Texas Forensic Science Commission

Justice Through Science

FINAL REPORT
NATIONAL MEDICAL SERVICES, INC. (NMS) DNA ANALYSIS IN CASE OF *U.S. v. Torney*

April 20, 2018

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I. SUMMARY OF THE COMMISSION'S STATUTORY AUTHORITY

A. Legislative Background and Membership

The Texas Legislature created the Texas Forensic Science Commission ("Commission") during the 79th Legislative Session by passing House Bill 1068 (the "Act"). The Act amended the Texas Code of Criminal Procedure to add Article 38.01, which describes the composition and authority of the Commission.[1] During subsequent legislative sessions, the Texas Legislature further amended the Code of Criminal Procedure to clarify and expand the Commission's jurisdictional responsibilities and authority.[2]

The Commission has nine members appointed by the Governor of Texas.[3] Seven of the nine commissioners are scientists or medical doctors and two are attorneys (one prosecutor nominated by the Texas District and County Attorney's Association, and one criminal defense attorney nominated by the Texas Criminal Defense Lawyer's Association).[4] The Commission's Presiding Officer is Jeffrey Barnard, MD. Dr. Barnard is the director of the Southwestern Institute of Forensic Science and the Chief Medical Examiner of Dallas County, Texas.

B. Accreditation Jurisdiction

The Texas Code of Criminal Procedure prohibits forensic analysis from being admitted in criminal cases if the entity conducting the analysis is not accredited by the Commission:[5]

> "…a forensic analysis of physical evidence under this article and expert testimony relating to the evidence are not admissible in a criminal action if, at the time of the analysis, the crime laboratory conducting the analysis was not accredited by the commission under Article 38.01."[6]

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[1] *See* Act of May 30, 2005, 79th Leg., R.S., ch. 1224, § 1, 2005.
[2] *See e.g.*, Acts 2013, 83rd Leg., ch. 782 (S.B.1238), §§ 1 to 4, eff. June 14, 2013; Acts 2015, 84th Leg., ch. 1276 (S.B.1287), §§ 1 to 7, eff. September 1, 2015, (except TEX. CODE CRIM. PROC. art. 38.01 § 4-a(b) which takes effect January 1, 2019).
[3] TEX. CODE CRIM. PROC. art. 38.01 § 3.
[4] *Id.*
[5] Until the 84th Legislative Session, the accreditation program was under the authority of the Department of Public Safety ("DPS").
[6] TEX. CODE CRIM. PROC. art. 38.35 § (a)(4).

The term "forensic analysis" is defined as follows:

> "Forensic analysis" means a medical, chemical, toxicologic, ballistic, or other expert examination or test performed on physical evidence, including DNA evidence, for the purpose of determining the connection of the evidence to a criminal action, except that the term does not include the portion of an autopsy conducted by a medical examiner or other forensic pathologist who is a licensed physician.[7]

The term "crime laboratory" is broadly defined, as follows:

> "Crime laboratory" includes a public or private laboratory or other entity that conducts a forensic analysis subject to this article.[8]

The forensic discipline discussed in this report is DNA analysis, a discipline subject to accreditation.[9] The laboratory that is the subject of this report, National Medical Services, Inc. ("NMS") is accredited by the Commission and the ANSI-ASQ National Accreditation Board ("ANAB") under the International Organization for Standardization ("ISO") accreditation standard 17025.[10]

C. Investigative Jurisdiction

Texas law requires the Commission to "investigate, in a timely manner, any allegation of professional negligence or professional misconduct that would substantially affect the integrity of the results of a forensic analysis conducted by an accredited laboratory, facility or entity."[11] The Act also requires the Commission to: (1) implement a reporting system through which accredited laboratories, facilities or entities may report professional negligence or professional misconduct; *and* (2) require all laboratories, facilities or entities that conduct forensic analyses to report professional negligence or misconduct to the Commission.[12]

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[7] *Id.* at § (a)(4).
[8] *Id.* at § (d)(1).
[9] Texas law exempts certain forensic disciplines from the accreditation requirement by statute or administrative rule. *Id at* §(a)(4).
[10] *See* http://www.txcourts.gov/fsc/accreditation/ for a list of accredited laboratories.
[11] TEX. CODE CRIM. PROC. art. 38.01 § 4(a)(3).
[12] *Id.* at § 4(a)(1)-(2).

As part of its accreditation authority, the Commission may also:

- Establish minimum standards that relate to the timely production of a forensic analysis to the agency requesting the analysis;
- Validate or approve specific forensic methods or methodologies; and
- Establish procedures, policies and practices to improve the quality of forensic analyses conducted in this State.[13]

The Commission may, at any reasonable time, enter and inspect the premises or audit the records, reports, procedures, or other quality assurance matters of a crime laboratory that is accredited or seeking accreditation.[14]

D. Important Limitations on the Commission's Authority

The Commission's authority contains important statutory limitations. For example, no finding by the Commission constitutes a comment upon the guilt or innocence of any individual.[15] The Commission's written reports are not admissible in civil or criminal actions.[16] The Commission has no authority to subpoena documents or testimony. The information the Commission receives during the course of any investigation is dependent upon the willingness of stakeholders to submit relevant documents and respond to questions posed. The information gathered in this report has ***not*** been subjected to the standards for admission of evidence in a courtroom. For example, no individual testified under oath, was limited by either the Texas or Federal Rules of Evidence (*e.g.*, against the admission of hearsay) or was subjected to cross-examination under a judge's supervision.

[13] *Id.* at § 4-d(b-1).
[14] *Id.* at § 4-d(b-2).
[15] *Id.* at § 4(g).
[16] *Id*. at § 11.

II. INVESTIGATIVE PROCESS

This report contains observations and recommendations regarding the DNA analysis performed by NMS in *United States v Torney*, a sexual assault case in the Superior Court of the District of Columbia Criminal Division (No. 2012 CF1 009423). Typically, the Commission would not consider issues raised in a criminal case in a court outside of Texas. However, on January 28, 2015, the Honorable Herbert B. Dixon, Jr. issued an order in the *Torney* case (the "Dixon Order") that if accurate, could substantially impact the reliability of other DNA cases analyzed by NMS, including Texas cases. As a result, during its August 18, 2017 quarterly meeting, the Commission voted to convene a team of subject matter experts to review the issues set forth in the Dixon Order. The review team includes D. Jody Koehler, the Commission's Senior Scientific Advisor, Dr. John Ballantyne, Associate Director (Research) at the National Center for Forensic Science and Dr. Timothy Sliter, Chief of the Physical Evidence Section at the Southwest Institute of Forensic Sciences. (*See* Ballantyne CV at **Exhibit A**; *See* Sliter CV at **Exhibit B.**) D. Jody Koehler, an ANAB Contract Lead Assessor also represented ANAB. (*See* Koehler CV at **Exhibit C**.)

III. SUMMARY OF THE INQUIRY AND CRIMINAL CASE

The January 2015 Dixon Order granted the U.S. Government's Motion In Limine to Exclude Expert Testimony regarding the DNA Profiles Generated by NMS Lab in the *U.S. v. Torney* case. The court also declined to credit as reliable the testimony of Dr. Phillip Danielson, an NMS advisor at the time the motion was adjudicated. (*See* Dixon Order at **Exhibit D.**) Dr. Phillip Danielson was retained by the defense to comment on NMS Lab's evidence and validations. At the time, Dr. Danielson was a consultant to NMS for DNA-related issues, including DNA validation studies and profile interpretation.

Other observations made in the Dixon Order included:

1. NMS failed to comport with accepted scientific principles in the interpretation of data generated from the anorectal swab (epithelial cell fraction) from the survivor in the case. Therefore, the laboratory's analysis was scientifically unreliable and inadmissible.

2. The language in the NMS report did not accurately capture the substance of the conclusions rendered. Therefore, the conclusions provided in the NMS report were also inadmissible.

NMS received a copy of the Dixon Order in February 2015 and requested a special assessment by ASCLD/LAB to review the lab's Forensic Biology Department DNA quantification and STR amplification and analysis standard operating procedures ("SOPs") and supporting validation studies to assess compliance with the requirements of the FBI's 2011 *Quality Assurance Standards for Forensic DNA Testing Laboratories* (FBI QAS).[17] The validation studies reviewed included the PowerPlex 16HS amplification kit and the Qiagen Investigator Quantiplex HYres quantification kit. The special assessment *did not include* a review of how these chemistries were utilized in any casework. No findings were assessed during the special assessment. (*See* ASCLD/LAB NMS special assessment report at **Exhibit E**).

Commission staff became aware of the *Torney* order during a presentation made by Assistant United States Attorney and Special Counsel for DNA and Forensics ("Special Counsel") at the National Forensic Science Symposium hosted by the National Association of Attorneys General Training and Research Institute in July 2017. Shortly after the presentation, the Commission sent an inquiry to NMS regarding the data shown by Special Counsel. The inquiry included a request for explanation regarding the following: the apparent use of "overblown" DNA data for interpretation; the potential impact on Texas casework performed by

[17] Quality Assurance Standards for Forensic DNA Testing Laboratories (effective 09-01-2011). https://www.fbi.gov/file-repository/quality-assurance-standards-for-forensic-dna-testing-laboratories.pdf/view

NMS; the assertion by a Promega Corporation representative, made in a sworn affidavit to the Honorable Judge Dixon's court, that Promega's amplification kit had been misused by NMS in the analysis of evidence in the *Torney* case; and the factual finding of the court that the NMS technical reviewer in the *Torney* case raised concerns regarding the overblown data during the course of the original testing but was overruled by the laboratory's DNA Technical Leader. On August 10, 2017 Dr. Christian Westring, the NMS Criminalistics Laboratory Director, responded to the Commission's inquiry disputing the findings of the court and the factual content of the Dixon Order. In the NMS response, Dr. Westring asserted that the DNA profile in question in the *Torney* case was not "overblown." (*See* NMS Response 08102017 at **Exhibit F.**) Dr. Westring appeared at the Commission's quarterly meeting on August 18, 2017 to respond to questions regarding the concerns raised in the Dixon Order.[18] During the meeting, Westring continued to maintain the data was not "overblown" even when faced with basic questions by Commissioners indicating the position was scientifically unsupportable.[19]

IV. OBSERVATIONS

A. Case Record

The Commission's subject matter expert panel reviewed the *Torney* case record generated by NMS. This was a comprehensive review that not only encompassed a review of the paper case record, but also analysis of the raw electrophoretic data generated by the laboratory.

1. DNA quantification

Quantification of DNA extracts for questioned samples is required by the Federal Bureau of Investigation Quality Assurance Standards ("FBI QAS"). Quantification kits and their

[18] Dr. Bruce Budowle, a member of the Commission and Director of the University of North Texas Health Science Center-Center for Human Identification, recused himself from this matter because he served as an expert for the Government in the *Torney* case.

[19] Video recordings of Commission quarterly meetings may be viewed at: http://www.txcourts.gov/fsc/meetings/.

associated software utilize a standard curve to generate estimated DNA quantities from forensic samples. The standard curve from the NMS quantification kit utilized standards ranging from 20 ng/uL to 0.004 ng/uL. Qiagen, the quantification kit manufacturer, guarantees linearity within the range of the standard curve. Qiagen's developmental validation of the quantification kit only looked at samples up to 100 ng/uL of DNA.

Sample 02021A was quantified prior to amplification as per the FBI QAS. The quantification value obtained was 223.16 ng/uL. This value was well outside of the linear range of the assay as guaranteed by the manufacturer, as established by the manufacturer during its developmental validation of the kit, or as demonstrated by NMS in its internal validation of the quantification kit. The case analyst did not attempt to dilute or re-quantify the sample. This remedial action was not expressly required under any published national standard or under NMS's quantification SOP. However, it should have been obvious to a qualified analyst that a quantification value so far outside the range of the standard curve was potentially unreliable and that dilution and re-quantification of the DNA extract would have led to the generation of more reliable quantification data.

2. Off-scale ("overblown") data

When an excessive amount of template DNA is amplified during the testing process, the electrophoretic instrument (CE) sends a signal to the firmware that the charge coupled device (CCD) camera is saturated at that data point(s), which is then written to the data file. When the data is analyzed utilizing the GeneMapper ID (or GeneMapper ID-X) software, the software will flag the data as off-scale. When a sample is overamplified, there will be issues with increased artifacts such as pull-up peaks, stutter peaks labeled as alleles due to increased stutter peak ratios, -A peaks, non-specific amplification products, and poor peak morphology. These artifacts may

compromise the interpretation of the profile. These types of issues can also indirectly impact the internal size standard utilized to ensure DNA fragments are assigned an appropriate allele call.

In the *Torney* case, the epithelial cell fraction from the survivor's anorectal swab was overamplified due to excessive template DNA in the amplification reaction. This was recognized by the analyst in the initial instrumental data that was observed from a 5-second injection, which was the standard injection time per laboratory protocol. The analyst repeated the electrophoresis of the sample using a 1-second injection time. This remedial action was in line with laboratory protocol. However, the resulting instrumental data was still off-scale. This led to the analyst noting approximately 71 artifacts on the electropherogram in question. (*See* Sample 02021A at **Attachment G.**) This data exhibited clear -A artifact peaks, increased baseline peaks due to non-specifically amplified products, possible elevated stutter peaks, and pull-up peaks, including pull-up peaks in the internal size standard that impacted the sizing quality of the sample. [20]

In the hands of the review team, the sizing quality of the sample had to be overridden during computer analysis because the pull-up peaks in the internal size standard prevented correct sizing of the data by the software. The analyst failed to recognize the impact these artifacts would have on data interpretation and failed to employ the appropriate methodology to correct the issues. The analyst followed NMS SOPs which did not require additional remedial steps. However, the final data as interpreted by the analyst was clearly unreliable as were the conclusions drawn from the data. This unreliable data was interpreted by the analyst and was reported to the client.

[20] The laboratory has hired an outside expert to determine why there were so many artifacts in the profile in question. Other contributing factors identified by the expert would be in addition to the finding that too much template DNA was amplified.

The practical impact on the criminal justice system of reporting peaks as authentic alleles when they are not can be significant for a case involving a sexual assault by an unknown assailant. For example, in this case NMS reported the anorectal swab from the survivor contained a mixture of "at least three" contributors. In a scenario where the survivor alleges sexual assault by an unknown person while claiming that she or he had no other sexual partners around the time of the assault, a DNA report indicating a mixture of "at least three contributors" would undermine the survivor's own account. This would not be because the survivor actually engaged in sexual activity with multiple partners but rather because the laboratory's failure to understand the proper relationship between casework protocol (and its limitations) and internal validation led to the generation of unreliable data. In other words, the impeachment of the survivor's testimony would be made possible not because of actual physical evidence of additional contributors, but because the laboratory used unreliable data to reach an incorrect conclusion regarding the number of contributors.

3. Lack of documentation for disagreement between technical reviewer, analyst and resolution of disagreement by the DNA Technical Leader

During technical review of a case record, another qualified analyst reviews the data generated, ensures SOPs have been followed to the extent possible while performing a paper review, reviews the report to determine if appropriate associations have been made between the questioned items of evidence and any known samples submitted, and ensures all appropriate documentation is collated within the case record as required by the laboratory's SOPs/quality manual. If an error is found, it is brought to the attention of the analyst and the analyst will correct the issue. If there is an unresolvable interpretational disagreement between the technical reviewer and the analyst, they follow the laboratory's SOP to resolve the disagreement. The NMS SOP in effect at the time stated:

> Prior to issuing a report, both individuals must agree on the interpretation of the data and the conclusions derived from the data. In the event of a disagreement, a third qualified individual (usually the Technical Leader or Criminalistics Director) will be involved to help resolve the dispute. The reviewer(s) may request, following authorization from the Technical Leader, that a sample be re-analyzed to resolve a disputed result. Generally, the most conservative result will be reported (usually "inconclusive" or "uninterpretable") if no agreement can be reached.

While the technical reviewer signed an affidavit in the *Torney* litigation stating she did not agree with the interpretation of the anorectal swab epithelial cell fraction sample and communicated this disagreement, there is no documentation in the case record to indicate a disagreement occurred or the Technical Leader's decision that the sample would be reported without reanalysis.

4. Lack of documentation of data reinterpretation for the amended report

When data is interpreted and a report is issued, the laboratory is required to document the interpretation in the case record as per ISO 17025:2005 4.13.2.2 which states "Observations, data and calculations shall be recorded at the time they are made and shall be identified to a specific task." This includes reinterpretations of data for the issuance of an amended report. There is no documentation for the reinterpretation of the data for the anorectal swab epithelial cell fraction that was communicated in the amended report issued by NMS on July 3, 2014. The laboratory has not supplied additional documentation to support the new interpretation.

B. Validation Review

1. Missing data from the PowerPlex 16HS stutter study

NMS performed a study to verify the published stutter percentages from Promega, the kit manufacturer. Upon examination of the data, it was noted that several data points were missing, all of which were higher than the manufacturer's suggested stutter percentages. (*See* Stutter Study Missing Data Points at **Exhibit H.**) The laboratory is currently reviewing and evaluating

the missing data and will be providing the results of its review in a subsequent report to the Commission.

2. Lack of validation data to support interpretation of off-scale data

While performing the review of the analyzed data for the PowerPlex Fusion 16HS kit performed by NMS, it was noted that only one sample at 4 ng of total input DNA was analyzed during the initial validation. The sample was not off-scale so there is a concern that the sample either was not quantified appropriately or when the amplification reaction was performed, 4 ng of input DNA was not added to the reaction tube. It is not an acceptable practice to only utilize one sample, especially one that exhibits no off-scale data, to ensure that an analyst may reliably interpret data that is greatly off-scale due to a high level of input DNA.

C. Staff Interviews

During staff interviews at NMS, the review team noted that analysts did not convey a clear understanding of the difference between re-amplification of a sample with too much template DNA and dilution of amplified product from a sample with too much template DNA. While both may lower peak heights to ensure data is within the linear range of the CE, diluting amplified product will not address other issues such as -A peaks or artifact peaks due to non-specifically amplified products. During a conference call with new DNA leadership, it was clear that training was provided to staff on this issue in early April 2018. (*See* **Exhibit K**.) Recommendations regarding follow-up on this initial training are discussed in **Section V** below.

Current NMS analysts and the current DNA Technical Leader reviewed the electropherogram for the anorectal swab epithelial cell fraction in *Torney* and agreed they would not be able to interpret the data as it is because there was too much template DNA in the sample. When asked if there were any concerns about losing data by re-amplifying the sample with less

template DNA, they all agreed that the sample was uninterpretable and they could not perform comparisons to it. However, when Dr. Westring was asked the same question, he responded that by re-amplifying the sample with less template DNA the laboratory was, in effect, "losing valuable data" that was present in the sample. This indicates a lack of understanding on the part of Dr. Westring regarding what constitutes reliable data when utilizing the Promega chemistry or indeed, any forensic DNA amplification chemistry. It also indicates a disconnect between the bench analysts and the individual who served as the DNA Technical Leader at the time *Torney* was analyzed.

D. Testimony of Dr. Phillip Danielson

The Dixon Order stated that Dr. Danielson's credibility was significantly undermined when he testified that the data from the anorectal swab epithelial cell fraction was not saturated and that the data should be interpreted. Dr. Danielson also testified that he was able to distinguish between "major" and "minor" split peaks in the data. He was unable to cite any peer-reviewed journal articles, SOPs, or textbooks to support his understanding. The subject matter experts on the review team have also never heard of these concepts and do not agree with Dr. Danielson's views. There were several other issues with Dr. Danielson's testimony. A few examples are as follows:

1. Dr. Danielson testified that "exclusion" can actually mean "inclusion," where the analyst just does not have sufficient data. He claimed there is not an industry-wide definition of what "included" and "excluded" means. This is incorrect information. Inclusion is defined by the SWGDAM guidelines as "**Inclusion:** a conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other). Exclusion is defined as "**Exclusion:** a conclusion that eliminates an individual as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other)."

2. Dr. Danielson testified that the Scientific Working Group for DNA Analysis Methods (SWGDAM) Guidelines for DNA Interpretation "list two times the peak to trough ratio as the way to calculate the analytical threshold." SWGDAM only lists this as one example and states that other methods may be utilized for calculating the analytical threshold. He also stated that the other methods in a scientific paper are inappropriate in light of the SWGDAM guidelines. These methods are not inappropriate, they are just not the same as the example given in the SWGDAM guidelines.

3. Dr. Danielson testified that allele 10 at TH01 at 7,313 RFU (relative fluorescence units) was within the linear range of the instrument. Peaks are determined to be off-scale by the instrument, not by the laboratory. In this instance, the peak in question was in fact labeled as off-scale by the instrument because the detector was saturated by the fluorescence signal from this peak.

4. In the same line of questioning, Dr. Danielson testified that because the peak was within the linear range of the instrument, the manufacturer's calculated stutter percentage would also apply. In this instance, the stutter percentage for the 9 allele to the 10 allele at TH01 is 6.7%. The manufacturer's calculated stutter percentage was 6%. It is well-known that increased stutter percentages will be observed with saturated data. In fact, the NMS DNA SOP (CR-915-01) states that off-scale data can result in elevated stutter.

5. In his testimony about determining an analytical threshold, Dr. Danielson stated that an analytical threshold is calculated utilizing negative controls. This is not always true. It is generally accepted in the forensic DNA community that samples with DNA can also be utilized for this calculation.

6. Dr. Danielson also testified that "none of the loci show an indication of saturation sufficient to invalidate the allele calls and the stutter thresholds that we use." As stated previously in this report, there are several empirical indicators of saturated data, including -A peaks (which is exhibited as split peaks), elevated stutter peaks, pull-up peaks, and an increased number of artifact peaks attributable to non-specifically amplified products. This profile exhibited split peaks, elevated stutter, pull-up and an increased number of artifact peaks. The analyst marked approximately 71 peaks as some type of artifact on the electropherogram.

IV. RELIANCE ON ACCREDITATION

As previously stated, ASCLD/LAB participated in a special assessment of NMS from March 5, 2015-April 5, 2015. During this limited special assessment the accrediting body focused on review and assessment of the following items: the procedure for the use of the PowerPlex 16HS chemistry in support of validation studies; the internal validation studies

including "signal detection linearity and DNA input linearity;" the procedure for the use of the Qiagen Investigator Quantiplex HYRes quantification kit; the internal validation studies for the quantification kit; and the interpretation protocol for PowerPlex 16HS. This review did not include any casework application.

Laboratory staff and criminal justice stakeholders rely on accreditation as an indication that the quality of the laboratory's work is sound. Analysts often testify that the accreditation process assesses scientific validity and acceptance. As an example, consider the following testimony from analysts in two different laboratories:

> *Q. Now, when we hear something like accredited, that sounds good, but what does that actually mean as far as the protocols that y'all have to follow in order to maintain that certification?*
>
> *A. Well, to be accredited, you're actually inspected by the accrediting agency, and they review your procedures to make sure that the procedures that you're following are scientifically valid, as well as accepted in the forensic community. They will come in and check out all of your operations, and then they routinely check—the accreditation cycle is actually a five-year cycle, but they do routinely check every year, or two years to make sure that you're following their guidelines and practices.*
>
> **********
>
> *Q. And y'all would be seeking that ASCLD accreditation?*
>
> *A. Correct, yes.*
>
> *Q. Correct? I mean, that's kind of the gold standard for certification of a laboratory doing the kind of DNA analysis that the lab does?*
>
> *A. Correct, yes.*

Stakeholders place strong emphasis on the accreditation process as an indicator of quality and accuracy of scientific procedures and outcomes. In fact, in one of NMS' letters to the Commission, management stated that "*NMS Labs has demonstrated to ASCLD/LAB and other assessors, on multiple occasions, its compliance with the appropriate accreditation standards,*

prior to, during, and after the Torney matter. NMS Labs has received written notices that we are fully compliant with the method validation requirements and the underlying standards recommendations of the forensic community." And, "*Representatives from ASCLD/LAB also conducted a "Special Assessment" upon my request, including all the data obtained through internal validation, including quantitation assays and STR profiles, SOPs, and NMS Labs' reporting guidelines as referenced in the Judge Dixon's order. NMS Labs passed the audit without findings, and the audit report was approved by the ASCLD/LAB Board of Directors."*

It is apparent that NMS upper management relied on the accrediting body to confirm the laboratory's approach to DNA analysis was appropriate despite the concerns set forth in the Dixon Order. When questioned about ANAB's special assessment at the quarterly Commission Meeting in August 2017, Pamela Sale, ANAB's Vice President for the forensic division, expressed her understanding that the assessor did not review the data in the *Torney* case because it was an active criminal case. This explanation contradicts common practice during assessments. Technical and lead assessors often review cases that have not been adjudicated and are still considered active. ANAB's explanation for the way the *Torney* special assessment was handled is problematic. They evaluated the laboratory's validation work without assessing the extent to which the validation results were being applied appropriately in actual casework. By signing off on NMS' validation work without reviewing the *Torney* case data or any other casework, ANAB's restricted review contributed to the misimpression that NMS had performed appropriate analyses when, at least with respect to the *Torney* case, it clearly had not. (*See* NMS Letter to Travis County District Attorney at **Exhibit I**).

V. CORRECTIVE ACTIONS AND RECOMMENDATIONS

Though NMS' initial response was to deny the factual findings and conclusions in the Dixon Order, NMS upper management initiated a major course correction after the review team's site visit in December 2017. The Commission commends Dr. Barry K. Logan, the Vice President for Forensic Science Initiatives of NMS, for providing his full support and commitment to the process during the period since the site visit. NMS has implemented many important changes in the last four months, including the following: (*See* NMS letters to the Commission dated February 14, 2018 and March 25, 2018 at **Exhibit J**.)

1. NMS modified its management structure and oversight of the DNA laboratory. Dr. Westring is no longer employed by the laboratory and Dr. Danielson is no longer a consultant.

2. The laboratory hired Dr. Charlotte Word as a technical expert to address the issues noted above. Dr. Word has already spent time in the laboratory with unlimited access to staff, records, and operating documents. Another visit is planned for late April 2018. (*See* NMS letter to Commission dated March 25, 2018 at **Exhibit J**, and letter report from Dr. Word to Dr. Logan at NMS, dated April 30, 2019 at **Exhibit L**.).

3. Several corrective actions have been implemented, including an investigation into the management issues contributing to quality issues, an investigation into missing stutter study data, and investigation into the issues identified in the *Torney* case.

4. NMS has identified all 88 Texas cases worked from 2010-2018 and Dr. Word has conducted an initial review of some of these cases. After she completes her review of all Texas cases, the laboratory will determine the extent to which the other approximately 1,200 DNA cases analyzed by NMS for other states may need to be reviewed as well.

