in support of any inclusion determined to be relevant in the context of the case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis."

In their conclusion, these authors emphasized the following:

> "…while this is the first published empirical study of potential DNA bias, Butler of the NIST laboratories has conducted extensive studies of mixture analysis over several years, wherein he supplies a large number of volunteer laboratories identical DNA mixture data and asks for their analysis. The results of these excellent studies have been presented at conferences and are available at the NIST webpages, but have never been published in a peer-reviewed journal. An interesting and perhaps the most critical point for this paper is that Butler's research findings show that inclusion statistics for the same profiles (using the same data) varied over 10 logs, that is from 1 in 434,600 to 1.18 x 10^{15}, using the exact same electropherograms."

There were widespread concerns that the FBI/SWGDAM efforts to improve DNA mixture interpretations were actually making matters worse. As law enforcement laboratories embraced the use of the binary threshold system, many scientists feared that valuable DNA results were frequently being disregarded by a profound increase in **'inconclusive'** comparisons between DNA mixtures, and

known reference profiles.

Due to these concerns, in 2013, NIST assessed the **'binary threshold'** strategy, by organizing a second series of inter-laboratory assessments—referred to as the NIST MIX13 Study. The outcome of the MIX13 study projected an unfavorable light on the binary approach. One hundred study participants were asked to assess a DNA mixture that included three contributors. One reference sample came from an individual who was known to be ***absent*** from this 3-person mixture. Seventy of the one hundred study participants incorrectly ***included*** this known individual. In addition to this appalling 70% rate of false inclusions, the random match probability of inclusion statistics ranged from **1 in 9** to **1 in 344,000**. Twenty-four of the one hundred study participants reported the comparison to the known reference as ***inconclusive***. Only six participants correctly excluded the ***'innocent'*** known individual. One of those participants utilized a probabilistic genotyping (PG) software system—which is currently marketed as **TrueAllele®**.

On August 1, 2018, the cumulative results of the MIX05/MIX13 studies were summarized in a peer-reviewed journal article. Dr. John Butler and his co-authors published the article[104], bearing the title: "**NIST Interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned."** Within this publication, the authors began their **"Conclusions"** section as follows:

> "The results described in this article provide only a brief snapshot of DNA mixture interpretation as practiced by participating laboratories in 2005 and 2013. Any overall performance assessment is limited to participating laboratories addressing specific questions with provided data based on their knowledge at the time. Given the adversarial nature of the legal system, and the possibility that some might attempt to misuse this article in legal arguments, we wish to emphasize that variation observed in DNA mixture interpretation cannot support any broad claims about 'poor performance' across ***all*** laboratories involving ***all*** DNA mixtures examined in the past."

This commentary, coming from the highly-regarded authors, is well-taken and agreeable. However, a contrasting perspective might be presented as follows: Those who manage law enforcement labs, as well as forensic DNA outsource labs, must be willing to openly acknowledge the fact that the comparative interpretation of complex DNA mixtures can present a formidable challenge to forensic biologists. They must also acknowledge that PG software technology has been developed—for the most part—with the objective of conquering the scientific concerns that have been propelled by the troubling, lengthy history of DNA mixture misinterpretations.

The leaders at NIST, and many others in the forensic DNA community, have embraced the development of the PG software systems. This technology will be discussed at greater length in the section of this chapter, entitled: **"Probabilistic genotyping systems replace the binary threshold methodology"**

In 2016, the Texas Forensic Science Commission (TFSC) issued a **'Clarification'**, bearing the title: **"Current and Proper Mixture Interpretation Protocols"**.[105] This document referenced the fact that—on May 8, 2015—the FBI

released a memorandum, acknowledging errors in DNA population frequency data. This memo is discussed in greater detail in the section of this Chapter entitled: **Population statistical calculations—giving weight to: 'cannot be excluded'.**

The TFSC document pointed out that—due to the FBI memo—Texas prosecutors with pending court proceedings were offered the option to have DNA statistics re-calculated for their cases. For a substantial number of these cases, prosecutors were alarmed to see unexpectedly profound changes in the statistical outcomes. When a number of these instances were brought to the attention of the TFSC, the tone of the inquiry intensified. As outlined in the TFSC **Clarification**:

> "The changes were attributable to the fact that the evidence was originally analyzed before certain important revisions were made in laboratory mixture interpretation protocols."

Further, the TFSC pointed out that:

> "Though DNA analysis is based on sound science, well defined guidelines for interpretation are necessary when analyzing DNA samples containing multiple contributors, because of the complexity of the samples and the possibility of missing data (e.g. allele dropout and other stochastic effects). The results of the Texas re-analysis requests highlighted in one state what has been an issue of concern in the forensic DNA community for years—that mixture interpretation is challenging; there can be wide variation from laboratory to laboratory and even within laboratories on how mixture evidence is interpreted; guidance on how to interpret mixtures properly was described in various journal publications and websites but it was not as centralized or proscriptive as it could have been; and efforts by the federal government (in particular the National Institute of Standards and Technology) to train laboratories and raise red flags regarding mixture interpretation problems they observed in two major studies (MIX05 and MIX13) took many years to transfer to the local level."

Finally, this TFSC **Clarification** established that:

> "Further information regarding implementation of these concepts is anticipated in an article by Drs. Frederick Bieber, John Buckleton, Bruce Budowle, John Butler and Michael Coble, …"

The TFSC cited article, Bieber, et al., was published August 31, 2016 in the peer-reviewed journal, ***BMC Genetics***, with the title: **"Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion."**[106] At the beginning of the article, the authors provide the following commentary:

> "The evaluation and interpretation of forensic DNA mixture evidence faces greater interpretational challenges due to increasingly complex mixture evidence. Such challenges include: casework involving low quantity or degraded evidence leading to allele and locus dropout; allele sharing of contributors leading to allele stacking; and differentiation of PCR stutter artifacts from true alleles."

Further into the article, the authors point out that:

> "There are concerns that methods utilized for interpretation of complex forensic DNA mixtures may not be implemented properly in some casework. Similar questions are being raised in a number of U.S. jurisdictions, leading to some confusion about mixture interpretation for current and previous casework."

As Buckleton and colleagues have pointed out, **"all DNA profiles should be considered as potential mixtures."**[107] The competent litigator must work intently with a consulting molecular biologist, in order to understand that this can be the case—even if only two alleles are observed at a given locus.

The fundamentals of assessing a possible DNA mixture.

Various fundamentals can be considered when an analyst is confronted with an apparent DNA mixture—without the benefit of PG software. These fundamentals are most effectively summarized within the previously described, January 12, 2017, SWGDAM guidelines. Refer to: **Section 2: Mixture Interpretation Overview and Strategies.** When a genuine DNA mixture is believed to be present on an evidence item, that mixture should be assessed for the possible presence of a notably strong subset of allelic signals (elevated RFUs), comprising a **'major'** profile. Also present, can be one or more additional profiles from a **'minor'** contributor(s). These are referred to as a **'major/minor mixtures'** or ***'distinguishable mixtures'***.

Alternatively, a presumed DNA mixture may lack any discernable major contributor. Instead, a number of minor, relatively equal sources of DNA signals appear to be present within the data. Such DNA mixtures are referred to as an ***'indistinguishable mixtures'***. Results of this evaluation are dependent upon a detailed assessment of the peak height landscape of the overall DNA mixture. Such an assessment might be conducted most effectively with PG software technology.

If three genuine alleles are present at two or more loci, the mixture includes at least two individuals. If five genuine alleles are present at one locus or more loci, the mixture includes at least three individuals. If seven alleles are present at one locus or more loci, the mixture includes at least four individuals, and so on.

A variety of scientifically sound considerations can contribute to the logical conclusion that a DNA mixture is not suitable for reliable interpretations or comparisons. These factors include, but are not limited to the following: **1)** The number of contributors within a mixture. As the total number of alleles increases, the potential for any scientifically-reliable interpretations becomes increasingly doubtful. **2)** When indistinguishable minor contributors are present in a DNA mixture, it can be quite challenging to interpret subtle imbalances between the intensities of allelic signals. **3)** Sometimes, alleles among certain individuals coincidentally overlap—as might be expected from individuals who are genetically related or from the same ethnic population pool. **4)** The likelihood of a misinterpretation increases as more and more allelic dropout events must be 'forgiven', in order to consider a specific person as a potential contributor.

In the event that a genuine DNA mixture is reported by a crime lab analyst, the number of allelic dropout instances should be cautiously evaluated for the potential exclusion of each suspected contributor. When a key suspect or victim reference profile is to be compared to a DNA mixture, the absence of each allele from the collection of signals provides evidence for a potential exclusion.

Beyond a fundamental knowledge of how DNA mixtures are evaluated—using only human intuition—and no PG software—the competent litigator should work with the consulting molecular biologist to understand the previously referenced

2011 ***Science and Justice*** study described by Dror and Hampikian. This article illustrated the degree of subjectivity involved in DNA mixture interpretations. These researchers argued that in mixture interpretation, "domain irrelevant information" has a strong potential to bias an analyst's conclusions and create false incriminations.

Probabilistic genotyping systems replace the binary threshold methodology.

Thus far, this chapter has discussed the advent of the binary threshold methodology for examining DNA typing data—including the often troublesome DNA mixture interpretations. This binary method employs analytical thresholds and stochastic thresholds.

Recent efforts have led to the development and validation of computerized software—referred to as probabilistic genotyping (PG) software systems. The objective of PG analysis is to begin with the broadly diverse assortments of signals, emerging from the DNA typing process. For each mixture of DNA, there is a computer-driven endeavor to separate out the individual genetic types within those mixtures. One of the developers of a leading PG analysis software **(TrueAllele®**) is Cybergenetics—based out of Pittsburgh, PA. Dr. Mark W. Perlin, is the Chief Scientific and Executive Officer at this company. In 2018, Dr. Perlin authored an extremely illuminating history of the DNA misinterpretation crisis—which predates the summary that has been provided in this chapter.[108] The article bears the title: **"When DNA Is Not the Gold Standard: Failing to Interpret Mixture Evidence."**

In this article—published in *The Champion*—Dr. Perlin voiced disapproval of the ***initial*** movement toward utilizing a simple inclusion/exclusion single threshold system—stating that **"There is no scientific basis, however, for this threshold approach to analyzing mixtures."** The article clarified that: **"…thresholds often gave "inconclusive" results on informative data…"**. Further, Dr. Perlin criticized the questionable logic, driving the belief that—when one threshold proves to be unsuccessful—perhaps ***two*** thresholds will resolve the issue. Specifically, the article reported that **"The second threshold greatly decreased their match statistics and increased inconclusive outcomes, eliminating needed DNA information."** Within the **"Conclusion"** section of this 2018 article in *The Champion*, Perlin wrote:

> "Unscientific, untested "statistical" analysis of DNA mixtures has led to incorrect results on hundreds of thousands of items of evidence."

Not long after the shockwaves subsided from the NIST MIX13 Study—leaders within the FBI, SWGDAM, and NIST acted upon the need to embrace various changes. Refer to a presentation from Dr. Perlin at the 2015 NIST Conference: **The International Symposium on Forensic Science Error Management: Detection, Measurement and Mitigation.** Within the abstract of his presentation, entitled **"Objective DNA Mixture information in the Courtroom: Relevance, Reliability and Acceptance"**,[109] Dr. Perlin explained the following—in reference to impending movement toward utilizing PG technologies:

> "The reliability of objective genotype separation has been extensively tested. Such extensive testing, error rate determination, and scientific peer review address FRE 702 and *Daubert* reliability factors. Courts have accepted this extensively validated computer approach, with admissibility upheld at the appellate level. Separated genotypes provide results that juries find easy to understand. Objective DNA analysis elicits identification information from evidence, while rigorous validation establishes accuracy and error rates."

In December, 2015, the FBI Crime Lab abandoned the binary methodology—no longer utilizing analytical and stochastic thresholds as their starting point for resolving DNA mixtures. Instead, our federal crime lab now utilizes **STRmix™**, a PG analytical software—that was developed in competition with **TrueAllele®**.

Refer to a May 17, 2017, FBI press release, bearing the title: **"FBI Validates STRmix™ for Use on Up to Five-Person Mixtures."**[110]—authored by Ray Weiss. Within the introduction of this PR article, Mr. Weiss wrote:

> "The findings show that STRmix™ – a sophisticated forensic software used by trained, experienced DNA experts to resolve mixed DNA profiles previously thought unresolvable – is sufficiently robust for implementation in forensic laboratories."

The PR article continued, pointing out that the FBI:

> "…has published its validation of STRmix™ for use on mixtures of up to five persons, as well as across a wide range of templates and mixture ratios."

The article continued:

> "The FBI's internal validation, published in FSI: Genetics, notes that STRmix™ offers numerous advantages over historical methods of DNA profile analysis and has greater statistical power for estimating evidentiary weight, all of which can be used reliably in human identification testing."

The article pointed out that the STRmix™ analytical software was developed by Dr. John Buckleton and Dr. Jo-Anne Bright, forensic scientists at the New Zealand Institute of Environmental Science and Research (ESR), in collaboration with Duncan Taylor, from Forensic Science South Australia (FSSA). The PR article also described the following:

> "Using standard, well-established statistical methods, STRmix™ builds up a picture of the DNA genotypes that, when added together, best explains the observed mixed DNA profile. STRmix™ then enables users to compare the results against a person or persons of interest and calculate a statistic, or "likelihood ratio," of the strength of the match."

At the STRmix™ website, we are informed of the following:

> "STRmix™ is expert forensic software that can resolve previously unresolvable mixed DNA profiles. Developed by global leaders in the field, it uses a fully continuous approach for DNA profile interpretation, resolving complex DNA mixtures worldwide."

STRmix™ can be used to resolve relatively simple DNA mixtures, as well as complex mixtures, prior to factoring in the data from any known reference samples. Using well-established statistical methods, the software builds millions of conceptual DNA profiles. It grades these profiles against the evidence sample, finding the combinations that logically justify the observations. Once this is accomplished, a range of likelihood ratio options are used for subsequent comparisons to the known reference profiles. Specifically, STRmix™ uses a Markov Chain Monte Carlo (MCMC) engine to model peak heights of potential allelic data.

The STRmix™ software also models various types of apparent stutter peak

data, and factors in the possibility of allelic drop-out events. All of these functions are performed rapidly by STRmix™. A MCMC statistical approach provides a means of sampling from any complicated distribution[111]. Complicated distributions—such as a collection of peak height results comprising a DNA mixture e-gram landscape—are often enormously challenging for probability calculations. Due to the fact that the performance of STRmix™ is supported by comprehensive validation studies—with these underlying mathematics readily accessible to DNA experts—the effectiveness of the software can be clearly summarized for juries.

In light of these profound developments in the landscape of DNA mixture interpretation, the competent litigator must be mindful of the following realities: **1)** Individual analysts—not PG analytics—are responsible for extracting DNA, quantifying DNA, and amplifying raw DNA typing results from the evidence items. **2)** Errors remain a distinct possibility—as human beings continue to play a key role in distinguishing between analytical artifacts, elevated background noise, and presumed genuine allelic signals. **3)** During the time frame within which analysts are generating and inputting the evidentiary DNA mixture data into the PG-software systems, it remains vital for the reporting scientists to have absolutely no knowledge of the genetic make-up within the ***known*** DNA standards to be used for DNA comparisons. This includes the known reference samples from victims, suspects, or other individuals associated with the case investigation. These fundamental concerns

were previously discussed in greater depth in the chapter section entitled: **"LCN, DNA mixtures, and the impact of cognitive bias on RFU thresholds."**

Refer to the same, May 2018, issue of *The Champion*, within which Dr. Perlin summarizes the history DNA misinterpretations. A related article bears the title: **"Mixing it Up: Legal Challenges to Probabilistic Genotyping Programs for DNA Mixture Analysis."**[112] Within the section of this article entitled **"DNA Analysis Going Automated.",** the authors reference the SWGDAM definition of PG analysis as follows:

> "…the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios (LRs) and/or infer genotypes for the DNA typing results of forensic samples…"[113]

The authors refer to a report issued in September 2016, from the President's Council of Advisors on Science and Technology. In what is known as the PCAST report, the highly-regarded scientists assessed the analysis of simple, as well as complex DNA mixtures. The PCAST report acknowledged that PG programs represent a marked improvement over earlier subjective methods. However:

> "…*they still require careful scrutiny* to determine (1) whether the methods are scientifically valid, including defining the limitations on their reliability [that is, the circumstances in which they may yield unreliable results] and (2) whether the software correctly implements the methods."

The authors refer to a highly publicized homicide in upstate New York—and the ensuing trial process—pertaining to the *People v. Hillary*. Most illuminating, the authors of this article in *The Champion* refer to *Hillary* as follows:

> "…an excellent example of the lack of consistency between probabilistic programs that are examining the same evidence. It is a reminder that probabilistic genotyping is far from being an established field where results are reproducible from program to program. In Hillary, the difference was stark: STRmix inculpated the defendant with a statistic of 335,000, while TrueAllele exculpated him with a likelihood ratio below 1. Hillary also makes plain that an executable version of a program might be necessary for mounting an admissibility challenge. An executable version of a program is a copy of the software that a defense expert could operate on her computer, much like a layperson would operate Microsoft Word or Excel. Using the executable version of the program, the defense expert could test how changing certain input values might change the overall likelihood ratio."

Deeper into the article, the authors emphasized the following:

> "…if two programs that have passed Daubert/Frye standards end up with discordant results in a particular case, without explanation, why should the jury hear about the higher, more damaging result?"

Before the end of 2020, the number of forensic DNA facilities utilizing some form of validated PG software will most likely exceed 100. Due to the growing prevalence of PG software analytical methods, litigators should respond appropriately—upon recognizing that these methods have been used—in part—to assist with the scientific investigation of the case evidence. In addition to consulting with an expert in forensic biology/DNA, it is worthwhile to also consider seeking input from an individual who has experience with the development and utilization of PG technology.

Population statistical calculations—giving weight to: 'cannot be excluded'.

The landscape of DNA signals observed on an evidence item—whether from a single source or a mixture of contributors—will have little meaning until comparisons can be made to the DNA profiles from known individuals. The calculation of a probability of inclusion (POI) statistic, or a likelihood ratio (LR) statistic is crucial, and litigators must be wary of off-the-cuff pronouncements.

These off-the-cuff pronouncements occur frequently when the DNA analysis is conducted with extremely limited, potentially degraded samples, or much worse—contaminated samples that are presumed to be derived from ***'touch DNA'***.[114] In these circumstances, Thompson and colleagues have argued that:

> "Analysts try to take these effects into account by being *more lenient about their standards* for declaring a match. They do not require that a suspect's DNA profile correspond exactly to an evidentiary sample because of stochastic effects."[115]

These researchers point to the turn-around of an early champion of forensic DNA analysis: Dr. Bruce Budowle. As discussed earlier in this chapter, Dr. Budowle has issued warnings that crime labs were dealing with mixtures and low copy number DNA analysis in ways that may be unreliable.[116]

Let us scrutinize the probability of inclusion (POI) statistic. By the end of August, 2020, the estimated world population will be approximately 7.8 billion.

Although it certainly might enhance criminal investigations to generate a DNA type for every single human being residing on earth, such an initiative would be excessively daunting and impractical.

Keeping this obstacle in mind, suppose that a single-source DNA profile is recovered from an evidence item. Also suppose that these data provide an exact, locus-by-locus match to a person who has already been typed for DNA. Lastly, suppose that this person does not have an identical twin. A partial DNA match—occurring at only 15 loci, among the currently tested 24 loci—might generate a probability of inclusion (POI) that is estimated, for example, to occur in 1 out of every quadrillion human beings. This would be written out as follows: 1 out of 1,000,000,000,000,000. It is useful to note that the value, 1,000,000,000,000,000, is about 128,000 times greater than the human population of our entire planet. By calculating and reporting such lofty POI values, forensic biologists can often testify confidently to the origin of a single source profile, or the source attribution[117] of the DNA revealed on the evidence. Such testimony can be enormously compelling to juries. However, the premise that identity is being indisputably confirmed has become the subject of intense debates. As David Balding points out, numbers greatly exceeding the population of the earth may very well be founded on what he calls the "uniqueness fallacy."[118]

The dynamics of the POI calculations can change dramatically when weaker,

partial DNA profiles and/or DNA mixture profiles are being reported by the crime lab analyst. Thus, the scientists become even more obligated to justify any report that a specific individual 'cannot be excluded' as a potential contributor of DNA on a specific evidence item. Statistical calculations must be carefully performed and included within the DNA reports, as a means of clarifying the statistical weight of such an inclusion statement.

Calculating the sometimes lofty random match POI values for a subset of alleles utilizes a statistical formula known as the product rule.[119] A visual example of how this formula works in population genetics might take shape as follows: Imagine using a deck of fifty-two playing cards, with alleles at a single genetic locus determined by a card that is dealt to an individual. Suppose that—among the mix of nations and racial groups on our planet—Allele A is the most common genetic marker. Suppose that this allele accounts for 25% of the observed alleles found from a number of DNA typing/population studies. Translating this into our 'playing cards' example, if a person is dealt an Allele A, that would be similar to being dealt one of the thirteen hearts, from the fifty-two card deck (a deck of cards is 25% hearts).

Let us now suppose that Allele B is profoundly less common than Allele A. Perhaps less than 2% of the population carries this unusual genetic marker. In our playing cards scenario, carrying Allele B would be like shuffling the fifty-two cards, and dealing the ace of clubs to an individual. The product rule applies when a

specific person—for example—is dealt Allele A (any heart), from mom, and Allele B (the ace of clubs), from dad. With the probability of getting a heart from a full, shuffled deck of cards at 25%, plus the probability of getting the ace of clubs at 1.923%. The probability of having the Allele A/Allele B genotype[120] in this specific example scenario is:

0.25 x 0.01923=0.0048

This genetic type would occur in 1 out of every 208 people. It is useful to keep in mind that this is a simplified playing card example—focusing on only one locus. Even when data are recovered from only 15 of the FBI-mandated, expanded set of 24 loci, a value resembling 208^{15} might result from the product rule if every single one of the 15 genetic loci includes at least one rare allele, such as Allele B. A DNA profile from an actual living person is likely to be comprised of mostly common alleles, with various rare ones mixed in.

Keeping all of the above in mind, POI numbers well beyond the quadrillion range are routinely observed from present-day DNA analysis. Competent litigators must be wary of misrepresentations of POI calculations. One form of misrepresentation is referred to as the ***'Prosecutor's Fallacy'***. The opposing form of misrepresentation is appropriately referred to as the ***'Defense Attorney's Fallacy'***. Both forms of misrepresentation are discussed on the website provided by highly-

regarded forensic DNA mathematician, Dr. Charles Brenner.[121]

Let us describe an example of how these fallacies might play out in the courtroom. First, the ***'Prosecutor's Fallacy'***: Suppose that a crime lab forensic biologist observes a limited, partial DNA profile on a key piece of evidence. When the analyst compares this partial DNA profile to the known profile of the defendant, a degree of consistency is revealed. However, due to the limited DNA data, the analyst must issue a report, attesting to a POI statistic of 1 in 2000.

Upon hearing this statistic, the prosecutor is disappointed. This is due to the fact that so many cases yield DNA consistencies with POI statistics in the range of 1 in several trillions, 1 in several quadrillions, or even higher. In order to fortify justification for a guilty verdict, the prosecutor decides to explore some convenient, supplemental calculations. The prosecutor contemplates that, among the 2000 theoretical, random test subjects, an estimated 1999 of those people would be excluded as possible contributors to the key evidence item. Upon dividing the value of 1 by 2000, the prosecutor achieves a resulting quotient of 0.0005. This result tells the prosecutor that 99.95% of the people within any randomly selected population can be eliminated as suspects. Feeling much better about the statistics—as part of the prosecutor's closing arguments to the jury—the following wording is presented:

> "Ladies and gentlemen, there is a 99.95% chance that the defendant's DNA is on that key evidence item. Based upon this fact, you must come back with a 'guilty' verdict."

Wikipedia provides an illuminating example of the fallacy associated with this twisted logic, under the subheading of **'Conditional Probability'**.[122] This example reads as follows:

> "Argument from rarity—Consider the case: a lottery winner is accused of cheating, based on the improbability of winning. At the trial, the prosecutor calculates the (very small) probability of winning the lottery without cheating and argues that this is the chance of innocence. The logical flaw is that the prosecutor has failed to account for the large number of people who play the lottery."

Similar to participants in a lottery, note the enormous number of individual profiles on our planet, or the very large number housed within searchable DNA databases.

In order to exemplify the ***'Defense Attorney's Fallacy'***, let us adhere to the same, previous example, employing the theoretical 1 in 2000 POI statistic. Upon hearing the misrepresentation of that statistic by the opposition, counsel for the defense rises in objection, and offers the following:

> "Your honor, that calculation is absolutely incorrect. Note that there are only 80,000 residents in our small county. Based on that, 80,000 divided by the 1 in 2000 statistic gives us an estimated 40 individuals residing in close proximity to the crime scene. Consider that these individuals clearly qualify as potential contributors to the partial DNA profile observed on the evidence. Therefore, we have an estimated 97.5% chance that the DNA came from one of those people, in comparison to the 2.5% chance that the DNA came from my client."

This example illustrates the defense attorney's fallacy. This nonsense recklessly ignores a variety of realities. Among the 40 potential suspects residing in that small county, several individuals would most likely be excluded, because they

are young children. A number of others are presumably immobilized/sickly senior citizens, or people suffering from a variety of handicaps. Still other individuals may have physical appearances that are profoundly contradictory to witness accounts, or may have alibis that eliminate them from consideration as suspects. The fact is, both fallacies effectively taint juries with incorrect and misleading information.

Both fallacies are further discussed in the 2004 issue of ***Nature Review Genetics.*** An article by Mark Jobling and Peter Gill is entitled **"Encoded Evidence: DNA in Forensic Analysis"**.[123] In this publication, the authors write as follows:

> "…interpretation in the courtroom has not been without controversy, and this is because of the way DNA evidence is sometimes presented."