5. The laboratory self-identified an additional unrelated issue regarding artifacts included in a Y-STR interpretation that led to an incorrect exclusion in a Harris County sexual assault case. The Harris County District Attorney's office has been notified. This was not an NMS-specific issue but rather one that has been observed in published journal articles and was identified and flagged by NMS in some of its casework. The laboratory will be reviewing other cases to assess whether additional notifications may be necessary.

NMS should continue the action items outlined in **Exhibit J**, including the various items for which outside consultants have been retained. In addition to these items, the review team recommends that any training provided to staff include a form of assessment to determine whether the staff has internalized the concepts presented. Dr. Word is planning a combination of competency sets and practice scenarios to achieve this objective. Finally, the Commission expects NMS to continue to provide Commission staff with quarterly updates regarding the progress made on the items outlined in **Exhibit J**.

CURRICULUM VITAE

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EDUCATION

1997	Ph.D. Genetics State University of New York (SUNY) at Stony Brook Stony Brook, NY, USA
1979	M.Sc. Forensic Science University of Strathclyde Glasgow, Scotland, UK
1976	B.Sc. (Hons) Biochemistry University of Glasgow Glasgow, Scotland, UK

CURRENT POSITION(S)

2009-present	Professor (tenured) Department of Chemistry University of Central Florida, Orlando, FL
1998-2009	Associate Professor (tenured) Department of Chemistry University of Central Florida, Orlando, FL
2000-present	Assistant Director (Biological Evidence) National Center for Forensic Science, Orlando, FL
2001-present	Associate Director (Research) National Center for Forensic Science, Orlando, FL
2009-present	Professor Biomolecular Science Center University of Central Florida, Orlando, FL

2003-2009 Associate Professor
Biomolecular Science Center
University of Central Florida, Orlando, FL

PREVIOUS EMPLOYMENT

1987-1998 Manager/Supervisor and DNA Technical Manager
Biological Sciences Section, Suffolk County Crime Laboratory, NY

1982-1987 Forensic Biochemist, Hong Kong Government Laboratory, Hong Kong

1979-1982 Forensic Biologist, Strathclyde Police Forensic Science Laboratory, Glasgow, UK

1977-1978 Inspector of Police, Royal Hong Kong Police, Hong Kong

1976-1977 Police Constable, Strathclyde Police, Glasgow, Scotland

CERTIFICATION AND LICENSURES

1993-2003 Diplomate of the American Board of Criminalistics (D-ABC)

1987-1997 Chartered Biologist and a Member of the Institute of Biology (U.K.) (CBiol, MIBiol)

OTHER ACADEMIC APPOINTMENTS

1997 Clinical Assistant Professor of Health Sciences, School of Health Technology and Management, SUNY, Stony Brook, NY (part time and voluntary)

1998 Clinical Associate Professor of Health Sciences, School of Health Technology and Management, SUNY, Stony Brook, NY (part time and voluntary)

HONORS

1976 Honors Degree in Biochemistry (B.Sc.) (University of Glasgow, U.K.)

1976 PMAS Book Prize and 7/70 Trophy, Scottish Police College

1979 Forensic Science Society Book Prize for the most meritorious student attending the M.Sc. Forensic Science program at Strathclyde University

1999 Directorate Merit Award for assistance given to Royal Canadian Mounted Police in connection with the Swissair 111 Aircraft disaster

1999	Commemoration award from the FBI for service to the FBI and forensic community as a member of the DNA Advisory Board
2002	Certificate of Appreciation from the Director, National Institute of Justice "for outstanding contributions as a member of the Kinship and Data Analysis Panel in support of the World Trade Center DNA effort"
2004	Received a Research Incentive Award (RIA) from the University of Central Florida in recognition of outstanding research accomplishments
2006	Inducted into the UCF Millionaires Club (for faculty members who have brought at least $1 million in external research funds into the University)
2008	Awarded an ESR (Institute of Environmental Science and Research), New Zealand, International Fellowship
2009	Received a Research Incentive Award (RIA) from the University of Central Florida in recognition of outstanding research accomplishments
2016	Inducted as an inaugural Member of the UCF Chapter of the National Academy of Inventors

SCIENTIFIC SOCIETY MEMBERSHIP

- American Academy of Forensic Sciences (AAFS)
- American Association for the Advancement of Science (AAAS)
- International Society of Forensic Genetics (ISFG)
- American Nano Society (ANS)
- National Academy of Inventors (NAI) (UCF Chapter)

CONSULTING ACTIVITIES

1998-2000	DNA Technical Leader (Consultant) for the Mississippi Crime Laboratory, Jackson, Mississippi
1998-2000	DNA Technical Leader (Consultant) for the State of Delaware Office of Chief Medical Examiner, Wilmington, Delaware
1999-2000	DNA Technical Leader (Consultant) for the South Western Institute for Forensic Science (SWIFS), Dallas County, Texas

2001-2002 Technical Leader (Consultant) for the Sedgwick County Regional Forensic Science Center, Wichita, Kansas

- National Forensic Science Technology Center, St. Petersburg, FL
- US Department of Energy, Washington DC
- Lakehead University, Ontario, Canada
- Onondaga County, NY
- Standards Council for Canada
- Lockheed Martin

CONTINUING EDUCATION / ADDITIONAL TRAINING

1988 Graduate credits in Analytical Separations (3cr. A) from the City University of New York (CUNY)

1989 DNA-Forensic Applications, University of New Haven, CT

1988-1989 Training in the use of molecular biology techniques in the laboratory of Dr. Paul Bingham, Dept. of Biochemistry, SUNY Stony Brook, NY

1989-1997 Training in the use of molecular biology techniques in the laboratory of Dr. Ken Marcu, Dept of Biochemistry, SUNY, Stony Brook, NY

1989 Forensic Application of DNA Typing Methods, FBI Academy, Quantico, VA (Graduate credits in Laboratory Applications of DNA (3cr. A) and Forensic Applications of DNA (3cr. A) from the University of Virginia, VA)

1992 Advanced DNA Typing School at the FBI, Forensic Science Research and Training Center, Quantico, VA.

1994 Statistical Methods in Forensic DNA Analysis, NEAFS Annual Meeting New York, NY

1995 Implementation and Consequences of New DNA Technologies: the Sequel, American Academy of Forensic Sciences, Seattle, WA

1995 Advanced PCR Applications, Florida Crime Laboratory Council and the Florida Forensic Advisory Committee, Orlando, FL

1995 Workshop in Statistics for Forensic Scientists, National Forensic Science Technology Center, St. Petersburg, FL

1995 Advanced DNA Technologies Workshop, American Academy of Forensic Sciences, Nashville, TN

1995	DNA Databanks and Repositories and CODIS Users Group Meeting, Tallahassee, FL (Armed Forces Institute of Pathology)
1995	Advanced DNA Technologies: Automation and Application, American Academy of Forensic Sciences, New York City, NY (invited speaker)
1997	Forensic Sciences Summit: Roadmap to the Year 2000. NIJ/NIST(OLES)/ASCLD workshop, Gaithersburg, MD. Workshop proceedings published by NIJ (1999) (Forensic Sciences: Review of Status and Needs)
1997	Presenting DNA Statistics in Court, Promega 8th International Symposium on Human Identification, Scottsdale, AZ.
1997	Statistics Training for DNA Scientists. Division of Criminal Justice Services, Albany, NY. Two day workshop conducted by Bruce Weir, North Carolina State University
1997	Florida DNA Training Session IV: STRs-The Next Generation. Florida Crime Laboratory Council and the Florida Forensic Advisory Committee, Orlando, FL
2000	ISO/IEC 17025 Assessor Training, Laboratory Accreditation Bureau
2001	SWGDAM, FBI Academy, Quantico, VA
2002	SWGDAM, FBI Academy, Quantico, VA
2003	SWGDAM, FBI Academy, Quantico, VA
2003	Low Copy Number DNA and Extracting DNA Profiles from Challenging Sample Materials Workshops, AAFS, Chicago
2004	Forensic Human Mitochondrial DNA Analysis, AAFS Annual Meeting, Dallas, TX
2004	Y-STR Analysis on Forensic Casework, AAFS Annual Meeting, Dallas, TX
2004	Applied Biosystems Annual User Forum, AAFS Annual Meeting, Dallas, TX
2004	SWGDAM, FBI Academy, Quantico, VA
2005	SWGDAM, FBI Academy, Quantico, VA
2006	SWGDAM, FBI Academy, Quantico, VA
2007	SWGDAM, FBI Academy, Quantico, VA
2007	Statistical Analysis of Real-time PCR Data, CHI Quantitative PCR Conference, San Diego, CA
2008	SWGDAM, FBI Academy, Quantico, VA

PRESENTATIONS (280)

1984 The ABO Typing of Hair as a Routine Casework Method. International Association of Forensic Sciences, Oxford, UK

1988 Quality Assurance in the Forensic Serology Laboratory. Northeastern Association of Forensic Scientists Annual Meeting, Mystic, CT

1992 Validation of AHSG as a Genetic Marker System in Forensic Science. Co-author with L.S. Remmert. Northeastern Association of Forensic Scientists Annual Meeting, Atlantic City, NJ.

1992 Extraction Strategies for Routine HLA DQα Analysis. Co-author with R.S. Jordan and L.S. Remmert. Northeastern Association of Forensic Scientists Annual Meeting, Atlantic City, NJ

1993 Use of a Semi-Automated Multiplex PCR Method to Evaluate Four Short Tandem Repeat Loci. Co-author with J.B. Sgueglia, A. Juston and J. Galdi. Northeastern Association of Forensic Scientists Annual Meeting, Springfield, MA

1994 Validation Studies on a Semi-Automated Multiplex Analysis of Four Short Tandem Repeat Loci, HUMVWA31, HUMTH01, HUMF13A1 and HUMFES/FPS. Co-author with J.B. Sgueglia, A. Juston and K. Galindo. Northeastern Association of Forensic Scientists (NEAFS) Annual Meeting, New York, NY

1994 The Efficacy of PM Analysis for Routine Forensic Biology Casework. Co-author with L. S-Reich and R. S. Jordan. NEAFS Annual Meeting, New York, NY

1994 A Sensitive Rapid Gender Identification Test Utilizing the X-Y Homologous Gene Amelogenin. Co-author with K. Galindo. NEAFS Annual Meeting, New York, NY

1994 Trace and DNA: A Hairy Experience. Co-author with J.B. Sgueglia, T. Zaveski, and L.S-Reich. NEAFS Annual Meeting, New York, NY

1994 Revising an Existing PGM ULPAGIF Method to Accommodate Pharmacia's Reformulated Ampholines. Co-author with C. Wagner, A. Juston, P. Dhawan, R. Baumann and D. Alia. NEAFS Annual meeting, New York, NY

1995 The Integration of HLA DQα and PM Analysis into an Operational Forensic Biology Setting. Amplitype Users Forum, AAFS, Seattle, WA

1995 The Evaluation of Chemiluminescent RFLP Probes for Forensic Casework. Co-author with J.B. Sgueglia, M. Philip and T.L. Ferguson. NEAFS Annual Meeting, Mystic, CT

1995 The Long Island Fingernail Phenomenon. Co-author with D. Alia, R.S. Jordan and L.S. Reich. NEAFS Annual Meeting, Mystic, CT

1995 Use of Bovine Serum Albumin (BSA) as a PCR Additive. Co-author with R. S. Jordan, J. Eberhardt, and L.S. Reich. NEAFS Annual Meeting, Mystic, CT

1996 Multiple STR Multiplexes Make for a Multitude of Possible Genotypes. Amplitype Users Forum, AAFS, Nashville, TN

1996 Quality Assurance in the DNA Laboratory. National Conference on the Future of DNA: Implications for the Criminal Justice System. Washington, DC

1996 Forensic Casework Analysis Using Multiple STR Multiplexes on a Multitude of Sample Types. Co-author with Sgueglia, J.B. and Juston, A.C. Seventh International Symposium on Human Identification. Scottsdale, AZ

1996 Forensic Casework Analysis Using Multiple STR Multiplexes on a Multitude of Sample Types. Co-author with Sgueglia, J.B.S. and Juston, A.C. NEAFS Annual Meeting, Poconos, PA

1996 TWA Mass Disaster-Identification of Human Remains. Co-author with Sgueglia, J.B., Juston, A.C., Reich, L.S., Jordan, R.S., Galdi, J. And Phillip, M. NEAFS Annual Meeting, Poconos, PA

1996 DNA Advisory Board, Eastern Analytical Symposium, Somerset, NJ

1997 TWA Flight 800 Mass Disaster-DNA Identification of Human Remains. Co-author with Sgueglia, J.B., Juston, A.C., Sherlock-Reich, L., Scioli-Jordan, R., Galdi, J. and Philip, M. AAFS Annual Meeting, New York, NY

1997 Multiple STR Multiplexes Make for a Multitude of Possible Genotypes. Co-author with Sgueglia, J.B. and Juston, A. AAFS Annual Meeting, New York, NY

1997 Validation and Casework Analysis Using a Megaplex STR System. Co-author with Sgueglia, J.B., Juston, A.C., Dooling, K.E. and Cannella, C. NEAFS Annual Meeting, White Plains, NY

1998 Casework Analysis Using a Megaplex STR System for Human Identification. Co-author with Sgueglia, J.B., Juston, A.C., Dooling, K.E., Sherlock-Reich, L., Scioli-Jordan, R. and Willard, J. M. AAFS Annual Meeting, San Francisco, CA

1998 The Use of DNA Analysis to Identify Victims of Mass Disasters: TWA Flight 800 and the Wyman-Gordon Forgings, Inc., Explosion. Co-author with Willard, J.M., Lee, D.A., Ross, J.P., Wilson, R.E. and Holland, M.M. AAFS Annual Meeting, San Francisco, CA

1998 Electrophoretic variation at the FGA Locus. Co-author with Sgueglia, J.B.,

Juston, A.C. and Essex,B. NEAFS Annual Meeting, Rhode Island

1998 Testing, Evaluation and Validation, CLIP Summit, NIJ, Washington, DC

2000 How Can DNA Research and Development Enhance Victim's Rights? The Fifth Annual Conference on the future of DNA: Implications for the Criminal Justice System. The National Institute of Justice, U.S. Department of Justice. New York, New York

2001 Development of a Panel of Y Chromosome Markers for Forensic Use. Co-author with Hall, A. AAFS Annual Meeting, Seattle, WA

2001 The Development of a panel of Y chromosome Markers for Forensic Use. Center for Bioinformatics, North Carolina State University, Raleigh-Durham

2001 The Development of an RNA Based Assay System To Supplant Conventional Methods for Body Fluid Identification. Co-author with Juusola, J. 12th International Symposium on Human Identification, Biloxi, MS

2001 The Role of the Crime Laboratory in Mass Fatality Incidents. American Society of Crime Laboratory Directors (ASCLD) Annual Meeting, Phoenix, AZ

2001 Forensic Identification by Nuclear and Mitochondrial DNA. Maples Center for Forensic medicine, University of Florida, Gainsville, FL

2002 Robust Multiplex Amplification of Y-STR Loci. Co-author with Hall, A. AAFS Annual Meeting, Atlanta, GA

2002 New ways of looking at old and old ways of looking at new DNA. Ancient DNA Training Program, Lakehead University, Thunder Bay, Canada

2002 The Development of an RNA Based Assay System for Body Fluid Stain Identification. Co-author with Juusola, J. AAFS Annual Meeting, Atlanta, GA

2002 Forensic Biometrics: The Determination of Individual Physical Characteristics by DNA Typing. Co-author with Kotkin, M. 13th International Symposium on Human Identification, Phoenix, AZ

2002 Body Fluid Identification by RNA Profiling. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2002 Y-Chromosome Markers. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2002 Assessment and Repair of Damaged DNA. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2003 Highly Discriminating Y-STR Multiplexes Suitable for Forensic Use to Permit the Determination of 49-loci Male Haplotypes. Co-author with Hansen, E. AAFS Annual Meeting, Chicago, IL

2003 DNA Identification of Mass Fatality Casualties. Florida Emergency Mortuary Response System Training Seminar, Orlando, FL

2003 A Mass Fatality Guide for Medical Examiners and Coroners. Co-author with Whitcomb, C. AAFS Annual Meeting, Chicago, IL

2003 The Design and Compilation of a US Y -STR Haplotype Reference Database. Co-author with Berdos, P., and Hansen, E. AAFS Annual Meeting, Chicago, IL

2003 Y-SNP Analysis by Pyrosequencing. Co-author with Fletcher, J. AAFS Annual Meeting, Chicago, IL

2003 Strategies for Typing DNA from Damaged Spermatozoa. Co-author with Hall, A. Extracting DNA Profiles from Challenging Sample Materials Workshop. AAFS Annual Meeting, Chicago, IL

2003 Innovative Uses of Y Chromosome Markers in Forensic Science. Ancient DNA Training Program, Lakehead University, Thunder Bay, Canada

2003 Assessment of Damaged DNA Templates. Co-author with Hall, A. NIJ fourth Annual DNA Grantees Workshop, Washington DC

2003 Streamlined Processing of Sexual Assault Kits: Programs and Early Applications. Co-author with Hall, A. NIJ fourth Annual DNA Grantees Workshop, Washington DC

2003 DNA Profiling of the Semen Donor in Extended Interval ($\geq$48 h) Post Coital Cervicovaginal Samples. Co-author with Hall, A. European Academy of Forensic Sciences of the European Forensic Science Institutes, Istanbul, Turkey

2003 Messenger RNA Profiling for Body Fluid Identification. Co-author with Juusola, J. FBI Symposium on Crime Laboratory Management. Minneapolis, MN

2004 Stability and Recovery of mRNA in Biological Stains. Co-author with Setzer, M. and Juusola, J. AAFS Annual Meeting, Dallas, TX

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Co-author with Juusola, J. and Miller, K. AAFS Annual Meeting, Dallas, TX

2004 Strategies for Low Copy Number (LCN) DNA Analysis. Co-author with Hanson, E. and Raker, V. AAFS Annual Meeting, Dallas, TX

2004 Mitochondrial DNA Analysis by Pyrosequencing. Co-author with Hastings, S. and Dugan, K. AAFS Annual Meeting, Dallas, TX

2004 The Design and Development of a Comprehensive 49 Locus Y-STR Database For Major U.S. Populations (poster). Co-author with Berdos, P. AAFS Annual Meeting, Dallas, TX

2004 The Design and Development of a Comprehensive 49 Locus Y-STR Database For Major U.S. Populations. Co-author with Berdos, P. Y-STR Analysis on Forensic Casework Workshop, AAFS Annual Meeting, Dallas, TX

2004 Getting Blood Out of Stone: Eking Out More Information from Physiological Stains. Applied Biosystems Annual Users Forum, AAFS Annual Meeting, Dallas, TX

2004 Assessment and *In Vitro* Repair of Damaged DNA Templates. Co-author with Hall, A. Florida Academy of Sciences Annual Meeting, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Co-author with Juusola, J. Florida Academy of Sciences Annual Meeting, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Mid West Association of Forensic Scientists (MAFS) Spring Workshop, Chicago, IL

2004 Pyrosequencing Applications in Forensic Science: Y-SNPs, mtDNA Analysis and Microbial Forensics. Mid West Association of Forensic Scientists (MAFS) Spring Workshop, Chicago, IL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Ancient DNA Internship Program, Paleo-DNA Laboratory, Lakehead University, Thunder Bay, Ontario, Canada

2004 The Molecular Genetics of the Y Chromosome and the Utility of Y-Chromosome Markers in Forensic Science. Forensic DNA Technology Workshop, Promega Corporation and Center for Forensic Sciences, Toronto, Canada

2004 Assessment and Repair of Damaged DNA Templates. Co-author with Hall, A. NIJ Fifth Annual DNA Grantees Workshop, Washington DC

2004 Determination of the Age of an Individual from Biological Samples Deposited at the Crime Scene. Annual Conference on Criminal Justice Research and Evaluation, Washington DC

2004 Assessment and Repair of Damaged DNA Templates. Co-author with Hall, A. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 A Modified Whole Genome Amplification Method for STR Analysis Using Single or Few Cell Equivalents of Input genomic DNA. Co-author with Hanson, E. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 Age Determination: The Identification of Newborns Using messenger RNA Profiling Analysis. Co-author with Alvarez, M. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex Real Time PCR. Co-author with Juusola, J. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 The Forensic Biology Program at the National Center for Forensic Science. The FRN/CLIP National Conference: Innovative Partnerships. Tampa, FL

2004 Principles of Nucleic Acid Biochemstry. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Y chromosome Biology. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Basic Population Genetics. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Inference of Human Geographic Origins Using *ALU* Insertion Polymorphisms. Co-author with Ray, D., Walker, J., Hall, A., Llewellyn, B., Christian, A., Turteltaub, K. and Batzer, M. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Assessment and *In Vitro* Repair of Damaged DNA Templates-Forensic Implications. Co-author with Hall, A. American Society for Microbiology Conference. DNA Repair and Mutagenesis: From Molecular Structure to Biological Consequences, Southampton, Bermuda

2005 A Lot from a Little: Forensic Genetics at UCF/NCFS. Midwest Research Institute (MRI), Palm Bay, FL

2005 Strategies for the Automation of Forensic Serology Operations. Quest for Automation and the Reality of Quality Standards Workshop. Sponsored by Fitzco Inc. and Quality Forensics. AAFS Annual Meeting, New Orleans.

2005 Age Determination: The Identification of Newborns Using Messenger RNA Profiling Analysis. Co-author with Alvarez, M. AAFS Annual Meeting, New Orleans

2005 Assessment and *In Vitro* Repair of Damaged DNA Templates. Co-author with Hall, A. AAFS Annual Meeting, New Orleans

2005 mRNA Profiling for Body Fluid Identification Using Multiplex Real-Time PCR. Co-author with Juusola, J. AAFS Annual Meeting, New Orleans

2005 mRNA Profiling: Body Fluid Identification Using Multiplex Real-Time PCR. Co-author with Juusola, J. Promega's 16th International Symposium on Human Identification, Grapevine, TX

2005 The Future of DNA Profiling in Sexual Assault Investigations. Keynote speech. International Symposium on Sex Crimes, Toronto Police Department, Toronto, Canada

2005 Future of DNA Including Strategies for the Automation of Forensic Serology Operations. External Lecture Series. Centre for Forensic Sciences, Toronto, Canada.

2005 DNA-STR Testing in Criminal Investigations and Mass Disasters. Department of Anthropology, University of Western Ontario, Canada

2005 An investigation of YSTR haplotype clustering among 298 Caucasian men in the US. American Society of Human Genetics Annual Meeting, Salt Lake City Utah. Co-author with Garvey, D., Berdos, P. and Sims, L.

2005 mRNA Applications in Forensic Genetics. Applied Biosystems Seminars, Foster City, CA

2006 The Biological Evidence Program at the National Center for Forensic Science, NIJ Applied Technologies and Partnerships Conference, Hilton Head, SC

2006 Age Identification by RNA Profiling: Validation of a Newborn Child- Specific Real-Time PCR Assay. Co-author with Alvarez, M. AAFS Annual Meeting, Seattle, WA

2006 Biochemical Repair and Lesion Bypass of Damaged DNA. Co-author with Hall, A, Woodgate, R and McDonald, J.AAFS Annual Meeting, Seattle, WA

2006 mRNA Profiling: Identification of Solid Tissues of Forensic Interest by Multiplex Real-Time PCR. Co-author with Juusola, J. AAFS Annual Meeting, Seattle, WA

2006 Development of a Speedy Rape Kit Screening Method. Co-author with Hall, A. AAFS Annual Meeting, Seattle, WA

2006 A Comparison of the Performance of Commercial Y-STR Kits for Operational Use with Challenging Samples: Extended Interval Post-Coital Samples, Mixtures and Environmental Insults Co-author with Press, K. and Hall, A. AAFS Annual

Meeting, Seattle, WA

2006 Population genetics of the Y chromosome and application of Y-STRs to casework. Future Trends in Forensic DNA Technology, Practical STR Statistics Workshop, Los Angeles, CA.

2006 mRNA Tissue Identification. The Bode Technology Group Third Annual Advanced DNA Technology Workshop, San Diego, CA.

2006 Ethnogeographic Profiling: The Development of a Hierarchical SNP Typing System to Predict Ethnogeographic Ancestry. Co-author with Sims, L. and Garvey, D. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL

2006 Taught Degree Courses: US Experience. International Forensic e-Symposium™ on Forensic Education, The Forensic Institute 2006 Series (www.e-symposium .com)

2006 The Compilation and Management of a Comprehensive US Y-STR Reference Database. Co-author with Fatolitis, L. Annual NIJ DNA Grantees Meeting, Washington DC

2006 The Determination of the Physical Characteristics of an Individual fromBiological Stains: Age Determination. Co-author with Alvarez, M. Annual NIJ DNA Grantees Meeting, Washington DC

2006 Human Identity Testing: A Biotechnology Based Revolution. Qiagen Investor and Analyst Meeting, New York City

2006 Mass Fatality Incident Management. Technologies for Critical Incident Preparedness Conference and Exposition. Atlanta, GA

2006 Burnett Honors College's Career Opportunities in the Biomedical Sciences. Forensic Science Careers. University of Central Florida, Orlando, FL

2006 The Use of Recently Phylogenetically Defined Y-SNPs in a Typing System to Predict Ethnogeographic Ancestry Using Pyrosequencing Technology. Sims, L., Garvey D. and Ballantyne, J. 17th International Symposium on Human Identification, Nashville, TX

2006 Strategies for Obtaining a DNA Profile of the Male Donor in Extended Interval (>72h) Post-Coital Cervico-Vaginal Samples Using Commercial Y-STR Multiplex Systems: Extraction Techniques, Post Amplification Clean Up and Novel Enzymes. Mayntz-Press, K. and Ballantyne, J. 17th International Symposium on Human Identification, Nashville, TX

2006 Dual Extraction of RNA and DNA from Human Body Fluids for Use in Forensic Casework. Hall, K., Kelly, A., Lin, M., Ballantyne, J., Craig, R. and Dugan, K. 17th International Symposium on Human Identification, Nashville, TX

2006 The SWGDAM Y Committee and the Consolidated National Y-STR Database. National CODIS Meeting, Crystal City, VA

2006 The Determination of Physical Features of the Donor of a Crime Scene Sample. National Conference on Science and the Law. St Petersburg, FL.

2007 The Differentiation of Sub-Populations within Y-SNP Haplogroup G. Sims, L., Klega, K., Garvey, D. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 Microbial Genetic Signatures. Donigan, M. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 Biochemistry of Dry State DNA: Comparison of Depurination Rates of Bases. Pope, A. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 The Development of a Highly Informative, Hierarchical Multiplex SNP Typing System to Predict Ethnogeographic Ancestry Using Pyrosequencing Technology. Sims, LM, Garvey, D and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 Simplified Low Copy Number (LCN) DNA Analysis by Post PCR Purification. Smith, PJ and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 Novel Techniques for Identifying the Semen Donor in Extended Interval Post-Coital Samples. Mayntz-Press, K, Sims, L and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 The Forensic Identification of Newborns using Messenger RNA Profiling Analysis. Alvarez, M. and Ballantyne, J. Cambridge Healthtech International Meeting on Quantitative PCR, San Diego, CA

2007 Alternative Strategies to Increased Cycle Number for Low Copy Number (LCN) DNA Analysis. Forensic e-SymposiumTM. Human Identification: Profiling of degraded and low amounts of DNA

2007 The Determination of the Physical Features of the Donor of a Crime Scene Sample. NIJ Applied Technology Conference, Orange County, CA.

2007 Getting Blood form a Rock: Getting More and More from Less and Less. International Society for Optical Engineering (SPIE) Defense and Security Symposium, Orlando, FL

2007 Y-STR Profiling in Extended Interval (> 3 days) Post Coital Samples. Future Trends in Forensic DNA Technology Seminar Series (Applied Biosystems HID University), Chicago, IL.

2007 Double Strand Break Repair of Damaged DNA Templates. Lamers, R and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 Forensic Resource Network Operational Casework Support Programs at the National Center for Forensic Science. The NIJ Conference. Arlington, VA

2007 A Genetic Eyewitness: The Determination of Physical Characteristics of the Donor of a Body Fluid Stain. The NIJ Conference. Arlington, VA

2007 Determination of the Age (Time Since Deposition) of a Biological Stain. Hanson, E. and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 The Determination of the Physical Characteristics of an Individual from Bloodstains: Biological Age Determination. Alvarez, M. and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 Y-STR Profiling in Extended Interval (> 3 days) Post Coital Samples. Future Trends in Forensic DNA Technology Seminar Series (Applied Biosystems HID University), Waltham, MA.

2007 Y-STR Operational Casework Support Programs at the National center for Forensic Science. Association of Forensic DNA Analysts and Administrators summer meeting, Austin, TX

2007 Long Term Ambient Temperature Storage, Stability, and Recovery Efficiency of RNA from a Reversible Porous Nanoparticle Matrix. Alvarez, M., Almazan, M., Hogan, M., Utermohlen, J. and Ballantyne, J. 18th International Symposium on Human Identification, Hollywood, CA

2007 Repair of Human DNA from Forensic Samples. Loseke, D., Carrano, J., Ballantyne, J., McDonald, J., Woodgate, R. and Hall, A. 18th International Symposium on Human Identification, Hollywood, CA

2007 Determining the Physical Characteristics of an Individual from Bloodstains: Biological Age Determination. Alvarez, M. and Ballantyne, J. 18th International Symposium on Human Identification, Hollywood, CA

2007 The Whys and Whatnots of Y-STR Casework Analysis. General Electric Global Research and the University of Albany Northeast Regional Forensic Institute, Forensic DNA Initiatives Seminar, Niskayuna, NY

2007 Biology of the Y Chromosome and Y-STRs. New technologies and applications

in forensic biology workshop. 2nd Tri-Division Educational Conference. Utah Division, Nevada State Division and the Arizona Identification Council of the International Association for Identification in conjunction with the Northwest Association of Forensic Scientists. Salt Lake City, UT.

2007 Getting Blood from a Stone: Getting More and More Forensic Evidence form Less and Less. Qiagen Corporation, Gaithersburg, MD.

2008 Incarcerations and Exonerations: The Key Role of the Forensic Sciences. Incarcerations and Exonerations-Criminalistics (DNA). AAFS Annual Meeting, Washington, DC.

2008 DNA Profiling of the Semen Donor in Extended Interval (> 72 h) Post Coital Cervicovaginal Samples. Ballantyne, J. and Hanson, E. NIJ Applied Technologies Conference, Point Clear, AL.

2008 Its 2008, what can the Crime Lab do for you: New Technologies and DNA? Ballantyne, J. and Hanson, E. NIJ Applied Technologies Conference, Point Clear, AL.

2008 Not your CSI DNA Profiling: Messenger RNA Profiling Applications in Bio-Molecular Forensics. Department of Chemistry Seminar Series, Florida International University, Miami, FL.

2008 Biology of the Y Chromosome and Y-STRs. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Messenger RNA Profiling: A Prototype Method for Body Fluid and Tissue Identification. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Messenger RNA Profiling: Prediction of the Age of an Individual from RNA Recovered from the Crime Scene. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 A 'Genetic Eyewitness': the Determination of the Physical Features of the Donor of a Crime Scene Sample. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Data Preparation for Forensic DNA Typing. Johnson, M. and Ballantyne, J. Discovery 2008 (the data exploration conference), Cary, NC.

2008 Double Strand Break Repair of Damaged DNA Templates. Ballantyne J. and Lamers, R. The NIJ Conference, Crystal City, VA.

2008 Hypsochromic Spectral Shifts of the Hemoglobin Soret Band Correlate with the Time since Deposition of Dried Bloodstains. Hanson, E. and Ballantyne J. The

NIJ Conference, Crystal City, VA.

2008 Improved Detection of Male DNA from Post-Coital Samples. Ballantyne J. and Hanson, E. The NIJ Conference, Crystal City, VA.

2008 DNA Profiling of the Semen Donor in Extended Interval Post-Coital Samples Ballantyne J. and Hanson, E. The NIJ Conference, Crystal City, VA.

2008 Y-STR Databases. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 Y-STR Interpretation Guidelines. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 New Y-STR Multiplexes. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 A Y-STR Mixture Frequency Estimator. Macmillan, K., Gefrides, L., Klein, C., Fatolitis, L., Ballantyne, J. and Kahn, R. 19th International Symposium on Human Identification, Hollywood, CA.

2008 Hypsochromic Spectral Shifts of the Hemoglobin Soret Band Correlate with the Time since Deposition (TSD) of Dried Bloodstains. Hanson, E. and Ballantyne, J. 19th International Symposium on Human Identification. Hollywood, CA.

2008 The Fundamental Biochemistry of Dry State DNA: Hydrolytic Reactions. Marrone, A. and Ballantyne, J. 19th International Symposium on Human Identification, Hollywood, CA.

2008 Research at the National Center for Forensic Science. ESR Forensic Group, Auckland, New Zealand.

2008 Research at the National Center for Forensic Science. ESR Headquarters, Wellington, New Zealand.

2008 Why the Y?: Y Chromosome Biomarker Applications in Sexual Assault Investigations. New Zealand Forensic Science Society, Auckland, New Zealand.

2008 Messenger RNA Profiling Applications in Bio-Molecular Forensics. Forensic Science Institute, University of Central Oklahoma, Edmond, OK.

2008 Y Chromosome Applications in Forensic Casework. Arizona Department of Public Safety, Phoenix, AZ

2008 Forensic Biology Research at the National Center for Forensic Science. The 20th EDNAP (European DNA Profiling Group) Meeting, Zurich, Switzerland (NR/I/I)

2008 Messenger RNA Profiling for Body Fluid Identification. The 29th ENFSI (European National Forensic Science Institutes) DNA Working Group Meeting, Zurich, Switzerland (NR/I/I)

2009 Determination of the Age (Time since Deposition) of a Biological Stain. Ballantyne, J. and Hanson, E. BrightTALK DNA Identification Summit. Webinar

2009 A Y-STR Mixture Frequency Estimator in Forensic Casework. MacMillan, K., Genfrides, L., Klein, C., Fatolitis, L., Ballantyne, J. and Kahn, R. AAFS Annual Meeting, Denver, CO.

2009 Post Coital Interval for DNA Testing. The Fifth National SART (Sexual Assault Response Team) Training Conference, Seattle, WA.

2009 Beyond Traditional DNA Markers: Predicting a Person's Appearance from DNA Evidence. The Annual NIJ Conference, Washington, DC.

2009 Sexual Assault: Obtaining DNA from Evidence Collected up to a Week Later. The Annual NIJ Conference, Washington, DC.

2009 De-Convolution of Body Fluid Mixtures: Cell Type Identification and Single Source Genetic Profiling of Micro-Dissected Cells. Ballantyne, J and Hanson, E. The Annual NIJ Conference, Washington, DC.

2009 Improved Detection of Male DNA From Post Coital Samples. Hanson, E., Korfhage, C., Loeffert, D and Ballantyne, J. The Annual NIJ Conference, Washington, DC.

2009 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. The Annual NIJ Conference, Washington, DC.

2009 Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs. Hanson, E., Lubenow, H and Ballantyne, J. 23rd World Congress, International Society for Forensic Genetics, Buenos Aires, Argentina

2009 Body Fluid Identification by RNA Expression Profiling. BrightTALK Forensic Science Community webcast

2009 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. 20th International Symposium on Human Identification. Promega, Las Vegas, NV

2009 Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs. Hanson, E. and Ballantyne, J. 20th International Symposium on Human Identification. Promega, Las Vegas, NV.

2009 Simultaneous Determination of the Time Since Deposition and Identification of Dried Bloodstains Using a Portable Spectrophotometer. Hanson, E. and Ballantyne, J. European National Forensic Science Institutes (ENFSI) DNA Working Group, Edinburgh, UK.

2009 Optimization of Isolation Strategies for the Simultaneous Recovery of DNA and RNA from Forensic Samples. Parker, C, Hanson, E. and Ballantyne, J. Joint Forensic Science Association Meeting (Southern Association of Forensic Science, Mid-Atlantic Association of Forensic Science, Midwestern Association of Forensic Science, Southwest Association of Forensic Science). Orlando, FL.

2009 Recent Research into Extending the Post Coital Time Interval for DNA Profile Recovery. Ballantyne, J. International Association of Forensic Nurses, Sexual Assault Forensic Examiner Technical Assistance (SAFEta) webinar on Timing Considerations for Sexual Assault Examination.

2010 Extending the Post Coital Time Interval for DNA Profile Recovery. Orange County SART (Sexual Assault Response Team), Orlando, FL

2010 MicroRNA Expression Profiling for the Identification of Forensically Relevant Biological Fluids. Cambridge Healthtech Institute's 17th International Molecular Medicine Tri-Conference, San Francisco, CA.

2010 Forensic Biology Research at the National Center for Forensic Science. EDNAP (European DNA Profiling Group) Meeting, The Hague, Netherlands

2010 New York City Frye Hearing 2008-2010 People v. Megnath. The 32nd ENFSI (European National Forensic Science Institutes) DNA Working Group Meeting, The Hague, Netherlands

2010 Not your CSI DNA Profiling: RNA Applications in Forensic Genetics. 12th annual Ancient DNA Training Program, Lakehead University Paleo-DNA Laboratory, Thunder Bay, Ontario, Canada

2010 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. The Annual NIJ Conference, Washington, DC.

2010 Identification of Forensically Relevant Body Fluids and Tissues by Small RNA Profiling. Hanson, E. and Ballantyne, J. The Annual NIJ Conference, Washington, DC.

2010 Body Fluid Identification by RNA Profiling. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2010 Use of the National YSTR database and YSTR Mixture Deconvolution. Current

and Future Advances in Human Identification Conference (hosted by the Virginia Department of Forensic Sciences), Hampton, VA.

2010 Forensic Biology Research at the National Center for Forensic Science. EDNAP (European DNA Profiling Group) Meeting, Kiev, Ukraine

2010 External Visible Trait, Kinship and Ancestry Profiling using Large Scale SNP Panels. European Network of Forensic Science Institutes DNA Working Group Meeting, Kiev, Ukraine

2011 From the Bed to the Bench: Defining the Vaginal and Cervical Environment for Post-Coital DNA Recovery. Speck, P., Faugna, D. and Ballantyne, J. AAFS Annual Meeting, Chicago, IL.

2011 Evolution of DNA Mixture Interpretation. DNA Mixture Interpretation Workshop organized by the National Forensic Science Technology Center, Clearwater Beach, FL.

2011 Interpretation of Y STR Mixtures and Statistical Applications organized by the National Forensic Science Technology Center, Clearwater Beach, FL.

2011 Forensic Biology Research at the National Center for Forensic Science. EDNAP (European DNA Profiling Group) Meeting, Brussels, Belgium

2011 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Hanson, E. and Kiavand, A. The Annual NIJ Conference, Washington, DC.

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2011 The Effects of Y-STR Research on Practice and Policy. The Annual NIJ Conference, Washington, DC.

2011 DNA Mixture Deconvolution by Binomial Sampling of Individual Cells. Ballantyne, J. and Perlin, M. International Conference on Forensic Inference and Statistics (ICFIS). Seattle, WA.

2011 Optimization of Dried Stain Co-Extraction Methods for Efficient Recovery of High Quality DNA and RNA For Forensic Analysis. Parker, C., Hanson E., Ballantyne, J. 24th World Congress of the International Society of Forensic Genetics, Vienna, Austria.

2011 Validation of the Hemoglobin (Hb) Hypsochromic Shift Assay for Determination Of The Time Since Deposition (TSD) Of Dried Bloodstains. Albornoz, A., Hanson E., Ballantyne, J. 24th World Congress of the International Society of Forensic Genetics, Vienna, Austria.

2011 Identification of Skin in Touch/Contact Forensic Samples by Messenger RNA Profiling. Hanson E., Haas, C., Jucker, R., Ballantyne, J. 24th World Congress of the International Society of Forensic Genetics, Vienna, Austria.

2011 Collaborative EDNAP Exercises on Messenger RNA/DNA Co-Analysis For Body Fluid Identification (Blood, Saliva, Semen) And STR Profiling. Haas, C., Hanson, E., Morling, N., Ballantyne, J. 24th World Congress of the International Society of Forensic Genetics, Vienna, Austria.

2011 Enhanced DNA Profiling of the Semen Donor Can Assist the Investigation of Late Reported (> 5days) Sexual Assaults. Hanson, E. and Ballantyne, J. American Society of Crime Lab Directors (ASCLD) Annual Symposium, Denver, CO.

2011 Determination of the Time Since Deposition (TSD) of Dried Bloodstains. Hanson, E. and Ballantyne, J. American Society of Crime Lab Directors (ASCLD) Annual Symposium, Denver, CO.

2011 The Definitive Identification of Biological Fluids and Tissues in Forensic Sexual Assault Evidence Using Highly Specific RNA Biomarkers. Hanson, E. and Ballantyne, J. American Society of Crime Lab Directors (ASCLD) Annual Symposium, Denver, CO.

2011 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Hanson, E. and Kiavand, A. American Society of Crime Lab Directors (ASCLD) Annual Symposium, Denver, CO.

2011 Identification of Highly Specific RNA Biomarkers for the Identification f Vaginal Secretions in Forensic Casework. Hanson, E. and Ballantyne, J. 22nd International Symposium on Human Identification, National Harbor, MD.

2011 Y-Chromosome Specific Nested PCR Pre-Amplification Method for Improved Detection of Male DNA. Hanson, E., Solivan, M., Strauss, S., Di Pasquale, F., Engel, H. and Ballantyne, J. 22nd International Symposium on Human Identification, National Harbor, MD.

2011 Y-Chromosome Biology and the National Y-STR Database. Ballantyne, J. Y-Chromosome Short Tandem Repeat (Y-STR) Analysis and Typing, California Criminalistics Institute, Richmond CA (webinar).

2011 Forensic Biology Research at the National Center for Forensic Science. Ballantyne, J. European DNA Analysis Profiling (EDNAP) Meeting, Athens, Greece

2011 Identification of Highly Specific RNA Biomarkers for the Identification of Vaginal Secretions in Forensic Casework. Hanson, E and Ballantyne, J. European National Forensic Science Institutes (ENFSI) DNA Working Group Meeting, Athens, Greece

2011 Enhanced DNA Profiling for Detection of the Male Donor in Trace DNA Samples. Hanson, E and Ballantyne, J. European National Forensic Science Institutes (ENFSI) DNA Working Group Meeting, Athens, Greece

2011 Identification of Fetal Blood Using Developmentally Regulated Gamma Hemoglobin Isoforms. Ballantyne J. Rapid Biological Screening & Analysis Methodologies for Improving Throughput Workshop, Technology Transition Workshop, National Forensic Science Technology Center (Webinar)

2011 Time Since Deposition of Dried Bloodstains Using Ultraviolet/Visible (UV-VIS) Spectrometric Analysis of Hemoglobin. Ballantyne J. Rapid Biological Screening & Analysis Methodologies for Improving Throughput Workshop, Technology Transition Workshop, National Forensic Science Technology Center (Webinar)

2011 Impact of restricted marital practices on genetic variation in a distinctive endogamous population. Pemberton TJ, Li F, Hanson EK, Mehta NU, Mendoza-Fandino GA, Ballantyne J, Belmont JW, Rosenberg NA, Tyler-Smith C, Patel PI. 12th International Congress of Human Genetics/61st Annual Meeting of The American Society of Human Genetics, Montreal, Quebec, Canada.

2011 Fact vs. Fiction: Forensics. Orlando Skeptics, Orlando, FL

2012 Post-Coital DNA Recovery Phase 2: Early Results From Participating Couples Speck, P., Ballantyne, J., Connor, P., Donohoe, M., Hanson, E., Likes, W. and Cashion, A. AAFS Annual Meeting, Atlanta, GA

2012 Development of Optimized Recovery and DNA Typing Methodologies for the Analysis of "Touch and Contact" DNA Samples. Hanson, E., Kelley-Primozic K., Vigil, B., Bisbing, R. and Ballantyne, J. AAFS Annual Meeting, Atlanta, GA

2012 Forensic Biology Research at the National Center for Forensic Science, Virginia Commonwealth University, Richmond, VA.

2012 Advanced Topics in Forensic DNA Analysis. Forensic Science Training for Capital Defense Attorneys: Advanced Issues. Bureau of Justice Assistance and the National Clearing House for Science, Technology and the Law, Las Vegas NV

2012 DNA Mixture Genotyping by Probabilistic Computer Interpretation of Binomially Sampled Laser Captured Cell Populations: Combining Quantitative Data for Greater Identification Information. Ballantyne J, Hanson EK and Perlin MW. NIJ Conference, Crystal City, VA.

2012 Identification of Forensically Relevant Body Fluids and Tissues by RNA Profiling. Presented at the 'Upstream Screenings for Downstream Savings at the

Front End of a Forensic Investigation' Session. Ballantyne J and Hanson EK. NIJ Conference, Crystal City, VA.

2012 Current Status and Future of Y-STR Analysis Workshop. Association of Forensic DNA Administrators and Analysts (AFDAA), San Antonio, TX

2012 Identification of Skin in Touch/Contact Forensic Samples by Messenger RNA Profiling. Ballantyne J and Hanson EK. Association of Forensic DNA Administrators and Analysts (AFDAA), San Antonio, TX

2012 SWGDAM Update. Association of Forensic DNA Administrators and Analysts (AFDAA), San Antonio, TX

2012 Enhanced DNA Profiling of the Semen Donor Can Assist the Investigation of Late Reported (>6 days) Sexual Assaults. Ballantyne J and Hanson EK. Green Mountain DNA Conference. Burlington, VT

2012 Y-STR Database Implementation, Usage and Considerations. Promega's Y-STR Analysis Seminar, Milwaukee, WI

2012 Forensic DNA Technology and Genetic Implications on Privacy, Canada National DNA Databank Advisory Committee, Ottawa, Canada

2012 EDNAP mRNA Profiling exercises 4 + 5. Haas C, Hanson E and Ballantyne, J. EDNAP (European DNA Profiling Group) meeting, Linkoping, Sweden.

2012 Y-Chromosome specific nested PCT pre-amplification method for improved detection of male DNA. Hanson E, Solivan M, Strauss S, Di Pasquale F, Engel H and Ballantyne, J. Presented by Scherer, M. DNA in Forensics 2012: Exploring the Phylogenies (5th EMPOP Meeting, 8th Y-Chromosomal User Workshop), Innsbruck, Austria.

2012 Post Coital DNA Recovery Phase 2: Early Results from Participating Couples. Speck P, Ballantyne J, Connor P, Donohoe M, Hanson E, Lee E and Likes W. 2012 IAFN Annual Scientific Assembly (20th Annual), Fajardo, Puerto Rico.

2012 EDNAP mRNA Profiling Exercise 5. Haas C, Hanson E and Ballantyne J. EDNAP (European DNA Profiling Group) meeting, Brussels, Belgium.

2012 Beyond DNA: Other Forensic Biology Applications to Legal Medicine. Visionen und Zukunft der Forensik, University of Zurich, Institute for Legal Medicine, Zurich, Switzerland

2012 The Role of Y-STR Profiling in the Investigation of Sexual Assaults. United States Criminal Investigation Laboratory (USACIL), Forest Park, Fort Gillem, GA

2012 Post Coital DNA Recovery Phase 3: Early Results from Participating Couples. Speck, P., Ballantyne, J., Lee, E.D., Hanson, E., Donohoe, M.L., Likes, W., Cashion, A. WI-IAFN 9th Annual Helen Kelly Forensic Conference: Advancing Our Knowledge. Fontana, WI.

2012 Post Coital DNA Recovery: Early Results from Participating Couples. Speck, P., Ballantyne, J., Lee, E.D., Hanson, E., Donohoe, M.L., Likes, W., Cashion, A. and Connor, P. UTHSC System Research Conference, Memphis, TN.

2013 DNA Identification in Criminal and Mass Fatality Investigations. Beta Beta Beta Society Guest Lecture Series, St. Leo University, St. Leo, FL.

2013 EDNAP mRNA Profiling Exercise 6. Haas,C., Hanson, E. and Ballantyne, J.. EDNAP (European DNA Profiling Group) meeting. Bratislava, Slovakia. April 23, 2013.

2013 Enhancing the Sexual Assault Workflow: Testing Next Generation DNA Assessment and Y-STR Systems. Ballantyne J, Hanson E, Green R, Holt A, Bormann Chung C and Molero J. Green Mountain DNA Conference, Burlington, VT.

2013 Not your CSI DNA Profiling: RNA Applications in Forensic Genetics. Cold Spring Harbor Laboratory Genomics Workshop, Seminole State College, Altamonte, FL.

2013 Enhancing the Sexual Assault Workflow: Testing of Next Generation DNA Assessment and Y-STR Systems. BallantyneJ, Hanson E, GreenR, HoltA and MuleroJ. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia. @figshare http://dx.doi.org/10.6084/m9.figshare.865673

2013 Binary Logistic Regression Models Enable miRNA Profiling to Provide Accurate Identification of Forensically Relevant Body Fluids and Tissues. Hanson E, Rekab K and BallantyneJ. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Multiplex High Resolution Melt (HRM) Messenger RNA Profiling Assays for Body Fluid Identification**.** Hanson E and BallantyneJ. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia. F1000Posters [English] http://f1000research.com/posters/1094686

2013 Robust Methods for Improving Challenging DNA Workflows. Life Technologies Lunch Symposium. Ballantyne J. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Implementation of Messenger RNA Body Fluid Testing in Forensic Case Work. Ballantyne J. Workshop. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Rapidly mutating Y-chromosomal STRs – a multi-center assessment of global male lineage and relative differentiation. Ballantyne K, Ralf A, Ballantyne J, Hanson E, and Kayser M. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Implementation of Messenger RNA Body Fluid Testing in Forensic Case Work. Ballantyne J. Workshop. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Y-STR Matching: a Population Genetic Perspective. Weir B, Ballantyne J, Bright J-A Buckleton J, Curran J, Laurie C, Moretti T and Myers S. 25th World Congress of the International Society of Forensic Genetics, Melbourne, Australia.

2013 Farash, K., Morgan, B., DeVore, A., Hanson, E.K., Ballantyne, J. Enhanced Genetic Analysis of Bio-Particles Isolated from Single- and Multi-Source Touch DNA evidence Using Micro-Volume DNA/RNA Profiling Strategies. 24th International Symposium on Human Identification. Atlanta, GA.

2013 Hanson, E.K., and Ballantyne, J. Multiplex High Resolution Melt (HRM) Messenger RNA Profiling Assays for Body Fluid Identification. 24th International Symposium on Human Identification. Atlanta, GA.

2014 Enhancing the Sexual Assault Workflow. Ballantyne J. Webinar presented by Forensic Magazine.

2014 Enhancing the Sexual Assault Workflow: Testing of Next Generation DNA Assessment and Y-STR Systems. Ballantyne J, Hanson EK, Green R, Holt A, and Mulero J. South African Police Service, 2nd National Forensic Services Conference, Johannesburg, South Africa.

2014 Enhancing the Sexual Assault Workflow: Testing of Next Generation DNA Assessment and Y-STR Systems. Ballantyne J, Hanson EK, Green R, Holt A, and Mulero J. American Academy of Forensic Sciences Annual Meeting, Seattle, WA.

2014 Emerging Sexual Assault Evidence Testing Technologies. Ballantyne J. SWGDAM (Scientific Working Group on DNA Analysis Methods) Meeting, Fredericksburg, VA.

2014 Rapid and Inexpensive RNA-based Body Fluid Identification. Ballantyne J and Hanson EK. Green Mountain DNA Conference, Burlington VT

2014 Keynote Speech. Best Practices for the National Response to Sexual Assault Investigations Policy Forum. NIJ Forensic Technology Center of Excellence, Washington DC

2014 Facile semi-automated forensic body fluid identification by multiplex solution hybridization of NanoString® barcode probes to specific mRNA targets. Danaher P, White RL, Hanson E and Ballantyne J. 25th International Symposium on Human Identification, Phoenix, AZ

2014 RNA Tissue Typing by Next Generation Sequencing (NGS). Ballantyne J. NGS Advances in Human Forensic Genomics Workshop. 25th International Symposium on Human Identification, Phoenix, AZ

2014 Detection of male donor DNA in simulated physical contact/assault mixture samples using enhanced one-step micro-volume DNA profiling of isolated bio-particles". Farash, K., Hanson, E.K. and Ballantyne, J. 20th World Meeting of the International Association of Forensic Sciences (IAFS), Seoul, South Korea

2014 Combined genetic and micro-chemical analysis of household dust as a definitive trace identifier of a room and its occupants. Farash, K., O'Brien, H., Hanson, E.K., Petraco, N. and Ballantyne, J. F1000Posters 2014, 5: 1670 (poster) [English 2014 http://f1000research.com/posters/1097111] 20th World Meeting of the International Association of Forensic Sciences (IAFS), Seoul, South Korea

2014 Facile semi-automated forensic body fluid identification by multiplex solution hybridization of NanoString® barcode probes to specific mRNA targets. Danaher P, White RL, Hanson E and Ballantyne J. 20th World Meeting of the International Association of Forensic Sciences (IAFS), Seoul, South Korea

2014 Forensic Biology Research at the National Center for Forensic Science. Ballantyne, J and Hanson E. European DNA Analysis Profiling (EDNAP) Meeting, Zurich, Switzerland

2014 Human specific RNA quantification. Haas, C., Hanson, E. and Ballantyne, J. European DNA Analysis Profiling (EDNAP) Meeting, Zurich, Switzerland

2015 Obtaining successful DNA profiles from challenging samples: enhanced profiling strategies for physical separation of bio-particles in touch and dust specimens". Ballantyne, J., Hanson, E.K., Farash, K. and Petraco, N. 67th Annual American Academy of Forensic Sciences (AAFS) meeting. Orlando, FL., 2015.