Perhaps this is why Benjamin Disraeli reportedly wrote that **"There are three kinds of lies: Lies, damned lies, and statistics."**[124]

As mentioned earlier in this chapter, the FBI released a CODIS bulletin on May 8, 2015.[125] This memorandum was entitled **"Amendment of the 1999 and 2001 FBI STR population data."** In part, the memo read as follows: **"…the FBI Laboratory has identified some errors in the data published in the Journal of Forensic Sciences…"** The memo went on to announce an upcoming erratum notice, projected to be published in the ensuing months of 2015, within a peer-reviewed journal. The FBI predicted that the erratum notice would establish that the errors from 1999 and 2001 caused no more than a nominal effect on profile probabilities.

The notice appeared in the June 2015 issue of the ***Journal of Forensic Sciences***.[126]

Although the statistical errors were responsible for no more than a minimal effect on DNA inclusion probabilities, it is troubling that these miscalculations went unnoticed for all of fifteen years. Even worse, the errors affected population statistical calculations in the majority of law enforcement labs and outsource DNA test facilities, located in every U.S. state. Individuals working within our criminal justice system should moderate their distress relevant to the potential impact of the errors upon the case-by-case assessment of innocence or guilt. However, within this context, scientists must continue emphasizing the necessity for an elevated sense of general awareness, regarding human errors and forensic casework.

Many forensic scientists favor the use of likelihood ratio (LR) calculations as statistical support for the reported inclusions. This is particularly true when DNA mixtures are involved. Despite the widespread scientific acceptability of this methodology, there are flaws in this strategy. Refer to a 2017 article authored by Steven P. Lund and Hari Iyer, with the Statistical Engineering Division, Information Technology Laboratory, National Institute of Standards and Technology.[127] In this article entitled: **"Likelihood Ratio as weight of forensic evidence: A closer look."** Lund and Iyer stated as follows:

> "Because the likelihood ratio is subjective and personal, we find that the proposed framework in which a forensic expert provides a likelihood ratio for others to use in Bayes equation is unsupported by Bayesian decision theory,

> which applies only to personal decision making and not to the transfer of information from an expert to a separate decision maker, such as a juror."

Expanding on this reality, we can find no examples of a forensic DNA expert articulating a fundamentally coherent accounting—for juries—of how LR statistical estimations are used to arrive at the reported conclusions. Indeed, the National Forensic Science Technology Center (NFSTC) once provided the definition:

> "The likelihood ratio is the ratio of two probabilities of the same event under different hypotheses. Thus for events A and B, the probability of A given that B is true (hypothesis#1), divided by the probability of event A given that B is false (hypothesis#2) gives a likelihood ratio. The likelihood ratio is a ratio of probabilities, and can take a value between zero and infinity. The higher the ratio, the more likely it is that the first hypothesis is true."

While this definition has disappeared from the NFSTC website, a savvy litigator should not hesitate with inquiries into whether or not each crime lab forensic biologist fully understands such a definition, regardless of the confusion that it unquestionably must create for jurors, judges, prosecutors and defense attorneys who have obviously enjoyed quite limited scientific training during their education and employment. The trier of fact is likely to understand the following basic steps:

- On this evidence item is the reported DNA profile (or DNA mixture).
- The defendant qualifies as a possible contributor to the reported DNA.
- Supposing that 10,000 randomly-selected people are tested, we estimate that one of them would ***also*** be considered a possible contributor of this DNA.
- The other 9,999 random people would be excluded as possible contributors.

Keeping the simplicity of the above-listed steps in mind, how does PG analytical software—and the resulting LR calculations—fit into the DNA mixture analysis landscape for courtroom presentations? In 2012, Thompson and colleagues referred to PG analysis in an attempt to illustrate an approach to this dilemma:

> "A Pittsburgh company called Cybergenetics has been marketing an automated system for interpreting DNA evidence that relies on high-powered computers, and a form of Bayesian analysis called Monte Carlo-Markov Chain (MCMC) modeling, to draw conclusions about the profiles of possible contributors to evidentiary DNA samples."[128]

This illustration is as challenging for litigators and jurors to digest as computer interpreted psychological test data. Thompson et al. explained that the TrueAllele® PG software depends on the accuracy of the underlying assumptions, and:

> "Based on the assumptions that are programmed into the system, it can predict the "output" of a forensic DNA test for any given set of "inputs." In other words, it can predict the probability that a forensic DNA test will produce electropherograms showing a particular pattern of peaks, given that the sample tested contained DNA of an individual (or individuals) who have specific DNA profiles, and given various other assumptions about the quantity and quality of the samples tested."[129]

The competent litigator, faced with PG analytical software-generated LR statistics, might consider Thompson, Mueller and Krane's 'rubber band' analogy:

> "The fundamental problem facing those who try to design statistical procedures for such cases is that no one knows how broad the net cast by the test really is. Estimating the percentage of the population who would be 'included' as a possible contributor is like estimating the length of a rubber band. Just as a rubber band may be longer or shorter, depending on how far one is willing to stretch it, the size of the 'included' population may be larger or smaller, depending on how leniently or strictly the analyst defines the criteria for an 'inclusion."[130]

It might be useful to inform jurors of the application concerns with TrueAllele®, STRmix™, and other emerging PG software systems. For example, in Regina v. Duffy and Shivers[131] Laurence Mueller and Dan Krane served as experts for the defendant. In that Northern Ireland case, testimony revealed that the company ran the software four separate times—and produced four different LRs for incriminating the defendant. These results were as follows: 389 million, 1.9 billion, 6.03 billion, and 17.8 billion.[132] Thompson, Mueller and Krane reported that:

> "These varying results illustrate the issue of reproducibility discussed above -- they show that there is an element of uncertainty (a margin of error) in the likelihood ratios generated by the system. How this uncertainty is handled, when reporting the results to the jury, is an issue on which experts may well differ. The dispute in the Belfast case about whether the company had cherry-picked its data might well have been eliminated had the company chosen which evidentiary samples were most 'informative' without having access to information about the profiles of any suspects."[133]

Recent developments in the utilization of probabilistic genotyping software.

An elevated degree of acceptability has been established for PG software—both in the forensic DNA analytical labs, as well as in courtrooms across the U.S. However, it is illuminating to examine the *Daubert* admissibility process corresponding to ***U.S.A. v. Daniel Gissantaner***.[134] The opinion on this case—delivered by U.S. District Judge, Janet T. Neff—addresses the fact that the defendant was charged with the offense of felon in possession of a firearm. The scientific aspect of the case rested entirely on a trace quantity of DNA detected on this firearm. On September 25, 2015, the weapon was found by police officers, in a locked cedar

chest. While the cedar chest was located in the home of Mr. Gissantaner, it was in a room that was occupied by a different male individual. This alternative suspect was the confirmed owner of the cedar chest, and also happened to be a convicted felon. This male was also the only person who possessed a key to the chest.

Later, the firearm was submitted to the Michigan State Police (MSP) for DNA typing. The MSP Crime Lab reported a DNA mixture from at least three contributors. The report indicated that Mr. Gissantaner could not be excluded—due to an estimated contribution of DNA that was approximately 7% of the total DNA present on the firearm swab sample. Using STRmix™, the MSP Crime Lab reported an LR statistic of 49 million. To be clear, this is an estimated ratio. The numerator reflects the weight associated with the hypothesis that the DNA mixture originated from Mr. Gissantaner—plus unknown contributors. The denominator reflects the weight of the hypothesis that the mixture came ***strictly*** from unknown individuals.

Legal counsel representing Mr. Gissantaner filed a *Daubert* motion—challenging the admissibility of the STRmix™ analysis and the MSP Crime Lab report. During an initial, two-day *Daubert* hearing in May, 2018, the Court heard testimony from numerous experts, including the following: Dr. John Buckleton, a co-developer of STRmix™ at the New Zealand Institute of Environmental Science and Research (ESR); Dr. Steven P. Lund, a statistical expert with NIST, and Nathan Adams, a systems engineer with Forensic Bioinformatics, Fairborn, Ohio.

As a consequence of a need for a deeper clarification of the complex issues associated with this scientific investigation, the Court encouraged recommendations of additional court-appointed experts. The Court received written reports from Dr. Michael Coble, as well as from Dr. Dan E. Krane. Dr. Coble is an Associate Director with the Center for Human Identification, University of North Texas Health Science Center, at Fort Worth, Texas. Dr. Krane is the President/CEO of Forensic Bioinformatics, and has been a Professor of Biological Sciences at Wright State University, in Dayton, Ohio, for over twenty-six years. In addition to the reports from these two highly accomplished scientists, on July 8, 2019, both sides were provided an additional day of testimony, in the continued *Daubert* process.

The defendant and his scientific team emphasized to the Court that—by using any form of PG software—a number of factors entered into the program are under the control of the reporting analyst, and their technical management, operating within the specifications determined at that crime lab facility. Consequently, these variables can affect the outcome of the analysis, and the potential for errors—as the process is being executed. While Judge Neff noted that:

> "…Dr. Coble and Dr. Krane agree that probabilistic genotyping is the new paradigm for DNA mixture analysis."

It was also noteworthy to the Court that:

> "…much divergence remains on the reliability of probabilistic genotyping software under the circumstances presented in this [Gissantaner] case—the

> likelihood ratio generated from the analysis of complex mixture of low-template touch DNA consisting of at least three contributors in which the person of interest is determined to be a minor contributor of only 7%."

Taking into account the STRmix™ estimation of a low level DNA contribution at merely 7%, Dr. Krane calculated for the Court—based upon testimony from the MSP analyst—that the mass contribution corresponded to a yield of 49 pg of DNA. Such a meager DNA quantity is expected from as few as 8 or 9 human cells. Based—in part—upon this revelation, the Court concluded that the evidence on record did not establish adequate testing and validation of the STRmix™ software system, under the conditions of the DNA evidence in this Gissantaner case. Adding clarity to this conclusion, the Court stated as follows:

> "…STRmix™ does have some general acceptance in the scientific community, particularly with respect to simple mixture or "mainstream" higher quality and quantity DNA. However, the application of probabilistic genotyping software, including STRmix™, to the interpretation of complex mixture low-template, low level DNA in the manner used in this case to present a likelihood ratio in a criminal prosecution, remains controversial. This factor does not add weight for a finding that the STRmix™ DNA analysis is reliable."

Deeper into Judge Neff's opinion document, the following is emphasized:

> "The concluding lesson from the extensive testimony and complex documentary evidence presented in this case is that the specific care required for low-template, low level DNA testing has largely faded into the background as the shortcomings and the technology and need for stringent controls on its use have been glossed over in the rush to embrace the technological advancements. With low-copy number typing, problems that can arise at every step of the sampling and testing process are amplified. As a result, a low-copy number typing profile is apt to contain greater instances of

> drop-in and drop-out, extreme peak imbalances and significant stutter imbalances. The high sensitivity testing that occurs with probabilistic genotyping software such as STRmix™ should be undertaken with extreme care."

And ultimately, Judge Neff ruled that:

> "Based on the entire record, the Court determines that the STRmix™ DNA report at issue does not meet the *Daubert* reliability standard for admissibility as evidence. This decision is not an indictment of probabilistic genotyping, and certainly not of STRmix™ software in particular. The Court does not question the usefulness of probabilistic genotyping software as a sophisticated tool in forensic DNA analysis. Rather, this decision is a conclusion based on the testimony and other voluminous evidence, presented over a year-and-a-half of hearings, briefing and examination by counsel, experts and the Court."

Whether or not PG software analysis is used, litigators should be mindful that of the journey from DNA evidence to a guilty verdict depends on key assumptions:

(1) The DNA evidence itself is ***reliable and accurate***,

(2) The DNA evidence ***identifies*** the defendant, complainant, or other party necessary to prove guilt;

(3) This identification means that the individual was ***present*** at the scene where the DNA evidence was recovered;

(4) The identified individual had the ***opportunity*** to commit the alleged action;

(5) The DNA evidence proves that the identified individual ***engaged in the specific acts alleged***; and

(6) The proof that the identified individual was present, had an opportunity, and did actually commit the act ***demonstrates guilt***.

By revealing these analytic steps and their assumptions, the competent litigator will provide the trier of fact an opportunity to consider, evaluate, and intelligently question the probative value of the proffered DNA evidence.[135]

"THE BAD" - WHEN GOOD INTENTIONS GO WRONG

Competent litigators will utilize the *reliability testing* methodology described in Chapter Two for *voir dire* and the relevant points from the checklist of forty-seven issues for direct examination. The trap for the unwary expert or the less than well prepared litigator will be the use of the material in these last two sections against them. While the forensic use of DNA has tremendous applicability in the search for truth, the terrible mistakes described in these last two sections must be taken into consideration for any comprehensive explication of the evidence in any case.

Despite its tremendous value when done correctly, DNA errors can result from sample mislabeling, sample switching, or from cross-contamination between samples in the same or different cases. Are these innocent lab errors or something else?[136] The competent litigator will work closely with the consulting molecular biologist to explore answers to that question.

Beyond the laboratory reports, it is essential to scrutinize various levels of underlying data. This is a consequence of the fact that thorough examinations often

reveal interpretive limitations or problems that are never going to be detectable in the reports themselves. These could include inconsistencies between purportedly "matching" profiles, evidence of additional unreported contributors to evidentiary samples, errors in statistical computations and unreported problems with experimental controls that raise doubts about the validity of the results.[137]

All litigators facing a forensic DNA expert should take note of the following: For sixteen years, German police hunted a treacherous serial killer. This killer was unlike any other, a woman suspected of larcenies and six murders. Despite finding her DNA on guns, cigarette packs, even nibbled biscuits at crime scenes and placing a 300,000 Euro reward on her head, she could not be found. The anguish and confusion rose when her profile was found on some documents belonging to an individual who had died in a fire, but repeat analysis failed to give a different result. No, this illusive killer, the "Phantom of Heilbronn", could not be found. After sixteen years and thousands of law enforcement hours, sharper forensic DNA minds noticed that swabs used for taking DNA from suspects were all tainted by a woman at the manufacturer's facility. It was contamination that was the Phantom.[138]

Every forensic DNA expert and litigator must know these cases. The work of many of tireless litigators has exposed bad laboratory practices and just bad labs all over the English-speaking world. For example, in the year 2005, the Illinois State Police cancelled a contract with Bode Technology Group, one of the largest

independent DNA labs in the United States for poor quality work.[139]

LabCorp, another independent laboratory was accused of botching simple DNA paternity tests.[140] In North Carolina, the *Winston-Salem Journal* published a series of articles documenting numerous DNA testing errors by the North Carolina State Bureau of Investigation.[141]

In 2003, the Houston Police Department (HPD) shut down the DNA section of its crime lab, after a television expose revealed serious procedural deficiencies that were confirmed by subsequent investigations.[142] The HPD analysts had been reporting the wrong statistic in mixture cases for a multitude of years. In January 2008, the HPD crime lab removed their technical leader, and shut down their facility—as a consequence of a DNA analyst proficiency test cheating scandal.[143]

In ***Forensic DNA Evidence: The Myth of Infallibility***, Thompson reports on lab errors resulting in false database matches at forensic laboratories in California, Florida, Nevada, New Jersey, New Zealand and Australia.[144] In England, in the wake of *R v. Broughton*, commentators argued about evidence which could be characterized as "wholly and obviously unreliable".[145] In Scotland, Brian Kelly's conviction was proven to be based on a laboratory accident and overturned by the High Court in 2004.[146] The conviction of Farah Jama in 2006 in an Australian court revealed a likely contamination event. Sperm resulting from a consensual sexual act was linked with a rape case. There appeared to be no possibility of contamination

within the laboratory, but a common link was found in a sexual offense examination suite and the examining doctor.[147] It seems that doubt was cast on a number of Australian convictions when a forensic scientist told the *Australian* newspaper that the lab in question often mixed up DNA samples from different cases.[148]

Ancient/cold case DNA and contamination.

Based upon the efforts of the Innocence Project,[149] the Northwestern Center on Wrongful Convictions[150], Centurion™ [151], and similar organizations, it is clear that we must remain cautious with regard to the interpretation of data generated from archived DNA in cold case evidence. Take note of a profoundly insightful June 2012 publication released by the U.S. Department of Justice (DOJ), Office of Justice Programs. The title of this publication is: **"DNA for the Defense Bar"**.[152] Within this DOJ release, refer to Chapter 9, **"Delayed Prosecutions, Cold Case Hits, and CODIS".** Section 9 is entitled, **"Contamination"**—which begins with the following passage: **"There have been several cold hit cases worldwide involving contamination."** This is an understatement. The U.S. DOJ was justified in positioning a discussion of DNA contamination events within a Chapter dedicated to the questionable investigation of various cold cases.

Nina Witt, and others, warn the users of polymerase chain reactions (PCR):

> "As one of the most sensitive methods available for detecting nucleic acids, the PCR is at risk of being affected by low levels of contamination. This susceptibility is compounded by the fact that PCR functions by generating

> billions of copies of the DNA sequence that is being analyzed. Consequently, conducting the PCR reaction generates products, which if not handled carefully, may contaminate later reactions. As PCR has developed over the last 20 years, specific practices have been introduced to reduce laboratory contamination, including physical separation of the different stages of the procedure, incorporating enzymatic or irradiation steps to remove contaminating molecules, and generating a careful approach to identify contamination risk during sampling, sample processing, and analysis."[153]

Vivien Marx, argues for vigorous lab hygiene:

> "Given that the most frequent source of contamination is the product of previous PCR runs, it is also important to separate the lab areas for PCR setup and PCR analysis." [154]

Many years ago, this mechanism of PCR contamination, known as ***'carry-over contamination'***, became an enormous problem for ancient DNA researchers.

Ermanno Rizzi et al., described DNA contamination issues in ancient DNA:

> "….due to the enormous power of PCR to amplify even a few copies of DNA sequences, modern DNA contamination has become a crucial problem. For this reason, many of the most extravagant reports on ancient DNA, including claims of DNA sequences surviving for millions of years in plants and dinosaur bones, have been disputed and actually disregarded." [155]

In the same paper, Dr. Rizzi and colleagues went on to instruct:

> "To deal with this issue, researchers have outlined a series of guidelines to ensure the quality of ancient DNA data and the reliability of consequent conclusions. Over the years, these guidelines have gradually evolved into a more detailed and extensive list of requirements, resulting in the nine 'gold criteria'…"[156]

These so-called "gold criteria" were outlined in one of the most highly-referenced articles in the field of ancient DNA research, authored by Cooper and Poinar and entitled: **"Ancient DNA: Do it right or not at all."**[157] In this article, the

authors sound the alarm that some ancient DNA researchers are unfortunately becoming overly optimistic that contamination issues might be finally under control. The authors point out that:

> "Ancient DNA research presents extreme technical difficulties because of the minute amounts and degraded nature of surviving DNA and the exceptional risk of contamination. The need to authenticate results became obvious in the mid-1990s when a series of high-profile studies were shown to be unrepeatable."[158]

Specifically, the authors suggest that in the absence of full compliance with all nine criteria, the reliability and authenticity of results remain uncertain.[159]

Although these disturbing issues prevailed for numerous years within the realm of ancient DNA research, it is clear that notable leaders in the field have launched a powerful movement with the purpose of—first—identifying that there is indeed a problem. Furthermore, the leaders of this movement believe that mechanisms are available for minimizing the potential for contamination. Mélanie Pruvost, and colleagues cautioned readers:

> "PCR analyses of ancient and degraded DNA suffer from their extreme sensitivity to contamination by modern DNA originating, in particular, from carryover contamination with previously amplified or cloned material."[160]

Concerning carry-over contamination, Pruvost and colleagues state:

> "….amplification of the degraded and modified DNA is not very efficient and sporadically contaminating intact modern DNA molecules can be preferentially amplified. Indeed, this contamination caused erroneous results.[161]

Lacking awareness of DNA contamination and corrective actions in crime labs.

Crime lab forensic biologists are often responsible for the examination of cold case evidence. Similar to the challenges faced by ancient DNA researchers, cold case samples are often compromised or severely degraded, as a consequence of prolonged exposure to time—and the elements. Forensic analysts assigned to these archived cases have much to learn from the progression of the ancient DNA contamination crisis—documented in the scientific literature. Unfortunately, parallel efforts to identify and control contamination errors in forensic DNA labs have stumbled dreadfully short of the successes we have witnessed in the field of ancient DNA.

In 1998, the FBI's DNA Advisory Board issued a corrective action guideline directed toward forensic DNA labs. That guideline, which was documented as Standard 14.1.1,[162] reads as follows:

> "The laboratory shall maintain documentation for the corrective action. Such documentation shall be retained in accordance with applicable Federal or state law."[163]

Despite the universal acknowledgement of this standard, too many accredited laboratories have failed to fully comprehend and embrace a necessary sense of urgency. Most disturbing, management within a minority of facilities have chosen to disregard the importance of effective corrective action policies. When evidence contamination issues inevitably afflict the reputations of these facilities, the consequences can be disastrous.

Unlike the agonizing problems that once plagued the ancient DNA research community, contamination failures in forensic DNA labs can set wrongful convictions into motion. Innocent human beings end up forfeiting their freedom. Keeping in mind that such catastrophes are a consequence of fundamental scientific errors, and the failure to institute simple corrective actions, perhaps the criminal justice system should demand corrective measures on a more universal scale.[164]

For countless experts in forensic biology/DNA, it is clear that cross-contamination events and carry-over contamination events are issues requiring much greater scrutiny and much stricter controls. It is also clear that rich sources of known DNA, such as oral swabs, blood stain cards, or saliva samples from known individuals, should not be brought into the same forensic facilities and analyzed where crime scene items are also brought in, opened up, and analyzed for DNA.

Practical minimization of DNA contamination events in crime labs.

The crucial stage of crime lab DNA evidence processing is **'amplification'** (molecular photocopying). For more fundamental information on this amazing technological process, refer to the previous sections of this chapter, bearing the titles: **"Processing evidence: Prior to the production of DNA typing data."** and **"The goal of the 'molecular photocopier': Comparative DNA matches."**

Suppose that a diligent litigator for the defense learns the following information from an expert consultant on forensic biology/DNA: Examination of the

case file bench notes and analytical worksheets from the crime lab show precisely how the amplification process was set up. Suppose that the known DNA from the defendant and the known DNA from the alleged victim were set up for DNA typing—at the same time, and on the same wallet-sized, plastic plate—as all of the evidence items. The vast majority of crime labs utilize **'96-well format plates'**[165] for this stage of the analysis.

It is important to emphasize that setting up an amplification plate marks the beginning of a profound, powerful series of molecular processes. Within each well on these amplification plates, many millions of pieces of DNA are manufactured over the course of just a few hours. These millions of DNA fragments provide the genetic foundation for human identification in crime labs. In addition to this process being highly sensitive to potential DNA cross-contamination events, the resulting **'post-amp products'** must be cautiously respected by crime lab personnel as dangerous ***sources*** of contamination. Considering these universally established contamination hazards, it is extremely improper to handle DNA from evidence samples at the same time and loading them onto the same plate—with ***'known'*** DNA samples from an accused defendant, a victim, or any other individual.

Refer to the document released by the FBI on September 1, 2011, entitled: **"Quality assurance standards for forensic DNA testing laboratories."**[166] Within this FBI document, examine **Standard 6**, entitled **"Facilities"**. This standard

addresses safeguards against contamination in DNA testing labs. Specifically, **Section 6.1.2** states the following:

> "…techniques performed prior to PCR amplification such as evidence examinations, DNA extractions, and PCR setup shall be conducted at separate times or in separate spaces from each other."

Based upon the implications of this standard, it is scientifically improper to exercise ***no separation*** between known DNA from the accused, and evidentiary DNA. It is also improper to exercise ***no separation*** between known DNA from the victim, and certain evidentiary items collected from a suspect. Similarly, it would be improper for the crime lab analyst to process—for example, from a rape case—the suspect's penile swab, at the same time, or within the same space, as the alleged victim's SANE kit.

Once the amplification process is completed, the sizes of the manufactured DNA fragments are eventually characterized—for the purpose of identifying DNA from a single human being—or perhaps DNA from multiple human beings within each evidence sample. Performing these amplifications, from known and evidentiary samples—within the same time and space—introduces an enormous, unnecessary risk of cross-contamination events. At this point, the primary thought from any diligent litigator should be as follows: ***"Why would any analyst do that? Surely, DNA amplifications are rarely set up this way."*** On the contrary, such gravely flawed practices are more common than one might suspect.

These ill-advised practices occur, despite specific standards/guidelines—warning crime lab analysts of the disturbing risks. Refer—again—to **Standard 6** from the FBI's **"Quality assurance standards for forensic DNA testing laboratories."** Specifically, **Section 6.1.3** states the following:

> "…amplified DNA product, including real time PCR, shall be generated, processed and maintained in a room(s) separate from the evidence examination, DNA extractions and PCR set-up areas. The doors between rooms containing amplified DNA and other areas shall remain closed."

Based upon the FBI's demand to process and maintain post-amplification DNA in ***separate rooms*** from all other processes, it defies all sense of logic—for example, in a rape case—to amplify ***his*** DNA at the exact same time—and separated by only an inch or so on a 96-well plate—from the DNA extracted from ***her*** intimate SANE kit items.

Forensic testing laboratories are frequently confronted with the challenge of LCN DNA. Refer to the 2010 article authored by Dr. Butler and Dr. Hill—**"Scientific Issues with Low Amounts of DNA."**[167]. These authors describe what has been referred to as the **"Enhanced Interrogation Approach"**. In part, this approach can include utilizing an advanced DNA purification/concentration step, for the purpose of **'pushing the envelope'**, by increasing the sensitivity of the DNA testing. Specifically, a skilled forensic biologist might attempt to circumvent LCN testing limitations by subjecting post-amplification DNA products to a ***'Microcon®—based DNA clean-up procedure'***. While this strategy might offer

significantly 'enhanced' analytical sensitivity, if these post-amp products are not handled with tremendous caution, the consequences can be disastrous. From crime lab casework performed in 2002, the enormous risks associated with ***'DNA clean-up'*** procedures most likely led to the wrongful conviction of Gary Leiterman. This case is discussed in greater detail in the section bearing the title: **"John Ruelas, Gary Leiterman, Contamination, and the Michigan State Police"**.