2015 Rapid loop-mediated isothermal amplification (LAMP) of RNA biomarkers for forensic identification of semen and saliva. Hanson, E.K, Neary, K., Waldeisen JR, Mitra D, Dimov, IK, Buoncristiani, MR, Steinberger, E.M., Orrego, C. J. and Ballantyne, J. 67th Annual American Academy of Forensic Sciences (AAFS) meeting. Orlando, FL. February http://f1000research.com/posters/1097550

2015 A study of the formation, collection and microscope trace material and genetic makeup of household dust specimens". Petraco, N., Ballantyne, J., Hanson, E.K., and Farash, K. 67th Annual American Academy of Forensic Sciences (AAFS)

meeting. Orlando, FL, 2015.

2015 Combined genetic and micro-chemical analysis of household dust as a definitive trace identifier of a room and its occupants. Farash, K., O'Brien, H., Hanson, E.K., Petraco, N., and Ballantyne, J. 67th Annual American Academy of Forensic Sciences (AAFS) meeting. Orlando, FL, 2015.

2015 Who and What: Providing Context to a DNA Profile". Ballantyne, J. and Hanson, E.K. 67th Annual American Academy of Forensic Sciences (AAFS) meeting. Orlando, FL, 2015.

2015 Why Y Chromosome biomarkers are an ever-expanding essential tool in sexual assault investigations. Ballantyne J and Hanson E.K. Human Identification Solutions conference (HIDS), Madrid, Spain.

2015 "Getting blood from a stone": forensic genomics initiatives at Florida's National Center for Forensic Science. Ballantyne J. Plenary lecture. 79th Annual Meeting of the Florida Academy of Sciences, Saint Leo University, Saint Leo, FL.

2015 mRNA quantification. Haas C, Hanson EK and Ballantyne J. European DNA Analysis Profiling (EDNAP) Meeting. April 2015. Copenhagen, Denmark

2015 Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing. Haas, C., Ingold, S., Hanson, E.K. , and Ballantyne, J. EUROFORGEN 4th General Assembly. Telfs/Tirol, Austria.

2015 Why Forensic Science Providers Assisting Sexual Assault Investigations Should Offer Y-Chromosome Testing Services. Ballantyne J, Hanson E and Fatolitis L. 2015 ASCLD Symposium Washington, D.C.

2015 Forensic Molecular Identification of Cell Type: Providing Context to a DNA Profile. Ballantyne J and Hanson E. International Society for Applied Biological Sciences (ISABS) Conference on Forensic, Anthropological Genetics and Mayo Clinic Lectures in Individualized Medicine. Bol, Island of Brac, Croatia.

2015 Mixture de-convolution by genetic analysis of physically separated individual cells. Ballantyne J, Hanson E, Farash K, Petraco N, Perlin M. Green Mountain DNA Conference, Burlington, VT.

2015 Human RNA quantification to enhance mRNA profiling in forensic biology. Zhao D, Hanson E, Zhu X, Feng S and Ballantyne J. International Conference on Evidence Law and Forensic Science, Adelaide, South Australia, Australia.

2015 Targeted multiplexed next generation RNA sequencing assay for tissue source determination of forensic samples. Hanson E, Ingold S, Haas C and Ballantyne J. 26th World Congress of the International Society of Forensic Genetics, Krakow, Poland.

2015 Beyond DNA Profiling: RNA profiling, transfer and persistence-what it is and how it got there. Ballantyne J and Hanson E. Workshop, 26th World Congress of the International Society of Forensic Genetics, Krakow, Poland.

2015 Messenger RNA profiling methods for body fluid identification. Ballantyne J and Hanson E. The 11th DNA Technology Educational Seminar. Forensic Services and Coroner's Complex, Toronto, Canada.

2015 Smart Trace DNA Analysis Applied to Touch DNA and Household Dust Analysis. Ballantyne J, Hanson E and Petraco N. The 11th DNA Technology Educational Seminar. Forensic Services and Coroner's Complex, Toronto, Canada.

2015 Amplification of whole mitochondrial genome from challenging samples via multiplex PCR assay. Peters Hickman, M., Burnside, E. S., Blintz, B.J., Grisedale, K.S., Petraco, N.,Hanson, E.K., Ballantyne, J. and Wilson, M. 26th International Symposium on Human Identification (ISHI, Promega). Grapevine, TX. October 12-15, 2015.

2015 Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing Haas, C., Ingold, S., Hanson, E. and Ballantyne, J. EUROFORGEN 4th Steering Committee Meeting. Santiago de Compostela, Spain. October 22, 2015.

2015 Body Fluid Identification by Transcriptomics: Providing Context to a DNA Profile. Ballantyne J and Hanson E. Advanced Topics in Human DNA Identification Workshop. The Center for Forensic Science Education and Research, Chemical Heritage Foundation, Philadelphia, PA. December 2015.

2016 Providing Context To A DNA Profile: The Use Of NGS RNA Profiling For Tissue And Body Fluid Identification In Forensic Science. Ballantyne J and Hanson E. Genetics in Forensics Congress, London, UK. March 2016.

2016 Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing: EUROFORGEN/EDNAP mRNA NGS exercise 1: Assay for body fluid identification. Haas C, Ingold, S, Hanson, E and Ballantyne J. European DNA Analysis Profiling (EDNAP) Meeting. April 2016. Warsaw, Poland.

2016 Evaluation of the Precision ID System for Targeted Sequencing of DNA and RNA Markers for Human Identity and Body Fluid Identification. Ballantyne J. Human Identification Solutions Conference (HIDS). May 2016. Barcelona, Spain.

2016 Ingold S, Haas C, Hanson E and Ballantyne J. Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing. IALM 2016 Intersocietal Symposium. Venice, Italy. June 24, 2016.

2016 A highly automated NGS system for targeted sequencing of DNA for human identity applications. Ballantyne J and Hanson E. Green Mountain DNA Conference, Burlington, VT.

2016 Evaluation of the Ion S5 NGS System for targeted sequencing of DNA and RNA markers for human identification and body fluid ID. Ballantyne J and Hanson E. Applied Biosystems Future Trends in Forensic DNA Technology HID University Seminar Series, Green Mountain DNA Conference, Burlington, VT.

2016 Cell Type Identification by RNA In Situ Hybridization. Turnbull E, Figueredo J, Fleming R, Harbison S, Lin M, Ballantyne J and Hanson E. ANZFSS 23rd International Symposium on the Forensic Sciences. Auckland, New Zealand. September 2016.

2016 The evolution of forensic household dust analysis during the last hundred years. Petraco, N., Hanson, E., Ballantyne, J., Petraco, N.D. and Eng, M. 2016 Eastern Analytical Symposium & Exposition. Somerset, NJ.

2016 Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing. Haas, C., Ingold, S., Dorum, G., Hanson, E. and Ballantyne, J. Euroforgen meeting. Nov 30 – Dec 2, 2016. Berlin, Germany.

2017 The Evolution of Forensic Household Dust Analysis During the Last Hundred Years. Petraco, N., Ballantyne, J., Hanson, E., Petraco, N.D., Farash, K. and Eng, M. American Academy of Forensic Sciences Meeting 69th Annual Meeting. February 2017. New Orleans, LA.

2017 NGS Approaches for Contextualizing DNA Profiles. Ballantyne, J. and Hanson, E. 2nd Annual Genetics in Forensics Congress. March 2017. London, UK.

2017 What YOU Need to Know! DNA Findings After Sexual Assault. Speck,P., Ballantyne, J., Hanson, E. and Sanchez, R. International Conference on Sexual Assault, Domestic Violence, and Systems Change, End Violence Against Women International (EVAWI), Orlando, FL.

2017 Genetic analysis of mixed samples through identification and recovery of sperm and epithelial cells with the DEParray digital cell sorting system. Ballantyne, J and Hanson, E. 2017 Human Identification Solutions (HIDS) Conference, Vienna, Austria.

2017 Human organ tissue ID by targeted RNA deep sequencing to aid the investigation of traumatic injury. Ballantyne J. and Hanson E. 21st Triennial Meeting of the International Association of Forensic Sciences (IAFS), Toronto, ON, Canada.

2017 Genotyping casework type samples using an integrated NGS STR analysis and interpretation system. Ballantyne J. and Hanson E. 21st Triennial Meeting of the

International Association of Forensic Sciences (IAFS), Toronto, ON, Canada.

2017 DNA analysis of mixed sexual assault and touch samples with the DEParray digital cell-sorting system. Ballantyne J. and Hanson E. 21st Triennial Meeting of the International Association of Forensic Sciences (IAFS), Toronto, ON, Canada. August 2017 (poster)

2017 Genetic and micro-chemical analysis of household dust as an identifier or a room and its occupants. Ballantyne J, Hanson E, Johnson J., Penn A., Petraco N, Petraco N.D. and Eng M. 21st Triennial Meeting of the International Association of Forensic Sciences (IAFS), Toronto, ON, Canada. August 2017. (poster)

2017 A novel DNA/RNA co-extraction method using EZ1 DNA investigator extraction 'waste'. Hanson E., Lopez J. and Ballantyne J. 21st Triennial Meeting of the International Association of Forensic Sciences (IAFS), Toronto, ON, Canada. August 2017. (poster)

2017 Seeking answers from cold cases – panel discussion. Ballantyne J., Podini D. and Schellberg T. ThermoFisher Scientific Luncheon Symposium. 21st Triennial Meeting of the International Association of Forensic Sciences (IAFS), Toronto, ON, Canada. August 2017.

2017 Association of a body fluid with a DNA profile by targeted RNA/DNA deep sequencing. Ingold S, Haas C, Dørum G, Hanson E and Ballantyne J. International Society of Forensic Genetics (ISFG), Seoul, South Korea

2017 Analysis of Sexual Assault Evidence, in Lunch Seminar: Enabling forensic genetic analysis of biological mixtures through the identification and recovery of pure cells with the DEPArray™ system. Ballantyne J. and Hanson E. 27th Congress of the International Society for Forensic Genetics (ISFG), Seoul, South Korea.

2017 Developmental Validation of the paraDNA Body Fluid ID System. Blackman S., Stafford-Allen B., Hanson E., Panasiuk M., Dodd L., Ballantyne J. and Wells S. Poster. 27th Congress of the International Society for Forensic Genetics (ISFG), Seoul, South Korea.

2017 Messenger RNA profiling for body fluid identification. Ballantyne, J and Hanson E. Towards Better Solutions for Body Fluid Workshop. International Symposium on Human Identification (ISHI), Seattle WA.

2017 Collaborative EDNAP exercises on mRNA profiling for body fluid identification. Ballantyne, J, Hanson E, Ingold S and Haas, C. Towards Better Solutions for Body Fluid Workshop. International Symposium on Human Identification (ISHI) Seattle, WA.

2017 Messenger RNA NGS exercise 2:Assay for body fluid/tissue identification and assignment to donor (s). Haas C, Ingold S, Dorum G, Hanson E and Ballantyne J. EUROFORGEN/EDNAP meeting, Athens, Greece

2017 A bloody 38 years in forensic science. Ballantyne, J. Centre for Forensic Science, University of Strathclyde, United Kingdom

JOURNAL/FUNDING AGENCY REVIEWS

Journal of Forensic Science, Forensic Science International, Biotechniques, Expert Reviews in Molecular Diagnostics, NSERC (Natural Sciences and Engineering Research Council of Canada), Trends in Biotechnology, PLosONE, Department of Justice, National Institute of Justice, Mutation Research

PROFESSIONAL ACTIVITIES

1988 Organizer of the Banbury Conference at Cold Spring Harbor Laboratory on DNA Technology and Forensic Science

1991-1998 Member of the NYS DNA User's Group

1992 Chairman/Organizer of the Serology/DNA Session at the Annual Northeastern Association of Forensic Sciences, Atlantic City, NJ

1992-1995 New York State Scientific Review Board

1992 Organizer of the Banbury Conference at Cold Spring Harbor Laboratory, NY on DNA Fingerprinting

1994-1998 Proficiency Review Committee (DNA-PRC) of ASCLD/LAB

1995-1998 ASCLD/LAB Accreditation Inspector

1995-1998 Appointed by the Director of the FBI to the DNA Advisory Board (established by the DNA Identification Act 1994)

1995-2001 Member of FBI's TWGDAM (Technical Working Group on DNA Analysis Methods)

1995-1997 New York State DNA Sub-committee (Chapter 737 of the Laws of 1994)

1996-1998 Participant in the FBI-sponsored STR Standardization project

1996-1998 Appointed by the National Institute of Justice to the National Forensic DNA Review Panel (NFDRP) (established by the DNA Identification Act 1994)

1997-present	Appointed as Chair of New York State DNA Subcommittee (Chapter 737 of the Laws of 1994)
1997	Training Committee Chairperson of NIJ/NIST(OLES)/ASCLD workshop 'Forensic Science Summit: Roadmap to the Year 2000'.
1998-2002	Member of the Credentials Review Committee of ASCLD (established as a result of the issuance by the Director of the FBI of the Quality Assurance Standards for DNA Testing laboratories)
1999-present	Technical Assessor for the Standards Council for Canada
2000-2003	Peer Review Panel Member, National Institute of Justice
2001-2003	Planning panel member, and Member, of NIJ/West Virginia University's TWGED, Technical Working Group on Forensic Science Training and Education
2001-2003	Planning panel member, and Member, of NIJ/NCFS's Technical Working Group on Mass Fatality Incidents (Publication: 'Mass Fatality Incidents: A Guide for Human Forensic Identification')
2001-present	Member of the Department of Defense DNA Quality Assurance Oversight Committee of the Armed Forces Institute of Pathology Scientific Advisory Board, Washington, DC (oversight of the quality assurance program of the Armed Forces DNA Identification Laboratory)
2001-present	Regular 'invited guest' to the FBI's SWGDAM group (Scientific Working Group on DNA Analysis)
2001-2006	Member of the Kinship and DNA Analysis Panel (KADAP). (Set up by NIJ to aid the NYC OCME in the DNA identification efforts in the NYC WTC terrorist incident)
2002-2004	Planning panel member and Member, Florida Emergency Mortuary Operations Response System (system set up by the State of Florida to respond to mass fatalities incidents within the state)
2002-2003	Member of the Scientific Advisory Board, the BODE Technology Group, Springfield, VA
2003-2006	Member of the NIJ/Forensic Resource Network Principles of Forensic DNA for Officers of the Court Technical Working Group
2004	Co-Chair of the Y-STR Analysis on Forensic Casework Workshop, AAFS Annual meeting, Dallas, TX

2004 Moderator, Applied Biosystems Annual User Forum, AAFS Annual Meeting, Dallas, TX

2004 Co-Chair of the Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2005-2006 Member of the Hurricane Victim DNA Identification Expert Group (HVDIEG). (Set up by the State of Louisiana to aid the DNA identification efforts in the hurricane Katrina incident)

2007-present Member of the NIJ/National Clearing House for Science, Technology and the Law on DNA Evidence for Defense Lawyers Technical Working Group

2007-present Member of the Editorial Board of the Open Forensic Science Journal (www.bentham.org/open/toforsj).

2008-2012 Member of the Editorial Board of the Journal of Forensic Sciences

2008 Organized and taught a workshop 'New Technologies and Applications in Forensic Biology' for the New Jersey State Police, Hamilton, NJ.

2008-present Member of the Advisory Council Committee of the National Clearing House for Science, Technology and the Law at Stetson University College of Law, Gulfport, FL

2008 Organized and taught a workshop 'Y chromosome marker applications in forensic genetics' to the Arizona Department of Public Safety, Phoenix, AZ.

2008 Member of the Scientific Advisory Board of GenVault, Corporation

2010-present Member of the Scientific Advisory Board of Identitas Corporation

2012 Member of the Molecular Biology/DNA committee of SWGDVI (Scientific Working Group on Disaster Victim Identification)

2012-present Member of Steering Committee of the Annual Green Mountain DNA Conference held in Burlington, VT.

2015-2016 Faculty Advisor to the Forensic Science Association (UCF)

2015-2016 Program Committee member of the *2016 Gordon Research Conference on Forensic Analysis of Human DNA.*

2016-present External Advisor, Forensic STR Sequence Diversity Database, NCSU, Raleigh, NC.

2015-present Advisory Board member of the Oxford Global Annual Genetics in Forensics Congress, London, UK

2017-present Member of the Scientific Advisory Board to the Swedish National Police (National Forensic Centre, NFC)

TEACHING ACTIVITY

STUDENT INSTRUCTION

SUNY, Stony Brook, NY

Seminar in Forensic Biology,	Spring,	1997	HAD 435
Seminar in Forensic Biology,	Spring,	1998	HAD 435

UCF, Orlando, FL

1998-1999

Forensic Serology, Class. Methds	Fall	1998	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	1998	CHS 6535
Lab. Methods for Mol. Biol.	Fall	1998	PCB 6407C
Forensic Serology, Mol. Methds	Spring	1999	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	1999	CHS 6535L
Thesis Research	Spring	1999	CHS 6971

1999-2000

Forensic Serology, Class. Methds	Fall	1999	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	1999	CHS 6535
Thesis Research	Fall	1999	CHS 6971
Forensic Serology, Mol. Methds	Spring	2000	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2000	CHS6535L
Intro. To Forensic Science	Spring	2000	CHS 3501
Thesis Research	Spring	2000	CHS 6971
Introduction to Forensic Science	Summer	2000	CHS 3530
Thesis Research	Summer	2000	CHS 6971

2000-2001

Internship	Fall	2000	CHS 4591
Thesis Research	Fall	2000	CHS 6971
Forensic Biochemistry I	Fall	2000	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2000	CHS 6535
Court Presentation Skills	Fall	2000	CHS 6908
Forensic Biochemistry II	Spring	2001	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2001	CHS6535L
Intro. To Forensic Science	Spring	2001	CHS 3501
Thesis Research	Spring	2001	CHS 6971
Court Presentation Skills	Spring	2001	CHS 6908
Internship	Spring	2001	CHS 4591
Thesis Research	Summer	2001	CHS 6971

2001-2002

Forensic Biochemistry I	Fall	2001	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2001	CHS 6535
Court Presentation Skills	Fall	2001	CHS 6908
Thesis Research	Fall	2001	CHS 6971
Struct. and Funct.of Biomolecules	Fall	2001	IDS 7691
Frontiers in Biomolecular Science	Fall	2001	IDS 7690
Doctoral Research	Fall	2001	IDS7919
Forensic Biochemistry II	Spring	2002	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2002	CHS 6535L
Intro. To Forensic	Spring	2002	CHS 3501
Thesis Research	Spring	2002	CHS 6971
Doctoral Research	Spring	2002	IDS 7919
Thesis Research	Summer	2002	CHS 6971
Doctoral Research	Summer	2002	IDS 7919

2002-2003

Forensic Biochemistry I	Fall	2002	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2002	CHS 6535
Frontiers in Biomolecular Science	Fall	2002	IDS 7690
Thesis Research	Fall	2002	CHS 6971
Dissertation Research	Fall	2002	IDS 7971
Forensic Biochemistry II	Spring	2003	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2003	CHS6535L
Intro. To Forensic Science	Spring	2003	CHS 3501
Thesis Research	Spring	2003	CHS 6971
Dissertation Research	Spring	2003	IDS 7971
Court Presentation Skills	Summer	2003	CHS 6908
Thesis Research	Summer	2003	CHS 6971
Dissertation Research	Summer	2003	IDS 7971

2003-2004

Forensic Biochemistry I	Fall	2003	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2003	CHS 6535
Frontiers in Biomolecular Science	Fall	2003	IDS 7690
Thesis Research	Fall	2003	CHS 6971
Dissertation Research	Fall	2003	IDS 7971
Forensic Biochemistry II	Spring	2004	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2004	CHS6535L
Intro. To Forensic Science	Spring	2004	CHS 3501
Thesis Research	Spring	2004	CHS 6971
Dissertation Research	Spring	2004	IDS 7971
Court Presentation Skills	Summer	2004	CHS 6908
Thesis Research	Summer	2004	CHS 6971
Dissertation Research	Summer	2004	IDS 7971

2004-2005

Forensic Biochemistry I	Fall	2004	CHS 3533C

Forensic Analysis of Biol. Mat.	Fall	2004	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2004	BSC 6432
Thesis Research	Fall	2004	CHS 6971
Dissertation Research	Fall	2004	IDS 7971
Forensic Biochemistry II	Spring	2005	CHS 4534C
Intro. To Forensic Science	Spring	2005	CHS 3501
Thesis Research	Spring	2005	CHS 6971
Dissertation Research	Spring	2005	IDS 7971
Intro. To Forensic Science	Summer	2005	CHS 3501
Thesis Research	Summer	2005	CHS 6971
Dissertation Research	Summer	2005	IDS 7971

2005-2006

Forensic Biochemistry I	Fall	2005	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2005	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2005	BSC 6432
Thesis Research	Fall	2005	CHS 6971
Doctoral Research	Fall	2005	IDS 7919
Graduate Seminar (Court Present.)	Fall	2005	CHS 6908
Directed Research	Fall	2005	CHS 6918
Dissertation	Fall	2005	IDS 7980
Forensic Biochemistry II	Spring	2006	CHS 4534C
Intro. To Forensic Science	Spring	2006	CHS 3501
Forensic Anal Biol Mat Lab	Spring	2006	CHD 6535L
Experimental Molecular Biology	Spring	2006	PCB 4529
Thesis Research	Spring	2006	CHS 6971
Doctoral Research	Spring	2006	IDS 7919
Directed Research	Spring	2006	CHS 6918
Independent Study	Spring	2006	CHS 6908
Directed Research	Spring	2006	CHM 7919
Dissertation	Spring	2006	IDS 7980
Doctoral Research	Summer	2006	IDS 7919
Dissertation	Summer	2006	IDS 7980
Thesis Research	Summer	2006	CHS 6971
Directed Research	Summer	2006	CHS 6918
Directed Research	Summer	2006	CHM 7919

2006-2007

Forensic Biochemistry I	Fall	2006	CHS 3533
Forensic Biochemistry I lab	Fall	2006	CHS 3533L
Str.Funct.Rel. Biomol. Sci.	Fall	2005	BSC 6432
Honors Directed Reading	Fall	2006	CHS 4903H
Directed Research	Fall	2006	CHS 6918
Independent Study	Fall	2006	CHS 6908
Thesis	Fall	2006	CHS 6971
Directed Research	Fall	2006	CHM 7919
Doctoral Research	Fall	2006	IDS 7919

Dissertation	Fall	2006	IDS 7980
Forensic Biochemistry II	Spring	2007	CHS 4534C
Thesis Research	Spring	2007	CHS 6971
Doctoral Research	Spring	2007	IDS 7919
Directed Research	Spring	2007	CHS 6918
Independent Study	Spring	2007	CHS 6908
Directed Research	Spring	2007	CHM 7919
Dissertation	Spring	2007	IDS 7980
Honors Undergrad Research	Spring	2007	CHS 4970
Doctoral Research	Summer	2007	IDS 7919
Dissertation	Summer	2007	IDS 7980
Thesis Research	Summer	2007	CHS 6971
Directed Research	Summer	2007	CHS 6918
Directed Research	Summer	2007	CHM 7919
Honors Undergrad Research	Summer	2007	CHS 4970

2007-2008

Str.Funct.Rel. Biomol. Sci.	Fall	2007	BSC 6432
Forensic Molecular Biology	Fall	2007	CHS 6535
Thesis	Fall	2007	CHS 6971
Directed Research	Fall	2007	CHM 7919
Doctoral Research	Fall	2007	IDS 7919
Dissertation	Fall	2007	IDS 7980
Doctoral Research	Spring	2008	IDS 7919
Dissertation	Spring	2008	IDS 7980
Dissertation	Spring	2008	CHM 7980
Forensic Anal Biol Mat Lab	Spring	2008	CHD 6535L
Thesis	Spring	2008	CHS 6971
Doctoral Research	Summer	2008	IDS 7919
Dissertation	Summer	2008	IDS 7980
Thesis	Summer	2008	CHS 6971
Directed Research	Summer	2008	CHS 6918
Dissertation	Summer	2008	CHM 7980

2008-2009

Forensic Biochemistry I	Fall	2008	CHS 3533
Str.Funct.Rel. Biomol. Sci.	Fall	2008	BSC 6432
Directed Research	Fall	2008	CHM 6918
Dissertation	Fall	2008	CHM 7980
Directed Research	Fall	2008	CHS 6918
Thesis	Fall	2008	CHS 6971
Doctoral Research	Fall	2008	IDS 7919
Dissertation	Fall	2008	IDS 7980
Directed Research	Spring	2009	CHM 6918
Forensic Biochemistry II	Spring	2009	CHS4534C
Doctoral Research	Spring	2009	IDS 7919
Dissertation	Spring	2009	CHM 7980

Directed Research	Spring	2009	CHS 6918
Directed Research	Summer	2009	CHM 6918
Doctoral Research	Summer	2009	IDS 7919
Directed Research	Summer	2009	CHS 6918
2009-2010			
Forensic Molecular Biology	Fall	2009	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2009	BSC 6432
Directed Research	Fall	2009	CHM 6918
Directed Research	Fall	2009	CHS 6918
Dissertation	Fall	2009	IDS 7980
Directed Research	Spring	2010	CHM 6918
Dissertation	Spring	2010	CHM 7980
Forensic Anal Biol Mat Lab	Spring	2010	CHD 6535L
Dissertation	Summer	2010	IDS 7980
Thesis	Summer	2010	CHS 6971
Research	Summer	2010	MCB 4912
2010-2011			
Str.Funct.Rel. Biomol. Sci.	Fall	2010	BSC 6432
Forensic Biochemistry I (lecture)	Fall	2010	CHS 3533
Directed Research	Fall	2010	CHS 6918
Thesis	Fall	2010	CHS 6971
Research	Fall	2010	MCB 4912
Forensic Biochemistry II	Spring	2011	CHS 4534C
Directed Research	Spring	2011	CHM 6918
Thesis	Spring	2011	CHS 6971
Research	Spring	2011	MCB 4912
Research	Summer	2011	MCB 4912
2011-2012			
Biomedical Sciences	Fall	2011	BSC 6432
Forensic Molecular Biology	Fall	2011	CHS 6535
Research	Fall	2011	CHS 4912
Directed Research	Fall	2011	CHS 6918
Thesis	Fall	2011	CHS 6971
Research	Fall	2011	MCB 4912
Research	Spring	2012	CHS 4912
For Anal Biol Mat Lab	Spring	2012	CHS 6535L
Directed Research	Spring	2012	CHS 6918
Thesis	Spring	2012	CHS 6971
Research	Spring	2012	MCB 4912
Directed Research	Summer	2012	CHS 6918
Research	Summer	2012	MCB 4912
2012-2013			
Forensic Biochemistry I	Fall	2012	CHS 3533