On January 12, 2017, new guidelines were approved by SWGDAM.[168] These guidelines, bearing the title: **"Contamination Prevention and Detection Guidelines for Forensic DNA Laboratories"**, comprise the most comprehensive, meaningful standards that have ever been placed into print by individuals dedicated to the integrity of the U.S. scientific/criminal justice system. On **Page 4, Section 2.1.1.**, this select group of scientists recommended that DNA labs should strive for prevention of contamination events as follows:

> "Separate work areas. Due to the high concentration of amplified DNA in a PCR sample, laboratories must have designated spaces for pre- and post-PCR activities (refer to QAS regarding facilities). Evidence examination, DNA extraction, and pre-amplification set-up activities must be restricted to the pre-PCR area while the post-PCR area is limited to PCR amplification and all analytical processes using the products of PCR amplification."

Refer to **Sections 2.1.1.1.3., 2.1.1.2.3.,** and **2.1.1.2.4.**, where it reads as follows:

> "Designated areas that house all necessary personal protective equipment, hooks for lab coats and operational sinks with soap and disposable towels. These areas may be immediately adjacent to, but physically separated from, the pre-PCR area."

This passage advises analysts that—for example—they must not leave their post-amplification work area, wearing a 'post-amp lab coat', and enter any other area of the facility. Similarly, analysts must not carry pens, notepads, pipette instruments, disposable gloves, or paper towels, etc. from the designated post-amp area, to any other analytical area.

At the top of **Page 6, Section 2.1.2.,** SWGDAM continues as follows:

> "Separate processing (e.g., handling and prep for DNA extraction) in pre-PCR areas by case type. Reference samples should be processed separately from evidentiary items by area and/or time."

This passage marks the clearest, most profound scientific mandate—condemning the practice of handling, storing, or processing known reference samples anywhere near the same time/location as evidence samples.

SWGDAM went so far as to dedicate the majority of **Page 5** to the importance of monitoring and controlling air pressure/air flow between various analytical areas within the crime labs. The cause for this concern is the potential generation of liquid aerosols during the processing steps used for DNA samples. This concern culminates in **Section 2.2.4.3.4**, where SWGDAM recommends that analysts:

> "Use only aerosol-resistant pipet tips for all procedural steps, particularly DNA extraction, pre-amplification set-up and post-PCR processing."

As remarkably powerful as DNA technology truly is, its utility can be neutralized by human carelessness, errors, and most important, a lack of attention to identifying and correcting problems that might surface at a multitude of levels. It is

the role of both prosecution teams and defense teams to recognize when our criminal justice landscape is plagued with erroneous science, and return the system to the universal objective—the truth.

[**Note:** The following vignettes are drawn from actual cases. With the exception of highly-publicized cases, the identities of individuals involved, and if at all possible, the geographic locations of these cases, are being kept confidential.]

VIGNETTE – Highly-publicized contamination of cold case evidence

On November 4, 1968, a 13-year-old girl, Jane Durrua, was murdered in Middletown, New Jersey. The child had been raped, beaten and strangled near a set of railroad tracks. Shortly after the homicide, a number of local suspects were questioned, but no reliable leads could be developed. The case went cold. Potential biological evidence from the case investigation remained in a law enforcement storage facility for 33 years. In 2001, cold case detectives realized that the 1968 medical examination had reported suspicious stains on the underpants collected from the young girl. The investigation team submitted a request for the item to be sent to a forensic DNA lab in Maryland. In 2002, Jerry L. Bellamy became a suspect after his genetic profile matched DNA detected within semen stains that had been discovered on Jane's underpants. In referring to this discovery from evidence originating in such an old case, John Kaye, the Monmouth County prosecutor, called the results "a miracle". An arrest warrant for Mr. Bellamy was issued in June 2004.

In early 2005, as prosecutors prepared for the inevitable trial, clues began to emerge, bringing the DNA match into question. The New Jersey State Police conducted a thorough review of the results. As the prosecution collaborated on the ongoing investigation of the DNA match, a remarkable coincidence was established. It turned out that clothing from the Jane Durrua murder case as well as clothing items from an Atlantic City rape case had both been opened up and examined on precisely the same day, September 15, 1999, by the exact same forensic biologist, within the State Police Eastern Regional Laboratory in Sea Girt, New Jersey. In both of these completely different cases, a profile matching Mr. Bellamy had been generated by DNA typing. In light of these enormously improbable events, and the glaring likelihood of a DNA cross-contamination error, a decision was eventually made to dismiss all charges against Jerry Bellamy.[169] Subsequent testing of DNA evidence revealed that suspected serial killer, Robert Zarinsky, was Jane's actual murderer.[170]

VIGNETTE – Another well-known instance of cold case contamination

In June of 1997, 1-year-old Jaidyn Leskie disappeared near Melbourne, in Victoria, Australia. The child's disappearance, and the subsequent missing persons search, was highly sensationalized throughout the Australian media. Tragically, on New Year's Day, 1998, the toddler's body was discovered near the shoreline of Blue Rock Lake, 90 miles east of Melbourne. The next day, the child's tracksuit pants, bib, and other clothing items were found in the lake—and delivered to the Victoria

Police Crime Lab. Tests from young Jaidyn's bib, conducted in February of 1998, revealed DNA from an unknown female.

More than five years later, in November of 2003, the investigation team finally realized that this female DNA matched a 22-year-old victim of a sexual assault. The young woman insisted that she was not at all connected to Jaidyn Leskie, or any person among the child's family and friends. Her sexual assault occurred in Altona, a west side suburb of Melbourne. Interestingly, young Jaidyn had disappeared from the Latrobe Valley area, a distant location to which the rape victim had never visited.

The more the police investigators scrutinized the circumstances, the more they became convinced that the young rape victim was entirely disconnected from the toddler's disappearance. Apparently, evidence items from her sexual assault case were taken out and tested on the very same day that Jaidyn's bib and other clothing items were out and about in the Victoria Police Crime Lab. Among all of the attending law enforcement officials, nobody could retrace the steps by which the obvious contamination event had occurred. Amidst the rapidly eroding confidence in the reliability of forensic DNA testing, many Australians were questioning law enforcement standards. One fundamental question: Why should ***'known'*** DNA sources, collected from anybody—especially an innocent victim—be analyzed, side-by-side—with vital evidence items from a homicide investigation?[171]

Limitations, misinterpretations, and misrepresentations.

As forensic biology methods advance to increasingly lofty new heights, one might begin to suspect that DNA technology has no limitations as an investigative resource. This concept is false. The fallibility of the technology enters into the equation when human beings are asked to scour the crime scenes, collect the evidence, examine the items, extract/quantify the DNA, and interpret the resulting comparative scientific data. Human errors and misrepresentations of the facts associated with these tasks are the points of origin that can ultimately lead to wrongful convictions. In the event of oddly distorted circumstances, any one of us might become a suspect—accused of perpetrating a serious crime. Regardless of our own knowledge of innocence, most of us would rather not entrust our future entirely to the scrutiny of scientific instruments and computers. With that established, as long as human individuals play a role in the investigative and/or scientific processing of each criminal case, there will always be potential for errors, flawed speculation, and misrepresentations of the truth.

In addition to this chapter, there are countless references that can supplement our understanding of the forensic use of DNA—and its impact upon our criminal justice system. Any documentation published by the **S**cientific **W**orking **G**roup on **D**NA **A**nalysis **M**ethods (SWGDAM) is extremely useful.[172] This includes—but is not limited to—SWGDAM guidelines covering the interpretation of STR-based

DNA typing, the validation of probabilistic genotyping systems, and the prevention of contamination in forensic DNA laboratories.

Among the most remarkable available resources, any conscientious litigator would benefit enormously by accessing the DOJ publication: "**DNA for the Defense Bar"**.[173] Yet another resource—published in November, 2017, by The Royal Society of Edinburgh—bears the title: **"Forensic DNA Analysis: A Primer for Courts**."[174] This publication is vastly informative, as well as very concise (only 60 pages).

[**Note:** The following vignette is drawn from an actual case. With the exception of highly-publicized cases, the identities of individuals involved, and if at all possible, the geographic locations of these cases, are being kept confidential.]

VIGNETTE - A Problematic Investigation

An elderly couple was murdered, in their own home, by unknown assailants. The woman, Mrs. A, was beaten and suffocated. The man, Mr. A, suffered a multitude of injuries, including fatal head injuries. Only four days after the crime scene was processed, biological evidence was examined, and initial DNA typing results were in the process of being compiled by the local crime lab. By all standards, the investigation was moving forward with blinding speed. Within another week, eleven additional items were examined and typed for DNA.

Two door-to-door salesmen, Mr. M and Mr. N, were arrested for the crime.

These arrests were the consequence of a malicious, faulty interrogation of Mr. M. The interrogation spawned a highly improbable confession. Although Mr. N was also aggressively interrogated, the man continually maintained his innocence. Unfortunately, for the sake of the investigative process, virtually no probative DNA results were discovered from the 'first wave' of DNA evidence examinations. Absolutely no physical evidence pointed to biological material from the two murder victims, on the person or possessions of the two incarcerated suspects, Mr. M and Mr. N. Similarly, no physical evidence pointed to biological material originating from either Mr. M or Mr. N, anywhere on the homicide victims, or within the residential crime scene. Despite the initial, intense flurry of investigative work, virtually no additional analytical efforts were conducted during the following thirteen weeks. Throughout that time frame, Mr. M and Mr. N remained in jail.

From an eventual 'second set' of eighteen evidence items, the analysis revealed no pertinent DNA profiling results from all but one of those items. Enormously profound DNA data emerged from the right-hand fingernails collected from the deceased, elderly male, Mr. A. It is important to note that these fingernails, initially, tested positive for blood. Based on this finding, the analyst was certainly aware that this blood ***must*** have originated from one of the following two sources: **1)** From the severely beaten man; **2)** From a perpetrator who had been scratched during the attack. In the event that the blood was indeed from the deceased victim,

Mr. A, the DNA type from this sample would have unquestionably turned out to be 100% victim-derived. Thus, the DNA results would have proved worthless. To the contrary, the observed DNA mixture ***clearly*** established that Mr. A must have scratched his attacker, drawing tiny remnants of blood, as he fought for his life. A total of forty-three alleles were identified from the fingernail sample. Upon subtracting out the alleles corresponding to the elderly male victim, eighteen unaccounted for DNA markers were observed. This indicated a clear, single source of DNA, from an unknown male.

Beyond all doubt, this unknown male DNA contributor was not Mr. M, the man who had confessed to the homicides. Nor was the DNA from Mr. N, the man who consistently maintained his innocence. Defying logic, the reporting analyst inexplicably delayed further activity for 65 days, rather than expedite an ***immediate*** request for a DNA database search. Considering the discovery of genetic results from an unknown male at a murder scene, one would expect a greater sense of urgency.

About one month after the database search was eventually initiated, a ‘supplemental report’ was released by the crime lab. In that report, the analyst summarized the examination of a total of sixty-eight evidence items. Sixty-seven samples provided virtually no useful results that might suggest the identity of the killers. However, buried in the report, the analyst revealed DNA conclusions

regarding Mr. O, a truly promising suspect, due the presence of his DNA on the elderly male victim's fingernails. With these results clearly pointing to Mr. O, note that this man had absolutely no personal connections with either of the two incarcerated door-to-door salesmen. The story emerged that, once the DNA database search was finally verified, investigators traveled to a prison facility, and spoke with Mr. O, a suspected serial killer. Mr. O indifferently informed the detectives that he and his buddy, Mr. P, killed the elderly victims during a residential break-in. Mr. O also verified that Mr. M, as well as Mr. N, were never at the residential crime scene in question, and played absolutely ***no role*** in the double homicide.

The catastrophe associated with this case lies in the fact that, five days prior to the excessively-delayed DNA database search, Mr. O had invaded the home of two newlyweds. Mr. O proceeded to murder yet another victim, a beloved husband. The man's widow was awarded a sizable judgment in civil court. Mr. N, the man who never surrendered in maintaining his innocence, was also awarded a large settlement, for a 15-month-period of wrongful incarceration. Mr. M, the man who confessed—received absolutely nothing.

Error rates and how errors manifest themselves in forensic DNA analysis.

Defining scientific error rates has proven elusive with regard to forensic DNA casework analysis. In a September, 2014 ***Forensic Science International*** article authored by Ate Kloosterman, Marjan Sjerps and Astrid Quak, the authors caution:

> "Forensic DNA casework is currently regarded as one of the most important types of forensic evidence, and important decisions in intelligence and justice are based on it. However, errors occasionally occur and may have very serious consequences. In other domains, error rates have been defined and published. The forensic domain is lagging behind concerning this transparency for various reasons." [175]

In an attempt to describe a methodology for dealing with error rates, Kloosterman and colleagues offered:

> "The error rates reported in this paper are useful for quality improvement and benchmarking, and contribute to an open research culture that promotes public trust. However, they are irrelevant in the context of a particular case. Here, case-specific probabilities of undetected errors are needed. These should be reported, separately from the match probability, when requested by the court or when there are internal or external indications for error. It should also be made clear that there are various other issues to consider, like DNA transfer. Forensic statistical models, in particular Bayesian networks, may be useful to take the various uncertainties into account and demonstrate their effects on the evidential value of the forensic DNA results."[176]

William C. Thompson has written extensively for the bar in the United States. In a 2003 article Thompson, Ford, Doom, Raymer and Krane[177] instructed that:

> "It is easy to assume that any past problems with DNA evidence have been worked out and that the tests are now unassailable. The problem with this assumption is that it ignores case-to-case variations in the nature and quality of DNA evidence. Although DNA technology has indeed improved since it was first used just 15 years ago, and the tests have the potential to produce powerful and convincing results, that potential is not realized in every case. Even when the reliability and admissibility of the underlying test is well established, there is no guarantee that a test will produce reliable results every time it is used. In our experience there often are case-specific issues and problems that greatly affect the quality and relevance of DNA test results. In those situations, DNA evidence is far less probative than it might initially appear. The criminal justice system presently does a poor job of distinguishing unassailably powerful DNA evidence from weak, misleading DNA evidence. The fault for that serious lapse lies partly with those defense lawyers who fail

to evaluate the DNA evidence adequately in their cases."[178]

VIGNETTE - Bad "Likelihood Ratio" Statistics

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). For countless years, a city police crime laboratory utilized LR statistics to assess inclusion/exclusion scenarios relevant to DNA mixtures from their case evidence. In early 2013, upon consulting with a visiting expert in forensic DNA statistics, this crime lab was notified that their forensic biologists were being improperly trained to calculate the LR statistics for their assigned criminal casework. Hence, any reports citing LR statistics were incorrect. For any of these cases proceeding toward a trial, supplemental reports were required to address and correct the errors. This city police crime lab ultimately abandoned the notion of utilizing LRs for assessment of any observed DNA mixture profiles. The following case exemplifies the disastrous impact of such faulty statistical strategies.

Not long after midnight, a homicide occurred within the humble residence of the unemployed adult male victim, Mr. B. This victim, an alcoholic and a drug addict, was asleep on his living room sofa when the crime occurred. Investigators arrested a 55-year old man, Mr. R, for the homicide. The arrest was made when authorities learned that Mr. R had initially lied, telling police he was not at the residence on the night of the murder. Mr. R ultimately admitted that he was indeed

present at the crime scene.

According to Mr. R's statement: Two men, one tall, the other much shorter, abruptly rushed into the home, approached the living room sofa, and began attacking the victim. Mr. R said that he ran from his bed, and into the dark living room. At first, he believed that the taller of the two intruders was flailing his arms, as he was striking Mr. B. The attacker was actually stabbing the victim with a knife. Mr. R screamed at the perpetrators, imploring them to leave the victim alone, that there was nothing in the home to steal. As this plea was ignored, Mr. R. reached around the taller attacker from behind. He was promptly stabbed on the top of his hand.

Mr. R quickly withdrew and rushed to the kitchen to turn on the light and tend to his wound. In the process, he deposited blood on the light switch, and into the kitchen sink. When Mr. R noticed that the two attackers had moved on to search the bathroom/bedroom area, he took that opportunity to hurry out the front door. As Mr. R fled the scene, he could hear the victim, Mr. B, moaning in pain. Mr. R could only hope that his friend would survive the attack, but had no way of knowing that the man had been mortally injured by approximately twenty-five stab wounds.

Mr. R was in trouble. In addition to his initial lie to the investigators about being present at the crime scene, the evidence eventually proved that he was indeed there. DNA analysis of blood drops on the floor of the residence, blood smudges on the kitchen light switch, and blood deposits in the kitchen sink, all matched the DNA

profile collected from Mr. R. In contrast to his initial false statement, Mr. R later offered information to the investigators about the taller of Mr. B's two alleged attackers. Mr. R described a 6-foot, 5-inch African American man, who weighed approximately 180 pounds. He also pointed out that the man had distinctive dreadlocks hanging down the back of his neck. Mr. R also told the detectives that this man could often be found traveling on foot, through a well-known, drug-infested area of the city. Remarkably, Mr. R went so far as to provide the police with a specific nickname, a villainous cartoon character. We will refer to this individual as **"The Claw"**. Despite the fact that narcotics detectives were fully aware of the identity of The Claw, little was done to pursue this lead.

While Mr. R sat in the county jail, awaiting the murder trial, the city crime lab analyst issued the first DNA report on the homicide. In that report, Mr. R could not be excluded as a possible contributor of the minor alleles associated with the victim's right hand fingernails. The major contributor within the DNA mixture was the victim himself, Mr. B. Unfortunately, the city police lab was using the faulty likelihood ratio (LR) method. The analyst reported that the DNA mixture was ***"1 billion times more likely"*** to have originated from Mr. B and Mr. R, by comparison to a mixture of Mr. B, and an unknown DNA contributor.

Later, upon recognizing that the LR statistics were entirely incorrect, the same analyst was compelled to issue an amended report, to rectify the faulty calculations.

This corrected report was issued over two and a half years after the initial, misleading report. The amended version reported that Mr. R could not be excluded as a possible contributor of the minor, foreign alleles observed on Mr. B's right hand fingernails. However, the profoundly more appropriate probability of inclusion (POI) statistics revealed that ***1 out of every 50*** random individuals would also qualify as a possible contributor. Within the local metropolitan area, there were more than 900,000 residents. Thus, based on the corrected calculations, we now had 18,000 possible new suspects who could have contributed the minor alleles reported on the fingernails of the victim.

If the investigators had the benefit of this information, 2½ years earlier, as opposed to the ***"1 billion times more likely"*** likelihood ratio nonsense, they might have listened more attentively to Mr. R's account of the incident. The facts later emerged that there truly was a male individual, commonly referred to as **'The Claw'**. Years earlier, that person was indeed prowling the drug-infested sections of the city.

Records revealed that, a few days prior to the homicide, a 6 foot 5, 180-pound African American man, known on the street as The Claw, checked in with a mental health facility. This mysterious man complained of hearing voices, urging him to **"hurt somebody"**. A few days after the homicide, that same man once again, checked in with the same facility and repeated his complaint that a voice was urging him to hurt people.

Mr. R spent 44 months in the county jail, before he was finally subjected to the murder trial. By that time, The Claw had removed himself from the city street/drug scene. At trial, the prosecution forged ahead and embraced the baffling strategy of addressing only the initial forensic DNA report—the report citing the absurdly erroneous LR statistics. Counsel for the defense eagerly questioned the analyst, establishing the existence of a corrected version of that report. The defense enthusiastically emphasized the ***"1 out of 50"*** POI calculation. The following day, a defense DNA expert testified to the fact that, either Mr. R, or one of 18,000 other residents in or near the metropolitan area, could have incidentally transferred DNA onto the fingernails of the victim. That same DNA expert testified that the blood trail leading into the kitchen, on the light switch, and in the sink, corroborated Mr. R's claim that he was stabbed in the hand. The jury deliberated for 4 hours before returning a "Not Guilty" verdict.

VIGNETTE - Substandard Investigations and Bad Crime Lab Interpretations

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Picture a dreary, dilapidated small-town motel. It's raining. Completely naked, a woman walks to the center of the run-down motel courtyard and screams out for all to hear: "Does anybody want to have sex with me?" Mr. C and his girlfriend were staying in a nearby motel room. They decided to rescue the disturbed, intoxicated woman from the elements. With some

resistance, the woman was carried, by Mr. C, to their motel room.

Many hours later, Mr. C and his girlfriend arose and noticed that the woman was no longer in their room. In order to retrieve some early morning snacks, the girlfriend walked to the nearby vending machines. She heard a faint, distressed moaning. Mr. C's girlfriend realized that the woman from their room had been severely beaten and dumped in a nearby corner. Mr. C and his girlfriend promptly contacted the police and reported the crime. They decided not to mention that the woman had spent the night in their room. Days later, the woman died in a hospital, as a result of her injuries. The crime lab revealed the presence of the woman's DNA in the room occupied by Mr. C and his girlfriend. When they also reported Y-STR DNA markers, consistent with those from Mr. C, on the woman's body, including some alleles on her vaginal area, the police charged Mr. C with the homicide. The flaws within this investigation and the Y-STR test results were abundant:[179]

1) The vaginal Y-STR profile never established any seminal material, not a single sperm cell;

2) The weak, partial Y-STR profile could have originated from approximately 1 out of every 16 Native Americans. The small town with the dilapidated motel was populated by a high percentage of Native Americans—including Mr. C. This revelation does not even account for the fact that the Native American Y-STR database originates in part from males from Oklahoma,

from Florida, and elsewhere. The data originate in part from Sioux, from Cherokee, and from numerous other tribes. There was no way of knowing whether or not the statistics might be even less informative upon comparing the data with Apache/Hispanic males from the geographic location of the homicide;

3) Only a few of the males staying at the dilapidated motel were tested for their Y-STR profile;

4) The same is true for countless males staying at nearby cheap motels on the highway near the crime scene;

5) The same holds true for many of the victim's recent sexual partners;

6) The same holds true for numerous males residing in a subdivision—located just a fraction of a mile from the motel;

7) The same holds true for various males lingering near a liquor store/cocktail lounge establishment located less than 200 feet from the crime scene;

8) The same holds true for a male who had deposited DNA found on a Vodka bottle, recovered in close proximity to the badly beaten female victim.

Charges against Mr. C were reduced from first-degree murder to a much lower level charge of criminal confinement. When Mr. C accepted a plea agreement, he was released for time served.

VIGNETTE - Substandard Investigation and Faulty Analysis

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Some cases illustrate the remarkably bizarre, substandard investigations and scientific efforts that we occasionally endure within our criminal justice system. The case described below demonstrates that sometimes, the prosecution will not hesitate to brazenly waste public resources, in order to pursue an inconsequential matter.

A woman in a small southwestern U.S. city arrived at her residence, and realized that her burglar alarm had been activated. As she telephoned law enforcement, she spotted a man walking down her street, and described him to the dispatch operator. The woman also noticed an open window, facing her backyard. A trash can had been positioned on the back porch, beneath the open window. The police located the stranger, Mr. D, as he walked through the neighborhood. Upon questioning the man, the officers decided that he had little justification for "going for a walk" in that neighborhood. This translated into 'behaving in a suspicious manner'. When the police searched the immediate area, they happened upon a pair of lime green gardening gloves that were stuffed into a gap in a nearby rock wall. The officers put their suspect into the back of a squad car and transported him to the allegedly burglarized home. When the complaining witness came to her front door, an officer held up the lime green gloves and asked

"Are these yours?" The woman asked the officer to hold that thought for a moment, and went to her backyard. She returned to the front door and told the officer, "Yes! My gardening gloves are missing, and they look exactly like those!"

Mr. D was placed under arrest. The prosecution's theory was that Mr. D, a professional burglar, had gained access to the victim's backyard. When he found the gloves on the porch, he allegedly put them on to avoid leaving fingerprints. Mr. D then moved the trash can to a nearby window and crawled into the home. As soon as the burglar heard the activated alarm, he vacated the house. A number of minutes later, Mr. D allegedly hid the gloves a few blocks away within a rock wall, in hopes of avoiding any connection to the break-in.

Months after his arrest, Mr. D was subjected to a criminal trial. During the trial, the defense harped on the fact that the gloves could have been tested for DNA—either to connect them to the defendant, or to clear him of the charges. The jury agreed that the lack of DNA testing was clearly an issue. However, they could not agree upon a verdict. After the jury was dismissed, the prosecution exclaimed that they were determined to ***"get their man"***.

Prior to the 2nd trial, they commissioned a local laboratory to test the gloves for DNA. The assigned defense lawyer brought in a DNA expert, in order to examine the lab reports and supporting documents. Imagine the indignation of the taxpayers, in light of the inflated cost of two trials, plus expensive DNA tests, as well as the

cost of a defense DNA expert. All of this, in order to get to the bottom of a stolen pair of filthy gardening gloves. The attending lab analyst properly turned each glove inside-out and carefully collected cotton swab samples. These swabs targeted various inner surfaces that certainly should have rubbed against the 'handling skin cells' of the wearer. Recall that the average-sized person, from head-to-toe, sheds approximately 2 million skin cells over the course of a single minute. Interestingly, the gloves each contained a single-source genetic profile, perfectly matching the DNA from Mr. D. Although the defense DNA expert readily agreed to the DNA match with the defendant, something was terribly wrong with this scientific picture.

The problem: Where was the DNA from the burglary victim, the owner of the lime green gloves? On each glove, the only genetic material was that one full set of alleles, demonstrating a perfect match to Mr. D. Note that this was in spite of the victim's testimony that she originally purchased the gloves, and used them quite frequently, throughout a multitude of months. While the gloves were heavily soiled from the abundance of heavy yard work, the woman adamantly stated that she had never washed them—***not even once***. Most interestingly, the investigators did not bother to collect a DNA reference standard from the glove owner, and the local analytical lab never questioned the whereabouts of such a sample from the woman. The verdict for Mr. D: "Not Guilty" on all counts.