Research	Fall	2012	CHS 4912
Directed Research	Fall	2012	CHS 6918
Thesis	Fall	2012	CHS 6971
Research	Spring	2013	CHS 4912
Forensic Biochemistry II	Spring	2013	CHS 4534C
Thesis	Spring	2013	CHS 6971
Research	Spring	2013	MCB 4912
Thesis	Summer	2013	CHS 6971
Internship	Summer	2013	CHS 4941
2013-2014			
Forensic Molecular Biology	Fall	2013	CHS 6535
Research	Fall	2013	CHS 4912
Directed Research	Fall	2013	CHS 6918
Forensic Anal Biol Mat	Spring	2014	CHS 6535L
Thesis	Spring	2014	CHS 6971
Research	Spring	2014	CHS 4912
Directed Research	Spring	2014	CHS 6918
Research	Spring	2014	MCB 4912
Thesis	Summer	2014	CHS 6971
2014-2015			
Forensic Biochemistry I	Fall	2014	CHS 3533
Research	Fall	2014	CHS 4912
Independent Study	Fall	2014	CHS6908
Directed Research	Fall	2014	CHS 6918
Thesis	Fall	2014	CHS 6971
Forensic Biochemistry II	Spring	2015	CHS4534C
Research	Spring	2015	CHS 4912
Directed Research	Spring	2015	CHS 6918
Thesis	Spring	2015	CHS 6971
Thesis	Summer	2015	CHS 6971
2015-2016			
Forensic Molecular Biology	Fall	2015	CHS 6535
Research	Fall	2015	MCB 4912
Directed Research	Fall	2015	CHS 6918
Forensic Anal Biol Mat	Spring	2016	CHS 6535L
Thesis	Spring	2016	CHS 6971
Research	Spring	2016	MCB 4912
Research Report	Spring	2016	CHM 6918
Independent Study	Spring	2016	CHS 6908
Directed Research	Summer	2016	CHM 6918
Thesis	Summer	2016	CHS 6971
2016-2017			
Forensic Biochemistry I	Fall	2016	CHS 3533

Thesis	Fall	2016	CHS 6971
Research	Fall	2016	MCB 4912
Forensic Biochemistry II	Spring	2017	CHS 4534
Directed Research	Spring	2017	CHS 6918
Independent Study	Spring	2017	CHS 6908
Directed Research	Spring	2017	CHS 6918
Research	Spring	2017	CHS 4912
Research	Spring	2017	MCB 4912
Directed Research	Summer	2017	CHM 6918
Doctoral Research	Summer	2017	IDS 7919

ADMINISTRATION

1998-2004 Program Coordinator for the Forensic Biochemistry Track within the MS in Industrial Chemistry

2004-2017 Program Coordinator for the Forensic Biochemistry Track/Concentration within the MS in Forensic Science

2014-2015 Interim Director, National Center for Forensic Science, UCF, Orlando, FL

THESIS/DISSERTATIONS SUPERVISED (Chair/PI)

Graduated:

PhD:
Jane Juusola (PhD, Biomolecular Science, 2005)
Ashley Hall (PhD, Biomolecular Science, 2005)
Michelle Alvarez (PhD, Biomedical Science, 2007)
Erin Hanson (PhD, Biomedical Science, 2008)
April Marrone (PhD, Chemistry, 2009)

MS
Charles Badger (MS, Molecular and Micro-Biology, 2000)
Ashley Hall (MS, Forensic Biochemistry Track, 2001)
Debra Glidewell (MS, Forensic Biochemistry Track, 2001)
George Shiro (MS, Forensic Biochemistry Track, 2001)
Jeffrey Ban (MS, Forensic Biochemistry Track, 2002)
Gigi Raker (MS, Forensic Biochemistry Track, 2003)
Stacey Smith (MS) (MS, Forensic Biochemistry Track, 2003)
Erin Hanson (MS, Forensic Biochemistry Track, 2003)
Darlene Daniels (MS) (MS, Forensic Biochemistry Track, 2003)
Paulina Berdos (MS, Forensic Biochemistry Track, 2004)
Mindy Banton or Setzer (MS, Forensic Biochemistry Track, 2004)
Jeremy Fletcher (MS, Forensic Biochemistry Track, 2004)

Susan Hastings (MS, Forensic Biochemistry Track, 2004)
Christine Sanders (MS, Forensic Biochemistry Track, 2005)
Katherine Press (MS, Forensic Biochemistry Track, 2006)
Pam Smith (MS, Forensic Biochemistry Track, 2006)
Kyle Parker (MS, Forensic Biochemistry Track, 2006)
Micah Halpern (MS, Forensic Biochemistry Track, 2008)
Charly Parker (MS, Forensic Biochemistry Track, 2011)
Brittany Morgan (MS, Forensic Biochemistry Track, 2013)
Christopher Comar (Broward County, FL) (MS, Forensic Professional Track, 2014)
Arlene Petrosky (Broward County, FL) (MS, Forensic Professional Track, 2014)
Katherine Farash (MS, Forensic Biochemistry Track, 2015)
Mariela Rivera (MS, Forensic Professional Track, 2015)
Stephanie Lucas (FDLE, Jacksonville) (MS, Forensic Biochemistry Track, 2016)
Nicole Masker (MS, Forensic Biochemistry Track, 2016)
Jamie Walsh (MS, Forensic Professional Track, 2017)

BS
Michelle Josey (BS Honors in the Major (Forensic Science), 2007)

Undergraduate Research
Mohid Mirza (BS, Biomedical Sciences)
Hayley O'Brien (BS, Forensic Science)
Alexandria DeVore (BS, Forensic Science)

Current:

PhD
Ashley Geraets (PhD, Chemistry)
Nikhita Shankar (PhD, Biomedical Science)
Kaitlin Huffman (PhD, Chemistry)

MS
Mary Margaret Daniel (MS, Forensic Science)

Undergraduate Research
Jaclyn Johnson (BS, Biomedical Science)
Amanda Penn (BS, Biomedical Science)
Jasmine Lopez (BS, Biomedical Science)

THESIS/DISSERTATION COMMITTEES (not as Chair)

2004-2007 Todd Castoe (PhD, Biomolecular Science)
2001-2004 Oscar Ruiz (PhD, Biomolecular Science)
2002-2004 Claudia Romero (PhD, Biomolecular Science)
2002-2003 Paul Cohill (PhD, Biomolecular Science)
2005-2006 Wang Yiqiang (Danny) (PhD, Chemistry)

2005-2009 Bongyong Lee (PhD, Biomedical Science)
2004-2010 Jose Salvatico (PhD, Biomedical Science)
2008-present Minpei Wong (PhD, Biomedical Science)
2008-2009 Sarah Parker (BS Nursing, Honors Thesis)
2010-2011 Eric Goldstein (Honors in the Major, Molecular Biology)
2010-2016 Aditya Reddy Kolli (PhD, Chemistry)
2011-2013 Emily Moore (Honors in the Major, Biology)

EXTERNAL EXAMINER

2005 Curtis Hildebrandt (MS, Lakehead University, Thunder Bay, Canada)
2010 Ursula Zipperer (MS Forensic Science, Virginia Commonwealth University, VA)
2011 Phuvadol Thanakiatkrai (PhD, Forensic Science, Strathclyde University, UK)
2013 Mohaimin Kasu (M.Phil Biomedical Forensic Science, Univ.of Cape Town, SA)
2016-present Sabrina Ingold (PhD Integrative Molecular Medicine (imMed), Univ. of Zurich, Zurich, Switzerland)
2016-present Andrea Salzmann (PhD Integrative Molecular Medicine (imMed), Univ. of Zurich, Zurich, Switzerland)
2018-present Stephanie Polifroni (PhD in Criminal Justice, John Jay College of Criminal Justice, NY)

PATENTS

2007 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,270,983, issued September 18, 2007.

2007 Age Determination from Biological Stains Using Messenger RNA Profiling Analysis. Co-inventor with Michelle Alvarez. United States Patent No: 7,276,340 B1, issued October 2, 2007.

2009 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,582,435, issued September 1, 2009.

2009 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Real Time --Polymerase Chain Reaction (Q-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,588,921, issued September 15, 2009.

2010 Age Determination from Biological Stains Using Messenger RNA Profiling Analysis. Co-inventor with Michelle Alvarez. United States Patent No: 7,704,693, issued April 27, 2010.

2014 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Real Time --Polymerase Chain Reaction (Q-PCR). Co-inventor with Jane Juusola. United States Patent No: 8,637,654 issued January 28, 2014.

2015 Method for Determining the Origin of a Sample. Co-inventor with Helge Lubenow and Erin Hanson. United States Patent No: 8,936,909 B2 issued January 20, 2015.

2015 Method for Determining the Origin of a Sample. Co-inventor with Helge Lubenow and Erin Hanson. European Patent No: EP 2 315 852 B1 issued January 28, 2015.

PATENT APPLICATIONS

2012 US Provisional Application No. 61/543,116
Title: Methods and Compositions for Detecting a Target DNA in a Mixed Nucleic Acid Sample
Inventors: Jack Ballantyne, Erin Hanson, Francesca Di Pasquale, Sascha Strauß, Holger Engel
Assignees: UCF, QIAGEN GmbH

PUBLICATIONS

A. Peer-Reviewed Journal Articles

1 Chromosomally Integrated Retroviral Substrates are Sensitive Indicators of an Antibody Class Switch Recombinase-Like Activity. Ballantyne, J., Ozsvath, L., Bondarchuk, K. and Marcu, K.B. *Curr. Top. Microbiol. Immunol.* **194**, 439-448 (1995)

2 Forensic Applications of a Rapid, Sensitive and Precise Multiplex Analysis of the Four Short Tandem Repeat Loci HUMVWF31/A., HUMTH01, HUMF13A1, and HUMFES/FPS. Robertson, J.M., Sgueglia, J.B., Badger, C.A., Juston, A.C. and Ballantyne, J. *Electrophoresis* **16**, 1568-1576 (1995)

3 The Applicability of Formalin Fixed and Formalin Fixed Paraffin Embedded Tissues in Forensic DNA Analysis. Romero, R., Juston, A.C., Ballantyne, J. and Henry, B.E. *J. Forensic. Sci.* **42**, 708-714, (1997)

4 Antibody Class Switch Recombinase Activity is B Cell Stage Specific and Functions Stochastically in the Absence of 'Targeted Accessibility' Control. Ballantyne, J., Henry, D. and Marcu, K. *Int. Immunol.* **9**, 963-974, (1997)

5 Mass Disaster Genetics. *Nature Genet.* **15**, 329-331 (1997)

6 Efficient Recombination of a Switch Substrate Retrovector in CD40-Activated B Lymphocytes: Implications for the Control of C_H Gene Switch Recombination. Ballantyne, J., Henry, D.H., Muller, J.R., Briere, F., Snapper, C.M., Kehry, M. and Marcu, K.B. *J. Immunol*., **161**, 1336-1347, (1998)

7 Immunoglobulins: Polyclonal and Monoclonal Antibodies. Ballantyne, J., Mandle, R. and Bing, D.H. Chapter 36 In Hematology: Basic Principles and Practice, Third Edition. Churchill Livingstone, New York, (2000)

8 Messenger RNA Profiling: A Prototype Method to Supplant Conventional Methods for Body Fluid Identification. Juusola, J. and Ballantyne J. *For. Sci. Int.* 135: 85-96 (2003)

9 The Development of an 18 Loci Y-STR system for Forensic Casework. Hall, A. and Ballantyne, J. *Anal Bioanal Chem* 376 1234-1246 (2003)

10 Novel Y-STR Typing Strategies Reveal the Genetic Profile of the Semen Donor in Extended Interval Post Coital Cervicovaginal Samples. Hall, A. and Ballantyne, J. *For Sci Int* 136: 58-72 (2003)

11 Strategies for the Design and Assessment of Y-STR Multiplexes for Forensic Use. Hall, A. and Ballantyne, J. *Forensic Sci Rev* 15(2) 137-149 (2003)

12 A Highly Discriminating 21 Locus Y-STR "Megaplex" System Designed to Augment the Minimal Haplotype Loci for Forensic Science Casework. Hanson, E. and Ballantyne, J. *J Forensic Sci* 49(1): 50-51 (2004)

13 SWGDAM Developmental Validation of a 19 locus Y-STR System for Forensic Casework. Daniels, D., Hall, A. and Ballantyne, J. *J Forensic Sci* 49 (4) 668-683 (2004)

14 Characterization of UVC-Induced DNA Damage in Physiological Stains: Forensic Implications. Hall, A. and Ballantyne, J. *Anal Bioanal Chem* 380 72-83 (2004)

15 An mRNA and DNA Co-Isolation Method for Forensic Casework Samples. Alvarez, M, Juusola, J and Ballantyne, J. *Anal Biochem* 335: 289-298 (2004)

16 Inference of Human Geographic Origins using *Alu* Insertion Polymorphisms. Ray, D., Walker, J., Hall, A., Llewellyn, B., Ballantyne, J., Christian, A., Turteltaub, K., and Batzer, M. *For Sci Int* 153 117-124 (2005)

17 Multiplex mRNA Profiling for Body Fluid Identification. Juusola, J. and Ballantyne, J. *For Sci Int* 152 1-12 (2005)

18 Whole Genome Amplification Strategy for Forensic Genetic Analysis Using Single or Few Cell Equivalents of Genomic DNA. Hanson, E. and Ballantyne, J. *Anal Biochem* 346 246-257 (2005)

19 DNA Identifications After the 9/11 World Trade Center Attack. Biesecker LG, Bailey-Wilson JE, Ballantyne J, Baum H, Bieber FR, Brenner C, Budowle B, Butler JM, Carmody G, Conneally PM, Duceman B, Eisenberg A, Forman L2, Kidd KK, Leclair B, Niezgoda S, Parsons TJ, Pugh E, Shaler R, Sherry ST, Sozer A, Walsh A. *Science* 310 1122-1123 (2005)

20 Comprehensive Annotated STR Physical Map of the Human Y Chromosome: Forensic Implications. Hanson, E. and Ballantyne, J. *Legal Medicine* (2006) 8 110-120

21 Laser Microdissection Separation of Pure Spermatozoa from Epithelial Cells for STR Analysis. Sanders, C. T., Sanchez, N., Ballantyne, J. and. Peterson, D.A *J. Forensic Sci* 51(4) 748-757 (2006)

22 Novel thermostable Y-family Polymerases: Applications for the PCR Amplification of Damaged or Ancient DNAs. McDonald, J.P., Hall, A., Gasparutto, D., Cadet J., Ballantyne J and Woodgate, R. *Nucleic Acids Res* (2006) 34 (4) 1102-1111

23 The Identification of Newborns Using Messenger RNA Profiling Analysis. Alvarez, M. and Ballantyne, J. *Anal Biochem* 357 21-34 (2006)

24 Testing and Evaluation of 43 'Non-Core' Y Chromosome Markers for Forensic Casework Applications. Hanson, E., Berdos, P. and Ballantyne, J. *J. Forensic Sci* 51(6) 1298-1314 (2006)

25 Y-STR Concordance Study Between Y-Plex™5, Y- Plex™6, Y-Plex™12, Powerplex®, Y-Filer™, MPI, and MPII. Gross, A.M., Berdos, P. and Ballantyne, J. *J. Forensic Sci* 51(6) 1423-28 (2006)

26 Sub-Populations within the Major European and African Derived Haplogroups R1b3 and E3a are Differentiated by Previously Phylogenetically Undefined Y-SNPs. Sims, L.M., Garvey, D. and Ballantyne J. *Human Mut* 28(1) 97 (2007)

27 Population Data for a Novel, Highly Discriminating Tetra-local Y-STR: DYS503. Hanson, E. and Ballantyne, J. *J. Forensic Sci* 52 (2) 498-499 (2007)

28 Simplified Low Copy Number (LCN) DNA Analysis by Post PCR Purification. Smith, P.J. and Ballantyne, J. *J. Forensic Sci* 52 (4) 820-829 (2007)

29 Performance Characteristics of Commercial Y-STR Multiplex Systems. Mayntz-Press, K.A and Ballantyne J. *J. Forensic Sci* 52 (5) 1025-1034 (2007)

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FUNDED PROJECTS

A. External Contracts and Grants
Summary: Since May 2001, 52 awards totaling ~$9.7 million (% PI: ~$8.9 million).

1 Title: **Validation of Y chromosome STR (Y-STR) Multiplexes for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $124,691

Beginning Date: May 2001
Status: new
Term: 1 year

2 Title: **National Y -STR Haplotype Reference Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $112,718
Beginning Date: May 2001
Status: new
Term: 1 year

3 Title: **Assessment of Damaged DNA Templates in Biological Stains**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2002-IJ-CX-K001 (UCF 11-64-6009)
Total Dollar Amount: $115,000
Beginning Date: January 2002
Status: new
Term: 1 ½ years

4 Title: **Validation of Y chromosome STR (Y-STR) Multiplexes for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $45,102
Beginning Date: May 2002
Status: continuation
Term: 1 year

5 Title: **National Y -STR Haplotype Reference Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $80,351
Beginning Date: May 2002
Status: continuation
Term: 1 year

6 Title: **Development of Novel Y Chromosome Markers for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $74,201
Beginning Date: May 2002
Status: new
Term: 1 year

7 Title: **mtDNA by Pyrosequencing**
PI: Jack Ballantyne
Sponsor: FBI
Grant Number: BAA-914497 (UCF 11-64-509)
Total Dollar Amount: $120,818
Beginning Date: November 02
Status: new
Term: 1 year
8 Title: **Validation of Y chromosome STR (Y-STR) Multiplexes for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $66,885
Beginning Date: May 2003
Status: continuation
Term: 1 year

9 Title: **National Y -STR Haplotype Reference Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $107,116
Beginning Date: May 2003
Status: continuation
Term: 1 year

10 Title: **Speedy Rape Kit Screening**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $116,885
Beginning Date: May 2003
Status: new
Term: 1 year

11 Title: **Development of Novel Y Chromosome Markers for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $100,885
Beginning Date: May 2003
Status: continuation
Term: 1 year

12 Title: **Age Determination from RNA**
PI: Jack Ballantyne
Sponsor: TSWG (Technical Support Working Group on Counter Terrorism)
Grant Number: DAAD05-03-C-0047
Total Dollar Amount: $117,526

Beginning Date: August 2003
Status: new
Term: 1 year

13 Title: **Development of a Panel of Y Chromosome STR Markers for Forensic Casework**
PI: Jack Ballantyne
Sponsor: The BODE Technology Group, Springfield,VA
Grant Number: 11-64-4305
Total Dollar Amount: $5,000
Beginning Date: July 1999
Status: new
Term: 3 months

14 Title: **Assessment of Damaged DNA Templates in Biological Stains**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2002-IJ-CX-K001 (UCF 11-64-6009)
Total Dollar Amount: $169,924
Beginning Date: September 2003
Status: renewal
Term: 1 ½ years

15 Title: **Messenger RNA Profiling: A Prototype Method to Supplant Conventional Methods for Semen Identification**
PI: Jack Ballantyne
Sponsor: FBI
Grant Number: JFB103287/A3C0328700 (UCF 11-64-6021)
Total Dollar Amount: $158,486
Beginning Date: November 2003
Status: new
Term: 1 year

16 Title: **Messenger RNA Profiling: A Prototype Method to Supplant Conventional Methods for Body Fluid and Tissue Identification**
PI: Jack Ballantyne
Sponsor: FBI
Grant Number: Modification to JFB103287/A3C0328700 (UCF 11-64-6021)
Total Dollar Amount: $300,000
Beginning Date: April 2003
Status: modification to
Term: 1 year

17 Title: **Validation of Y chromosome STR (Y-STR) Multiplexes for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $124,921
Beginning Date: May 2004
Status: continuation

Term: 1 year

18 Title: **National Y -STR Haplotype Reference Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $133,616
Beginning Date: May 2004
Status: continuation
Term: 1 year

19 Title: **Speedy Rape Kit Screening**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $136,476
Beginning Date: May 2004
Status: continuation
Term: 1 year

20 Title: **Development of Novel Y Chromosome Markers for Operational Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $124,921
Beginning Date: May 2004
Status: continuation
Term: 1 year

21 Title: **Determination of Physical Characteristics of an Individual from Biological Stains**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2005-MU-BX-K075
Total Dollar Amount: $224,776
Beginning Date: September 2005
Status: new
Term: 2 years

22 Title: **Determination of Age (Time since deposition) of a Biological Stain**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2005-MU-BX-K071
Total Dollar Amount: $124,753
Beginning Date: October 2005
Status: new
Term: 2 years

23 Title: **Evaluation of Whole Genome Single Cell Amplification; Sperm Cells Isolated from Vaginal Smears**

PI: Jack Ballantyne
Sponsor: FBI
Award Number: J-FBI-05-177
Total Dollar Amount: $428,267
Beginning Date: September 2005
Status: new
Term: 1.5 years

24 Title: **Development and Validation of Novel Y Chromosome Markers for Forensic Use**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $113,717
Beginning Date: June 2004
Status: continuation
Term: 1 year

25 Title: **Management of a Comprehensive US Y-STR Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $145,145
Beginning Date: June 2005
Status: new
Term: 1 year

26 Title: **Compilation of a Comprehensive US Y-STR Reference Database**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $119,566
Beginning Date: June 2005
Status: continuation
Term: 1 year

27 Title: **Forensic DNA Sourcebook**
Sponsor: National Institute of Justice
Grant Number: 98-IJ-CX-K003 (UCF 11-65-6006)
Total Dollar Amount: $121,571
Beginning Date: June 2005
Status: new
Term: 1 year

28 Title: **Compilation and Management of a Comprehensive US Y-STR Reference Database**
PI: Jack Ballantyne
Sponsoring Agency: National Institute of Justice
Grant Number: 2005-MU-MU-K044 Supplement 1 (UCF 24-07-6017)
Total Dollar Amount: $253,697
Beginning Date: June 2006

Status: continuation
Term: 1 year

29 Title: **Forensic DNA Sourcebook**
PI: Jack Ballantyne
Grant Number: 2005-MU-MU-K044 Supplement 1 (UCF 24-07-6017)
Total Dollar Amount: $116,110
Beginning Date: June 2006
Status: continuation
Term: 1 year

30 Title: **Optimization, Testing, and Validation of Novel-DNA Technology**
PI: Jack Ballantyne
Grant Number: 2005-MU-MU-K044 Supplement 1 (UCF 24-07-6017)
Total Dollar Amount: $230,193
Beginning Date: June 2006
Status: new
Term: 1 year

31 Title: **Double Strand Break Repair of Highly Integrated DNA**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2006-DN-BX-K005 (UCF 24-06-6033)
Total Dollar Amount: $174,025
Beginning Date: June 2006
Status: new
Term:2 years

32 Title: **DNA Profiling of the Semen Donor in Extended Post Coital-Coital Samples**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2007-DN-BX-K148 (UCF # 24-07-6018)
Total Dollar Amount: $271,504
Beginning Date: October 2007
Status: new
Term: 2 years

33 Title: **Improved Detection of Male DNA from Post-Coital Samples**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2007-DN-BX-K147 (UCF # 24-06-6040)
Total Dollar Amount: $324,705
Beginning Date: October 2007
Status: new
Term: 2 years

34 Title: **Management of a National Y-STR Database**
PI: Jack Ballantyne
Sponsor: NFSTC (National Institute of Justice)

Grant Number: 2007-MU-BX-K008 (UCF # 24-07-8003)
Total Dollar Amount: $150,000
Beginning Date: November 2007
Status: continuation
Term: 1 year

35 Title: **Deconvolution of Body Fluid Mixtures: Cell Type Identification and Genetic Profiling of Micro-dissected Cells**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2008-DN-BX-K007 (UCF # 24-07-6027)
Total Dollar Amount: $415,776
Beginning Date: October 2008
Status: new
Term: 2 years

36 Title: **Y-STR National Population Statistics Database**
PI: Jack Ballantyne
Sponsor: NFSTC (National Institute of Justice)
Grant Number: 2008-MU-MU-K003 (UCF # 24-07-8004)
Total Dollar Amount: $150,000
Beginning Date: November 2008
Status: continuation
Term: 1 year

37 Title: Rapid **STR Genotyping of Forensic Crime Scene Samples**
Co-PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2008-DN-BX-K012 (UCF # 24-07-8005)
Total Dollar Amount: 20% of $491,261 = $99,968
Beginning Date: October 2007
Status: new
Term: 2 years

38 Title: **Identification of Forensically Relevant Fluids and Tissues by Small RNA Profiling**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2009-DN-BX-K255 (UCF # 24-07-6031)
Total Dollar Amount: $328,962
Beginning Date: November 2009
Status: new
Term: 2 years

39 Title: **Predicting the Biological Age of a Bloodstain Donor**
PI: Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2009-DN-BX-K179 (UCF # 240-07-6030)
Total Dollar Amount: $300,450
Beginning Date: October 2009

Status: new
Term: 2 years

40 Title: **Y-STR National Population Statistics Database**
PI: Jack Ballantyne
Sponsor: NFSTC (National Institute of Justice)
Grant Number: 2007-MU-BX-K008 (UCF # 24-07-8010)
Total Dollar Amount: $150,000
Beginning Date: November 2009
Status: continuation
Term: 1 year

41 Title: **Molecular Characterization of Trace Biological Evidence for the Optimized Recovery and Analysis of 'Touch DNA'**
PI: Jack Ballantyne (100% share)
Sponsor: National Institute of Justice
Grant Number: 2010-DN-BX-K139 (UCF # 24-07-6035)
Total Dollar Amount: $304,657
Beginning Date: November 2010
Status: new
Term: 2 years

42 Title: **Post Coital DNA Recovery**
PI: Jack Ballantyne (20 % share)
Sponsor: National Institute of Justice
Grant Number: 2009-DN-BX-0023 (UCF # 24-07-8011)
Total Dollar Amount: $149,495 (Ballantyne share)
Beginning Date: November 2010
Status: new
Term: 2 years