How the prosecution/defense might respond to the claim: "We have DNA"

The forensic biological/DNA analysis of a criminal case often reaches a logical stage for the crime lab scientist to pause the progression of the analytical work. At this point, the case investigators and the scientists can benefit from taking the opportunity to communicate about the initial analytical strategy, as well as the results. Typically, counsel for the prosecution is briefed on the status of the case investigation. At this stage, the crime lab/prosecution team might assertively pre-warn the defense team with the claim: ***"We have DNA."***

Upon hearing those three words, an alarming percentage of defense teams might humbly initiate discussions of a conciliatory plea agreement. This response could be embarking upon a grave professional error. This is not a suggestion that the technologies currently being used for crime scene analysis, evidence examination, body fluid identification, and DNA typing are anything short of remarkable. However, challenges can emerge when the crime scene provides what seems to be evidence worthy of DNA testing. Even when some clearly perceptible DNA results are generated, the scientific value of the data may fall miserably short of any value in the criminal justice system. The case investigation and the subsequent legal proceedings will become vastly problematic if forensic biology experts, either for the prosecution or the defense, allow themselves to speculate beyond the reaches of the genuine nature of the scientific results.

Let us scrutinize this "We have DNA" declaration by exploring the following checklist of sensible responses:

- Of course there is DNA. DNA is ubiquitous—essentially everywhere. But whose DNA did you actually find?
- Was DNA from the defendant found anywhere that might be incriminating?
- Was the victim's DNA found anywhere—incriminating the defendant?
- How much DNA was found?
- Was the deposit of DNA from *one* human source, or a mixture of multiple individuals?
- Are there any clues suggesting *how* this DNA arrived where it was eventually found?
- Are there any clues suggesting *when* this DNA arrived in that location?
- If the scientist has clues regarding how/when this DNA arrived where it was found, what types of incidental activities—unrelated to the crime—might justify the location, quantity, and typing information corresponding to the observed DNA mixture, or the single source deposit?
- Were some vital evidence items *not* examined? If so, was potentially

valuable DNA information available on those items—results that could have cleared the defendant of any guilt?

VIGNETTE - A bungled investigation. But "We have DNA"

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). A young adult male died in a hospital—mostly from head injuries inflicted as he was beaten and kicked by an unidentified perpetrator. During the opening statements at the homicide trial, the first words from the prosecution team were: …***"We have DNA…"***

The case for the prosecution went downhill from there. Most notably, the prosecution's initial, primary witness was a diagnosed schizophrenic. At the time of the homicide, this male individual was a confirmed daily-use crack cocaine addict. Making matters worse, the witness was known to rarely bother with taking any of his prescribed mental health medications. The next key witness for the prosecution offered no improvement. The young adult female suffered from bipolar disorder, in addition to her schizophrenia. She was a daily-use heroin addict, and worked regularly as a prostitute. This woman also chose not to follow doctor's orders with her prescribed mental health medications. Both of the two key witnesses admitted to hearing imaginary voices on a routine basis. The woman sobbed uncontrollably throughout her time on the witness stand. Ultimately, she begged to halt the process, saying that she was hearing voices, ***during her testimony***.

There were three crime scenes associated with this homicide. The first crime scene was the unknown location at which the male victim was beaten nearly to death—and subsequently anally raped. Although investigators theorized that the assault/battery/sexual assault location was within an apartment, a search warrant for that specific residence was not executed until over ***sixteen weeks*** after the homicide. Regardless of whether or not that residence resembled a crime scene immediately after the criminal incident, the biological information recovered after all of that time had expired, was unfortunately useless.

The second crime scene was a parking lot where the dying victim was dumped after the brutal crime. Analysis of this crime scene was also bungled. Emergency medical responders removed clothing from the victim, and set it aside on the asphalt. This clothing sat in the snow/sleet for a protracted period of time—which was never precisely calculated for the jury. The garments became soaking wet, before being lumped together and haphazardly stuffed in a plastic bag. An unknown time passed before these items were transported to the appropriate facility, later to be dried and examined. Again, biological analysis of the victim's clothing provided little more than ambiguous, unfortunately useless DNA results.

The third crime scene was the heavily damaged anal/rectal area of the dying adult male victim. Defying logic, the case investigation team delayed their request for a SANE exam. The SANE nurse was not able to examine the victim until after

physicians thoroughly cleaned, and repaired the physical damage to the anal/rectal area. Although seminal material and DNA evidence may have been lost as a result of this non-lifesaving medical procedure, the leader of the investigation team clearly documented a request for DNA typing on the anal swab that was eventually collected by the SANE nurse. The crime lab forensic biologist conducted a presumptive test for semen on the anal swab. When that test was found to be negative, DNA typing was inexplicably left unexplored.

Despite two mentally-compromised key witnesses, and despite the complete obliteration of all three crime scenes, the jury found the accused man guilty of second degree murder. This scenario establishes the enormous power behind the opening three words of the trial, …..**"We have DNA…"**

Speculation about how or how much

It is scientifically irresponsible to speculate on how a DNA deposit may have arrived where it was detected—or that DNA might be present, but in undetectable quantities. Let us suppose that either a single source DNA profile, or perhaps an interpretable DNA mixture profile has been detected on a crime scene evidence item. It is a very precarious, dangerous proposition to speculate as to how this source of DNA may have arrived on the surface of the item. Some scientific clues might be useful in illuminating the circumstances of a DNA deposit. For example, suppose that DNA typing establishes that a source of genetic material is consistent with a

specific male. Let us also suppose that the evidence item is a vaginal swab collected from a woman who has voiced allegations of rape. If the crime lab photographed numerous sperm cells from this same vaginal swab, logic dictates that the DNA arrived in the vaginal cavity as a consequence of sexual intercourse. Similarly, suppose that DNA typing establishes a source of genetic material to be from a specific person. Suppose that person claims to have received a cut on the hand and presents a fresh wound, in support of that claim. If a drop of reddish brown material provides a positive test for blood—once again—we possess a compelling scientific clue as to how the source of DNA may have arrived on the DNA test surface.

Without the support of scientific clues, such as confirmation of semen, blood, or saliva, it is scientifically flawed and misleading to suggest how DNA arrived onto an evidence item. In 2004, forensic biologists Carole Peel and Peter Gill instructed:

> "Scientists reporting body fluid cases in court are frequently requested to provide their expert opinion regarding the origin of any DNA profile obtained. It is well documented that, with the recent development of low copy number (LCN) profiling techniques, DNA profiles can be obtained from minute amounts of biological material. Forensic laboratories now routinely analyse samples yielding less than 100 picograms DNA. The recovery of genetic profiles from touched objects and the transfer of DNA from one individual to another in the process of shaking hands has been demonstrated. It has also been shown that a full profile can be recovered from secondary transfer of epithelial cells (from one individual to another and subsequently to an object) at 28 cycles. This sensitivity increases the chance of detecting extraneous cells deposited in an event unrelated to a crime by the standard processing of body fluid stains. Precautions taken in the reporting of LCN cases may therefore be applicable to all cases involving low levels of DNA, such as minute blood stains on touched objects, even when amplified using standard 28 cycle

profiling techniques."[180]

Unsupported scientific reports, or speculative courtroom testimony can propagate information that is much more prejudicial than it is useful. The same concept applies to scientifically flawed and misleading speculation regarding when DNA may have arrived upon an evidence item. Today's state-of-the-art DNA typing technology, by itself, simply cannot reveal the history or timing of DNA transfer events.

VIGNETTE - Interpretations can be faulty—even from the FBI Crime Lab

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Mr. Q was wrongfully accused of sexually assaulting his own young male child. The evidence examined by an FBI Crime Lab analyst consisted of nothing more than four cotton swabs. These swabs were collected from the anal area of Mr. Q's young son. The FBI report stated ***"...semen identified"***. In conferring with his defense attorney, Mr. Q insisted that he would never hurt his child, and that the lab report had to be blatantly wrong.

In 2010, when a defense DNA expert assessed the FBI Crime Lab documents, he noticed that the reporting analyst referred to an ***"FT Positive"*** presumptive semen test result on two of the four anal swabs from the boy. The test was for prostate specific antigen (PSA), a protein that is abundantly present in semen. Within the case file, the defense expert discovered that this mysterious ***"FT"*** designation was

shorthand for ***"Faint"***. It seems that the FBI Crime Lab utilized a $1.05 PSA detection cartridge (similar to a pregnancy test strip). Upon doing so, the PSA test strip revealed nothing more than a faint positive result. No effort was made to conduct a microscopic search for sperm cells. Instead, the FBI Crime Lab proceeded to test one of the four swabs for DNA. This effort revealed only the boy's DNA, and absolutely no data suggesting the presence of any cellular material from the child's father, Mr. Q.

The defense expert recommended retesting on not one, but all four swabs. The swabs were sent to a qualified independent lab in the Chicago area. The Chicago lab was equipped with a more accurate, more specific, screening test for semen called 'RSID-Semen'. This lab also utilized a more sensitive, more thorough DNA testing strategy. The Chicago lab reported absolutely no indication of semen, and supported the FBI Crime Lab's finding of no DNA from Mr. Q.

There is nothing defective about the notion of utilizing PSA test cartridges to search evidence items for seminal material. However, it is highly problematic to lean heavily on such tests—as if they 'somehow' offer absolute proof that sexual activity has indeed occurred. This is especially true in the absence of any supporting tests for sperm cells or DNA from an accused individual. PSA does indeed exist in body tissues and fluids other than semen. For this reason, a nationwide controversy was brewing in 2010. Is PSA a presumptive test, or a confirmatory test? The state of

Minnesota Bureau of Criminal Apprehension (BCA), just as one example, weighed on this topic in 2015—by publishing the following comments on their website:

"…p30 test is a presumptive test for the presence of semen &/or seminal fluid."

The Minnesota BCA website also reports the following:

> "Positive identification of sperm microscopically is the only confirmatory test for semen identification used at the BCA."[181]

PSA and similar diagnostic tools were meant to provide clues toward the ultimate goal—which will ***always*** be DNA. In Mr. Q's case, FBI Crime Lab management refused to back off from their outlandishly ardent speculation of ***"semen identified"***.

Up until the week of the trial, Mr. Q had been sitting in jail for over sixteen months. What's worse, the man was facing 30 additional years in prison—in the event of a conviction. Mr. Q was offered an opportunity for no more than 'time served'. However, the man would have been required to accept a guilty plea. Rather than consider this, Mr. Q maintained his innocence and refused to make any deals. After the jury endured the trial, they deliberated for only 2½ hours, before finding Mr. Q not guilty on all counts. The man was immediately released.

The take home lesson from Mr. Q's case was that, sometimes, the prosecution's case is highly dependent upon key scientific aspects of the investigation. An enormous obstacle materializes when the corresponding scientific data are fundamentally weak. As a consequence of bias, the laboratory analysts

might over-emphasize the strength of the results, in order to maintain good favor with the prosecution. This activity is both ill-conceived, and dangerous.

DNA in Sexual Assault Cases

We can all agree on two fundamental truths. First, there are documented cases of flawed criminal investigations and misguided prosecutions, often leading to Wrongful Convictions.[182] Second, any circumstance involving harm to the children within our society is certain to cause a powerful response of revulsion and outrage. Within our criminal justice system, these two fundamental truths often collide.

Current estimates reveal that about 20% of the adult women in the U.S. claim that they were sexually abused during their childhood.[183] About one half of that percentage applies to U.S. men, also claiming that they were sexually abused as children. Additional sources claim that these estimated percentages are most likely way too conservative. As a consequence of the enormous level of emotion experienced by the victims of these crimes, many cases are never reported.

Imagine a call coming into a law enforcement emergency dispatch unit. Shortly after the call, law enforcement resources are mobilized, and they arrive at a home. Officers are confronted by a hysterical female and a withdrawn child. A finger is pointed at a male suspect. Perhaps this suspect is standing in front of the officers. Perhaps he is sound asleep in a nearby bedroom, unaware of the confusion and

consternation. Perhaps the accused is not even present at the scene. After statements are collected from various individuals, a scenario such as this often leads to the immediate incarceration of the accused. Such circumstances also lead to a medical examination, further subjecting the child to traumatic events. Often, such distressing medical examinations are quite necessary.

Suppose that an attorney is assigned to defend a client who has been accused of inappropriate sexual activity with a young child. Let us also suppose that the accused person has consistently emphasized that he has never had any contact with the child, and has never set foot in the home of the child. When DNA testing establishes the presence of genetic material—originating from the defendant—on the underpants of the child in question, what are the chances for an effective defense strategy? We can all agree that the accused is in deep trouble. We can equally agree that the circumstances are different when the accused lives in the same home, is a caretaker for the child, and handles all of the laundry responsibilities.

Competent litigators must be aware of these ***residential effects***. Among the most illuminating peer-reviewed scientific articles centering on this concept of residential DNA transfer events, refer to the 2016 publication entitled: **"DNA transfer during laundering may yield complete genetic profiles."**[184] Sarah Noel and contributing authors established that sufficient quantities of DNA for complete

genetic profiles could be transferred from clothing item to clothing item—during routine laundry cycles. The study revealed that such events were commonplace with semen deposits, as well as vaginal secretions. Equally important, this series of studies sought a degree of insight into fundamental concerns frequently plaguing defense teams that are presented with this issue of potential residential effects. The study was designed as follows: Underwear was collected from female children—living within homes with absolutely no history of intrafamilial sexual abuse. A total of 168 biological evidence cuttings were collected from 24 pairs of underwear, donated from the homes of 11 different 'control families'. The requirements for these garments were; 1) They needed to have been owned and worn by the child for at least six months; 2) They needed to be regularly washed with clothing from the other individuals residing in the home; 3) They needed to be submitted to the DNA testing lab after being washed and dried. When these 168 cuttings from these 'control' garments were extracted for DNA, 24% of the samples did not yield sufficient DNA to meet the lab's customary threshold for analysis. An additional 11% of the samples failed to provide an interpretable DNA profile. An additional 13% provided sufficient DNA for an attempt at typing. However, only the female child's profile could be detected. Interestingly, the authors reported that:

> "The remaining 52% (or 87 cuttings) yielded interpretable mixtures of DNA corresponding to multiple family members. The quantity of male obtained varied greatly and reached up to 6.7 ng."

The lesson revealed by this illuminating series of studies informs litigators that jurors may not be properly advised to conclude that foreign DNA on any garment from a child—even a very intimate region within their undergarments—signals an indication that crimes are occurring within the residence in question.

VIGNETTE - Residential Effects and a Failure to Consider the Evidence

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Mr. Y lived for several years with a platonic female friend, and her young daughter, who had grown from a small child to a young teen. One day, the teen inexplicably reported to her mother, a multitude of inappropriate actions, allegedly committed by Mr. Y.

Law enforcement was immediately brought to the residence. This created a multitude of opportunities for forensic investigators to corroborate the statements from the young female. Alternatively, the prompt arrival of the police could have led to evidence casting doubt upon the allegations. The young female claimed that Mr. Y had forced hand-to-penis contact. She also claimed that Mr. Y pulled down her underpants and rubbed his penis against her buttocks. Defying logic, no penile swab was collected from Mr. Y. Competent litigators know that in countless cases, forensic biological tests of penile swabs have led to the conviction of sex offenders. In countless additional cases, lack of evidence from penile swabs have cast an enormous cloud over the legitimacy of the allegations.

There were allegations that Mr. Y kissed the young female, pulled up her shirt and bra, and spread more of his saliva across her chest area. Samples could have been collected from all of these areas of contact, and potential saliva deposits. However, the young female's lips, as well as the skin near her breasts, were never sampled. In light of the allegations, this oversight was inexcusable. Recall that a single drop of saliva contains approximately 500,000 salivary epithelial cells. Tests indicated nothing on the bra. No swabbing was collected from the female's buttocks area and no foreign DNA was found on the anal swab. The young female reportedly witnessed Mr. Y masturbating and ejaculating onto tissue papers. She alleged that Mr. Y placed them into a specific trash container. The discarded tissues, paper towels, and napkins in that container were all recovered by the crime scene investigators.

Tests from all of these materials failed to detect the slightest indication of semen/or DNA from the accused man. Recall that a single drop of semen contains approximately 3 million spermatozoa. Despite the abundance of available cells/DNA from a multitude of potential sources, taken together with the need for only 100 cells to achieve a DNA profile, the case investigation uncovered a complete absence of scientific support for each and every allegation. Each attempt to test evidence that might incriminate Mr. Y, failed to suggest any hint of criminal activity.

Just prior to the start of the trial, an expert forensic biologist arrived at the office of the defense team for a discussion of the case. The attorneys described bizarre events that had occurred earlier that day. They informed their DNA expert that they had decided to conduct one final check on a copy of the Child Protective Services (CPS) file. Although the defense team was aware of a CPS audio recording with the alleged victim, they were shocked to find a DVD labeled "Video file"—referencing the name of the young female. Considering that they were only hours away from the start of the trial, the attorneys frantically inserted the disk into the nearest laptop. They soon observed the young female, providing a statement to a CPS interviewer. Point-by-point, the presumed victim recounted each of her very specific, detailed allegations. Further into the video record, the young female mentioned "…then, Mr. U did this, …". Later, she continued "…then, Mr. U did that..." The defense attorneys turned to each other, and exclaimed, **"Mr. U!? Who's that?"** Further review of the file revealed that approximately one year prior to the allegations targeting their client, Mr. Y, the same young female had voiced remarkably similar allegations against a ***first*** alleged perpetrator, **Mr. U.**

Not surprisingly, the Court granted a continuance. Months later, another continuance was granted, and so on. The trial was finally set to get underway in earnest, about 15 months after the discovery of the young female's multiple, nearly identical allegations. Again, the defense team decided to play it safe and revisit

various file materials—just to ensure that there were no more 'buried surprises'.

This time, the attorneys uncovered an odd series of communications, which were dated a few months prior to the latest trial date. The prosecutor and the reporting crime lab DNA analyst were embroiled in an e-mail quarrel. The analyst was trying to accentuate the fact that—long after completion of the casework in question—she had decided to make some changes in her life. The analyst had returned to college, and was now comfortably pursuing a new career. The prosecutor was arguing that the former DNA analyst was thoughtlessly side-stepping an important case, at the height of the state's need for scientific testimony. The analyst conceded that she was overwhelmed by her responsibilities at the DNA lab, and was inadequately equipped to testify in such a daunting process. When the defense team filed a new motion, demanding all communications associated with the case, the prosecution decided to dismiss the matter. The nightmare was over for Mr. Y.

The take home lesson from Mr. Y's ***residential effects*** case was that, sometimes, as a consequence of a profoundly substandard investigative effort, the prosecution should abandon the case. Regardless of the reckless justification for not doing so, the defense team must remain energetic in their commitment to standing up for their client's freedom. Sometimes, despite the degree to which the investigative effort is faulty—and despite the resolve of the defense—the jury arrives at an unfortunate conclusion.

VIGNETTE - Residential Effects and the FBI Crime Lab

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Mr. X arose from bed early one day, and went to work. Sometime later, one of his young nieces experienced painful urination. The child's mother, the sister of Mr. X, became hysterical and convinced herself that "something horrible must have happened". A few hours later, Mr. X's life was turned upside down. He was arrested in front of his co-workers.

The reporting FBI Crime Lab analyst found a DNA mixture profile on a pair of shorts collected from Mr. X's bedroom. The major DNA contributor to this mixture was Mr. X himself. The minor DNA profile on the shorts may have been from the child in question, or perhaps from her sister.

The household, which was owned by Mr. X's sister and her husband, was a mess. Mr. X fit right in as he too, was quite untidy. He frequently wore those same shorts, over-and-over, and he rarely washed them. It is notable that Mr. X was routinely asked to babysit his nieces/nephews in his downstairs bedroom. When he was left to watch the children, Mr. X would recline in his messy room with the kids, watching TV, playing video games, and consuming snacks.

The FBI lab analyst also reported a PSA positive test on a sample from the child's underpants. In an attempt to confirm this presumptive positive test, the

analyst collected more material from the underpants. However, this did not lead to the detection of a single sperm cell. The FBI analyst had to admit at trial that ***zero*** sperm cells and ***zero*** DNA from Mr. X was found on the child's underpants.

Mr. X sat in jail for nearly 2 years the before the trial. When it was finally over, the jury deliberated for less than two hours and found him "Not Guilty".

VIGNETTE - Residential Effects and Domain Irrelevant Information

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). A similar series of allegations surfaced in another case involving ***residential effects***. Here again, the prosecution team was able to claim "We have DNA, so, he must be guilty." Despite the fact that DNA was indeed observed, the reporting crime lab analyst offered only warped scientific interpretations. Fortunately, in the case described below, the defense team effectively illuminated the distinctions between fact and speculation.[185]

After a protracted on-and-off, hot-and-cold courtship, Mr. F and Mrs. F, decided to get married. Upon agreeing to the marriage, Mr. F had rescued his new bride and her daughter from a life bordering on poverty. After the wedding ceremony, Mr. F became the legal step-father to his 8-year-old stepdaughter. To most observers, Mr. F seemed to be maintaining an affable, appropriate stepfather/stepdaughter relationship with the child.

A number of weeks after the wedding, the stepdaughter voiced allegations that Mr. F entered her bedroom and forced her to perform oral sex on him. The child also alleged that, after Mr. F ejaculated into her mouth, she spat the ejaculate onto the floor near her bed. The State's team obtained warrants and when crime scene technicians visited Mr. F's stately home, they utilized a special, multi-wavelength analytical "crime scope". The investigators collected a substantial section of the bedroom carpet, with various marked areas of staining.

Once this section of carpet reached the crime lab, the evidence was further scrutinized, utilizing a similar crime scope. The analyst assigned to the case tested a variety of carpet areas with a presumptive semen test. Awhile after the investigators took the carpet from Mr. F's home, they discovered the defendant's extensive rental history of movies featuring young-girl-oral-sex themes. The prosecution then assembled a large team of investigators, litigators, forensic laboratory personnel, and Children's Advocacy Center interviewers, trainers and therapists.

Having collected the carpet, the semen and the video rental history, the State's team believed they had a rock solid case. Although various tests were available for the detection of saliva, no such analysis was conducted on any area of the carpet. Regardless of the preliminary tests, or the lack of certain tests, the lab was undoubtedly able to locate semen on the carpet. That semen was conclusively typed to Mr. F. This semen was, in some instances, mixed with an extremely low level of

DNA originating from a female source. Initially, the crime lab compared this minor, partial DNA profile only to the 8-year-old female child. The lab report concluded that they could not rule out the possible presence of DNA from the child.

As devastating as the above-described synopsis might seem on the surface, there were three glaring flaws in these observations. The flaws were as follows:

1) The extremely weak female DNA profile, with similarities to the child, were found in the room where that same child lived, slept, walked, talked, played, coughed, and sneezed.

2) A single drop of saliva contains about 500,000 salivary epithelial cells. With that in mind, note that only a few hundred cells are needed for a complete DNA profile. It is hardly compelling that only a partial profile was achieved.

3) Mrs. F, the biological mother of the child, lived in the same home, but was not initially typed for DNA, for comparative purposes with the carpet samples.

Two months after the finding of Mr. F's semen and the DNA mixtures in the young girl's room, statements emerged that, on more than one occasion, witnesses were aware that Mr. F and Mrs. F had engaged in sexual activity in the child's bedroom. The crime lab analyst finally typed Mrs. F for her DNA profile. Four additional months elapsed before the crime lab ***finally*** issued a report, revealing that the minor, partial DNA profile could have actually originated from either the

mother or the child. Curiously, while the initial crime lab report referred to the child by her actual name as a possible contributor to the carpet stains, the lab's subsequent report listed the potential DNA mixture of contributors as "…the victim, Mr. F, and Mrs. F".

Apparently, the crime lab was weighing in with a verdict. Perhaps the crime lab members of this large prosecution team were influenced by domain irrelevant information such as the video rental history. The defense DNA expert pointed out that a few of the alleles found in the mixture could not have originated from the 8-year-old child, but were consistent with Mrs. F, the mother of the child. After 6 hours of deliberation, the jury found Mr. F. "Not Guilty".

"THE UGLY" - FOOLS - FRAUD - and the FBI

Approximately 2.3 million persons in the United States; 84,000 persons in the U.K.; 40,000 persons in Canada and 43,000 persons in Australia are incarcerated in jails and prisons.[186] If only one out of every 100 of these cases involves disputable biological/DNA interpretations, this translates into approximately 25,000 problematic cases.

Since the mid-1990s, television and news reports have provided a number of accounts regarding gross negligence, scientific misconduct, and fraud in forensic laboratories.[187] The instances of misconduct often involve forensic biologists who

skew the scientific findings, in order to make them more consistent with what the analyst 'hopes' to be true. Certainly, bias can develop into scientific misconduct, when analysts begin suppressing or misrepresenting their findings. Investigators looking into the Houston Police Department Crime Laboratory, found many instances of this type of misrepresentation.[188] The Las Vegas, Nevada lab was found to have numerous problems as well.[189] A number of cases at the Victoria Police Forensic Services Centre in Melbourne have shown cross-contamination of samples causing false cold hits. Two of those cases led to false convictions.[190] There have also been a number of dishonest serology and DNA analysts who have been responsible for serious miscarriages of justice.

For example, Thompson reports that in Virginia, Earl Washington, Jr. was falsely convicted of capital murder and came within hours of execution when post-conviction DNA testing contradicted DNA tests on the same samples performed earlier by the State Division of Forensic Sciences. In this case, an independent laboratory investigation found that the state lab had botched the analysis of the case, failing to follow proper procedures and misinterpreting its own test results.[191]

Garrett and Neufeld report that in the Texas case of Josiah Sutton, the victim had been raped by two men in the back seat of her car. The investigators found semen in the vaginal swab taken during a rape exam and on a stain removed from the back seat where the rape occurred. Unfortunately for all concerned, the report

authored by the Houston Police Department Crime Laboratory and the trial testimony of laboratory analyst, Christy Kim, presented invalid DNA results.[192] Garrett and Neufeld report that the raw data and the analyst's bench notes indicated that the vaginal sample reflected a mixture of the victim's DNA, as well as DNA from two male donors. However, the semen stain on the car seat suggested it came from a single source of male DNA. That lone male could not have been Sutton.[193] Garrett and Neufeld make the point that, making matters worse for Mr. Sutton, at trial, Kim presented no statistics but gave testimony that implied uniqueness for each DNA pattern. The analyst testified that Mr. Sutton's DNA pattern was detected in the evidentiary samples. The jury was left with the mistaken impression that the DNA evidence uniquely identified Sutton as the rapist.[194]

The Texas case of Timothy Durham provides additional fodder for the litigator of DNA expertise. In this matter, Mr. Durham was accused of raping a young girl in Oklahoma City. At his trial, Durham produced eleven alibi witnesses, including his parents, who all testified that he was with them attending a skeet-shooting competition in Dallas at the time when the rape occurred. Durham also produced credit-card receipts for purchases he made in Dallas on that day. But the prosecution had something stronger: the young victim's identification and DNA evidence. Durham was convicted and sentenced to 3,000 years in prison.[195]

Dogged determination, and a family who could afford a competent defense, found that a portion of the incriminating evidence was still available. The new DNA analysis not only excluded him as the source of the semen found on the victim, but also showed that the previous DNA test had been misinterpreted.[196]

The competent litigator will use these case histories to better understand how to confront the ugly reality of misconduct and misrepresentation. It happens all too frequently. Here are some more recent examples:

VIGNETTE - A Failure to Explore DNA from a Presumed Getaway Vehicle

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Near midnight, a sheriff's department officer, Deputy C, was on patrol in a mountainous area a few miles outside of a city. The deputy was tragically and mysteriously shot dead at close range, several feet away from his police car. The assumption was that Deputy C was killed by the driver of a vehicle, corresponding to the deputy's last license plate call to the dispatch operator. Investigators tracked down the current owner of the vehicle, Mr. V. This made sense as law enforcement officials were keenly aware that Mr. V was wanted for questioning on various other matters, including another homicide. Adding fuel to the fire, Mr. V, upon hearing that the authorities were searching for him, attempted to evade the police. A highly-publicized manhunt resulted in his eventual capture.

The attention to the manhunt should not have diminished other aspects of the murder investigation. However, the facts of the case clearly suggest that this may have occurred. Once Mr. V's gold 1991 pickup truck was located, it received less attention than it deserved. The investigative hypothesis was that Deputy C, first called in the license number to the dispatch operator, then the deputy signaled Mr. V to pull over, as Mr. V was driving the truck. When the license plate number came back with the name of an innocent, previous owner of the truck, the deputy exited his police car and walked alongside the vehicle, unaware that the person behind the wheel might present a threat to his safety. Investigators believe that when Deputy C approached the driver's side window, the driver rolled down the window, leaned out and shot the officer in the face with the muzzle of the firearm only 18-24 inches from the point of impact. Apparently, the investigative/forensic team conducted an examination of the outer/driver's side of Mr. V's pickup truck and detected virtually ***no*** evidence of blood. This analysis took place during the time that law enforcement was searching and seeking to capture Mr. V.

It is important to note that, when Deputy C called in to the dispatch operator with the license plate number from the pickup truck, he referred to the vehicle as "…a silver pick-up truck". It is also notable that a witness subsequently reported "…a silver or white truck" speeding away from the scene. Mr. V's 1991 pickup truck was not silver, …not white, …but gold. It is also notable that, years after the early

stages of the investigation, witnesses testified that during the precise time of the homicide, Mr. V was not driving around in the mountains, but was actually at a residence on the other side of the city.

The prosecution pursued the death penalty. On June 4, 2010, a jury found Mr. V guilty of first degree murder. Months later, in anticipation of the death penalty phase of the process, the defense team for Mr. V initiated added investigative steps. Independent forensic biologists examined Mr. V's gold 1991 pickup truck. This examination was exhaustive, front to rear, inside and out. Despite the fact that the scientists scrutinized every crack and crevice on the vehicle, and regardless of the remarkable sensitivity of state-of-the-art blood/DNA detection systems, not a speck of blood and no DNA from the murdered deputy could be found.

During the death penalty trial, the astonishing truth was revealed that Deputy C was not actually pulling over the vehicles corresponding to the license plates that he was calling in to the dispatch operator. A defense team investigator visited the owner of the vehicle that was called in immediately prior to the pickup truck license plate dispatch call. The owners of that small black sedan recalled that they were in their vehicle, at that precise location, around midnight, on the date of the murder. When asked about a traffic stop, the black sedan owners assured the investigator "No, we were not pulled over. But we remember hearing about the shooting incident on the news, the next day."

Audio dispatch records demonstrated that Deputy C called in Mr. V's license plate number, shortly after running the license plate corresponding to the small black sedan. A brief time after that, the audio dispatch recording clearly revealed the deputy's voice as he returned to his radio. Deputy C announced: ***"10-8"***. In police code, "10-8" notifies the dispatch operator that the officer is back ***"In-service"***.

Keep in mind that Deputy C was shot at close range—only inches from the vehicle. In light of the conspicuous absence of biological material/DNA on Mr. V's gold 1991 pickup truck, a scientific observer might consider the hypothesis that the truck was never anywhere near the scene of this homicide. Consider that the license plate from Mr. V's truck could have been removed and placed onto a different vehicle, perhaps justifying the previously mentioned reports of a "silver or white pickup truck". Lastly, consider that, after the homicide, the driver of this unknown silver/white vehicle returned to Mr. V's gold pickup truck, and put the license plate back where it belonged. Interestingly, when law enforcement investigators found Mr. V's gold 1991 truck, the license plate was located inside the truck cab, inserted into the interior back window molding of the vehicle. Both Mr. V and his spouse (the primary driver of the gold truck) recall that the license plate was always attached at the traditional location, bolted onto the center of the back bumper.

Based upon the above-outlined hypothesis, the defense forensic biologists carefully removed the license plate from the window molding and

collected evidence swab samples from its surface. DNA typing from these sample swabs revealed the presence of eleven alleles. This incomplete DNA profile was a mixture of at least two unknown individuals. Both Mr. V and Deputy C were excluded as possible contributors to this DNA mixture.

Consider the hypothesis that Deputy C and the other witness were mistaken about the color of the pickup truck. Consider that the getaway vehicle from the scene of the homicide was indeed Mr. V's gold 1991 pickup truck, not a silver truck, and not a white truck. Perhaps, in the dark of night, similar vehicle colors are too difficult to distinguish with accuracy. With this assumption in mind, around midnight on the night of the incident, the weather was cold. Light snow flurries were beginning to accumulate in the mountain area outside of the city. Imagine an individual driving the gold 1991 truck, as it was pulled over by Deputy C. As the officer approached along the driver's side of the pickup truck, the murderer needed to roll down the window of the vehicle. Note that this particular gold 1991 pickup truck has no power windows, only a manual crank knob. The perpetrator's next step would be to lean out and fire his weapon at the victim.

As the killer speeds away from the scene, he may choose to let volumes of cold, midnight air rush into the cab of the pickup truck. Logic dictates that the killer would feel compelled to again grasp the window control knob and crank the window shut. Based on this hypothesis, an evidence swab sample was collected from the

surface of that driver's side window crank knob. DNA typing from this sample revealed the presence of seven alleles. Again, both Mr. V and Deputy C were excluded as possible contributors to this partial DNA profile. The death penalty phase jury sentenced Mr. V to life in prison, rather than the death penalty. Various jurors cited their doubts that Mr. V had committed the homicide in the first place.

VIGNETTE - Failure to Explore DNA from A Murder Weapon

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). One would presume that no homicide case evidence item could be more important than the actual weapon used to commit the crime. The following two cases cast some doubt on this notion.

Many years ago, a wealthy businessman, Mr. E, was killed by a remote-detonated explosive device. Both the defense and the prosecution agreed on the nature of the murder weapon. It was also agreed that fragments from the explosive device could be important components for identifying the bomber. The defense argued that Mr. E's death was a consequence of a revenge-motivated professional hit, possibly involving organized criminals.

In contrast to this hypothesis, the prosecution took Mr. E's ex-wife to trial for conspiracy to commit murder. It seems that the former Mrs. D had benefitted from a $2 million life insurance policy on her ex-spouse. Although both sides agreed that

the former Mrs. D was at least 800 miles away at the time of the bombing incident, the prosecution presented evidence that Mrs. D may have utilized a male accomplice to set up the deadly device. Prosecutors were able to convince jurors to disregard DNA results recovered from remnants of material from the bomb. Despite the fact that the prosecution's presumed male accomplice had virtually zero experience with explosives, and was equally clueless regarding remote control technology, juries convicted both of the accused individuals for their presumed roles in conspiracy and murder. Most compelling, DNA from the explosive device parts implicated a person who, to this day, remains unidentified, and excluded DNA typing data from the convicted accomplice.

VIGNETTE - Failure to explore DNA from yet another murder weapon

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). A tragic quintuple homicide occurred in one of the most brutal crimes in the history of a major U.S. city. Mr. W was accused of beating his entire family to death with a metal pipe. Mr. W consistently maintained his innocence. Both the defense and the prosecution agreed on the identity of the murder weapon. Although the city crime lab analyst boasted on the witness stand, regarding the astonishing sensitivity of DNA technology for the detection of trace genetic material, the business end of the metal pipe was never tested.

Results showing a variety of mixtures of blood from the victims were indeed

reported on one end of the metal pipe. However, the question of "Who was killed?" had already been answered by the five dead bodies at the residence. The vital question was: "Who gripped the metal pipe, in order to beat those five people to death?"

That vital question was inexplicably disregarded by the so-called 'scientists' at the city police laboratory. Not surprisingly, that same city police facility at all levels, has since been permanently mothballed, as a consequence of sloppy work and egregious procedural errors. The multi-discipline shutdown of the entire forensic facility took place only three years and nine months after Mr. W. was convicted and sentenced to life in prison without parole.

The improperly tested murder weapon—the metal pipe, is now in storage within a state police facility. Interestingly, state police authorities and the prosecution have brazenly evaded inquiries regarding the precise location of this crucial evidence item. This activity effectively avoids further testing of the 'handling DNA', which could reverse Mr. W's conviction and 'embarrass' individuals working within the state criminal justice system.

VIGNETTE - Residential Effects in a Bungled Investigation

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). Mr. Z was the victim of a ***residential effects***

accusation. He lived in a humble mobile home with his wife, their one-year old son, and his wife's three daughters from a previous marriage. One evening, Mr. Z broke his wife's rules by arriving at home in an intoxicated condition. After a few unpleasant exchanges, Mr. Z retired to bed. Some amount of time later, his bed was being kicked by somebody. To his surprise, it turned out to be a local police officer. As Mr. Z was loaded into a squad car, he noticed that one of his stepdaughters was being escorted away to a hospital for a sexual assault examination.

No hint of semen could be found on: a vaginal swab, a vaginal slide, an oral swab, an oral slide, an anal swab, an anal slide, or a swab from a pair of underpants, all collected from the young stepdaughter. DNA testing of the same samples showed the presence of only the young female's DNA, nothing else. The only exception was the underpants. Although no semen was detected on any of the surfaces of the underpants, a DNA mixture was reported. The majority of the DNA in the mixture was from the young female. There was a 32.7 to 1 ratio of female DNA to male DNA on the swab from the underpants. Thus, this scientific information provided to the prosecution was, by itself, acceptable. However, the interpretation of those data was warped, beyond all standards of scientific logic.

DNA reference profiles, for comparison to the DNA mixture results from the underpants, were determined only from Mr. Z and from the young female. No genetic information was ever gathered from the mother of the four children, the

young girl's two female siblings, or most important, the one-year old half-brother. It is vital to emphasize that this toddler was the biological son of Mr. Z. Not testing this male child's DNA was a catastrophic oversight on the part of the investigative team. Less than 2 billionths of a gram of male DNA was found on these underpants.

Picture the young female complainant, in the confined environment of a small, cluttered mobile home, often clad in little more than a pair of underpants and a tee shirt. Imagine her wrestling around and playing with her one-year old male sibling. Imagine this youngest member of the household, a toddler, and his many daily encounters with saliva-caked toys, snacks, sippy cups, and every other intriguing item he could get his hands on. Also, try to picture the toddler's lingering encounters with respiratory infections. Now, revisit the fact that no responsible individual, associated with this investigation, bothered to test the boy for his DNA profile.

Most profound, note the astounding fact that a portion of the male DNA profile detected on the young girl's underpants could not have originated from either Mr. Z, or his one-year old male child. Detection of DNA from an unknown male upon such a disturbing location, on the underpants of the alleged victim, emphasized numerous inescapable facts. An unknown male, perhaps five-years-old, or perhaps eighty-five years old, had—at some point in time—ventured into the mobile home. Once inside the home, a source of DNA from this mysterious male somehow ended up on the surface of the underpants worn by the young female complainant.

Tragically, the trier of fact never knew whether the 2 billionths of a gram of male DNA originated from Mr. Z, or his toddler son. The prosecution shrugged off these facts as "irrelevant" and enthusiastically forged ahead with the poorly-conceived case. Mr. Z was found guilty and sentenced to 18 years in prison.

The Tendency of Jurors to Harbor Unrealistic Confidence in Crime Labs

At the beginning of this chapter, litigators were warned that many prospective jurors embrace a media-driven, preconceived concept that forensic biology is flawless. Even some of the crime lab scientists themselves believe that, when DNA technology generates results that appear 'miraculous', those data should be considered immune to criticism. The driving force behind this atmosphere of overconfidence begins, for example, with the fact that most contamination events and other laboratory errors take place without the reporting scientist having any knowledge of any 'red flags', in the first place. When a forensic DNA consultant, brought in by the defense, is asked to review the forensic biology discovery documents, indications of game-changing errors and misinterpretations may not be transparently ***advertised*** by the reporting crime lab analyst.

The following case example illustrates the incidence of inadvertent, undetected errors, and the peril associated with the rationalization that 'red flags' are absent—and thus, mistakes are impossible.

VIGNETTE - When the 'Miracle' Is Simply a Contamination Event

(Note: The identities of individuals involved in this case and the geographic locations have been kept confidential). In 1980, Ms. X was having some renovations done on her home. During this period, she was staying in a small trailer, which was located in a position adjacent to her main residential structure. When neighbors realized that they had not seen Ms. X enter or exit her trailer for quite a few days, they became concerned and notified law enforcement. The poor woman had been dead for an unknown number of days.

There appeared to have been some kind of scuffle in the tiny trailer. However, limited evidence of blood was observed. The victim was naked, lying on the floor, with her robe positioned nearby. She had been strangled to death. According to the medical examination/investigation team, there was no indication of any sexual component to the homicide. Over the many months to come, a significant number of potential male suspects were questioned and scrutinized. All of those men were eventually discounted as potential primary suspects. One of those initial suspects was Mr. J.

Thirty-three years later, in 2013, the police decided to reopen Ms. X's homicide investigation, as a cold case. It was somehow decided that Mr. J should be considered as a particularly viable suspect. In 1980, Mr. J had been working to renovate the bathroom in the main residential structure owned by Ms. X. The new

law enforcement team speculated that Mr. J could have entered the woman's small trailer and killed her as a consequence of an argument, or perhaps an attempted robbery. All agreed that, due to the lack of evidence of any sexual assault, the genuine motive was uncertain.

A DNA standard saliva sample was collected from Mr. J, and delivered to the local crime laboratory. This extremely DNA-rich known sample was handled and processed, along with various 33-year-old crime scene evidence items, which were also out and about in the lab for the purpose of analysis. Testimony established that Mr. J's freshly-collected standard—was in the hands of the ***very same analyst*** who had also removed the much older evidence items from storage, on the ***very same day***.

During testimony, the analyst admitted that, in the recent past, the reporting crime lab did occasionally experience contamination events. However, the analyst emphatically insisted that the Mr. J/Ms. X case was handled without any issues. This testimony included a claim that all of the negative control blanks tested clean—free of any unwanted sources of DNA. The analyst also testified regarding the foundation of the prosecution's case, ***a single, thirty-three year old hair root.***

Ms. X's medical examiner, at the 1980 autopsy, noted two hairs in the vicinity of the woman's thigh/pubic area. It was uncertain whether or not these hairs had originated from the victim. Both hairs were placed into the same airtight glass vial. Although this attempt at preservation was entirely inappropriate for DNA, in 1980,

there was virtually no such thing as DNA typing. Thus, there were no training standards for proper handling and storage.

Even with DNA typing being developed in the 1990s, and proceeding to today's vastly more sophisticated level, it is not possible to successfully obtain an STR typing profile from any part of any hair, except for the root, where the hair follicle is attached at and beneath the surface of the skin. Mitochondrial DNA typing can be achieved from the 'shaft' of a human hair. However, that technology was never used during the course of Ms. X's homicide investigation.

STR-based DNA typing offered extremely unusual data from ***one*** of the two hairs collected from Ms. X's thigh/pubic area. The result was a DNA mixture from at least two individuals. The diligent scientist should pause here and consider the obvious, perplexing question. How might one achieve a DNA mixture from the root of a single hair? Recall that the majority of any hair root exists below the surface of the skin. Regardless of this bizarre observation of a DNA mixture on a single, 33-year-old hair root, a comparison to the known DNA profile from Mr. J yielded a 'miraculous' result. The analyst observed a pristine, full, matching DNA profile to the accused man. The remaining remnants of degraded allelic information within this hair root DNA mixture showed some consistency with Ms. X. However, those data were not suitable for any reliable scientific conclusions.

Interestingly, the second hair from the glass vial provided nothing beyond the expected, uninterpretable DNA data. Only a few, weak allelic signals were observed, presumably as a consequence of enzymatic DNA degradation, occurring over the course of the 33-year storage period. This observation unveils another disturbing question, which is as follows: If the DNA on ***one*** hair root suffers severe degradation during long-term storage, can the DNA from a ***second*** hair root—stored millimeters apart from the ***first*** hair root, under identical conditions in the same glass vial—provide a pristine DNA profile? Before attempting to answer that, the diligent scientist must also consider that within the very same ***first*** hair root, the DNA from Ms. X was heavily degraded, whereas the DNA from Mr. J. allegedly survived the 33-year storage period—miraculously intact. These observations defy the Laws of Thermodynamics, as they apply to biological systems and enzymatic reactions.[197]

Hair roots, even from human hairs that have been subjected to an extremely brief storage period, are notoriously pitiful sources for DNA recovery. This fact is thoroughly discussed in the literature, but may be most clearly established in a 2013 publication released by Australian researchers—with contributions from the Australian Federal Police.[198] In this publication, the authors report that about two-thirds of the STR-tested telogen hairs[199] provided ***zero*** callable alleles.

From 998 hairs analyzed in the Australian study, not a single DNA mixture was observed. In addition to the fact that the reporting analyst in the Mr. J/Ms. X

homicide case alleged legitimate recovery of a ***DNA mixture*** from the 33-year old evidentiary hair, the total DNA yield was claimed to be 18 nanograms. Adding to this outlandishly peculiar scientific scenario, a closer look at the DNA quantification data revealed that approximately 70% of the DNA was derived from a female source, whereas only 30% could be accounted for by a male source. Yet another question emerges: If these estimates were reliable and accurate, how could the female fraction of the DNA appear so degraded, whereas 30% of the genetic material from the hair root provided an immaculate, full male DNA profile—implicating Mr. J? The analyst responded to this puzzle by testifying that the real-time PCR process used to quantify female:male DNA ratios is prone to substantial inaccuracies.

In reality, the real-time PCR process did indeed estimate a total DNA yield of 18 nanograms. This yield translates into a starting estimated total of 3,600 DNA-containing cells. The prosecution team was confronted with the question of how all of these cells, from two different people, could remain for 33 years, within a few millimeters, along a single hair root. Interestingly they responded, as the case entered into the trial, by changing their theory—as to how/why the crime was committed.

Suddenly, the thinly-veiled suggestion emerged. The assault/strangulation may have included a sexual component, after all. This shift in strategy raised ***yet another*** perplexing question. In the event of suspected sexual activity associated this homicide, and the presumed presence of saliva or semen, where were the crime lab

tests for these body fluids? Furthermore, in the event that the crime lab analyst chose not to risk consumption of any material from the hair root, where were the results from microscopic analysis of the alleged 3,600 cells attached at this hair root? No such body fluid tests or microscopic observations were ever provided to the jurors.

In 1980, when the medical examiner collected the two hairs in one glass vial, he also collected a sample of blood from Ms. X, and placed that blood into a similar, sealed glass vial. The reporting analyst testified that bench notes were recorded, at the time of handling and processing that vial of blood from the victim. As soon as the screw cap was loosened on the vial, a horrible odor was released. This was the unmistakably foul stench that comes with decomposition of human cells or tissue. Upon closer observation of the contents within this glass vial, the analyst realized that there was little or no liquid present. Instead, there was only a smelly, disgusting blood clot. The analyst testified that it was immediately apparent that ***zero*** DNA would ever be recovered from this 33-year-old blood sample, as a result of severe degradation. Thus, the analyst did not even bother to attempt recovering any DNA.

Please recall that every drop of human blood contains approximately 400,000 DNA-containing white blood cells. If such a vial, filled with countless drops, untold millions of cells, becomes worthless after 33-years of storage, how is it possible for any scientist to achieve a miraculous ***18 nanogram DNA yield*** from a single hair root, stored for the identical amount of time, in a similar, sealed glass tube?

The genuine answer to all of these disturbing questions is simple. It is enormously improbable that the DNA matching Mr. J was anything other than a contamination event—a laboratory error. This contamination event occurred within the reporting law enforcement facility, as the 'fresh' reference standard from Mr. J was handled by the same analyst on the same day as the vial containing the two hair samples—collected during the 1980 autopsy. The defendant was simply ***not*** present at the 1980 crime scene. Unfortunately, the defendant was convicted of the homicide, and sentenced to live out the remainder of his life in prison.

From Incompetence to outright Fraud

Every litigator seeking to be prepared for a DNA expert's cross-examination should be mindful of the rogues of serology and DNA analysis. It is understandable when a scientist commits an error, and seeks to rectify the problem. The following are examples of pure treachery in crime labs:

Jacqueline Blake and the FBI

Jacqueline Blake had a long career with the FBI Crime Lab.[200] There were numerous indications that something was wrong, but it seems these signs of trouble caused little concern, among her FBI supervisors. The first indications of problems with Blake occurred in 1991, and again, in June 1994. She received an overall job rating of "Unsatisfactory". Her performance appraisal stated that her "examinations

are not conducted according to acceptable laboratory practices," and that she generated false positive serology testing results during proficiency testing and "inaccurate documentation of examinations conducted for blood and semen." Nevertheless she was promoted to the GS-11 grade level in 1996 and promoted again to the position of GS-12 Biologist in April 1998.

Ms. Blake took 6 months to complete the PCR training course; approximately 2 months longer than average. Her instructor noted that she seemed to have a difficult time with simple math. When left on her own to process crime scene DNA materials, she prepared extraction blanks along with other samples and recorded the creation of these samples in her notes. According to the investigation into her conduct by the Office of the Inspector General (OIG), from 2000 to 2002 she failed to process the negative controls in 90 out of 92 cases where DNA was detected on the evidence.

Blake's misconduct was not discovered by the FBI until April 8, 2002. She initially denied omitting any negative controls, even though it appeared that she had routinely thrown out the portion of DNA evidence samples that might have contained contamination, prior to sending the samples through the computer-operated genetic analyzer.

When confronted, Blake left the FBI's building and did not report to the laboratory again for work. Believing that Blake was an untrustworthy employee, who manipulated the FBI's procedures and lied about her conduct, an OIG attorney

and an investigator interviewed Blake at her home. Blake admitted that she knew that she was not processing the negative controls that were required by the protocols. She also revealed that she knew she was misrepresenting the status of the negative control samples when she did not properly prepare them for injection into the DNA typing instrument. Regardless of this, she initialed the related injection worksheet.

Ms. Blake explained to the OIG that she wanted her cases to run smoothly and show no hints of contamination. The OIG investigation concluded that Blake was a sophisticated, calculated, and cunning liar. She was clever enough to experiment with her technique in the PCR training program—perhaps to determine if anyone would detect her deception. As Blake has stated to OIG investigators, she knowingly misrepresented her work in laboratory documents that she knew other DNA Unit employees would rely upon. The OIG determined that Ms. Blake's misconduct had rendered over two years of her STR work scientifically invalid and unsuitable for use in court.

In a May 27, 2004, announcement,[201] the FBI claimed that their laboratory "….detected discrepancies, within Blake's analysis, regarding the proper use of negative controls for DNA testing." But this self-serving announcement was less than forthright. The OIG report makes it clear that the discovery of Blake's misconduct was inadvertent. The report notes that Ms. Blake was not discovered earlier for two primary reasons: **1)** she was adept at lying to her supervisors; and

2) the DNA Unit had in place a shortsighted policy that failed to require Unit Examiners to routinely scrutinize GeneScan® data.

The OIG investigators were deeply concerned with the FBI Crime Lab's position that no additional inquiry was warranted on the cases handled by Ms. Blake, during her 12-year tenure as a serologist and RFLP technician. These concerns were primarily due to the fact that Blake's major failing was limited to her aversion to running STR negative controls. The FBI supervisors argued that there was no indication that Blake ever intended to manipulate test results. They asserted that any procedural controls in place in their lab would have detected any misconduct of that nature. However, the OIG investigators and attorneys were inclined to consider the totality of circumstances surrounding the actions of Ms. Blake—including her 1994 performance appraisal and training history. They emphasized that Blake had been confirmed as an untrustworthy employee, who manipulated the FBI DNA Unit's procedures, and doubled down, by lying about her conduct.