43 Title: **Compilation and management of a Comprehensive US Y-STR Reference Database**
PI: Jack Ballantyne (100 % share)
Sponsor: RTI International, Forensic Center of Excellence
Grant Number: Subaward number 4-321-0213168 (UCF # 24-07-8012)
Total Dollar Amount: $120,535
Beginning Date: April 2012
Status: new
Term: 2 years (renewed 2 additional years)

44 Title: **Who and How: Comprehensive RNA-based BodyfluID Assay to Provide Context to a Recovered DNA Profile**
PI: Jack Ballantyne (100 % share)
Sponsor: Department of the Army
Cooperative Agreement Number: W911NF-12-2-0055 (UCF # 24-07-6037)
Total Dollar Amount: $301,173
Beginning Date: September 2012
Status: new
Term: 2 year

45 Title: **Combined Genetic and Micro-chemical analysis of household dust as a definitive trace identified of a room and its occupants**
PI: Jack Ballantyne (50 % share)
Sponsor: National Institute of Justice
Grant Number: 2013-DN-BX-K025 (UCF # 24-07-6038)
Total Dollar Amount: $188,198
Dollar Amount (Ballantyne share): $94,099
Beginning Date: January 1 2014
Status: new
Term: 1 year

46 Title: **Methodologies for Rapid Sexual Assault Forensic Evidence Screening**
PI: Jack Ballantyne (100 % share)
Sponsor: Department of the Army; Sub-contract from LGC
Cooperative Agreement Number: W911NF-13-R0011 (UCF # 24-07-8013)
Total Dollar Amount: $179,148
Dollar Amount (Ballantyne share): $179,148
Beginning Date: December 1 2014
Status: new
Term: 21 months

47 Title: **The physical separation and single source DNA profiling of individual mixture components by RNA in situ hybridization-based cell type identification**
PI: Jack Ballantyne (50 % share)
Sponsor: National Institute of Justice
Grant Number: 2014-DN-BX-K018 (UCF # 24-07-6040)
Total Dollar Amount: $530,426
Dollar Amount (Ballantyne share): $265,213
Beginning Date: January 1 2015
Status: new
Term: 2 years

48 Title: **How it got there: associating individual DNA profiles with specific body fluids in mixtures using targeted digital gene expression and RNA-SNP identification**
PI: Jack Ballantyne (50 % share)
Sponsor: National Institute of Justice
Grant Number: 2014-DN-BX-K019 (UCF # 24-07-6041)
Total Dollar Amount: $436,457
Dollar Amount (Ballantyne share): $218,228.50
Beginning Date: January 1 2015
Status: new
Term: 2 years

49 Title: **Combined Genetic and Micro-chemical analysis of household dust as a definitive trace identified of a room and its occupants**
PI: Jack Ballantyne (50 % share)

Sponsor: National Institute of Justice
Grant Number: 2013-DN-BX-K025 (UCF # 24-07-6042)
Total Dollar Amount: $188,198
Dollar Amount (Ballantyne share): $94,099
Beginning Date: January 1 2016
Status: continuation (phase II)

50 Title: **Optimization of RNA Body FluID Assays: Differential Co-extraction for Sperm Analysis and Rapid Direct Lysis for High-Throughput Evidence Screening**
PI: Jack Ballantyne (100 % share)
Sponsor: Department of the Army
Grant Number: W911NF-16-2-0018 (UCF # 24-07-6044)
Total Dollar Amount: $219,149
Dollar Amount (Ballantyne share): $219,149
Beginning Date: January 13 2016
Status: new
Term: 15 months

51 Title: **Human Organ Tissue Identification by Targeted RNA Deep Sequencing to Aid in the Investigation of Shooting and Other Traumatic Bodily Injury Incidents**
PI:Jack Ballantyne
Sponsor: National Institute of Justice
Grant Number: 2016-DN-BX-0165
Total Dollar Amount: $424,799
Dollar Amount (Ballantyne share 50%): $212,399.50
Beginning date: January 1, 2017
Status: new
Term: 2 years

52 Title: **Compilation and management of a Comprehensive US Y-STR Reference Database**
PI: Jack Ballantyne (100 % share)
Sponsor: RTI International, Forensic Center of Excellence
Grant Number:
Total Dollar Amount: $51,883
Beginning Date: June 2017
Status: new
Term: 1 year (renewable 4 additional years)

EXPERT TESTIMONY
Testified as an expert witness in Courts of Law in US, Scotland, England and Hong Kong

REFERENCES
Available upon request

Curriculum Vitae

Timothy J. Sliter, Ph.D.

Contact Information

Southwestern Institute of Forensic Sciences
2355 North Stemmons Freeway
Dallas, Texas 75235
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Current Professional & Academic Positions

- Chief of Physical Evidence, Dallas County Criminal Investigation Laboratory, Southwestern Institute of Forensic Sciences, Dallas, TX
- Associate Professor, Department of Pathology, University of Texas Southwestern Medical Center, Dallas, TX

Employment History

1998-2004	DNA Unit Supervisor, Southwestern Institute of Forensic Sciences, Dallas, TX
1991-1998	Assistant Professor, Department of Biology, Southern Methodist University, Dallas, TX
1988-1991	Postdoctoral Research Associate, Department of Biology, University of North Carolina at Chapel Hill, Chapel Hill, NC
1986-1988	Postdoctoral Fellow, Curriculum in Neurobiology, University of North Carolina at Chapel Hill, Chapel Hill, NC

Education

1973-1977	Harvard College, Cambridge, MA. Degree: A.B., *cum laude*
1977-1978	Harvard University, Graduate School of Arts and Sciences Cambridge, MA
1979-1986	University of California at Irvine, School of Biological Sciences Irvine, CA. Degree: Ph.D. (Developmental & Cell Biology/Genetics)

Other Training

- 1998 - Training course: Mitochondrial DNA Sequence Analysis for Forensic Scientists, Armed Forces Institute of Pathology, George Mason University, Manassas, Virginia
- 1998 - Workshop, Expert Witness Testimony, 9th International Symposium on Human Identification, Orlando, Florida
- 1998 - FBI/SWGDAM STR Training Workshop, Austin, TX
- 1998 - Annual CODIS User's Workshop, Washington, DC
- 1999 - SWGDAM Forensic Statistics and Population Genetics Workshop, Austin, TX
- 2000 - American Academy of Forensic Sciences Annual Meeting, Reno, NV
- 2000 - Training workshop: Forensic DNA Analysis, American Academy of Forensic Sciences Annual Meeting, Reno, NV
- 2000 - National Institute of Justice, DNA Grantees Workshop, Washington, DC
- 2000 - Training course: Bloodstain Pattern Interpretation, Bloodstain Institute, Corning NY (Instructors, Herb MacDonell, Paul Kish)
- 2000 - Training course: Advanced Blood Stain Analysis, Mesquite Police Department, Mesquite, TX (Instructor: Bob Henderson)
- 2001 - American Academy of Forensic Sciences Annual Meeting, Seattle, WA
- 2001 - Training workshop: Short Tandem Repeat Analysis, American Academy of Forensic Sciences Annual Meeting, Seattle, WA
- 2002 - National Institute of Justice, DNA Grantees Workshop, Washington, DC
- 2003 - Technical seminars: Tools for Gene Expression Analysis, SNP Genotyping, DNA Sequencing, and Fragment Analysis, University of Texas, Southwestern Medical Center, Dallas, TX
- 2003 - Federal Bureau of Investigation DNA Auditors Training, Texas Department of Public Safety, Austin, TX
- 2004 - Federal Bureau of Investigation, Combined DNA Index System (CODIS) Training, Vienna, VA
- 2004 - AAFS Annual Meeting, Dallas, TX
- 2005 - 33rd Annual Crime Laboratory Development Symposium, Ann Arbor, MI
- 2005 - Training course: Scanning Electron Microscopy & X-ray Microanalysis, Lehigh University
- 2006 - 34th Annual Crime Laboratory Development Symposium, Atlanta, GA
- 2006 - Federal Bureau of Investigation, Mitochondrial DNA Training Course, Quantico, VA
- 2006 - National Institute of Justice, DNA Grantees Workshop
- 2007 - NIJ Conference 2007/DNA Grantees Conference, Arlington, VA
- 2007 - DNA Summit Meeting, Arlington, VA
- 2008 – American Academy of Forensic Sciences Annual Meeting, Washington, DC
- 2008 – NIJ Conference & DNA Grantees Workshop, Arlington, VA
- 2009 – NIJ Conference & DNA Grantees Workshop, Arlington, VA
- 2009 - NFSTC Mitochondrial and STR DNA Analysis by Mass Spectrometry Workshop, San Diego, CA
- 2010 – NIJ Conference & DNA Grantees Workshop, Arlington, VA
- 2012 - NIJ Conference & DNA Grantees Workshop, Arlington, VA

- 2012 – Current Status & Future of Y-STR Analysis, AFDAA Workshop, San Antonio, TX
- 2013 – Outdoor Recovery Workshop, Forensic Anthropology Center, University of Tennessee, Knoxville, TN
- 2013 – ASCLD/LAB Measurement Confidence Level 100 Training
- 2013 – ASCLD/LAB Level 200 Uncertainty of Measurement Training for Firearms
- 2014 – STRmix DNA Statistics Training Workshop, Las Vegas, NV
- 2015 – Fiber Analysis Training Workshop, Skip Palenik, Fort Worth, TX
- 2015 – Hair Analysis Training Workshop, Skip Palenik, Fort Worth, TX
- 2015 – NIJ 2015 Impression Pattern and Trace Evidence Symposium, San Antonio, TX
- 2015 – 2015 Association of Firearm and Tool Mark Examiners Annual Training Seminar, Dallas, TX
- 2015 – Texas Forensic Science Commission DNA Mixture Interpretation Training, Fort Worth, TX
- 2015 – NIST International Symposium on Forensic Science Error Management, Washington, DC
- 2015 – Texas Forensic Science Commission Root Cause Analysis Training, Austin, TX
- 2015 – International Symposium on Human Identification, Grapevine, TX
- 2015 – Association of Forensic DNA Analysts and Administrators, Summer Meeting, Dallas, TX
- 2016 – Texas Forensic Science Commission DNA Mixture Interpretation Training, Fort Worth, TX

Presentations

- 2009 – Panel Presentaton: "Systematic DNA Testing," Innocence Network Annual Meeting, Houston, TX.
- 2011 – Presentation: "Forensic Analysis, DNA and CODIS," Texas Bar Association, Advanced Criminal Law Course, Houston, TX.
- 2017 – Workshop: "Texas Forensic Scientist Licensing Program," American Society of Crime Laboratory Directors, 2017 Annual Meeting, Dallas, TX.
- 2018 – Presentation: "DNA in Criminal Investigations," Eastfield College, Mesquite, TX.
- 2018 – Presentation: "DNA 101 and Emerging Technologies," Center for American and International Law, Plano, TX.

Other

- 2005 - Witness, hearing on state forensic DNA issues, Texas Senate Criminal Justice Committee, Houston, TX
- 2010 - Witness, hearing on state crime laboratory issues, Texas Senate Criminal Justice Committee, Austin, TX
- 2016 –Texas Forensic Science Commission Licensing Advisory Committee

Professional Organizations

- American Society of Human Genetics

- Genetics Society of America
- Royal Statistical Society (UK)
- Association of Forensic DNA Analysts & Administrators
- Texas Society of Crime Laboratory Directors
- ASTM Committee E11 (Quality & Statistics)
- ASTM Committee E30 (Forensic Sciences)

Grant History

Project Director, FY2017 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 627,301.

Project Director, FY2016 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 594,061.

Project Director, FY2015 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 592,042.

Project Director, FY2013 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 698,382.

Project Director, Enhancement of Local Crime Lab and Medical Examiner Services, FY2012 Paul Coverdell Forensic Science Improvement Program, National Institute of Justice. Award amount: $ 174,410.

Project Director, FY2012 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 682,135.

Project Director, FY2011 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $ 849,881.

Project Director, FY2008 Forensic DNA Backlog Reduction Program - Dallas County, National Institute of Justice. Award amount: $822,502.

Project Director, DNA Backlog Reduction & Enhancement of DNA Analysis Services, FY2007 Forensic DNA Backlog Reduction Program, National Institute of Justice. Award amount: $809,929.

Project Director, Development of an Enhanced Electronic Casework Record System, FY2007 Paul Coverdell Forensic Science Improvement Program, National Institute of Justice. Award amount: $94,361.

Project Director, Enhancement of Firearms Analysis Services, FY2006 Paul Coverdell Forensic Science Improvement Program, National Institute of Justice. Award amount: $95,000.

Project Director, Enhancement of Firearms Analysis Services, FY2005 Paul Coverdell Forensic

Science Improvement Program, National Institute of Justice. Award amount: $95,000.

Project Director, Enhancement of Forensic DNA Testing Capabilities, FY2005 DNA Capacity Enhancement Program, National Institute of Justice, 2005-2006 (current). Award amount: $372,193.

Project Director, Reduction in DNA Casework Backlog, FY2005 Forensic Casework Backlog Reduction Program, National Institute of Justice, 2005-2006 (current). Award amount: $288,660.

Project Director, Training of Forensic Scientists & Death Scene Investigators, Criminal Justice Division, Office of the Governor (Texas), FY2004 Coverdell Grant Program, 2005. Award amount: $47,355.

Project Director, Enhancement of Forensic DNA Testing Capabilities, FY2004 DNA Capacity Enhancement Program, National Institute of Justice, 2004-2005. Award amount: $479,806.

Project Director, Enhancement of Firearms Analysis Services, FY2004 Paul Coverdell Forensic Science Improvement Program, National Institute of Justice, 2004-2005. Award amount: $80,233.

Project Director, FY2001, FY2003 No Suspect DNA Backlog Reduction Program, National Institute of Justice, 2002-2004. Award amount: $420,000.

Project Director, STR Validation and Implementation, Criminal Justice Division, Office of the Governor (Texas), 1998-2003. Award amount: $461,385.

Project Director, Forensic DNA Laboratory Supervision and Validation of Mitochondrial DNA Sequence Analysis, Criminal Justice Division, Office of the Governor (Texas), 1998-2002. Award amount: $484,000.

Project Director, STR Validation and Implementation, National Institute of Justice, 1998-1999. Award amount: $151,068.

Project Director, Molecular Genetics of Insect Steroidogenesis, National Research Initiative, U.S. Department of Agriculture, 1993-1998. Award amount: $345,000.

Publications

Sliter, T.J. (1987). A reevaluation of the map location of the *ecdysoneless* mutation. Drosophila Information Service 66:130.

Sliter, T.J., B.J. Sedlak, F.C. Baker and D.A. Schooley (1987). Juvenile hormone in *Drosophila melanogaster*: identification and titer determination during development. Insect Biochemistry 17: 161-165.

Richard, D.S., S.W. Applebaum, T.J. Sliter, F.C. Baker, D.A. Schooley, C.C. Reuter, V.C. Henrich and L.I. Gilbert (1989). Juvenile hormone bisepoxide biosynthesis *in vitro* by the

ring gland of *Drosophila melanogaster*: a putative new juvenile hormone in the higher Diptera. Proceedings of the National Academy of Science (USA) 86:1421-1425.

Sliter, T.J. (1989). Imaginal disc autonomous expression of a defect in sensory bristle patterning caused by the *lethal(3)ecdysoneless*^{1} (*l(3)ecd*^{1}) mutation of *Drosophila melanogaster*. Development 106:347-354.

Sliter, T.J., V.C. Henrich, R.L. Tucker and L.I. Gilbert (1989). Genetics of the *dras3-Roughened-ecdysoneless* chromosomal region (62B3-4 to 62D3-4) in *Drosophila melanogaster*: analysis of recessive lethal mutations. Genetics 123: 327-336.

Henrich, V.C., T.J. Sliter, D.B. Loubahn, A. MacIntyre and L.I. Gilbert (1990) A steroid/thyroid hormone receptor superfamily member in *Drosophila melanogaster* that shares extensive sequence similarities with a mammalian homologue. Nucleic Acids Research 18: 4143-4148.

Bidmon, H. and T.J. Sliter (1990). The ecdysteroid receptor. Invertebrate Reproduction and Development 18: 13-27.

Sliter, T.J. and L.I. Gilbert (1992). Developmental arrest and ecdysteroid deficiency resulting from mutations at the *dre4* locus of *Drosophila melanogaster*. Genetics 130: 555-568.

Sliter, T.J., K. Sudhivoraseth and J.L. McCarthy (1996). Quantitation of ecdysteroid synthesis during short-term organ culture. Methods in Enzymology 272: 292-304.

Bassett, M.B., J.L. McCarthy, M.R. Waterman and T.J. Sliter (1997). Sequence and developmental expression of Cyp18, a member of a new cytochrome P450 family from *Drosophila*. Molecular and Cellular Endocrinology 131: 39-49.

D. JODY KOEHLER

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EDUCATION

Southwest Texas State University
M.S. in Biology **1996**
Minor: Biochemistry
Thesis: "Use of Random Amplified Polymorphic DNA (RAPD) to Identify Largemouth Bass Subspecies and Their Intergrades"

Southwest Texas State University
B.S. in Aquatic Biology **1993**
Minor: Chemistry

AWARDS

Graduate Stipend, Southwest Texas State University	January 1994 – December 1994
Academic Excellence Award, Southwest Texas State University	May 1993, May 1996
Fred and Yetta Richan Aquatic Biology Award, Southwest Texas State University	May 1993
Dean's List, Southwest Texas State University and Texas A&I University	May 1989, May 1992, May 1993
Honor Roll, Texas A&I University	September 1989
Livestock Show and Rodeo Scholarship, Texas A&I University	December, 1988
Alpha Chi-Member	
Houston Golden Key National Honor Society –member	

TEACHING EXPERIENCE

Southwest Texas State University
Laboratory Instructor-Introductory Botany/Aquatic Biology **1994**
Taught laboratory sections of Introductory Botany and Aquatic Biology.

Austin Community College
Adjunct Instructor-Introductory Biology/Microbiology **2002-2005**
Taught lecture and laboratory sections of Introductory Biology and Microbiology. Graded all written work and developed course curriculum.

Concordia University
Adjunct Instructor-Introductory Biology/Forensic Science **2005-2009**
Taught lecture and laboratory sections of Introductory Biology. Taught Forensic Science. Graded all written work and developed course curriculum.

RELATED EXPERIENCE

Texas Forensic Science Commission
Senior Scientific Advisor **November 2017 – Present**
Provide technical expertise to the Texas Forensic Science Commission investigations, assist with t he Commission's laboratory accreditation program and provide vital support to the Licensing Advisory Committee tasked with implementing the forensic analyst licensing program.

ANSI-ASQ National Accreditation Board (ANAB)
Contract Lead Assessor **January 2017-Present**
Lead assessment teams to determine if forensic laboratories are in compliance with international accreditation standards, including standards set by the International Organization for Standardization.

Laboratory Manager, Capitol Area Regional Laboratory **March 2017 – October 2017**
Lead the Capitol Area Regional Laboratory, performing performance reviews, implementing process improvement to ensure the laboratory is meeting the needs of our clients by producing high quality casework in a timely manner, testifying in court, compiling grant progress report data, meeting with employees to ensure their needs are met, working with under-performing employees to ensure they are can perform the job duties that are required of them, serving as the Quality Manger and DNA Technical Leader, and approving expenditures required to operate the laboratory

Texas Department of Public Safety Crime Laboratory

DNA Section Supervisor II/III, Austin Laboratory **November 2006 –March 2017**

Lead a team of 20 DNA analysts, performing performance reviews, implementing process improvement to ensure the section is meeting the needs of our clients by producing high quality casework in a timely manner, testifying in court, compiling grant progress report data, meeting with employees to ensure their needs are met, working with under-performing employees to ensure they are can perform the job duties that are required of them, serving on a subcommittee to standardize the way DNA mixture profiles are interpreted within the crime laboratory, serving as the Technical Leader for our Weslaco Regional laboratory, mentoring new Technical Leaders/supervisors in the Crime Laboratory system, coordinating and overseeing the CODIS review project with private laboratories, and approving expenditures required to operate the DNA Section.

Texas Department of Public Safety

DNA Technical Leader/DNA Section Supervisor **May 2004 – November 2006**

Provided oversight for the technical operations of the DNA section, trained new analysts, provided oversight for proficiency testing of the analysts, troubleshooting instrumentation, evaluated employees' abilities and recommended remedial training if required, conducted administrative review on DNA cases, validated new equipment, performed DNA casework, and investigated crime scenes.

Austin Independent School District

Teacher **August 2002-August 2003**

Taught 7th grade Magnet Science, Medical Technology, and Marine Biology. Supervised the work of 28 students in a biology classroom. Kept accurate records of attendance, students' grades, and documentation of conversations with students and parents. Met the students' and parents' needs on a daily basis in a professional manner. Planned lessons to ensure TEKS guidelines were satisfied.

Texas Department of Public Safety

Criminalist/DNA Technical Leader **November 1996-July 2001**

Trained new employees to perform DNA analysis for the Austin laboratory as well as the regional laboratories. Provided oversight for proficiency testing, quality assurance and quality control, troubleshooting instrumentation, and instrument validation. Testified in court as an expert witness, investigated contamination incidents, and performed DNA analysis on forensic cases. Served as a team member on the system-wide DNA Advisory Board.

Texas Parks and Wildlife Department

Microbiologist **December 1994-November 1996**

Established two DNA laboratories within the Inland Fisheries Division. Performed genetic analysis on fish populations within Texas using protein and DNA analysis methods. Investigated fish health issues.

PUBLICATIONS AND PAPERS

Kathryn Oostdik, Kristy Lenz, Jeffrey Nye, Kristin Schelling, Donald Yet, Scott Bruski, Joshua Strong, Clint Buchanan, Joel Sutton, Jessica Linner, Nicole Frazier, Hays Young, Learden Matthies, Amber Sage, Jeff Hahn, Regina Wells, Natasha Williams, Monica Price, D. Jody Koehler, Melisa Staples, Katie L. Swango, et al. 2014. Developmental validation of the PowerPlex® Fusion System for analysis of casework and reference samples: A 24-locus multiplex for new database standards. FSI: Genetics, Vol. 12: 69-76

Jonelle M. Thompson, Margaret M. Ewing, William E. Frank, Jill J. Pogemiller, Craig A. Nolde, D. Jody Koehler, Alyssandra M. Shaffer, Dawn R. Rabbach, Patricia M. Fulmer, Cynthia J. Sprecher, Douglas R. Storts. 2013. Developmental validation of the PowerPlex® Y23 System: A single multiplex Y-STR analysis system for casework and database samples. FSI: Genetics Vol 7 (2): 240-250.

Johnson, S.K., L.T. Fries, D.J. Williams, and D.G. Huffman. 1995. Presence of the parasitic swim bladder nematode, Anguillicola crassus, in Texas aquaculture. World Aquaculture 26(3):35-36.

Fries, L.T., D.J. Williams, and S.K. Johnson. 1996. Occurrence of Anguillicola crassus, an exotic parasitic swim bladder nematode of eels, in the southeastern United States. Transactions of the American Fisheries Society 125 (5): 794-797.

Williams, D.J., S. Kazianis, and R.B. Walter. 1998. Use of Random Amplified Polymorphic DNA (RAPD) for the Identification of Largemouth Bass Subspecies and Their Intergrades. Transactions of the American Fisheries Society 127 (5): 825-832.

MEMBERSHIPS

American Society of Crime Laboratory Directors
Association of Forensic DNA Analysts and Administrators

AUDITOR QUALILFICATIONS

ANSI-ASQ National Accreditation Board-Lead Assessor (2017)
American Society of Crime Laboratory Directors-Laboratory Accreditation Board-*International* Assessor (2006)
American Society of Crime Laboratory Directors-Laboratory Accreditation Board-Legacy Inspector (2005)
The FBI Quality Assurance Standards for Forensic DNA Testing Laboratories Auditor (STR and Y-STR)-2005, updated training as required

REFERENCES

Available upon request

SUPERIOR COURT OF THE DISTRICT OF COLUMBIA
Criminal Division – Felony Branch

UNITED STATES OF AMERICA	)	
	)	**Case No. 2012 CF1 009423**
v.	)	**Judge Herbert B. Dixon, Jr.**
	)	
CARDELL TORNEY	)	

FINDINGS OF FACT, CONCLUSIONS OF LAW, AND ORDER

(**Granting** the Government's Motion *in Limine* to Exclude Expert Testimony;
Granting the Government's Motion for Findings of Fact and Conclusions of Law;
Vacating Protective Order; and **Granting** New IPA Hearing to Defendant to Exercise His Right to Request or Waive DNA Testing)

This matter is before the court on the government's *Motion* in Limine *to Exclude Expert Testimony regarding the DNA Profiles Generated by NMS Labs* filed on July 12, 2013. The motion was supported with an affidavit by Dr. Bruce Budowle. The defendant's *Opposition to Government Motion to Exclude NMS DNA Results* was filed on August 21, 2013, supported with affidavits by Dr. Phillip Danielson and Dr. Christian Westring.

In preparation for hearings on the underlying motion *in limine*, the government requested the protocols relied upon by NMS Labs to support the conclusions reflected in the NMS report dated March 18, 2013. In response to an objection by the defendant, the court issued a protective order dated August 28, 2013 limiting those protocols to be disclosed to the government. Subsequently, the court issued a substitute protective order dated September 2, 2013, with expanded language, on request of the defendant, to properly limit the people who should be allowed to view NMS's retrials and "reasonably limit the purpose of their review to the litigation in this case."

Thereafter, the court conducted several days of evidentiary hearings, as follows:

- November 1, 2013: testimony of the government's expert, Dr. Bruce Budowle;

- December 13, 2013: testimony of the defendant's expert, Dr. Phillip Danielson;
- March 18 – 19, 2014: the continued testimony of the defendant's expert, Dr. Phillip Danielson.

On June 16, 2014, the defendant orally moved for additional testing of the DNA evidence by NMS Labs because of the government's criticisms of the DNA testing conducted and protocols followed by NMS Labs. The court gave an oral ruling denying that motion on the same day.

On June 17, 2015, the defendant filed a motion requesting the court to appoint an independent expert to conduct further DNA testing. The court orally denied that motion at a hearing on June 24, 2015.

On July 7, 2014, in accordance with prior rulings of the court requiring the government to give notice of any rebuttal witnesses, the government filed a notice of rebuttal experts Margaret M. Ewing and Dr. Budowle.