The FBI went further with their self-serving May 27, 2004, announcement, claiming that they conducted an "expeditious and thorough review." Again, the OIG investigators and attorneys expressed concerns, regarding the time it took to generate a sufficient notification letter to those affected by Ms. Blake's scientific fraud. The OIG documented the results of their analysis—stating that the FBI Crime Lab wasted nearly two years—beyond the discovery of Blake's misconduct. According to this

claim, there were still 42 cases within which the evidence contributors had not received a letter notifying them that Ms. Blake had failed to properly process the evidence that they submitted. Twenty of these contributors received no notification at all—regarding the status of their evidence. The OIG report made it clear that Blake's misconduct and the FBI Crime Lab's failure to respond to any red flags for over two years, has damaged the credibility of our nation's forensic DNA facility.

Ms. Blake plea-bargained to enter a guilty plea to criminal charges. Within her plea records, Blake admitted that, from approximately August 1999 to June 2002, she authored and submitted over 100 casework reports containing false statements regarding the DNA analysis she performed. Specifically, Blake admitted she had falsely certified that she properly completed several control tests, knowing that she had, in fact, neglected to perform them.[202]

Orchid Cellmark and Sarah Blair

Orchid-Cellmark is one of the world's largest private DNA testing laboratories. Cellmark does laboratory analysis for law enforcement agencies throughout the world and has worked on a number of prominent investigations, including the O.J. Simpson, Jon Benet Ramsey, and Unabomber cases. As a large private concern, Cellmark rarely allowed a look into their procedures or even disclosure of their electronic files in criminal cases.

Chemist Sarah Blair was hired by Cellmark in June 2002 and completed her training to perform independent testing on individual cases in November 2003. Sometime later, it was discovered that Blair electronically manipulated the analysis in at least 20 tests.[203] It seems that Blair had done independent work at the lab for many months and the internal peer review or quality control process thoroughly failed. **The lab was forced to admit that Blair had engaged in "professional misconduct" by improperly substituting control samples that are the scientific basis for comparison, with actual DNA evidence.**

Ms. Blair manipulated the computer files produced by the company's genetic analyzers, replacing the computerized results for problematic control samples with the results of "clean controls" from other cases. The Director of the Technical Forensic Services at the Cellmark lab where Blair worked wrote in a sworn affidavit that . . . "Blair was terminated when it was discovered that she substituted profiles from controls or allelic ladders *not associated with the particular case*, in place of a positive amplification control, negative amplification control, reagent blank control or allelic ladder, *which belonged with the case.*"

We will never know how many of Blair's cases resulted in false convictions. But we do know, as Thompson instructs, that Sarah Blair's misconduct might have been noticed earlier by independent analysts, had Orchid-Cellmark been more transparent about the details of their casework.[204]

Fred Zain - The Lying Chemist

Fred Zain was a West Virginia State Police forensic expert who testified in hundreds of criminal cases.[205] Over the years, Zain rose to the position of Chief of Serology at the West Virginia Department of Public Safety. His testimony helped convict hundreds of defendants across a dozen states. As he became a forensics "star," prosecutors who wanted to win convictions in difficult cases used him more and more frequently. Zain's stature in West Virginia, and his fame as an expert in serology/DNA analysis, led to an elevated job offer—as chief of physical evidence for the medical examiner in Bexar County, Texas.

Back in West Virginia, two fellow lab workers complained about Zain's bias against defendants. They informed their superiors that they had seen Zain record results from blank test plates. Kenneth Blake, the director of the West Virginia State Police Criminal Identification Bureau, admitted that he never questioned Zain's academic background, when recommending him for employment. Blake explained that he looked into the allegations voiced by the two lab colleagues and dismissed the issue as nothing more than an office squabble. "They didn't like Zain, and Zain didn't like them," Blake said at the time. A subsequent investigation into Mr. Zain's college transcripts revealed that he was a mediocre scholar who had failed organic chemistry. It also seems that no one reviewed the notes from Zain's alleged analysis, before qualifying him as an expert witness. Nobody scrutinized any of Zain's

academic transcripts or his lab notes until his house of cards came tumbling down.

Mr. Zain's work in West Virginia was discredited in 1993 by the state Supreme Court—which stated that Zain may have lied or fabricated evidence in dozens of rape and murder cases. When word of this review reached Texas, Zain was promptly terminated by Bexar County. It seems the review by the West Virginia Supreme Court also found that Zain was systematically faking scores of test findings in a 16-year career of cases. In many instances, innocent defendants were victimized, and the state was defrauded of justice. The West Virginia Supreme Court noted, after a review of 189 of Zain's cases, **''any testimony or documentary evidence offered by Zain at any time should be deemed invalid, unreliable and inadmissible.''** Subsequently West Virginia has paid at least $6.5 million to settle lawsuits by wrongfully convicted defendants.

In one of Zain's West Virginia cases, he testified regarding blood and other body-fluid evidence. Zain's statements helped to convict Glen Dale Woodall, a cemetery worker, of kidnapping and rape. At Mr. Woodall's trial, Zain testified that—based upon his scientific analysis of semen recovered from the victims—**"[t]he assailant's blood types ... were identical to Mr. Woodall's."** Glen Woodall was convicted and sentenced to a prison term of 203 to 335 years. His conviction was overturned in 1992 after he demanded a DNA test that contradicted Mr. Zain's expert testimony. Woodall sued the State of West Virginia for false imprisonment,

and received a $1 million settlement. It was this million dollar verdict that prompted the State's Supreme Court to look deeper into Mr. Zain's crime lab transgressions.

Another of Zain's notorious cases involved the conviction of Gilbert Alejandro in Texas. In that case, Zain testified that he had conducted DNA testing and obtained results inculpating Alejandro. Mr. Zain told the jury, **"the banding patterns that were identified from these items that you mentioned were identical to the banding patterns of Mr. Alejandro. As I stated in the report, they could only have originated from him."**[206] Interestingly, Zain offered no random match criteria for this alleged DNA inclusion. He falsely testified to the jury that **"DNA typing is a hundred percent identity as to whether a blood or body fluid may have originated from a particular donor or not."**[207] A subsequent internal laboratory inquiry concluded that Zain had—at best—compared only partial banding pattern results visually; later tests excluded Alejandro.[208] In 1998, Zain was charged in Hondo, Texas with aggravated perjury, evidence tampering, and fabrication connected to the 1990 rape conviction of Gilbert Alejandro.

The *State of West Virginia vs. William Harris* was another Zain case pursued by the West Virginia Public Defender's office. In the case against 17-year-old William Harris, Zain lied, telling the jury that the genetic markers in the semen left by the assailant matched those of Harris and only 5.9 percent of the population. Subsequent DNA testing revealed that William was not the donor of the semen

involved in the rape. A detective in this same case was later convicted of perjury.

In West Virginia and Texas, criminal charges were brought against Fred Zain in 2001, after seven convictions relying on his testimony were overturned as a result of challenges. Millions of dollars in settlements were paid to those who complained of deliberate injustice in the two states. In a Texas case involving a convicted axe murderer, Mr. Zain invoked his Fifth Amendment right against compelled self-incrimination. The cause for this was that Zain was questioned, regarding the finding of a defense expert, that the ax had actually never been tested for blood. This finding contradicted Zain's previous testimony that the axe bore conclusive blood evidence. In 2002, Fred Zain died of colon cancer. This occurred before any criminal cases could be concluded against the lying chemist.[209]

Pamela Fish and the Chicago Police Department Crime Laboratory

For years, Pamela Fish was a star analyst for the Chicago Police Department Crime Lab. Later, she was equally notorious with the Illinois State Police Crime Lab.[210] Over the years, Ms. Fish rose through the ranks within the Chicago lab. Later in her career, she was promoted to oversee the serology section, and eventually the biochemistry section—within the State Police facility. Fish obtained her doctorate in biology from the Illinois Institute of Technology and became the training coordinator for the state police lab's DNA section. Throughout the course of her career, she testified at trials and hearings, on approximately one hundred occasions.

In the early 1990's, some very unusual assaults began to occur in the Chicago area. Dubbed the "beauty shop rapist" a man would arrive at a salon, have his hair done and then pull out a gun. He would herd customers and staff into a room and pick out a woman to attack on the premises. After he left one beauty shop, a victim caught his semen on a toilet paper wrapper.

John Willis, a man from the Arkansas delta area, had never finished the fourth grade. He was arrested and charged with the series of beauty shop assaults. Willis could barely read or write, and grew up chopping and picking cotton, instead of going to school. Despite the beliefs of the police investigators, Willis knew that he was innocent. "I didn't be quiet," stated Willis. "I jumped up and I started screaming. . . . I kept hollering about the DNA".

In a sworn deposition, Willis insisted as follows: "I knew it would free me because I hadn't did nothing." But gaining approval of DNA testing did not turn out to be easy. At the time, serology, which analyzed blood types, was the primary tool used in Chicago sexual assault cases. Pamela Fish, the scientist in charge of the police department's serology unit, was their "star witness".

Before trial, Willis' defense attorney made a standard request for documents. The defense team received Fish's typewritten lab report. At Willis' trial, Dr. Fish took the witness stand and told the jury that the serology tests were inconclusive. Thanks to the intensive and suggestive interviews of the Chicago police, victims

identified Willis as their attacker. Willis was convicted and sentenced to 100 years.

It seems that while awaiting trial, Willis learned about DNA analysis from television, and insisted that he would be proven innocent, if only he could be tested. In fact, Willis discovered who the actual rapist was. While Willis was in the Chicago jail, fellow inmates informed him that a man named Dennis McGruder had been arrested on rape charges. Added to that, McGruder's sexual assaults bore a striking resemblance to the crimes for which Willis was serving time.

While Willis was languishing in prison, something very strange was happening in Chicago. The methods of the "beauty shop rapist" continued with a minor modification. The rapist changed his choice of crime scene to neighborhood bars in the very same area of the city as the beauty shop crimes.

Greg O'Reilly, from the Public Defender's office in Chicago, with assistance from volunteers with the Innocence Project, began to push the courts on Willis' behalf. In 1998, Willis' attorneys had a breakthrough. Responding to a subpoena specifically asking for the test results, a clerk in the Chicago crime lab sent a fax to the defense team. The fax included Dr. Fish's report, ***and her lab notes***. On a single sheet within that file, the defense team noticed a notation, apparently from Dr. Fish, revealing that she never did find Willis' blood type in semen recovered from the crime scene. This would have been a powerful piece of evidence for his defense. However, Dr. Fish kept it hidden and said nothing about it during the trial—seven

years earlier. Indeed, Willis' blood type was clearly ***different*** from the source of the semen. Willis had blood/semen type B, whereas the evidentiary sample was contributed by a man who was carrying the type A blood/semen marker.

The day after John Willis was released from prison, in February 1999, Chicago Tribune reporters noted that Dr. Pamela Fish was the guest speaker at an Illinois judge's seminar in Chicago. Her role: explaining DNA profiling and evidence to the jurists. A few weeks later, she was promoted to oversee biochemistry testing at the lab. The DNA tests ultimately secured by those representing Willis had excluded him. Those same tests nailed Dennis McGruder. How many women were raped by McGruder between the time he was set free from the Chicago jail, and his eventual guilty plea to the "Beauty Shop Rapist" charges?

Former defendants who had been exonerated by careful scientific testing, repeatedly sued Dr. Fish and her crime laboratory employers. For example, Dr. Fish testified in the prosecution of four teenagers in the 1986 rape and murder of medical student, Lori Roscetti. After the trial and conviction of those four teenagers, a DNA expert, Dr. Ed Blake, assessed her testing, and concluded that she should have excluded all of the defendants. In a report for the defense, he called her testimony "scientific fraud." DNA testing later cleared all four men after they spent as much as 15 years in prison. After they were pardoned in 2002, Chicago police linked two other men to the murder. Both suspects gave videotaped re-enactments of the crime.

For years, Dr. Fish was the focus of criticism by defense attorneys and state legislators, because her testing was at the center of major wrongful conviction cases. In the summer of 2001, a state legislative committee holding hearings on prosecution misconduct questioned state police director Sam Nolen about Dr. Fish's work. At the time, State Representative James Durkin (R-Westchester) urged Nolen to transfer Dr. Fish—due to the questions regarding her faulty analysis. Instead, lab management relocated her into a research position, where she would no longer have a role in criminal casework. In 2004, after Willis settled his lawsuit against Chicago and Dr. Pamela Fish, her contract was not renewed. She left the agency.[211]

Joyce Gilchrist and the Death Penalty

Ura Alma Thompson, a 76-year-old woman, lived alone in an Oklahoma City apartment. On October 27, 1981, her nephew discovered her body. At first, her death appeared to have been from natural causes. However, the medical examiner ruled that it was a homicide after discovering bruises and evidence of rape. The police arrested Malcolm Rent Johnson and charged him with the crime. Although Johnson had a criminal record, he steadily maintained his innocence. At his trial, Oklahoma City police lab expert, Joyce Gilchrist, testified regarding six slides that she had examined. Gilchrist reported the presence of semen and hair matching Mr. Johnson. She also testified that Malcolm Johnson's blood type matched the sperm collected from a bedspread and a pillowcase in the victim's apartment. Despite his protests,

Ms. Gilchrist's testimony convinced the jury that Malcolm was at the crime scene.[212]

Oklahoma City defense attorney Douglas Parr offered that ''She was extremely important to the Oklahoma County district attorney's office . . . . She was one of their star witnesses.'' Indeed, concerning the trial and the prosecutor working the case, Oklahoma County district attorney, Robert H. Macy offered: ". . . Joyce Gilchrist gave him the testimony that firmly erased any reasonable doubt, any doubt at all in this case.'' Malcolm Rent Johnson was convicted of rape and murder and was executed by the State of Oklahoma on January 6th, 2000. However, Mr. Johnson was convicted on the basis of scientific evidence that never existed.

Despite complaints from her colleagues at the lab, Joyce Gilchrist was promoted. Various Oklahoma prosecutors used her work in thousands of cases, including 23 that resulted in sentences of death. Everything changed when a July 31, 2001, memorandum was reported by *The Daily Oklahoman* and *The Associated Press*. The memo, which was written by Laura Schile, an Oklahoma City Police Department chemist, made it clear that there was no sperm on those six slides. Schile's finding was endorsed by three other chemists in the laboratory. One of those chemists, Kyla Marshall, confirmed to the press that when the slides were retested, they revealed no sperm at all.

A few days after her release of the memo, Ms. Schile resigned because of what her lawyer described as a hostile work environment within the police department.

Soon after her resignation from the laboratory, Ms. Schile's memo prompted attorneys to call for investigations as Joyce Gilchrist, the Oklahoma City police "star witness", had aided the prosecution in roughly 1,200 cases. In fact, Mr. Johnson was one of 12 people who were put to death in Oklahoma, after Ms. Gilchrist's testimony helped convict them. Among all of the cases scrutinized by state officials, 99 were quickly singled out for further examination. These 99 included the cases of three death row inmates.

As the inquiry grew, larger laboratories were called in to review Gilchrist's work. The FBI found that she gave misleading testimony in five of eight cases. As the review of Gilchrist's work proceeded, Jeffrey Pierce, who was imprisoned for 15 years on a rape conviction, was released after DNA testing disproved Joyce Gilchrist's pivotal testimony against him. Malcolm Johnson wasn't that lucky.[213]

Recent developments in the forensic use of DNA.

It would be quite impractical to construct a section of this chapter—centering on the last few decades—with the objective of adequately illuminating the most influential developments in the utilization of DNA technology. Hundreds of crimes, and the resulting scientific investigations, could potentially be addressed here. Examples would be cases associated with the following suspects: Colin Pitchfork[214], Ron Williamson/Dennis Fritz[215], Kirk Bloodsworth[216], Timothy Cole[217], Kenneth Waters[218], O.J. Simpson[219], Timothy Spencer[220], Michael Morton[221], Glen Woodall[222], Tim Masters[223], Ray Crone[224], David Camm[225], Gary Ridgway[226], Amanda Knox[227], and of course, whoever killed JonBenét Ramsey[228]. The number and complexities of cases pertinent to DNA technology are beyond the scope of this chapter. As an alternative, the following five cases are the focus of this section:

The Lukis Anderson case: A 'perfect storm' for incidental DNA transfer.

Prior to midnight, on November 29, 2012, a group of men broke into a mansion located about 10 miles southwest of San Jose, California, in the quiet community of Monte Sereno. The owner of the mansion was 66-year-old Raveesh Kumra[229]. A successful Silicon Valley investor, Mr. Kumra lived in the home with his ex-wife, Harinder Kumra. The intruders tied up Raveesh, blindfolded him, and placed duct tape around his mouth/nose area. Harinder was struck in the face by one of the men. She was also tied up, and positioned next to Raveesh.

The brutal men ransacked the mansion for valuables, and eventually fled the scene. Shortly after the intruders were gone, Harinder managed to make her way to the kitchen phone, and dialed 9-1-1. When law enforcement officers and paramedics arrived, they realized that Raveesh was deceased. At the crime scene, it was noted that everything was in disarray. Dressers had been emptied, the refrigerator door was ajar, and a cell phone had been tossed into one of the toilets. The homicide victim, Raveesh, was on the floor near the kitchen. His body was transported to the morgue for an autopsy. The medical examination established that excessive duct tape had caused the man to suffocate. In addition to a thorough scouring, and the collection of over 100 potentially relevant items throughout the crime scene, fingernail samples were collected from the victim.

Among the first few rounds of evidence examination, a Santa Clara County

forensic analyst found various unknown DNA profiles. This included DNA results recovered from a pile of used, soapy, latex gloves, found in the kitchen sink at the mansion. DNA results were also found on a portion of the duct tape. A third DNA profile was recovered from those fingernail samples collected from Raveesh Kumra. When DNA profiles were compared to the CODIS database, there were three hits to known individuals. Those hits were 22-year old DeAngelo Austin, 21-year-old Javier Garcia, and from the fingernails samples, 26-year-old Lukis Anderson.

Three and a half weeks after the home invasion/homicide, Lukis Anderson was arrested and charged with murder. In the fall of 2012, Mr. Anderson was homeless, a hardcore alcoholic, and had lengthy record of petty criminal activity. Lukis spent the majority of his time intoxicated, wandering the streets of downtown San Jose, and hustling for spare change.

The investigation team found that it was not very challenging to build a solid case against Mr. Austin and Mr. Garcia. Both young men were suspected gang members—operating out of Oakland, California. Cell phone records from both Austin and Garcia demonstrated that—on the night of the homicide—their phones were connecting with cell towers located in close proximity to Monte Sereno.

Meanwhile, the case against Lukis Anderson was not developing very successfully at all. There were no clear connections with any gangs. There were also no supporting cell phone records for the night of the home invasion/homicide. It is

also notable that—many months after the initial DNA database hits, DNA from a fourth man, Marcellous Drummer, was also discovered on crime scene evidence.

After Lukis remained in jail for a number of weeks, his assigned public defender, Ms. Kelley Kulick, started to gain some traction, in an unexpected way. As a consequence of the fact that the homicide charge could readily develop into a death penalty case, Ms. Kulick asked a defense investigator to collect all medical records, pertaining to Mr. Anderson. This effort would include any documentation of mental health issues associated with the accused man. The records confirmed that Lukis was frequently admitted to various hospitals in Santa Clara County.

Ms. Kulick and the investigator found that—during one of his recent hospital stays—Lukis was transported in an ambulance, to the Santa Clara Valley Medical Center, in San Jose. His blood alcohol test results estimated that he must have consumed the equivalent of 21 beers. Lukis spent that entire night detoxing at the medical facility. Kelley Kulick and her investigator were baffled by the date of record for this 'detox event'—November 29, 2012. Lukis was not discharged until the morning of November 30th. If accurate, these records confirmed that Lukis Anderson was unconscious, in a hospital bed, a 20-minute drive northeast of Monte Sereno, California. The time frame of this detox event spanned long before, and long after the time frame of the home invasion, and the death of Raveesh Kumra.

Aware that the prosecution would justifiably have doubts regarding this

astonishing revelation, the defense team set out to make sure that the admission records were not somehow erroneous. Although the documents were signed and dated by members of the hospital staff, it was possible that some other person had stolen the identity from Mr. Anderson, or perhaps the detox treatment was for a different man—with the same name. It was also a remote possibility that the repeated documented references to November 29, 2012, were simply off, perhaps by one day.

The defense team carefully investigated every detailed move that Lukis made during that vital time frame. Their efforts revealed that—at 7:54 p.m.—a 7-Eleven clerk called a dispatcher, reporting that Lukis was panhandling near the store. By the time the police arrived, Lukis was gone. According to a clerk at the S&S Market, an intoxicated Lukis Anderson arrived and sat down in front of this establishment at about 8:15 p.m. Lukis was continuing to consume alcohol. About two hours later, the heavily intoxicated man stumbled into the S&S Market, and collapsed within one of the aisles. Shortly after this was reported, law enforcement officers were the first to arrive at the scene. A San Jose Fire Department truck, including their paramedic, arrived next—with more documentation of the incident being generated. Two other paramedics arrived in an ambulance. The paramedics placed Lukis onto a stretcher, and transported him to the Santa Clara Valley Medical Center. The hospital records confirmed that Mr. Anderson was admitted at 10:45 p.m. on November 29, 2012. Within the murder investigation records, Harinder Kumra established that the

murderers entered and ransacked her home between 11:30 p.m. and 1:30 a.m. Lukis had an air-tight alibi.

The Santa Clara County district attorney's office tried to sort out how the alibi could be so remarkably enduring, whereas the presence of DNA from Lukis was irrefutably in such an incriminating place. Upon reviewing how the crime lab handled the DNA evidence, there were no obvious indications of contamination risks. The investigative team found no indications that DNA from Lukis Anderson may have been a component of other cases that the crime lab had recently processed. Additional inquiries offered no indications of possible contact between Raveesh Kumra and Lukis Anderson during the days leading up to November 29, 2012. An instance of previous incidental contact could have explained how the DNA from Lukis ended up on the fingernails of a murder victim.

Ultimately, yet another careful review of the medical records finally unveiled a remarkable coincidence. There were two names—two paramedics—who administered aid to the nearly comatose Lukis Anderson at the S&S Market, in downtown San Jose. Three hours later, those same two names appeared again—on documents from the initial response at the Kumra homicide scene. Two paramedics were in close contact with Lukis Anderson, around 10:30 p.m. Not long after 1:30 a.m., those very same two paramedics were in close contact with the body of the murder victim, Raveesh Kumra. It is uncertain as to precisely how the contact with

the paramedics, their fingers, their uniforms, their medical instruments, vectored a 10-mile DNA transfer event from San Jose to Monte Sereno. However, no person with any credibility disputes the scientific fact of such an event.[230]

In a statement to a reporter with the *San Francisco Chronical*, Deputy District Attorney, Kevin Smith, hypothesized that this event "…had to be a freak accident." Experienced forensic DNA scientists might characterize the Lukis Anderson case circumstances more appropriately—pointing out the fact that there is no practical means of calculating the frequency or rarity of such events. ***We simply do not know.***

Joseph DeAngelo: The Golden State Killer.

During the 1970s and 1980s, the state of California was terrorized by over 100 burglaries, at least 50 sexual assaults, and thirteen brutal homicides—all committed by the same male individual[231]. The most disturbing aspect of this reign of terror was the shadowy, elusive nature of the perpetrator. Over the many years, law enforcement investigators had assessed over 8,000 possible suspects. As the remarkable identifying power of DNA typing continually evolved throughout the 1980s and beyond, a vast collection of case evidence accumulated. Regardless of their dedicated efforts, investigation teams were unable to connect the DNA results to any specific individual.

The landscape of the investigation began to change in 1994, when a man

named Paul Holes took it upon himself to begin searching for this elusive criminal—also known as the East Area Rapist. Detective Holes served as an investigator for the Contra Costa County District Attorney's Office. Due to the countless evidence items, there was no shortage of genetic material for comparisons against the DNA databases. However, in early 2017, when Detective Holes recognized that CODIS resources might never move his investigation forward, he began developing a remarkably innovative DNA strategy.

Rather than using STR results to compare against law enforcement DNA databases, crime scene sample results were compared to data from various ancestral DNA analysis websites. The turning point of this strategy was the investigation team's use of GEDMatch, a Florida-based website that sorts out DNA profiles from individuals who have chosen to upload and publicly share their genetic information. This approach led to the identification of pools of people who appeared to be interconnected to various family trees. To be clear, Detective Holes was pursuing the hypothesis that these ancestral DNA inquiries might identify a web of connections between various, 2nd cousins, 3rd cousins, and other related individuals, who might be genetically connected to that one individual for which he had been searching for over two decades—a hideous rapist/killer .

As the information accumulated, the investigators were faced with a myriad of old-fashioned, tedious law enforcement tasks. It became necessary to sift through

countless family tree members, and attempt to eliminate individual males who ***could not*** be the Golden State Killer. These elimination events were a consequence of various factors such as their ages, their residential locations over many years, and a complex pool of other circumstantial clues. After the extensive, game-changing ancestral DNA inquiries, and the painstaking sifting of related males, investigators spent another six weeks, examining a shortlist of potential suspects—males who could not be ruled out. One of those men was a former member of the police force in Auburn, California—a suburb of Sacramento. Investigators were eventually able to collect discarded material from this suspect. The man's DNA was clearly a match.

On April 24, 2018, Joseph DeAngelo, the East Area Rapist, the Golden State Killer, was captured and incarcerated. Less than a month earlier, Detective Holes had retired as a law enforcement investigator. Without a doubt, various layers of controversy are beginning to develop and unfold as a consequence of how genetic information was used to bring closure to this prolonged, difficult investigation.[232]

On April 1, 2007, a segment of ***CBS News-60 Minutes*** was broadcast, bearing the title: **"A Not So Perfect Match: How Near-DNA Matches Can Incriminate Relatives of Criminals."**[233] During this segment, Lesley Stahl pointed to the reality that searches of the DNA databases often fail to provide an exact match to the results at all of the genetic loci. However, the search process might unveil an unmistakable series of genetic similarities to a specific individual. While these comparative results

establish that this individual did not deposit DNA at the crime scene, the similarities provide a clue, which might lead to a close relative. ***60 minutes*** cited a study showing that 51% of state prison inmates have family members who are also incarcerated.