Thereafter, on July 14, 2014, the defendant filed a *Notice of Withdrawal of Expert Notice*. At a hearing on July 28, 2014, the defendant personally consented on the record to the withdrawal of expert notice and the government indicated in response that it would not object if the defendant requested testing by another laboratory. Subsequently, on August 21, 2014, the government filed its *Motion for Findings of Fact and Conclusions of Law*, supported with affidavits by Dr. Bruce Budowle, Margaret Ewing of Promega Corporation, and Laura Cronin, formerly of NMS Labs, requesting that the court to rule as follows:

- That the report generated by NMS Labs is inadmissible;
- That NMS Labs' validation data and protocols *not* be the subject of a protective order, because these data are integral to illustrating how the interpretation protocols are not grounded in NMS Labs' validation data; and

- That the defendant was entitled to a new IPA hearing to be given the opportunity to request DNA testing by a laboratory that will comport with accepted scientific principles.

FINDINGS OF FACT

Upon consideration of the entire record of this case, the court makes the following findings of fact:

1. The DNA test kit utilized by NMS Labs (Promega's PowerPlex® 16HS System) is generally accepted within the relevant scientific community; however, NMS Labs' application of its methodology and interpretation of the data generated by the testing was not conducted in accordance with accepted practices within the forensic DNA scientific community.

2. **Dr. Bruce Budowle**

The government's position is supported by Dr. Bruce Budowle, Executive Director of the Institute of Applied Genetics and Professor in the Department of Molecular and Medical Genetics at the University of North Texas Health Science Center in Fort Worth, Texas. The court finds that Dr. Budowle is uniquely qualified to review and evaluate the work of NMS Labs because, *inter alia*, Dr. Budowle: (1) was previously employed for twenty-six years at the Federal Bureau of Investigation's Laboratory Division where he was involved in the research, development, and validation of numerous methods of DNA analysis; (2) led the team that developed forensic DNA typing capabilities at the FBI Laboratory in Quanticao, Virginia; (3) authored the Quality Assurance Standards that are followed by DNA laboratories throughout the country; (4) formerly served as the Chair of the Scientific Working Group on DNA Analysis Methods (SWGDAM); (5) has extensive experience in all aspects of forensic DNA analysis, including analysis of low level samples, mixture analysis, population genetics, statistical interpretations, and various genetic marker systems; (6) is one of the most published forensic DNA scientists in the world with over 500 publications on the subject of forensic DNA; and (7)

his publications have been relied upon by courts around the nation in deciding a number of pivotal issues that have arisen in the area of forensic DNA since the advent of forensic DNA analysis. The court credits Dr. Budowle's testimony and makes the following findings based on Dr. Budowle's testimony and sworn statements:

- In interpreting DNA profiles generated for casework, NMS ignored its own validation data and has not applied sound practices for evaluating DNA profiles which are grounded in necessary validation studies.
- There is little evidence that NMS's protocols are grounded in NMS's own validation data or those of the scientific community.
- Dr. Phillip Danielson's position that casework can be interpreted differently than validation samples is incomprehensible and out of step with accepted principles within the forensic DNA field.
- Dr. Danielson's interpretation of SWGDAM guidelines is inconsistent with the manner that members of SWGDAM themselves and the vast majority of laboratories in the United States interpret the guidelines and practice DNA interpretation.
- The language used in the report issued by NMS does not accurately capture the substance of the conclusions rendered. In fact, the report is uninformative about the evidence and particularly misleading. In particular, making allele calls when a peak "may or may not be true DNA" does not provide investigators or fact finders with valid and reliable information to properly interpret the DNA evidence or the findings of the analysis. Even more troubling was Dr. Danielson's disclosure that NMS's interpretation may not be DNA as there was no statement in its report or its protocol about the serious degree of uncertainty related to NMS's findings. Thus, the language in the NMS report fails to reveal this serious flaw in the interpretation of DNA evidence, *i.e.*, the findings of

contributors to the evidence may be erroneous. Such practices are out of step with those accepted within the relevant scientific community of generating and reporting reliable and accurate results.

- Regarding NMS Ex. 2.2-1A, the court further finds that:
    - NMS did not perform the quantitation assay appropriately. The improper use of the assay resulted in far too much DNA being used in the amplification process.
    - The DNA results were not within the linear range of the instrument, which would make any previous criteria established by NMS for interpretation invalid for the results generated.
    - Stutter was not analyzed in accordance with accepted industry practices and NMS's own validation data were not applied. Thus, results being attributed to the presence of alleles are invalid and unjustified.
    - All of the warning indicators for off-scale data were present in this sample and yet ignored.
    - Interpretation of the type of data generated here was not appropriate because the PowerPlex® 16HS System (PP16HS), the commercial kit used by NMS for DNA testing in this case, was not designed to be used in such a fashion. Therefore, NMS, with its protocol used in this case, cannot reliably distinguish between true DNA and artifacts.
    - Although DNA analysts endeavor to determine the quantity of DNA and use amounts within a particular range to avoid all of the problems that occurred here, NMS did not follow accepted practices to attempt to use an appropriate quantity of DNA in connection with its testing in this case.

3. **Margaret M. Ewing**

Margaret Ewing is currently employed as a research scientist at Promega Corporation, the manufacturer of the PowerPlex® 16 HS System (PP16HS). Promega is the first and one of the largest manufacturers of DNA multiplex kits in the world. Had the hearing on the admissibility of DNA testing by NMS Labs gone to its conclusion, Ms. Ewing would have been sent by Promega to testify on behalf of Promega as a company designee. According to her sworn statement, Ms. Ewing would have testified to the proper use of PP16HS, the misuse of this Promega product by NMS Labs, and that Promega has relied upon the advice and guidance of the leaders in the scientific community (such as Dr. Bruce Budowle). Promega's position is based on the opinions of persons who designed and conducted the developmental validation of PP16HS. It is particularly noteworthy to the court that this is the first time in the history of Promega Corporation, where it was prepared to send a representative to testify in a criminal trial that one of its products had been misused by a DNA laboratory.

Promega Corporation is uniquely qualified to opine on the application of its manufactured product. Based on the sworn statement of Ms. Ewing, the court finds that NMS misused PP16HS by interpreting the data generated in the second run for NMS Exhibit 2.2-1A. In particular, the court adopts the following factual assertions by Ms. Ewing on behalf of Promega:

- PP16HS was not designed to interpret data in the relative fluorescence units (RFU) range exhibited in the electropherogram produced by the second run for NMS Exhibit 2.2-1A. PP16HS was designed for use in the linear range of the instrument.
- The data in NMS Exhibit 2.2-1A was outside the linear range of the instrument.
- Characteristics of the electropherogram for Exhibit 2.2-1A indicate that NMS failed to hit the amplification target for proper quantity of DNA. These characteristics were

the high RFU values for alleleic peaks and the large number artifacts, including high background noise and an increased amount of stutter and pull-up.

- There are a number of factors that illustrate why interpretation of data produced in NMS Exhibit 2.2-1A was clearly inappropriate, including the fact that the peak heights of the minor alleles designated by NMS were comparable to artifacts in the sample, the substantially high noise levels, the saturation indicators, and an excess of DNA in the amplification process.
- Contrary to Dr. Danielson's testimony, Promega would not expect the Promega stutter percentages to remain linear with off-scale data exhibited in NMS Exhibit 2.2-1A.
- Given all the indicators of saturation in the data for NMS Exhibit 2.2-1A, no qualified DNA analyst would have interpreted the minor alleles in that sample. However, in a deviation from accepted practice in the industry, NMS Labs reported an interpretation of these minor alleles.
- There is no support within the scientific community for Dr. Danielson's assertion that there is a substantive distinction between "major" and "minor" split peaks when interpreting data generated by PP16HS.
- Various factors illustrate the absence of any interpretable autosomal male DNA in NMS Exhibit 2.2-1A, such as the failure to detect male DNA with the quantitation system and the comparison of the total human DNA to male DNA for the epithelial and sperm fractions.

4. **Laura Cronin**

Laura Cronin is a former employee of NMS Labs. She worked at NMS labs for over six years with the title of Forensic Biologist 3. Her supervisor at NMS labs was Dr. Christian Westring.

Ms. Cronin was the technical reviewer for the DNA report issued by NMS Labs in this case. Upon her initial review of the data, she recommended to the DNA analyst, Jillian Fesolovich, that the sample be reamplified. It was her opinion that NMS Exhibit 2.2-1A needed to be reamplified because:

- It appeared as though the analyst had not performed the quantitation assay appropriately which, in turn, caused too much DNA to be used into the amplification process.
- The ectropherogram was overblown.

Because the DNA analyst disagreed with her opinion, the technical leader -- Dr. Westring -- was made aware of the disagreement. Ms. Cronin explained to Dr. Westring the reasons she believed that the quantitation data and the dilution factor did not seem to be appropriate and the electropherogram was overblown. Ms. Cronin recommended to Dr. Westring that NMS re-amplify the sample (which would have taken no more than an hour), but Dr. Westring made the decision that the sample would not be retested.

Ms. Cronin specifically remembered this case because her gut reaction was that NMS Exhibit 2.2-1A should have been retested. Importantly, Ms. Cronin did not feel confident that the profile developed by NMS was accurate. Additionally, Ms. Cronin indicated that she could not trust the eletropherogram because a significantly higher amount of DNA was amplified than is recommended.

Ms. Cronin is not familiar with the terms "major split peaks" or "minor split peaks." During her time at NMS Labs, she never received any training designed to assist with distinguishing between major and minor split peaks.

5. **Dr. Phillip Danielson**

The court does *not* credit the testimony of Dr. Phillip Danielson. In addition to the above-mentioned findings, the court finds that Dr. Danielson's credibility was significantly undermined by the following:

- Dr. Danielson initially testified that it was his opinion that the data in NMS Exhibit 2.2-1A was not saturated and that there was agreement within NMS that these data should be interpreted. Danielson 3/18/14 Testimony at 128-29. When pressed on whether there was any internal disagreement within NMS as to whether the data should be interpreted, Dr. Danielson asserted that he was not able to comment. Danielson 3/18/14 Testimony at 129. According to the sworn statement of Laura Cronin, the NMS employee who conducted the technical review of NMS Exhibit 2.2-1A, she notified the DNA analyst (Jillian Fesolovich), and later the technical leader (Dr. Westring), that the sample needed to be re-amplified because, in her view, the data should not have been interpreted due to the fact that it was overblown. It is troubling that internal disagreement within NMS Labs over interpretation of the very DNA results at issue never came to light in Dr. Danielson's statement or testimony, or in the sworn statement of Dr. Christian Westring. The court does not find it credible that Dr. Danielson would have been unaware of the internal disagreement within NMS Labs over the interpretation of the very data at issue in this case.
- The court does not credit Dr. Danielson's assertion that it was proper to interpret the data in NMS Exhibit 2.2-1A. In particular, the court discredits Dr. Danielson's

assertion that he was able to distinguish between "major" and "minor" split peaks. In particular, Dr. Danielson was not able to cite to a single journal article (Danielson 3/19/14 Testimony at 141), any reference in Dr. John Butler's textbook (Danielson 3/19/14 Testimony at 143), or the practices of a single accredited DNA laboratory (Danielson 3/19/14 Testimony at 144) to support his theory. More troubling, Laura Cronin, a former NMS Labs DNA analyst, stated that she had never heard of the terms "major" or "minor" split peaks, much less received training or guidance on how to distinguish between the two.

CONCLUSIONS OF LAW

In accordance with the above findings of fact, the court concludes as a matter of law that:

- NMS Labs failed to comport with accepted scientific principles in the interpretation of data generated for NMS Exhibit 2.2-1A and, therefore, the conclusions set forth in connection with NMS Exhibit 2.2-1A are scientifically unreliable and inadmissible;
- The language used in the report issued by NMS does not accurately capture the substance of the conclusions rendered (*i.e.*, alleles "may" or "may not" represent true DNA) and, therefore, the conclusions contained in the NMS Report are inadmissible for this reason as well; and
- The validation data and protocols produced by NMS Labs in support of the DNA testing conducted in this case SHALL NOT be the subject of a protective order because these data are integral to the record herein and to the testimony of Dr. Bruce Budowle that NMS Labs ignored its own data and that NMS Labs' protocols are not grounded in NMS Labs' validation data.

ORDER

THEREFORE, in accordance with various rulings made on the record in the presence of the parties, and the above findings of fact and conclusions of law, it is by the court this 28th day of January 2015 *nunc pro tunc*

ORDERED, that the government's *Motion for Findings of Fact and Conclusions of Law* shall be and is hereby **GRANTED**; and it is further

ORDERED, that the government's *Motion to Exclude NMS DNA Results* shall be and is hereby **GRANTED** and the report generated by NMS Labs is deemed inadmissible; and it is further

ORDERED, that the protective order governing NMS Labs' validation data and protocols shall be and is hereby **VACATED** because the validation data and protocols are integral to illustrating how the interpretation protocols are not grounded in NMS Labs' validation data; and it is further

ORDERED, that the defendant, Cardell Torney, is entitled to a new IPA hearing pursuant to D.C. Code § 22-4132 (b) to exercise his right to request or waive DNA testing by a DNA laboratory that will conduct DNA testing in accordance with accepted scientific principles.

HERBERT B. DIXON, JR.
JUDGE
(Signed in Chambers)

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ASCLD/LAB-*International*

Special Assessment Report

National Medical Services, Inc.
dba NMS Labs Criminalistics Laboratory

Willow Grove, Pennsylvania

This ASCLD/LAB report is in response to a special request from the director of the NMS Labs Criminalistics Laboratory and represents the results of an independent, expert review of certain validation data and the resulting protocols. This report contains conclusions about those validation studies conducted by the laboratory and the laboratory's use of the resulting validation data for developing protocols for interpreting mixed DNA profiles and establishing limits to conclusions that can be drawn from the data. This very focused assessment by an ASCLD/LAB representative was not intended to include, and in fact did not include, a review of how the protocols in question were or were not applied to any actual casework.

INTRODUCTION

On March 4, 2015, American Society of Crime Laboratories Laboratory Accreditation Board Executive Director John Neuner requested the assistance of a technical expert for a special assessment/review of validation studies performed by the Forensic Biology Department of NMS Labs.[1] The *Curriculum Vitae* of the selected expert was provided to the laboratory for review and the reviewer was notified by Director Neuner on March 6, that she was approved by NMS Labs' Criminalistics Laboratory Director, Dr. Christian Westring, to conduct this special assessment. The expert auditor's self-certification, as normally provided for all FBI DNA QAS audits, is provided as **Attachment 4**.

NMS Labs (National Medical Services, Inc. / dba NMS Labs Criminalistics Laboratory) has been accredited under the ASCLD/LAB-*International* Program in the disciplines of Biology (Categories 3.1, DNA Nuclear and 3.3, Serology) and Controlled Substances (1.0, General Controlled Substance Analysis) since April 20, 2010 (Certificate No. ALI-112-T). Prior to accreditation in the ASCLD/LAB-*International* program, the laboratory was accredited continuously in the ASCLD/LAB Legacy program from August 26, 2003 through April 20, 2010.

METHOD

NMS Labs' Criminalistics Director, Dr. Christian Westring, requested an independent review of NMS Labs' Forensic Biology Department DNA quantification and STR amplification and analysis standard operating procedures (SOPs), and supporting validation studies, to assess compliance with the requirements of the FBI's 2011 *Quality*

[1] www.nmslabs.com.

Assurance Standards for Forensic DNA Testing Laboratories (FBI QAS).[2] Although not considered auditable standards or requirements, validation guidelines and recommendations developed by and for the forensic community worldwide [Scientific Working Group for DNA Analysis Methods (SWGDAM), European Network of Forensic Science Institutes (ENFSI)][3],[4] also were consulted for this review. Documents reviewed included laboratory SOPs, validation summaries, PCR data (.sds files), and STR electropherograms (.pdf), and in some cases the STR sample files (.fsa), validation review/approval memoranda from the technical leader, and external FBI QAS audits documenting review and approval of the validation studies by qualified external auditors. On a few occasions the assigned auditor communicated with Dr. Westring through email or telephonically for clarification and/or additional documentation, which was promptly provided. It is also important to note that data files provided for review were reorganized and in some instances, re-named for clarity.

RESULTS AND DISCUSSION

Listed in Dr. Westring's letter (**Attachment 1**) are the specific requests (reproduced below in italics) below which is a brief summary of the studies followed by a discussion of the results of the review.

1. *Review and assessment of the procedure (CR-320-10, DNA AMPLIFICATION BY POLYMERASE CHAIN REACTION) for the use of the PowerPlex 16HS chemistry employed by NMS Labs in support of internal validation studies.*

   The PowerPlex® 16 HS System instructions are incorporated into a general laboratory Standard Operating Procedure (SOP) that combines instructions for setting up samples for amplification for all STR kit chemistries used on casework by NMS Labs' Forensic Biology Department. Both versions provided by Dr. Westring were reviewed: that which was in use in 2013 (*CR-320-10, DNA AMPLIFICATION BY POLYMERASE CHAIN REACTION*; copyright 2012), and the current version (CR-320-15, copyright 2014). Specifically with regard to the PowerPlex® 16 HS amplification procedure there appears to be only one change in the procedure: a DNA template concentration adjustment from 50 pg/µL to 30 pg/µL equal to or below which the maximum volume (17.5 µL) of DNA template is to be added. Impacting all amplification kit procedures included in this SOP is the addition of a witness step requiring that a second analyst verify all samples against the amplification worksheet. The low end DNA concentration adjustment was first mentioned in version 13 of the SOP (CR-320-13) in response to observations that the input optimum of DNA

[2] Quality Assurance Standards for Forensic DNA Testing Laboratories (effective 09-01-2011). http://www.fbi.gov/about-us/lab/biometric-analysis/codis/quality-assurance-standards-for-forensic-dna-testing-laboratories.

[3] SWGDAM Validation Guidelines, December 2012. (Original published in Forensic Science Communications in July 2004; available at http://www.fbi.gov/about-us/lab/forensic-sciencecommunications/fsc/july2004/index.htm/standards/2004_03_standards02.htm)

[4] ENFSI, Recommended Minimum Criteria for the Validation of Various Aspects of the DNA Profiling Process. Issue 001, November 2010, http://www.enfsi.eu/sites/default/files/documents/minimum_validation_guidelines_in_dna_profiling_-_v2010_0.pdf

template was lower than when the PowerPlex® 16 HS kit was originally validated (communication from Dr. Westring). This adjustment to the optimal range resulted in a lower end of approximately 0.5 ng of DNA.

The instructions for setting up the PowerPlex® 16 HS System amplification in both 2012 and 2014 SOPs, which are based on the kit manufacturer's developmental validation, recommended protocol, and NMS Labs' internal validation studies, are detailed and clear. They describe the specific controls and standards that must be used, the reagents, supplies, and instrumentation required to perform the tests. The amplification reagents and instrumentation are monitored for contamination and functionality by the incorporation of at least one negative and one positive template control, respectively, with every amplification batch.

The 2012 and 2014 copyrighted versions of the Laboratory SOP conform with ASCLD/LAB-*International* accreditation requirements and the FBI QAS (September 2011), and have been assessed for conformance with the requirements/standards of both documents by qualified laboratory assessors/auditors as part of the *ASCLD/LAB-International* accreditation program and as required by the FBI QAS.

2. *Review and assessment of the internal validation studies conducted by NMS Labs of the PowerPlex 16 HS chemistry including known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies (thresholds), signal detection linearity and DNA input linearity, range for peak interpretation, stutter thresholds, mixture studies, and contamination assessments – including documentation and summary reports.*

   Soon after the release of the PowerPlex® 16 HS System in 2009, the FBI QAS (July 2000)[5] -compliant, multi-laboratory developmental validation was published by the kit manufacturer, Promega, in 2010.[6] For the seven years leading up to adopting this newer kit, NMS Labs provided human identification (HID) DNA services with the PowerPlex® 16 System. NMS Labs also provided PowerPlex® 16 validation data for this review. Both PowerPlex® 16 and PowerPlex® 16 HS kits target the same genetic loci using identical dye-labeled primer sets, allelic ladders, and internal size standard. The HS System features a proprietary "enhanced" reaction buffer chemistry and a *Thermus aquaticus* (*Taq*) enzyme engineered for heat activation (*Hot-Start*). Promega Corporation, the manufacturer of the kit, advertises that the major benefit of the PowerPlex® 16 HS System over the PowerPlex® 16 System is an increased

[5] Quality Assurance Standards for Forensic DNA Testing Laboratories (effective July 1998). *Forensic Science Communications Vol: 2* (3) July 2000.

[6] Ensenberger MG et al. 2010. Developmental validation of the PowerPlex® 16 HS System: An improved 16-locus fluorescent STR multiplex. FSI Genetics 4 (4) 257-264.

sensitivity to lower template concentrations and a greater resistance to inhibitors of PCR amplification.[7]

During the month of September 2002, NMS Labs conducted an FBI QAS (effective date July 1998) - compliant validation using PowerPlex®16 on the ABI Prism® 310 Genetic Analyzer and using Genescan®/Genotyper® for the data analysis (see PP16_2002). These studies varied annealing temperatures, cycle numbers, and extension times, and analyzed male/female mixture ratios, species specificity, and known and non-probative casework samples, sensitivity, reproducibility and precision. Although the capillary platform, software, and kit no longer are in use by the Laboratory, it is pertinent to this review to highlight the Laboratory's extensive experience analyzing data derived from the PowerPlex 16/16 HS genetic loci.

To maintain conformance with ASCLD/LAB-*International* accreditation and FBI QAS requirements, the Laboratory conducted internal validation studies of the PowerPlex® 16 HS System according to ASCLD/LAB-*International* requirement 5.4.5 (and subcategories)[8],[9] and the FBI QAS (effective dates July 1998 and September 2011). Below is a brief summary of the Promega PowerPlex® 16 HS System validation studies reviewed. It is important to note that all of the validation studies conducted by the Laboratory included an assessment of contamination by the use of no template controls in all tests run.

The Laboratory's initial validation of the PowerPlex® 16 HS System was completed and brought on line with the ABI Prism® 310 (Genescan®/Genotyper® software) and Applied Biosystems® 3130 (GeneMapper®*ID software*) genetic analyzers in **January 2010:**

- Challenged Sample Study using samples treated with PCR inhibitors hematin, tannic acid, and humic acid, comparing the performances of the PowerPlex® 16 HS, PowerPlex® 16, AmpFLSTR® Identifiler®, and AmpFLSTR® MiniFiler™ DNA kits (September 2009).

- Known/Non-Probative Casework/Concordance Study on both ABI Prism® 310 (Genescan®/Genotyper®) and AB® 3130 (GeneMapper® *ID*) capillary electrophoresis platforms using casework and proficiency test samples [organic and DNA IQ™ (Promega) -extracted DNA] assessing concordance between PowerPlex® 16 HS, PowerPlex® 16, AmpFLSTR® Identifiler®, and AmpFLSTR® MiniFiler™ kits (January 2010).

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[7] Ensenberger MG, Fulmer PM. The PowerPlex® 16 HS System. Profiles in DNA, March 2009.(https://www.promega.com/~/media/files/resources/profiles%20in%20dna/1201/the%20powerplex%2016%20hs%20system.pdf?la=en)

[8] ISO/IEC 17025 *General requirements for the competence of testing and calibration laboratories* (Second Edition 2005-05-15, http://www.iso.org/iso/home/store/catalogue_tc/catalogue_detail.htm?csnumber=39883)

[9] *ASCLD/LAB-International* Supplemental Requirements for the Accreditation of Forensic Science Testing Laboratories, 2011 Edition (Effective 11-22-2011, http://www.ascld-lab.org/board-interpretations-and-guidance-documents/)

- Mixture Study (2, 3, and 4 contributors) using NIST SRM 2391- certified reference samples on both ABI Prism® 310 (Genescan®/Genotyper®) and AB® 3130 (GeneMapper® *ID*) capillary electrophoresis platforms, 5 and 10 second injections (December 2009) .

- Sensitivity/Stochastic Study on both ABI Prism® 310 (Genescan®/Genotyper®) and AB® 3130 (GeneMapper® ID) capillary electrophoresis platforms using inputs ranging from 1 pg to 4 ng of DNA template (December 2009).

- Reproducibility/Precision was assessed by comparing results between two genetic analyzers and by assessing results from graded inputs from the same DNA source and multiple injections of the same sample.

August 2012 the Laboratory performed additional PowerPlex® 16 HS studies on two AB® 3130 (GeneMapper® *ID*) genetic analyzers ("Watson" and "Crick"; the AB Prism® 310 genetic analyzer was retired from service in 2011). The following were addressed in conformance with the FBI QAS (effective September 2011).

- Analytical/Stochastic Threshold Study and Template Input Optimization Study including repeatability (5 replicates), reproducibility (two analyzers), accuracy (profile match) and precision (bp length) when inputs of 15.63 pg to 4 ng of DNA template (5 replicates) and applying 1, 5, and 10 second injections.

September 2012 the laboratory conducted an additional PowerPlex® 16 HS study. The DNA input used in this and all studies that follow are based on results obtained with the Investigator® Quantiplex HYres kit (see below). Studies prior to this used DNA extracts quantified with Quantifiler ® Human DNA Quantification Kit, Quantifiler® Y Human Male DNA Quantification Kit, and with the earliest studies, QuantiBlot® Human DNA Quantification Kit:

- Mixture Study assessing a range of male: female mixture ratios using an input of 500 pg of DNA template.

June through July 2013 the Laboratory conducted supplemental studies to assess the impact on PowerPlex® 16 HS System performance when using a reduced scale reaction volume (below the 25 µL volume recommended by the kit manufacturer protocol). From these studies, the Laboratory determined in their hands, that optimal kit performance was obtained with the full scale reaction volume and to date their SOP maintains the use of a 25 µL reaction volume.

- Mixture Study assessing 2, 3, and 4 male and female contributors at varying ratios using inputs of 250 - 500 pg of DNA template.
- Mock Casework Study using challenged samples consisting of diluted blood stains exposed to bleach, detergent, soil, gasoline and rust, semen on cotton and denim, cigarette butts, and swabbings of a pistol grip and slide.

The Laboratory conducted additional supplemental studies on stability of PowerPlex® 16 HS amplified DNA when stored refrigerated for six months to determine if the method used for denaturing the amplified DNA caused artifacts in the PowerPlex® 16 HS electropherograms (see PP16 HS_2013-2014).

All PowerPlex® 16 HS validation studies conducted by NMS Labs employed the analysis software stutter filter settings validated by Promega as part of the developmental validation. This is not unusual as many laboratories adopt the stutter percentages recommended (and developmentally validated) by the manufacturers of STR kits. There is neither a requirement in the FBI QAS nor a recommendation in the SWGDAM Validation Guidelines for the laboratory to re-validate stutter thresholds as long as the manufacturer's recommended thresholds are proven to perform appropriately when the laboratory's validated SOP is followed.