The issue at hand back in the year 2007, was: **"…should police start investigating those family members, or is that going too far?"** In the year 2018, a related question emerged: **"Should we direct some investigations toward the available genetic results housed on public databases, or is *that* going too far?"**

John Grega: An Innocent Husband.

On February 28, 2011, Michael J. Spence, Ph.D., had been working for three years as an independent consultant in forensic biology/DNA. He was contacted by Ian P. Carleton, an attorney located in Burlington, Vermont. During that initial call, Dr. Spence was asked to assist with a 1994 homicide case.

The client, Mr. John Grega, was accused, and later convicted, of the horrific beating, rape, and strangulation of his wife—Christine Grega. Throughout the entire investigative process, as well as his 18 years of incarceration, John Grega persistently maintained the fact that he was an innocent man. Dr. Spence was asked if he would be willing to examine the case documents, and provide an assessment in the form of an affidavit. The purpose would be to persuade the Windham County (Vermont) Court's approval of post-conviction DNA testing. Before agreeing,

Spence asked Mr. Carleton to explain the detailed circumstances of the homicide, the investigation, and the conviction. Mr. Carleton offered the description as follows:

John Grega, an educated man, was a partner in his father's window-washing business. John, his wife Christine, and their 2-year-old son, John Henry Grega Jr., lived in the Long Island town of Lake Grove, New York. The Grega's traveled to West Dover, Vermont, for a family vacation. On September 12, 1994, the Grega family was staying at a small condominium complex called Timber Creek. On that day, John decided to take his toddler son out to a local playground.

When John returned to the condo, his child was sound asleep in the backseat of the vehicle. Shortly after entering the residence, John found Christine, dead in the downstairs whirlpool bathtub.

After unsuccessfully attempting to revive Christine, John hurried next door to have the neighbors call an ambulance. Although John believed that Christine might have still been alive, the medical examiner later determined that the woman was already deceased—from asphyxiation. She had also been brutally assaulted. Her body showed signs of more than 100 distinct injuries, including irrefutable evidence of a sexual assault. The investigators and the prosecution fixated on the fact that there was no sign of forced entry into the condo. They theorized that John Grega—in fear that his wife intended to abandon an allegedly troubled marriage—killed his wife, and then left the condo with his son, in order to create an alibi.

John Grega had no criminal record. He had no history of mental illness, and no history of violence—sexual, or otherwise. There were no witnesses to the crime, and virtually no physical evidence was introduced at the trial. Regardless of these facts, and based upon nothing beyond a purely circumstantial case—John Grega was charged with Christine's murder. Less than a year later, on August 4, 1995, a jury convicted John Grega of aggravated murder and aggravated sexual assault. John became the first person ever, to be sentenced by the state of Vermont, to life in prison without any future opportunities for parole.

Upon assessing this case synopsis, Dr. Spence agreed with Mr. Carleton. There were questions left to be answered, regarding the scientific investigation of this case. Along with two other qualified scientists, Dr. Spence provided a careful examination of the various relevant forensic biology/DNA documents. Those scientists were Shelley Johnson, a DNA analysis Group Leader at Fairfax Identity Labs (Richmond, Virginia), and Steven Laken, Ph.D., CEO of Cephos Corporation (Tynsboro, Massachusetts).

On March 29, 2011, affidavits from the three scientists were provided to the Windham County Court. All three scientists agreed that there was an urgent need to utilize DNA technological resources—which were entirely unavailable in 1995. Such state-of-the-art tests held the potential to reveal previously elusive results from 'intimate' items recovered from a variety of crime scene samples.

A passage from Dr. Spence's affidavit—referring to Y-STR-based testing—was as follows: **"The YFiler system (trademark of Applied Biosystems, Inc.) has proven to be an extraordinarily effective diagnostic tool in criminal case investigations—particularly sexual assaults and child molestations. The reason for this effectiveness is the fact that, regardless of the load of DNA present from any female contributors, the Y Chromosome-based Y-STR system provides typing data only from any male DNA that is present within the detection limits. Y-STR based DNA typing was not available at the time that this crime occurred. This technology would be particularly valuable for the analysis of any intimate swabs taken from Mrs. Grega's body—specifically, oral, anal, and vaginal swabs."** Later in the affidavit, Dr. Spence wrote: **"…in the event that such a test reveals the presence of as little as one or a few unknown male genetic markers—alleles that cannot be accounted for by John Grega's Y chromosome—this would conclusively establish the presence of an unidentified male. Logic dictates that such a discovery would point to this individual as a person who engaged in intimate contact with Mrs. Grega, sometime immediately prior to her death."**

On September 2, 2011, the Vermont Court ordered the prosecution and the Vermont Attorney General's Office to arrange for DNA testing of evidence from John Grega's case. On May 14, 2012, a laboratory report was released—

summarizing the truly ***extraordinary*** DNA test results. On the anal swab collected during the 1994 medical examination—from the deceased body of Christine Grega, **"The major DNA profile originated from an unknown male."** In the event that there is any confusion here: Within that DNA mixture ***THE MAJOR DNA PROFILE ORIGINATED FROM AN UNKNOWN MALE***. This was a male who was clearly ***not*** the husband—Mr. John Grega.

As of 2021, this mysterious male has yet to be identified. The Y-STR profile from this male cannot be used to conduct familial searches, for the purpose of possible identification of the perpetrator, or any close relatives.

Prosecutors working on the Grega case in 2012 reluctantly agreed that—in light of these remarkable DNA results—Mr. John Grega was entitled to a new trial. On August 22, 2012, John Grega was finally released, after serving 18 years in prison, for a crime that ***he did not commit***. John walked out of the Southern State Correctional Facility—and into the arms of his family and friends.[234]

In a subsequent motion crafted by Mr. Carleton and the defense team, they wrote: **"It is difficult to overstate the game-changing nature of this new evidence, especially in a case where, as here, the evidence of Mr. Grega's guilt has at times been purely circumstantial…"** They added: **"Put simply, we now have compelling evidence that John Grega did not commit the crime for which he has served nearly two decades in jail."**

John Grega's tireless efforts to prove his innocence were facilitated by the Innocence Protection Act—passed by the Vermont Legislature in 2008. This legislation has allowed individuals convicted of certain crimes, to petition the court for various types of forensic tests—including DNA.[235]

Defying logic, the Vermont prosecution team continued to subject Mr. Grega to this seemingly endless ordeal. They continued—over the course of an additional year—to try to salvage their case, in anticipation of a new trial. On August 21, 2013, the prosecution finally abandoned their poorly-conceived denial of the glaring truth. All charges were dismissed against this innocent husband. John Grega became the first person in Vermont's history to be exonerated—based on DNA evidence.[236]

On January 23, 2015, near Ronkonkoma, Long Island, New York, John Grega died in a car crash.

Steven Avery, Brendan Dassey, Manitowoc County Wisconsin, and Netflix.

The Steven Avery/Brendan Dassey case centered upon two criminal case investigations—encompassing crimes that occurred over twenty years apart. The remarkable depth and complexities of these two cases was at the vortex of a controversial documentary series, bearing the title: **"Making a Murderer"**.[237] This profoundly interesting project aired on ***Netflix***, December, 18, 2015.

On the afternoon of July 29, 1985, Penny Ann Beernsten was jogging along

the Lake Michigan shoreline, in the state of Wisconsin. She was confronted by an unknown male, forced into a wooded area, and sexually assaulted. As soon as law enforcement investigators became convinced that Steven Avery (age 22) fit the description of the attacker, he was promptly arrested and charged with rape and attempted murder.

According to local police records, a known serial rapist, Gregory Allen, was under police surveillance during the thirteen-day period leading up to the attack on Penny Ann Beernsten. Records also revealed that two years earlier, Gregory Allen had been prosecuted for a sex-related crime on that same section of the Lake Michigan shoreline. Mr. Allen's 1983 rape case was handled by the same district attorney who prosecuted Steven Avery in 1985. Despite the fact that Gregory Allen had an enormous rap sheet, little was done to further investigate the possibility that ***he*** may have been the actual perpetrator of the brutal sexual assault.

During the trial, a forensic examiner testified for the prosecution—informing jurors that a hair recovered from Mr. Avery's shirt was ***"consistent"*** with Ms. Beernsten. Years later, a multitude of similarly corrupt misrepresentations of hair comparisons became part of the most widespread scandal in the history of the FBI Crime Laboratory.[238]

The defense team responded to the forensic inaccuracies by presenting sixteen alibi witnesses for Steven Avery. Despite all of this testimonial support, on

December 14, 1985, the jury needed only four hours to convict Mr. Avery of the sexual assault. The man was sentenced to 32 years in prison.

In 1995, ten years into Mr. Avery's 32-year sentence, a detective from Brown County, Wisconsin, placed a momentous call to the Manitowoc County Sherriff's Department. Brown County is adjacent to Manitowoc County—to the immediate northwest. During that fateful phone call, the detective informed the attending sergeant that Brown County had the known serial rapist, Gregory Allen, in custody—as part of an investigation into a recent, sexual assault. While in custody, Mr. Allen confessed to the Lake Michigan shoreline rape of Penny Ann Beernsten. In response to this ominous case development, the attending sergeant—a sworn law enforcement officer—***did nothing***. The Manitowoc County Sheriff's Department then proceeded to conceal the existence of the call, …altogether.

In April, 2002, seven years after the Brown County phone call, the Wisconsin Innocence Project facilitated an initiative to conduct DNA testing on thirteen hairs collected during Penny Ann Beernsten's sexual assault examination. The state crime lab found a hair that produced a CODIS database match. ***Finally***, a CODIS hit linked none other than ***Gregory Allen*** to the crime that victimized Ms. Beernsten. At the time, Mr. Allen was serving a 60-year prison term for a sexual assault in Green Bay.

On September 11, 2003, the charges against Steven Avery were dismissed, and the clearly innocent man was released. This came almost eighteen years after

the initial wrongful conviction. On October 12, 2004, Mr. Avery filed a $36 million federal wrongful conviction lawsuit. Steven Avery named the defendants as follows: the Manitowoc County Sheriff's Department, the Sheriff himself, the officers implicated in the cover-up of the 1995 Brown County phone communication, and the prosecutor who—in the beginning—had chosen to disregard the known serial rapist, Gregory Allen, as the logical suspect in the Beernsten sexual assault case.

By October, 2005, attorneys for the plaintiff—Steven Avery—had conducted about thirty-five depositions, to illuminate the abysmal truth—regarding Avery's wrongful conviction. Clearly, this included the details surrounding that 1995 phone call from the Brown County detective. Depositions targeting the former Manitowoc County Sheriff, as well as for Mr. Avery's prosecutor, were scheduled for mid-November, 2005. All of this occurred shortly before what would become the most remarkable, bizarre homicide investigation in the history of the state of Wisconsin.

On October 31, 2005, Teresa Halbach disappeared. At age 25, Ms. Halbach was employed as a photographer for ***AutoTrader*** magazine. Her last known appointment was with none other than Steven Avery, at his home on the grounds of Avery's Auto Salvage. Three days later, on the afternoon of November 3, 2005, Teresa Halbach's mother informed police that her daughter appeared to be missing.

Later that same day, a sergeant with the Manitowoc County Sheriff's Department placed a call to the local dispatcher. He provided a license plate number

that had been relayed to him from a fellow law enforcement officer. When the dispatcher confirmed that Teresa Halbach—the missing photographer—was the owner of the vehicle, the sergeant asked: **"99 Toyota, right?"** The dispatcher affirmed the year and make of the vehicle.

Also that same day, local police questioned Steven Avery, as well as individuals from two of Ms. Halbach's earlier vehicle photography appointments. Coincidentally, the sergeant who placed the November 3rd dispatcher call was the very same Manitowoc County Sheriff's Department sergeant who fielded (and covered-up) that infamous 1995 call from Brown County—regarding capture of the serial rapist, Gregory Allen.

Regardless of the sergeant's mysterious November 3rd call to dispatch, law enforcement officers spent the majority of the daylight hours—throughout November 4th—continuing their search for Ms. Halbach. They canvassed numerous areas, including Avery's Auto Salvage property. These efforts included multiple helicopter flyovers. There was no sign of Ms. Halbach—or her 1999 Toyota RAV4—which ***somehow*** remained missing.

The following day, at 10:15 a.m., November 5, 2005, volunteer searchers discovered the 1999 Toyota RAV4, on Avery's Auto Salvage property. During the days that followed, the case investigation shifted intensely toward Steven Avery, and become increasingly twisted and peculiar—with each passing hour.

During the vital early stages of the investigation, a sensible decision ***seemed*** to have been made. Due to the enormous conflict of interest linked to Mr. Avery's $36 million federal lawsuit—Manitowoc County needed to relinquish ***100%*** control of the Halbach homicide investigation to the neighboring Calumet County Sheriff's Department. Resources from Manitowoc County would be available—but strictly to support Calumet County investigators. While these ***proposed*** measures made perfect sense—in theory—these restrictions were scandalously disregarded.

Steven Avery's residence—a trailer located on the Auto Salvage property—was subjected to a multitude of thorough searches. On November 8, 2005, four days after the very first of many searches, the keys to Ms. Halbach's 1999 RAV4 were suddenly found on the floor of Steven Avery's bedroom. Present at the time of this search were Manitowoc County law enforcement officers. Among them were individuals who had been named as defendants in Mr. Avery's lawsuit.

DNA testing of the RAV4 keys indicated the presence of Steven Avery. Although Ms. Halbach owned the RAV4, and handled her own vehicle keys on a daily basis, no hint of her DNA was detected on that evidence item. Although no fingerprints from Mr. Avery were found on the RAV4, investigators theorized that he may have worn gloves. Bloodstains recovered from the interior of the vehicle appeared to be a result of transfer events—perhaps from the killer handling the vehicle. The blood smudges provided yet another match to Steven Avery. However,

these observations raised the question: If the use of gloves prevented Mr. Avery's fingerprints, how was blood transferred from his hands to the areas that he had 'theoretically' touched?

On November 11, 2005, Steven Avery was arrested and charged with the homicide. Investigators eventually found charred bone fragments and teeth—reported to be from Ms. Halbach—in a burn pit near Mr. Avery's trailer. Oddly, these remnants were not in one location, but spread out across multiple parts of the Auto Salvage property. The homicide investigation team theorized that Mr. Avery sexually assaulted and murdered Teresa Halbach, sometime after 3:00 p.m., on October 31st. He then moved the victim's RAV4 to a remote section of the Auto Salvage property, and attempted to cover it with branches and vegetation. He then allegedly attempted to conceal the crime by incinerating the remains of the victim.

This theory appeared to be contradicted by a delivery man, who stated that he was putting fuel into his vehicle near the Avery property on October 31st. This witness reported that—at about 3:30 p.m.—he saw an SUV resembling the one owned by Ms. Halbach, leaving Avery's Auto Salvage property. The delivery man was unable to see the driver of the vehicle. Assuming the accuracy of these statements, and it was the RAV4 in question, a serious flaw emerges: If Steven Avery actually committed the homicide, why would he choose to drive away from the Avery Auto Salvage property, only to come back later in the same vehicle, to

burn the remains of the victim, and leave the RAV4 a short distance from his home?

An eventual hypothesis proposed that Ms. Halbach may have been killed by a gunshot to the head. After several careful searches of the Avery property revealed no projectiles, a projectile was fortuitously discovered in the garage near Steven's residence. Once again, the same Manitowoc County law enforcement officers—named as defendants in Mr. Avery's lawsuit—were present at this search.

When DNA testing was conducted on this projectile, the analysis was handled by the very same technician who falsely reported the 'match' to Penny Ann Beernsten's hair—in 1985—from the shirt worn by Steven Avery. The DNA analyst completely consumed this projectile sample. Although the results indicated consistency with the DNA from Teresa Halbach, it was also clear that the analyst had contaminated the typing process with her own DNA. In every crime lab across the U.S., this finding disqualifies the reliability of the results altogether. This would have eliminated the utility of the bullet fragment, since the DNA sample had been entirely consumed. To circumvent this error, the analyst simply wrote up a ***'deviation request document'***. In one step, the crime lab was able to disregard universally-accepted scientific standards, and ignore their own published procedural limits. DNA testing results were presented to the jury—despite the contamination.

During preparation for Steven Avery's trial, his defense attorneys discovered a box of evidence—collected in 1996—as part of the appellate investigation into the

sexual assault that victimized Penny Ann Beernsten. In addition to the fact that the seal on the box had been breached at some unknown point in time, the attorneys found a vial of Steven Avery's blood within the box. Most alarming, they noticed a puncture hole in the closure fitted into the top of the blood vial.

Mr. Avery's defense attorneys, reinforced by the accusatory tone of the ***Netflix*** presentation, **"Making a Murderer"**, emphasized this mysteriously punctured stopper as a profound 'red flag'. This tone centered on the potential that numerous 'astonishing' observations were most likely a consequence of evidence tampering. These observations were as follows: **1)** Teresa Halbach's RAV4 was 'called in' by law enforcement on November 3, 2005—but inexplicably remained 'undiscovered' until two days later—when the vehicle turned out to be on the Avery Auto Salvage property; **2)** The RAV4 keys were overlooked—despite countless previous searches. Oddly, these keys materialized in Steven Avery's bedroom—discovered by defendants in his lawsuit; **3)** From those RAV4 keys, the crime lab reported DNA from Mr. Avery, but not so much as a hint of biological material from Ms. Halbach; **4)** The projectile was also somehow repeatedly overlooked—but miraculously discovered during a subsequent search of a garage located near Steven Avery's residence. Again, defendants named in the $36 million law suit were present on the property—at the time of this garage search; **5)** A source of Steven Avery's blood/DNA was found, with a puncture hole in the vial closure.

The prosecution countered the blood/DNA vial tampering allegations by pointing out the fact that the majority of forensic blood/DNA vials contain an additive called ethylenediaminetetraacetic acid (EDTA). To bolster their argument, the prosecution hastily arranged for testimony from an FBI technician. The FBI witness attempted to affirm that no detectable EDTA was present within the blood deposits recovered from Teresa Halbach's RAV4. Defense expert witness testimony established that the FBI tests for EDTA failed to include appropriate controls—which were necessary to validate the observed RAV4 negative EDTA results. The legal battle centering on this EDTA detection issue is far from over.[239]

The investigative mishaps and scientific confusion summarized thus far are aside from a multitude of added concerns associated with Steven Avery's nephew, Brendan Dassey. During the 2005 homicide investigation, Mr. Dassey was 16-years-old, with an estimated IQ of 73. The investigators hounded the young man into a patently flawed account of events—allegedly occurring on October 31, 2005. It was established that young Mr. Dassey was abandoned by his own legal counsel, and coerced into affirming a series of enormously questionable statements. Later, Dassey recanted his statements, and refused to testify at Steven Avery's murder trial. Regardless of this, on March 18, 2007, Mr. Avery was found guilty. Six weeks later, he was sentenced to life in prison without the possibility of parole.

Despite all of the odd twists and turns, the vulnerable Brendan Dassey was

convicted on April 25, 2007, for his supposed participation in the Halbach homicide. He was sentenced to life in prison, with eligibility for parole in the year, 2048. However, on August 12, 2016, this conviction was overturned by a federal judge—on the grounds that Mr. Dassey was coerced by law enforcement, to make statements that were 'suggested' by the police, rather than being founded upon actual events witnessed by the teenager.[240] On November 14, 2016, this federal judge ordered the release of Brendan Dassey—to occur within 90 days. As a consequence of an appeal filed by Wisconsin prosecutors, in December 2017, the 7th Circuit voted 4-to-3, to uphold Brendan Dassey's original conviction. Additional filings from Mr. Dassey's legal counsel will be forthcoming in the years to come.

In light of the seemingly endless complexities associated with the Avery/Dassey case, the most notable, irrefutable facts can be enumerated as follows: **1)** Regardless of any carefully formed assessment of the ***Netflix*** **"Making a Murderer"** docuseries, the presentation clearly triggered passionate responses from individuals with loyalties originating from all extremes of the social spectrum. Shortly after the December, 2015, airing of this story, ***Netflix*** reported an unprecedented 8% spike in new subscribers to their services.[241] **2)** Whether a person's inclination is to empathize with law enforcement, or with the accused, or with both sides, everyone can agree that Steven Avery was wrongfully convicted of the 1985 sexual assault that victimized Penny Ann Beernsten. **3)** After 18 years of

wrongful imprisonment—Mr. Avery was undoubtedly on a path—in October, 2004—toward collecting untold millions of dollars, as compensation for the damage that was done to his life.[242] **4)** If Steven Avery was genuinely responsible for Teresa Halbach's death, the man looked millions of dollars in the face, and threw it all away—along with his newly found freedom. In February 2006, Mr. Avery settled his $36 million lawsuit for $400,000. The majority of this settlement went to the attorneys who were preparing to defend him against the Halbach homicide charges. Meanwhile, the remainder was collected by the man's civil lawsuit attorneys. Steven Avery did not receive so much as a dime. **5)** Regardless of Mr. Avery's innocence or guilt in the Halbach homicide, there were conspicuous beneficiaries of the fact that murder charges were filed, and convictions were achieved. Beginning in early November, 2005, Mr. Avery's civil lawsuit was all but forgotten. No additional depositions were conducted. All of the defendants were suddenly forgiven from any threats to their careers or their personal finances. **6)** Considering this miraculous deliverance from potentially catastrophic consequences, the diligent observer might scrutinize the obvious. One feels compelled to explore any degree of involvement of these defendants in the processes that advanced the Halbach homicide investigation. The obvious conclusion has to be that these specific 'investigative participants' were either quite foolish—or perhaps they were remarkably brilliant.

In light of the well-publicized, $36 million civil action, why would any ***listed***

defendant choose to position themselves anywhere near the vicinity of the homicide investigation? Doing so opens the door for the social masses to raise allegations against the most subtle appearance that influencing the process could be an objective.[243]

John Ruelas, Gary Leiterman, Contamination, and the Michigan State Police.

During the early morning hours of March 21, 1969, Jane Mixer—a 23-year-old University of Michigan law student—was shot to death in Ann Arbor, Michigan. Due to the absence of any investigative leads over a protracted time frame, the murder of Ms. Mixer was assumed to be part of a series of homicides occurring in the Ann Arbor/Ypsilanti Michigan area between July 1967 and July 1969. Those well-known ***'Michigan Murders'*** were later attributed to the known serial killer, John Norman Collins—also known as the ***'co-ed killer'***.[244]

In early 2002, cold case investigators took possession of the 33-year-old evidence items—collected from the Jane Mixer murder investigation. Beginning in March 2002, forensic examination of these items was conducted by a Michigan State Police Crime Lab DNA analyst. The analyst reported two distinctly different male DNA profiles from two evidence items. A number of months later, these two unknown male profiles were uploaded into the Combined DNA Indexing System (CODIS) for comparison to other DNA profiles—housed within this database.

In December 2003, a database match was achieved from a DNA profile within a blood deposit that had been scraped from Jane Mixer's left hand—thirty-three years earlier—as part of the woman's autopsy. This DNA profile matched the DNA from a convicted offender by the name of Mr. John Ruelas. The known DNA profile for Ruelas had been entered into CODIS database—as a consequence of his 2002 conviction for murdering his mother—Ms. Margaret Ruelas.

Eight months later, in August 2004, a 2nd CODIS database hit suggested an association between the Jane Mixer case evidence and the known DNA profile from Mr. Gary Leiterman. The reason Mr. Leiterman's DNA profile had been placed within the CODIS database was as follows: In 2001, Gary Leiterman became addicted to the prescription drug, Vicodin. The pain killer was initially prescribed for Gary's severe back pain. An unfortunate drug addiction led to a prescription fraud charge against the man. In December, 2001, Gary successfully completed a 3-month drug rehabilitation program in a private clinic. He also completed the required one year court sponsored drug rehabilitation program which ultimately cleared him of the felony conviction arising from his drug-related charges.

Despite being cleared of the felony conviction, Gary Leiterman's CODIS DNA reference sample arrived at the MSP Crime Lab on February 22, 2002. The arrival of this ***first*** DNA reference sample from Mr. Leiterman was within 24 hours after the Margaret Ruelas murder case items were initially opened for analysis in the

very same section of the MSP Crime Lab.

When the December 2003, CODIS hit identified John Ruelas as a potential perpetrator of the Jane Mixer homicide, the cold case investigation team had to be exceptionally pleased with the DNA breakthrough. However, the enthusiasm faded when the MSP Crime Lab realized that John Ruelas was only 37-years-old. This exposed the fact that—in March, 1969—young Ruelas was a 4-year-old child.

Initially, it was hoped that Ms. Mixer's left hand scraping of blood/DNA—matching John Ruelas—did indeed come from the 4-year-old child, who was inexplicably present at the 1969 homicide scene. However, the facts overwhelmingly contradicted this outlandish hope. From the moment that the John Ruelas CODIS hit was discovered, through the present date, exhaustive investigative efforts have failed to reveal any hint of a personal connection between young Ruelas, Mr. Leiterman, or Ms. Mixer.

The facts were inescapable. Jane Mixer was shot twice in the head. Logic dictates that the blood on her hand most likely originated from her own head wounds. Copious deposits of blood from Ms. Mixer were observed all over the woman's body—as well as her clothing. Despite the coherence of the logic associated with these facts, the prosecution team—as they prepared for Gary Leiterman's trial—embraced an enormously outlandish notion—that young Ruelas was somehow present at the homicide—regardless of what anybody else suggests. Thus, perhaps

the 4-year-old boy merely experienced a nosebleed at this murder scene. This wildly irrational hypothetical ignores all of the following: **1)** No connection could ever be found between Jane Mixer, young John Ruelas, or any individuals within the Mixer or Ruelas families. **2)** Gary Leiterman traveled to Ann Arbor for the purpose of murdering a complete stranger. **3)** Despite the absence of any connection between Mr. Leiterman, young John Ruelas, or any individuals with the Leiterman or Ruelas families, Gary recruited the 4-year old child for the purpose of witnessing the crime he was preparing to commit. **4)** Gary somehow allowed this small child to drip his blood onto the hand of his gunshot victim. **5)** Despite the bizarre nature of Gary's decision to include a complete stranger, a child at this scene, no individual among the family or friends of young John Ruelas has any recollection that the child was ever missing on ***any*** night, around March of 1969. And this was despite the fact that Jane Mixer's time of death was believed to be between midnight and 3:00 a.m. **6)** Keeping in mind Mr. Leiterman's unprovoked brutality against a woman he did not know, the man somehow lost his appetite for committing such random crimes—and was never arrested or convicted of a single, subsequent, violent event—between March 1969, and the date of his well-publicized 2004 arrest—as a suspect in the Jane Mixer homicide. This was a span of ***thirty-five years***; **7)** Young John Ruelas grew up to—himself—become a murderer; **8)** Most astonishing, we arrive at the crown jewel of all coincidences. While one 2002 homicide investigation targeted 37-year-

old John Ruelas, a 2nd 2002 homicide investigation targeted the 1969 Jane Mixer cold case homicide. The forensic biology/DNA analytical phases of ***both*** of these investigations were conducted at the same time, and within the very same crime lab in Lansing, Michigan. Ridiculously, observers of these facts are expected to trust that it is more likely that all of these spectacular coincidences somehow became perfectly aligned.[245] Alternatively, we can choose to suspect that—not one, but ***two***—DNA cross-contamination events occurred during the processing of evidence from one MSP Crime Lab case.[246]

In 2005, Gary Leiterman was sentenced to life in prison without the possibility of parole. From the moment of his arrest in 2004, throughout his trial, and throughout all of his years of wrongful imprisonment, Mr. Leiterman maintained that he had nothing to do with the murder of Jane Mixer. During Gary's trial, the jury heard testimony from the MSP Crime Lab analyst who was assigned to analyze the Ruelas homicide case. This analyst was questioned about receiving a call from her supervisor—shortly after the realization that DNA linked to her case had ***somehow*** ended up on evidence that was being examined by one of her co-workers. The Ruelas case analyst was commanded to return from her current MSP-Grand Rapids Lab location, to discuss concerns about the timing and details of her analysis. Again, her supervisor's principle concern—undoubtedly—was a consequence of the potentially catastrophic detection of an out-of-place 4-year-old on the Jane Mixer homicide

evidence—from 1969.

Transcripts from her testimony reveal the following[247]: **"My supervisor telephoned me and asked me to come to Lansing to review my notes from my analysis from this homicide that I received from Jackson and to make a timeline as to when I performed the steps of my analysis in order to—for him to make a comparison to the timing of the analysis of the samples for the Mixer case."** Question from Gary's defense counsel: **"All right, and are you aware of when there was an overlap in those timelines?"** Response from the Ruelas case analyst: **"I believe there was an overlap in some of the sample handling, but I'm not exactly sure what the dates are or what the overlap of the sampling would be."**

These statements are disturbing on various levels. Most important, it is alarming to observe such vague testimony—regarding recorded dates/times documented within a DNA testing laboratory. Refer to the rigorous standards for maintenance of records, which have been established by the Federal Bureau of Investigation (FBI)[248] and the Scientific Working Group for DNA Analysis Methods (SWGDAM).[249] Within that context, the Ruelas case analyst stated that she was **"…not exactly sure…"** when specific stages of her analysis were conducted. Equally important, this acknowledged that a lack of attention to detail can be taken together with the fact that the analyst was commanded by her supervisor to travel 68 miles, in order to discuss **"..what the overlap of the sampling would be.."** relevant

to the Ruelas case—versus the timing of the Jane Mixer cold case evidence analysis.

Referring to the testimony records from Gary Leiterman's trial, it is illuminating to note that the Jane Mixer homicide DNA analyst testified that his evidence analysis began on March 22, 2002. This establishes that evidence item handling, sampling, and analysis—from ***both*** the Mixer and Ruelas cases—took place during overlapping timeframes, in early 2002.[250] These processing steps also occurred within the exact same crime lab facility, on laboratory bench spaces that were separated by no more than a few feet. Even more important, CODIS DNA sample extractions—the source of material from which Gary Leiterman was typed for his known DNA profile—were routinely conducted on a bench immediately adjacent to the laboratory area used for the analysis of the Jane Mixer case evidence.

Blood/DNA collected from any victim's hand, onto a cotton swab, and stored within unknown locations, under undefined conditions of temperature and humidity, ***for thirty-three years***, is certain to undergo a substantial degree of decomposition. There is no doubt that the introduction of pristine, non-degraded DNA from John Ruelas was due to evidence mishandling and case-to-case cross-contamination of biological material—at the MSP Crime Lab. It is also clear that any quality control/quality assurance measures—designed to alert analysts of potential DNA contamination errors—failed to provide any clues that this specific cross-contamination event had occurred.

The MSP Crime Lab—throughout 2002—was prone to quality control malfunctions and defective analysis. One vital indication of this was verified when the Jane Mixer homicide DNA analyst documented that he had subjected post-amplification polymerase chain reaction (PCR) products to what is referred to as a ***'Microcon®—based DNA clean-up procedure'***.[251] This supplemental step in the process was conducted at the urging of Charles Barna—the infamous MSP Crime Lab DNA Unit Director—during the time that these cases were handled/analyzed in early 2002. In addition to being enormously ill-advised, this DNA ***clean-up step*** was never validated by the MSP Crime Lab for use on post-amplification PCR products. Clearly articulated FBI and SWGDAM warnings—regarding potentially catastrophic problems with manipulation of post-amplification PCR products—have been discussed in this Chapter, in more detail (refer to the section entitled: **"Practical minimization of DNA contamination events in crime labs."**).

As a consequence of attempting this problematic DNA clean-up process, Charles Barna and the Jane Mixer homicide DNA analyst recklessly introduced an enormous, unnecessary risk of DNA cross-contamination within the MSP crime lab. This risk was compounded by the fact that utilizing ***any*** non-validated method is an inexcusable violation of universally-recognized quality control standards for DNA analysis laboratories. The jurors assigned to the Leiterman trial were completely unaware of these facts.

During Gary Leiterman's trial, MSP Crime Lab analysts and supervisors insisted that no DNA contamination events were ever detected. These claims were inaccurate and patently misleading to the jurors. Within the case file documents was an electropherogram bearing the label, ***"Negative Control 041902"***.[252]

This control sample was analyzed by the Jane Mixer homicide DNA analyst on Tuesday, May 7, 2002. Near the bottom of this data printout, a handwritten note revealed the following information:

"<u>Note</u>: Contaminant detected in ProfilerPlus microconed product (~15 μl)-However, not detected in Cofiler microconed product (~15 μl)-Lab personnel excluded-Co-amplified samples excluded-Action—microcon remaining product."

This notation established that yet another contamination event (other than the John Ruelas blunder) ***did*** indeed occur during analysis of the Jane Mixer homicide case. It also establishes multiple instances of the Jane Mixer homicide DNA analyst, subjecting post-amplification products to the **'Microcon®—based 'DNA clean-up'** procedures that had been encouraged by Charles Barna. These clean-up procedures were carried out in close proximity to the lab benches where various CODIS samples—including Gary Leiterman's DNA reference sample—were processed for DNA. It is noteworthy that the tenure of Charles Barna came abruptly to an end—as a consequence of an MSP Internal Affairs investigation into questionable laboratory

practices, including allegations that proficiency tests were falsified.[253]

Despite Mr. Barna's elevated position as the Director of the MSP Crime Lab DNA Unit, he was apparently unaware of the following realities of forensic DNA casework (topics covered in previous sections of this Chapter): **1)** Post-amplification PCR products require handling with extreme caution.[254] **2)** Genetic typing efforts from '**L**ow **C**opy **N**umber' (LCN) quantities of DNA, provide notoriously unreliable data.[255] **3)** Contamination disasters are being invited into your crime lab, when attempts are made to overcome LCN DNA quantity limitations, by directing analysts to resort to non-validated post-amplification manipulations of DNA.[256]

Individuals doubting the innocence of Mr. Gary Leiterman might point to the fact that the CODIS hit came from a relatively incriminating location—on a pair of pantyhose recovered from the Jane Mixer homicide scene. Despite the prosecution's speculation that the 'discolorations' sampled from these pantyhose were from drops of the killer's perspiration—there are ***no*** forensic biological tests for sweat deposits. Although those discolorations could have been from the perpetrator's spittle, it is interesting to note that the CODIS reference sample collected from Gary Leiterman was indeed ***also*** a deposit of saliva. The attending analyst failed to test the pantyhose stains for indications of human saliva.

Those in support of Gary Leiterman's conviction can also argue that contamination from a male who was only 4-years-old in 1969, as well as the

contamination of ***Negative Control 041902***, does not establish that additional contamination events ***must have*** occurred. The validity of this argument would be noteworthy, if it could be verified that the two known Jane Mixer homicide case DNA contamination events were a consequence of isolated MSP Crime Lab incidents. On the contrary, the facts relevant to long-running quality control malfunctions at the MSP Crime Lab establish a pattern of sobering causes for concern that have persisted—***for over 15 years.***

One is encouraged to refer to the July 14, 2005, testimony from the Margaret Ruelas homicide DNA analyst. The transcript record shows the following question from the defense:[257] **"And then, when all of that is done, I would assume that there is a log kept, or some sort of overall record to show the lab's proficiency in handling these samples?"** The analyst responded: **"I'm not certain that an error log is kept. I've never seen one in the laboratory."** Question: **"Who was your supervisor in 2002?"** The analyst responded: **"Charles Barna."**

The absence of an appropriate, centralized corrective action/quality assurance system within the MSP Crime Lab—as well as the lack of a compilation of error logs—represents a catastrophic deviation from the **DNA Advisory Board Quality Assurance Standards**, outlined in **Appendix II, Section 14.1.1** of that document.[258] Without the benefit of any centralized corrective action documentation—no crime laboratory can effectively identify and resolve systematic patterns of problems that

might negatively impact the data from the scientific investigation of each case.

At the forefront of such challenges resides the issue of ***contamination***. Within the testimony record from Gary Leiterman's trial, various MSP Crime Lab analysts and supervisors failed to provide any illuminating commentaries—regarding how their facility effectively addresses problems with contamination.[259]

To this day, no such mechanisms exist in that facility. Like countless other accredited facilities, the MSP Crime Lab utilizes procedures that incorporate negative controls, reagent blanks, and amplification blanks. Relying on these controls—without any centralized documentation of corrective actions—embraces a false sense of security, suggesting that effective quality control measures are in place. In numerous instances of crime lab casework across the U.S. and abroad—these laboratory quality control monitoring systems have repeatedly failed to detect acute DNA contamination problems. Such failures have afflicted countless DNA testing facilities—including instances that have already been cited within this chapter. The affected labs include—but are not necessarily limited to—facilities in the following locations: Victoria, Australia (1998)[260]; Houston, Texas (2003, 2008, and 2014)[261]; Sea Girt, New Jersey (2003)[262]; Seattle, Washington (2004)[263]; Detroit, Michigan (2007)[264]; San Francisco, California (2010)[265]; Manchester, England (2011)[266]; and St. Paul, Minnesota (2012)[267].

In 2008, a classic example of these ubiquitous failures to detect contamination

issues emerged within the Baltimore City Police Crime lab. In August 2008, it was discovered that analysts working within that facility had been unknowingly contaminating evidence with their own DNA—as well as DNA from co-workers—***for over seven years***. This finding led to the firing of Edgar Koch, the Baltimore City Police Department's crime lab director.[268] All of the above-listed accredited laboratories experienced acute DNA contamination problems that were ***not*** revealed by any negative control measures, reagent blanks, or amplification blanks.

During a January 2017, trial in Traverse City, Michigan, the reporting MSP Crime Lab analyst admitted that her facility was ***continuing*** to process forensic DNA cases without any centralized corrective action/quality assurance system.[269] Rather than maintain a readily accessible compilation of error logs, analysts are directed—upon observation of any contamination events—to simply make a note ***somewhere*** in the case file. This practice gives the appearance of ***burying, or hindering the discovery*** of multiple-case patterns of contamination events. Presumably, it is frowned upon for accrediting agencies, visiting auditors, and other individuals to have an unobstructed window into the extent of the contamination problems that might be plaguing the MSP facilities. Most important, it reveals a glaring deviation from the **DNA Advisory Board Quality Assurance Standards**[270] and the **FBI Standards for Forensic DNA Testing Labs.**[271]

Recall that DNA, presumed to be 'sweat' from Gary Leiterman, was reported

on the pantyhose recovered from the Jane Mixer homicide scene. A multitude of facts and a multitude of additional disturbing coincidences point to this finding as—yet another carefully concealed MSP Crime Lab cross-contamination malfunction. Accordingly, it is quite improbable that in 1969—Gary Leiterman contributed ***any*** genetic material to the evidence collected from the crime scene.

First, the reader should refer back to the information provided in previous sections of this chapter, bearing the titles: **"Ancient/cold case DNA and contamination"** and **"Lacking awareness of DNA contamination and corrective actions in crime labs"**. Some illuminating observations emerge when one examines the wealth of information contained within a publication released in June 2012 by the United States National Institute of Justice (NIJ). The 177-page publication is entitled: **"DNA for the Defense Bar"**.[272] Within the forward of this document, the authors—speaking on behalf of the NIJ—establish that the publication is **"…designed to increase the field's understanding of the science of DNA and its application in the courtroom."**

Refer to **Chapter 9**, which covers **"Delayed Prosecutions, Cold Case Hits and CODIS"**. Within this chapter, refer to Page 125—where the authors state as follows: **"To participate in NDIS, states must sign a Memorandum of Understanding verifying that the submitting laboratory is in compliance with the FBI's quality assurance standards."** Recall that—during the timeframe of the

John Ruelas contamination event, in 2002—the fundamental policy of the MSP Crime Lab was to rebuff their responsibility of maintaining a centralized compilation of corrective actions. Recall that in 2016 and beyond, MSP Crime Lab management has continued to direct their analysts to respond to contamination events by doing nothing beyond an informal notation—***somewhere*** in that specific case file.

As of late 2016, MSP Crime Lab management has continued to allow analysts to conduct DNA extractions and amplifications—while maintaining ***no separation of time or space*** between evidence from alleged victims, and DNA from accused defendants. These facts demonstrate a disturbing pattern of a continuing lack of compliance with the FBI's quality assurance standards.[273]

> Further into **Chapter 9**, Section 5 bears the title: **"Review the Match Report Carefully"**. Within this section, on Page 127—the authors emphasize the following:
>
> **"If the match is to a suspect profile generated and entered by the same LDIS lab, be sure to compare when the client's DNA was originally entered into the databank and when the evidence profile was entered. Was the evidence profile generated before the client's profile was generated for *any* case? Or was it generated before the client's profile was generated for the *present* case? The development of the evidence profile before the client's profile minimizes the risk that the evidence was mistyped or cross-contaminated."**

In the instance of the DNA match to Mr. Gary Leiterman, the operative questions were never illuminated: **"Was this DNA match reviewed carefully by the MSP Crime Lab? Was it carefully reviewed by counsel for Mr. Leiterman's defense, by counsel for the prosecution—and most important—by the jury?"**

Profoundly, the answers to these questions are addressed in the 2012 NIJ **"DNA for the Defense Bar"** document. Refer to **Chapter 9**, **Section 9**, which bears the title: **"Contamination"**. On Page 137, this section of the document reveals the following:

> **"Questions remain about the 1969 murder of a Michigan woman. In December 2003, police received a DNA match based on a cold hit of an evidence sample, but the matched person was only 4 years old at the time of the woman's death. A sample from another convicted offender was tested at the same lab and matched another item of evidence in the case. Police have failed to come up with an explanation for the first match; there was no obvious evidence of laboratory contamination. The second match was eventually tried and convicted on the basis of his DNA match. The case is currently under appeal."**[274]

Without a doubt, this ***contamination*** case example refers to none other than the John Ruelas contamination event—as well as the enormously questionable conviction of Mr. Gary Leiterman. Interestingly, the NIJ authors avoided identifying the specific facility responsible for this dismal attempt at scientific analysis. Most mystifying, Mr. Leiterman remained incarcerated—as the faulty scientific aspects of the Jane Mixer homicide investigation continued to evade the appropriate scrutiny.

Let us assume that the detection of Mr. Leiterman's DNA was—yet another, a third instance—of a DNA contamination event—during analysis of the Jane Mixer homicide evidence. But how exactly did this happen? Recall that the Leiterman CODIS DNA reference sample arrived at the MSP Crime Lab facility on February 22, 2002. ***Coincidentally***, this arrival date was only one day after the Ruelas murder case evidence items were first laid out for examination in the MSP Crime Lab.[275]

The initial test date for Mr. Leiterman's CODIS DNA reference sample was presumed to be sometime between July 17, 2002 and July 23, 2002. In addition to the glaring fact that the precise date of testing remains unclear, it is intriguing to refer to the July 14, 2005 testimony from one of the MSP Crime Lab's CODIS sample analysts. The testimony transcript reads as follows:[276] **"We do maintain dates about when tests were performed but we don't typically generate any paperwork when we just process a convicted offender sample to go into CODIS. So, any dates regarding when a sample was handled are stored in various databases at the stations where the action would be performed."** Further into the transcript, the same analyst continued: **"All of the information is electronic. We don't generate any paperwork from the receipt of an offender sample through the input into CODIS."** A bit later, defense counsel asked: **"Who actually handled Gary Leiterman's DNA sample or buccal sample?"** Answer: **"In this instance, the information that I retrieved from the databases to bring with me today indicates the date that certain samples were handled, but it doesn't give me any indication as to which individual handled the sample."** In yet another astounding coincidence, this CODIS sample analyst admitted in open court that there was no identifiable person available to question—regarding the detailed steps, or the integrity of the timing/handling of Gary Leiterman's CODIS DNA reference sample, in the MSP Crime Lab, between February 22, 2002 and July, 2002.

Most profound, no available analyst could be questioned about the overwhelming revelation that this early 2002 effort ***failed to generate a DNA profile*** from the Leiterman CODIS DNA reference sample. At this point, the diligent litigator, or the diligent juror, must ask: **"Should such a lack of accountability in handling a CODIS DNA reference sample be considered 'compliant' with the FBI's Quality Assurance Standards?"** Additionally, it is logically important to ask: **"During ~~the~~ Mr. Leiterman's trial, was it feasible for any juror, or any other individual, to 'Review the Match Carefully'?**

Keeping in mind that the initial attempt ***failed*** to generate a DNA profile from Gary Leiterman, it is remarkable that further testimony from the MSP Crime Lab CODIS analyst reveals the following:[277] **"The first time the card was processed, it did not yield a DNA profile. This is not completely uncommon because we are using saliva. ----Sometimes there's an area that was colored white that really contains mostly saliva and very few cells."**

Testifying under oath—it is a disgrace to suggest that such a DNA typing failure could be anything short of a profound, unexpected event. Note that this CODIS sample analyst was never asked to provide any hint of scientific data, regarding this ***imagined*** prevalence of failed saliva standards. Regardless of this ludicrous testimony, such failures are—in the real world—enormously rare events.

Recall the scientific fact that a single drop of saliva from the average human

being contains approximately 500,000 salivary epithelial cells. Consider the possibility that as little as only three drops of Mr. Leiterman's saliva were present on his CODIS DNA reference sample that was collected and delivered to the MSP Crime Lab on February 22, 2002. The projected DNA yield from this quantity of saliva should have been sufficient to conduct DNA typing nearly ***10,000 times over***. Based upon this reality, the vital question persists: **"What actually became of Mr. Leiterman's initial, saliva-soaked CODIS sample—within the MSP Crime Lab?"** Although the precise mechanism of mishandling remains unknown, it is probable that this reference sample was the source of the contamination event—leading to the arrest and conviction of an innocent man—Mr. Gary Leiterman. No CODIS sample from Mr. Leiterman was typed for DNA until 18 months after the initial sample mysteriously failed, sometime around July 2002.

After learning of the John Ruelas contamination event in 2002, one of the MSP Crime Lab DNA Unit supervisors attempted to duplicate the initial findings. This initiative ***failed*** to demonstrate reproducibility of the first round of results. In addition to observing ***no*** DNA consistent with John Ruelas, this DNA supervisor was unable to confirm any added conclusions that might have provided support for the highly-questionable, incriminating results against Gary Leiterman.

Added troubling coincidences are notable. From both the initial and supplemental rounds of analysis of the pantyhose, plus analysis of the blood spot on

the victim's hand, plus additional evidence items (bloody clothing from Ms. Mixer), detection of DNA from Jane Mixer herself was either weak, or completely compromised. Although blood is an enormously rich source of DNA, there is no mystery in the fact that DNA is highly prone to degradation—during ***thirty-three years*** of handling/storage under undefined conditions.

Despite these facts, the DNA on the pantyhose miraculously generated pristine DNA typing results—as well as a CODIS hit. The difficulties with finding Ms. Mixer's intact DNA from the clothing items and blood deposits might be attributed to the fact that the crime scene evidence was improperly packaged and improperly stored. It is an established fact that the Mixer cold case evidence was packaged, sealed and stored for all of those decades—***in plastic containers.*** It is a universally-discouraged DNA handling error to package any biological evidence in a closed, plastic system that allows a limited exchange of atmospheric gases.

When the Jane Mixer homicide DNA analyst was questioned about his failed attempt to characterize DNA from the presumed blood on the victim's hand—his testimony was as follows: Question from the prosecutor:[278] **"Did you compare with the presumed sample of Jane Mixer's blood?"** Analyst: **"In terms of—I didn't do it in terms of the report. In looking at it, you could look at the types, and the types are not the same. When the types are not the same, that's a non-match, therefore Jane Mixer could be excluded. In terms of, well excuse me, in terms**

of—it was inconclusive because you had additional activity. Excuse me, she could not be excluded. You had additional activity at one of the genetic markers that was a minor donor and it was inconclusive because it did not meet reporting standards, so what that means is that there is not opinion formed to whether she is included or excluded as a possible donor of this sample."

Perhaps the analyst could have minimized confusion by simply telling the jurors: **"No data confirmed the presence or absence of DNA from Ms. Mixer."** The prosecution continued: **"Is it—are the results that you are seeing in that particular sample consistent with or inconsistent with this spot of blood having been scraped off Jane Mixer's hand?"** Analyst: **"The DNA types that are present are consistent with a, basically, a single source biological sample. In this case, identified as blood."** Note that—with this testimony—the analyst further confused the jurors by disingenuously avoiding clarification that this 'single source' was a ***match to John Ruelas***, the 37-year-old suspect from a 2002 homicide case—whose DNA was being analyzed at a work station—located just a few feet away.

A diligent litigator should not find fault with the actions of the individuals who collected and packaged the Jane Mixer case evidence—with no aversion to 'sealing in' the high humidity atmosphere that persists in the state of Michigan. In 1969, crime scene investigators had no means of predicting the crucial role that DNA recovery and analysis might play in future 'cold' cases. Similarly, these technicians

had no means of gaining awareness that residual moisture would become the universally-recognized arch enemy of future DNA testing. Keeping these facts in mind, it would not have been a surprise to recover virtually no usable DNA from all of the items—33 years after collection of evidence from the Jane Mixer homicide scene. This statement is true—despite the fact that the examination of the deceased woman revealed an abundance of blood deposited on her body and her clothing.

Blood is a profoundly rich source of DNA. Indeed, a single drop of blood contains—on average—400,000 DNA-containing white blood cells. Regardless of the DNA-rich nature of blood, the inescapable fact is the 33 years of evidence handling/storage—and the profound potential for DNA degradation. Upon reviewing the DNA typing electropherograms, the evidence of DNA degradation was quite conspicuous.

By contrast, it is extremely illuminating to observe the much more pristine nature of the DNA results—establishing the presence of John Ruelas—which was clearly the product of a 2002 contamination event. Similarly, the DNA data corresponding to Gary Leiterman—as a 'presumed' contributor to the pantyhose—was also extraordinarily pristine. Considering the 33-year time span between evidence collection and DNA testing, these observations defy the previously referenced Laws of Thermodynamics, as they apply to biological systems and enzymatic reactions.[279] When DNA from Ms. Mixer is highly degraded and nearly

undetectable after 33 years, DNA deposited by other individuals—at the same time, on the same evidence—cannot miraculously escape the same forces of degradation. The only notable DNA types from the Jane Mixer homicide case samples tested by the MSP Crime Lab were indeed introduced strictly as a consequence of ***recent evidence mishandling, and contamination events***.

Crime lab contamination events and other errors should be compiled and organized into transparently accessible, centralized, corrective action files. When crime lab management endorses a paradigm of denial and concealment, as opposed to a policy of adherence to universally-embraced standards, their casework—and the lab itself—demands careful scrutiny. The John Ruelas DNA detection was ***clearly*** a contamination event. Scientific proof that the detection of Gary Leiterman's DNA on the pantyhose was yet another cross-contamination event will most likely never be indisputably established. However, such proof should not be required—as a precursor for re-examining the hideous fallacies associated with this investigation, the scientific analysis, and the prosecution's distortion of the truth—during the trial of Mr. Gary Leiterman. When the NIJ goes so far as to reference ***this specific case*** as a historically relevant example of DNA contamination, and when the trial testimony of the scientists create multiple layers of doubt—regarding the integrity/timing of handling the defendant's CODIS reference source of DNA—the entire conviction process requires a careful, comprehensive re-examination.

In 1992, the Innocence Project—New York, was founded by the attorneys, Barry Scheck and Peter Neufeld, at the Cardozo School of Law, within Yeshiva University, in New York City, New York.[280] In March, 2018, this outstanding organization agreed to accept Gary Leiterman's case. On July 4, 2019, Gary Leiterman passed away, in the custody of the Michigan Department of Corrections.

ENDNOTES:

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