The ENFSI validation document recommends checking stutter ratios and also states: *In general, stutter peaks have to be lower than the % of the allele peak height indicated by the manufacturer of the kit to be ignored as a biological artefact of the sample* (page 8). To further improve their interpretation SOP, NMS Labs investigated peak height linearity, saturation, and heterozygote allele balance, using graded quantities of DNA and various injection times, while also monitoring the conditions under which stutter and parent peak amplitudes became disproportionate, causing stutter percentages to exceed the kit manufacturer's recommended filter settings. Further, the Laboratory also analyzed the incidence and amplitude of plus-stutter from the PowerPlex® 16 HS kit loci. The studies conducted by NMS Labs on the PowerPlex® 16 HS kit verified that the kit developer's recommended stutter settings perform well when tests are conducted according to the instructions provided in NMS Labs' SOP. Further, these studies equip the laboratory with a foundation of data essential for an informed analysis and interpretation of STR profiles containing multiple contributors, which is reflected in the laboratory's interpretation SOP (see Request #5, below).

3. *Review and assessment of the procedure (CR-914-01, RT QUANTITATION ASSAY BY QIAGEN) for the use of the Qiagen Investigator Quantiplex HYres chemistry employed by NMS Labs in support of internal validation studies.*

Investigator® Quantiplex HYres protocol (version *CR-914-01,* RT QUANTITATION ASSAY BY QIAGEN; copyright 2012) as well as the current version (CR-914-04, copyright 2015) were reviewed per NMS Labs' request. The original procedure appears not to have changed significantly between the 2012- and 2015- copyrighted

versions except for the following additions to the 2015 copyrighted version: 1) a method for quantifying known and questioned samples on the same quantification plate, and 2) the option to validate an External Standard Curve. The current SOP provides a detailed standard operating procedure for the preparation of the External Standard Curve including how it is verified, and incorporated into the quantification assay of casework samples, and further describes conditions under which an External Standard Curve must be revalidated. Both 2012 and 2015 SOPs have the same lower thresholds for the Human (0.00488 ng/µL) and Male (0.00163 ng/µL) targets, which correspond to the lowest concentrations of human and male DNA in the standard curve.

NMS Labs provides detailed instructions on interpreting quantification data in both 2012 and 2015 SOPs, which are based on the kit manufacturer's developmental validation, recommended protocol and standard curve metrics, and NMS Labs' internal validation studies. The quantification reagents are monitored for contamination by the incorporation of at least one negative template control on each quantification plate and to verify successful amplification a positive human DNA standard also is included. The basic methodology used by the lab follows the kit manufacturer's recommended protocol with the exception that the laboratory validated and implemented a reduced scale reaction (half volume; see request 4 below) as well as the option to use the External Standard Curve.

The 2012 and 2015 copyrighted versions of the Laboratory SOP conform with ASCLD/LAB-*International* accreditation requirements (5.4.1, 5.4.2) and the FBI QAS (September 2011) and have been assessed externally for conformance to both documents by qualified laboratory assessors as part of the *ASCLD/LAB-International* accreditation program.

4. *Review and assessment of the internal validation studies conducted by NMS Labs for the Qiagen Investigator Quantiplex HYres chemistry including known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies, mixture studies, and contamination assessment – including documentation and summary reports.*

   The laboratory validated the QIAGEN Investigator® Quantiplex HYres kit to replace Quantifiler® Human DNA Quantification Kit and Quantifiler® Y Human Male DNA Quantification Kit methods that were in place in the laboratory. The benefits of adopting the QIAGEN kit included concomitant quantification of both total human and male DNA in a single test, and a greater sensitivity/lower detection limit for both human and male DNA.

   The QIAGEN Investigator® Quantiplex HYres kit was developmentally validated according to recommendations made by both the SWGDAM and ENFSI, and in full compliance with Standard 8.2 of the FBI QAS. QIAGEN's validation summary

document and validation certificate are available for download from their web site.[10,11]

To maintain conformance with ASCLD/LAB-*International* accreditation and FBI QAS requirements, the laboratory conducted an internal validation of the Investigator® Quantiplex HYres kit according to ASCLD/LAB-*International* requirement 5.4.5, and FBI QAS Standard 8.3, respectively, and as with the PowerPlex® 16 HS System validation studies, with guidance from SWGDAM and ENFSI recommendations. The studies were completed, reviewed, and approved by the Technical Leader in August 2012. Below is a brief summary of the QIAGEN Investigator® Quantiplex HYres validation studies reviewed (see HYres).

- Sensitivity/Limit of Detection vs. Reaction Volume Study; The laboratory's validation study initially compared the sensitivity/limit of detection of total human vs. male DNA in a dilution series of male DNA using "Full", 20 µL reaction volumes (kit manufacturer's suggested protocol) vs. "Half" reaction volumes scaled down to 10 µL. Because no significant difference between the two reaction volumes was observed in this preliminary study, the remainder of the validation studies were performed using the reduced scale reaction volume of 10 µL.

- Repeatability/Precision Study assessing variation between replicates from a series of samples tested by a single analyst. Four dilutions of a 1:1 mixture of male and female DNA tested the limit of detection of the male component to the mixture (Table 2).

- Reproducibility to assess whether there is significant variation between tests conducted independently by two analysts.

- Correlation between quantification results and STR profile: PowerPlex 16HS DNA profiles derived from a series of Investigator® Quantiplex HYres kit-quantified samples from a Sensitivity/Limit of Detection Study were examined to correlate HYres-quantified DNA results with STR profile characteristics assessing any possible nonconformities with expected results. This study also helped establish a range of DNA input concentrations for optimal STR kit performance.

- Inhibition Study using boiled human blood as a source of hematin. To assess the sensitivity of the quantification system to this known inhibitor of PCR.

[10] Qiagen Validation Report: Developmental validation of the Investigator® Quantiplex HYres Kit. November 2011 (file:///C:/Users/Allison/Downloads/Investigator-Quantiplex-HYres-Developmental-Validation-Report-EN%20(1).pdf).

[11] Validation Certificate: Developmental validation of the Investigator® Quantiplex HYres Kit, (file:///C:/Users/Allison/Downloads/Prom-5693CERT_ValidationQuantiplexandQuantiplexHYres_0113_WW.pdf)

- Mixture Study in which a series of graded ratios of male/female DNA admixtures were quantified including samples in which the limit of detection of male DNA was determined in the presence of excess female DNA.

- Simulated Casework Study quantifying a variety of body fluid stains, including body fluid mixtures (semen/vaginal fluid, vaginal fluid/saliva, saliva/semen, blood/saliva) from multiple donors and extracted from a range of substrates (cotton, denim, leather, condom).

- Contamination Assessment in which negative template controls from each validation test were applied to monitor the possible DNA contamination of the kit reagents and/or by the kit user.

5. *Review and assessment of the procedure (CR-915-01, DNA INTERPRETATION GUIDELINES AND POLICIES) for DNA interpretation employed by NMS Labs for the PowerPlex 16HS chemistry, reflecting the data obtained through internal validation prior to use in forensic casework. Specifically, this includes valid procedures to address stutter interpretation in mixed DNA profiles – particularly in the cases where minor contributors may be present; handling off-scale data; and reporting language to address uncertainty of conclusions, especially exclusions (see associated Addendum notes for reporting).*

   DNA Interpretation Guidelines and Policies, CR-915-01 (copyright 2012) and CR-915-08 (copyright 2014) are similarly organized and specifically address each of the recommendations listed in the SWGDAM Interpretation Guidelines.[12] The focus in this review is on aspects of the protocol that impact interpretation of PowerPlex® 16 HS data. To this end differences are minor and consist of slight adjustments in stochastic thresholds used with different injection times (shown in Table 1 of each protocol), and slight adjustments to expected heterozygous allele balance per injection time (reflected in Table 2 of each protocol). Parameter adjustments over time are to be expected as stochastic thresholds and peak balance are critical parameters that need to be re-verified occasionally with supplemental studies as the laboratory environment, equipment, consumables, and kits do not necessarily have consistent performance over extended time periods (i.e. gradual changes in instrument sensitivity, variation between reagent lots, etc.). The need to make these adjustments was supported by supplemental validation studies conducted by the laboratory in 2013. The importance of periodic re-validation is best described by Dr. John Butler:[13]

[12] SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories, January 14, 2010. http://swgdam.org/Interpretation_Guidelines_January_2010.pdf

[13] Butler J. 2006. Debunking Some Urban Legends Surrounding Validation Within the Forensic DNA Community. Profiles in DNA. http://cstl.nist.gov/strbase/pub_pres/Validation_UrbanLegends_ProfilesInDNA_902_03.pdf

URBAN LEGEND #8: ONCE A VALIDATION STUDY IS COMPLETED YOU NEVER HAVE TO REVISIT IT

In a certain sense, validation is never complete because it is part of a good quality assurance program. Instruments (e.g., laser power, CCD camera response) may change slightly over time and impact sensitivity of DNA tests. Environmental conditions that impact STR allele-sizing precision, such as room temperature, may also change over time. Ongoing monitoring (essentially "re-validation") should be performed regularly to verify that results are within the expected range.

An additional change in the laboratory interpretation guidelines (not impacting PowerPlex® 16 HS specifically) is a change to the preferred use of the likelihood ratio statistic over the use of the Combined Probability of Exclusion. It is likely this change was adopted by the Laboratory in response to recommendations promulgated to the forensic community by qualified experts in the areas of DNA mixture interpretation and forensic statistics. The changes in the protocol clearly indicate that NMS Labs keeps abreast of advancements in forensic DNA analysis.

Overall the Laboratory's interpretation SOP is very well-written, educational, detailed but easy to follow, and conforms with all applicable Standards and accreditation requirements of the FBI QAS (2011) and *ASCLD/LAB-International*, respectively. The SOP includes example conclusion statements to be used in the final report to the customer and annexed to the laboratory test report is a document from the Forensic Biology Department that provides definitions to terms, describes tests and their limitations, and clearly explains the statistical analyses utilized and their limitations (**Attachment 2**).

CONCLUSION

The Laboratory's validation studies were well planned and summarized, and the summaries were traceable back to the original data. The studies were well thought out and carefully evaluated, particularly the more detailed and complex studies conducted on PowerPlex® 16 HS kit including linearity, stochastic behavior, heterozygote peak balance, and stutter variation. These and other studies conducted by the lab provided a foundation for developing a sound protocol for interpreting mixed DNA profiles and establishing limits to conclusions that can be drawn from the data. It was clear that trends observed in the validation studies translated to improvements and/or adjustments to the laboratory SOPs. The validation studies and laboratory SOPs follow guidelines recommended by experts from the forensic community, were (and continue to be) subjected to external review by qualified auditors/assessors (**Attachments 3 and 4**), and

conform to all standards and requirements for accreditation by *ASCLD/LAB-International.*[14]

Attachments

1. Letter from Dr. Christian Westring (2 pages)
2. Annex to NMS Labs' Forensic Biology Department reports (2 pages)
3. QAS Audit Document (4 pages)
4. QAS Audit Document Appendix C (Allison Y. Eastman)

[14] The FBI Quality Assurance Standards Audit for Forensic DNA Testing Laboratories. September 2011. http://www.fbi.gov/about-us/lab/biometric-analysis/codis/forensic-qas-audit-9-1-11

Attachment 1

CRIMINALISTICS

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John K. Neuner
Executive Director
ASCLD-LAB
139 J Technology Drive
Garner, NC 27529

Date: 03/04/2015
Cc: Pamela Bordner, Senior Accreditation Program Manager

Director Neuner:

It has been brought to our attention that a ruling from the District of Columbia was recently issued in regard to the admissibility of DNA testing by NMS Labs' Forensic Biology Department. The opinion suppressed the results of tests performed in 2013 on the grounds that NMS Labs did not comport with the generally accepted methods and quality standards of the forensic community.

NMS Labs disputes both the findings of the court and the factual content of the order. We also contest the irregularities of the court proceedings – especially the fact that as the NMS Labs' Criminalistics Laboratory Director and Quality Manager, I was not provided an opportunity to testify regarding the validity of our procedures and our accreditation history. Regardless, NMS Labs stands by the validity as well as the scientific and forensic defensibility of the analytical procedures in place at the time, and in place today.

Having no legal standing to challenge the opinion, we now seek to verify that our validation studies, methods and reporting for those technologies comport with the recognized quality standards in the forensic community. Specifically, I am requesting that ASCLD/LAB perform an independent assessment of the following procedures employed by NMS Labs to the FBI's 2011 "Quality Assurance Standards for Forensic DNA Testing Laboratories":

- Review and assessment of the procedure (CR-320-10, DNA AMPLIFICATION BY POLYMERASE CHAIN REACTION) for the use of the PowerPlex 16HS chemistry employed by NMS Labs in support of internal validation studies.

- Review and assessment of the internal validation studies conducted by NMS Labs of the PowerPlex 16HS chemistry including known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies (thresholds), signal detection linearity and DNA input linearity, range for peak interpretation, stutter thresholds, mixture studies, and contamination assessments – including documentation and summary reports.

- Review and assessment of the procedure (CR-914-01, RT QUANTITATION ASSAY BY QIAGEN) for the use of the Qiagen Investigator Quantiplex HYres chemistry employed by NMS Labs in support of internal validation studies.

- Review and assessment of the internal validation studies conducted by NMS Labs for the Qiagen Investigator Quantiplex HYres chemistry including known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies, mixture studies, and contamination assessment – including documentation and summary reports.

- Review and assessment of the procedure (CR-915-01, DNA INTERPRETATION GUIDELINES AND POLICIES) for DNA interpretation employed by NMS Labs for the PowerPlex 16HS chemistry, reflecting the data obtained through internal validation prior to use in forensic casework. Specifically, this includes valid procedures to address stutter interpretation in mixed DNA profiles – particularly in the cases where minor contributors may be present; handling off-scale data; and reporting language to address uncertainty of conclusions, especially exclusions (see associated Addendum notes for reporting).

For more than 40 years, NMS Labs has demonstrated an unwavering commitment to the highest quality of laboratory testing services. We do this with integrity, accuracy, and a keen awareness of the continuous advances in forensic science and the associated quality standards.

Given the critical role of quality assurance in the forensic testing community, your prompt assistance in support of our commitment to independent evaluation and continual quality improvement will be greatly appreciated.

Respectfully,

Christian G. Westring, Ph.D.
Criminalistics Laboratory Director
christian.westring@NMSLABS.COM

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ADDENDUM 1: Supplemental Information on Item Examination, Analysis and the Meaning of Test Results

The following supplemental information is to provide our clients with a more comprehensive description of the methods used by our laboratory for the examination and analysis of items submitted for forensic testing. Also provided is a plain-language explanation of the meaning of results given in NMS Forensic Biology Laboratory Reports. Please note that not all sections of this addendum are necessarily applicable to the specific testing performed by NMS for your case. This information is provided as a courtesy to our clients and should not to be construed as being a component of your official NMS Forensic Biology Laboratory Report.

Definitions

Examined: Items that are examined are those that are evaluated for testing based on the ability to detect and/or recover possible biological material (*e.g.*, through visual inspection under normal light or by use of an Alternate Light Source (ALS) or the collection of evidentiary material(s) of interest for serological and/or DNA testing). Not all examined items, however, are necessarily forwarded for testing.

Analyzed: Items that are analyzed are those that are subjected to serological testing and/or microscopy (to characterize possible biological material) or to DNA testing (to develop genetic profiles) for the purpose of individualizing biological material or excluding potential contributors.

Examination Techniques for Detecting Possible Biological Material

Visual Examination under a Normal Light Source: Some body fluids (*e.g.*, blood, semen, urine and fecal matter) produce areas of discoloration that may be visually evident under a normal light source. This makes it possible to visually examine large items of evidence to locate possible biological stains.

- The visual detection of an area of discoloration may indicate the presence of stains containing biological material. Collected stains are typically subjected to further serological testing for specific body fluids and/or DNA analysis.
- The absence of a visually detectible area of discoloration may indicate either the absence of biological material or the presence of less than a detectible amount of biological material. It is not possible to distinguish between these two alternatives. Samples of evidentiary material without a visually detectible area of discoloration may still be collected at the discretion of the analyst for further serological testing and/or DNA analysis.

Visual Examination under an Alternate Light Source (ALS): Some body fluids (*e.g.*, semen, saliva and urine) will fluoresce under a UV or near-UV light source. This makes it possible to visually examine large items of evidence to locate possible biological stains.

- The visual detection of fluorescence may indicate the presence of stains containing biological material. Collected stains are typically subjected to further serological testing for specific body fluids and or DNA analysis.
- The absence of visually detectible fluorescence may indicate either the absence of biological material or the presence of less than a detectible amount of biological material. It is not possible to distinguish between these two alternatives. Samples of evidentiary material without detectible fluorescence may still be collected at the discretion of the analyst for further serological testing for specific body fluids and/or DNA analysis.

Serological Tests and Result Interpretation

Serological analyses for the characterization of biological stains (*i.e.*, blood, seminal fluid, spermatozoa, saliva, urine, fecal matter and species group identification) employs the following tests at the discretion of the analyst and results are interpreted as follows:

Blood

Hemastix® (HS), Hemochromogen (HC) and HemDirect (HD) Tests:

- A **Positive** result provides a presumptive indication of blood. A positive result is typically characteristic of (but not unique to) blood. Specimens testing positive should be regarded as possible blood stains.
- A **Negative** result indicates that no presumptive indication of blood was detected on the tested item. A negative result should be regarded as indicating either the absence of blood or the presence of less than a detectible amount of blood. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

Seminal Fluid

Acid Phosphatase (AP) and Combined Semenogelin / Prostate Specific Antigen (SG/p30) Tests:

- A **Positive** result provides a presumptive indication of seminal fluid. A positive result is typically characteristic of (but not unique to) seminal fluid. Specimens testing positive should be regarded as possible seminal fluid stains.
- A **Negative** result indicates that no presumptive indication of seminal fluid was detected on the tested item. A negative result should be regarded as indicating either the absence of seminal fluid or the presence of less than a detectible amount of seminal fluid. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

Sperm Cells / Spermatozoa

Direct visualization by microscopy is used to confirm the presence of sperm cells (spermatozoa). Sperm cells are unique to the fluids (*e.g.*, semen) and tissues of the male reproductive system.

- A **Positive** result is confirmatory for the presence of sperm cells. Specimens testing positive should be regarded as containing sperm cells. Combined with a positive test result for seminal fluid, a positive result for sperm cells should be interpreted as further indicating the possible presence of semen.
- A **Negative** result indicates that no sperm cells were detected on the tested item. A negative result should be regarded as indicating either the absence of sperm cells or the presence of less than a detectible number of sperm cells. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

Saliva

RSID Saliva (RS) Test:

- A **Positive** result provides a presumptive indication of saliva. A positive result is typically characteristic of (but not unique to) saliva. Specimens testing positive should be regarded as possible saliva stains.
- A **Negative** result indicates that no presumptive indication of saliva was detected on the tested item. A negative result should be regarded as indicating either the absence of saliva or the presence of less than a detectible amount of saliva. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

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Urine

Combined Urea/Creatinine Test:

- A **Positive** result provides a presumptive indication of urine. A positive result is typically characteristic of (but not unique to) urine. Specimens testing positive should be regarded as possible urine stains.
- A **Negative** result indicates that no presumptive indication of urine was detected on the tested item. A negative result should be regarded as indicating either the absence of urine or the presence of less than a detectible amount of urine. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

Fecal Matter

Urobilinogen Test:

- A **Positive** result provides a presumptive indication of fecal matter. A positive result is typically characteristic of (but not unique to) fecal matter. Specimens testing positive should be regarded as possible fecal matter stains.
- A **Negative** result indicates that no presumptive indication of fecal matter was detected on the tested item. A negative result should be regarded as indicating either the absence of fecal matter or the presence of less than a detectible amount of fecal matter. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

Species Group Identification

Ouchterlony Double Immunodiffusion Test:

- A **Positive** result provides a presumptive indication of species source. A positive result is typically characteristic of (but not unique to) a target species group. Based on the anti-serum used (*e.g.*, anti-primate, -canine, -bovine), specimens testing positive should be regarded as being of possible human (primate), dog (canine) or cow (bovine) origin, respectively.
- A **Negative** result indicates that no presumptive indication of species source was detected on the tested item. A negative result should be regarded as indicating either the absence of biological material from the target species group or the presence of less than a detectible amount of biological material from the target species group. Based on the testing performed, it is not possible to distinguish between these two alternatives.
- An **Invalid** result indicates that the test failed to perform in accordance with manufacturer-specified and/or laboratory validated parameters. An invalid test result cannot be interpreted as either positive or negative. Invalid tests are repeated after the cause of the test failure has been resolved (or an alternate test may be employed) if sufficient evidentiary material is available.

DNA Tests and Result Interpretation

DNA (Deoxyribonucleic Acid) analyses for the individualization of biological stains employ two basic types of STR (Short Tandem Repeat) testing:

- Autosomal-STR testing offers the greatest potential for individualization. It detects both male and female DNA equally but an excess of female DNA (typically >20:1) may render a male profile undetectable.
- Y-STR testing detects only male DNA. As a result, a male DNA profile can be detected even in the presence of an excess of female DNA. Since all paternally-related males (and an unknown number of males in the general population) have identical Y-STR profiles, a stain cannot be individualized to a single male.

General Categories of Testing Conclusions

- An **Inconclusive** result indicates that the sample failed to yield a minimal DNA profile. This may be due to the absence of amplifiable DNA or the presence of a less than detectible amount of DNA. Based on the testing performed, it is not possible to distinguish between these two alternatives. No conclusions can be drawn regarding the potential source of such samples
- An **Uninterpretable** result indicates that there is a lack of sufficient genetic information on which to base a statistically supported inculpatory conclusion. This may be due to an insufficient amount of amplifiable DNA, a failure of associated quality controls or an irresolvable mixture in the case of a Y-STR profile. No inculpatory conclusions should be drawn regarding the potential source of such samples. The data may be used, however, for exculpatory and/or non-probative purposes.
- A **Cannot be Excluded** result indicates that a DNA profile for a questioned sample is consistent with the known DNA profile from a reference or reference-type sample. This should be interpreted to mean that the known genetic profile is a potential source of or contributor to the questioned sample. This conclusion may include assumptions regarding missing data (*i.e.*, allele drop out); shared alleles (*e.g.*, when a known or major contributor is identified) and/or; the association of observed alleles with a specific profile (*e.g.*, when a mixture cannot be resolved into individual DNA profiles). Based on the testing performed, it is not possible to test these assumptions.
- A **Can be Excluded** result indicates that a DNA profile for a questioned sample is not consistent with the known DNA profile from a reference or reference-type sample. This should be interpreted to mean that either the known DNA profile is not present in the sample or that there is insufficient data on which to base a statistically supported inculpatory conclusion (esp. in the case of mixed DNA profiles). Based on the testing performed, it may not be possible to distinguish between these two alternatives.

Additional Cautionary Notes

- Partial autosomal-STR and Y-STR profiles should be interpreted with caution. Missing data may either confirm or refute a findings based on the interpretation of a partial profile.
- Irresolvable DNA Mixtures do not allow for the identification of individual DNA profiles. A failure to exclude a known DNA profile from a mixture, therefore, should be interpreted with caution. It should be interpreted to mean either that the known profile is a component of the mixture or that alleles from more than one contributor can be combined to yield a profile that is coincidentally consistent with that of the known contributor. Based on the testing performed, it is not possible to distinguish between these two alternatives.

General Categories of Statistical Conclusions

- The **RMP** (Random match Probability) statistic indicates how common/rare a DNA profile is in the general population. It does not indicate how common/rare a DNA profile is among persons who are biologically related. This statistic is not the probability that a given individual is the source of the DNA in a specific sample.
- The **LR** (Likelihood Ratio) Compares the relative support for two competing hypotheses under a specific set of assumptions. LRs can range from 0 to ∞. Alternate hypotheses and/or assumptions will typically change the LR value. An LR is not the probability that the underlying assumptions of either hypothesis are true/false.
- The **CPE** (Combined Probability of Exclusion) statistic indicates the percentage of the general population that can be excluded as a potential contributor to a mixed DNA profile. This statistic is not the probability that a given individual is an actual contributor to a mixture.
- The **2P Frequency** statistic is used as a conservative means of compensating for the possibility of autosomal-STR allele drop out. 2P is used with data that fall between the analytical and stochastic thresholds. 2P frequencies may be combined with RMP or CPE statistics.
- A **Y-STR** statistic reflects the number of times that a given Y-STR profile is observed in a national Y-STR database. This statistic is not the probability that a given male is the source of the male DNA in a specific sample.
- A **CPI** (Combined Parentage Index) statistic is a ratio of probabilities under the assumption that an alleged parent is the source of obligate alleles in a child versus the assumption that a randomly selected person from the general population is the source of the obligate alleles. Based on a 0.5 prior odds, the CPI can be expressed as a **POP** (Probability of Paternity).

THE FBI QUALITY ASSURANCE STANDARDS

AUDIT FOR

FORENSIC DNA TESTING LABORATORIES

IN ACCORDANCE WITH

THE QUALITY ASSURANCE STANDARDS

FOR

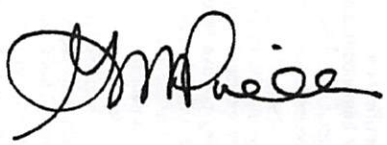
FORENSIC DNA TESTING LABORATORIES

EFFECTIVE SEPTEMBER 1, 2011

An Audit of: NMS Labs

Dates of Audit: June 19-21, 2013

Auditor(s):

Gina Pineda	
(Name)	(Signature)
(Name)	(Signature)
(Name)	(Signature)

Checklist of General Laboratory Information

1. Name of Laboratory: NMS Labs

2. Federal / State / Regional / County / Local / Other: Private
   Laboratory (Choose one)

3. Approximate Population Size Served: Nationwide

4. Uses a Contract Laboratory ☐ Yes ☒ NO
   Name of Contract Laboratory(ies): _____

5. NDIS Participant: ☐ Yes ☒ NO

6. Applying for NDIS Participation: ☐ Yes ☐ NO ☒ N/A

7. Technologies Used: (Choose those that apply)
   STRs X
   YSTRs X
   MtDNA
   Other: _____

8. Number of staff:
   DNA analysts: Staff: 5 Contract employees: _____
   DNA trainees: Staff: 0 Contract employees: _____
   DNA technicians: Staff: 0 Contract employees: _____
   Laboratory support personnel: Staff: 1 Contract employees: _____
   DNA technical leader: Britton Morin
   On site: ☒ Yes ☐ NO
   Casework CODIS administrator: N/A

9. Last audit conducted on: September 27, 2012
   ☐ External ☒ Internal Audit

10. Audit Document Discussion Used (Revision Date): September 1, 2011

Appendix C: Auditor Self-Certification for QAS Audits

Section 1 – to be completed by the laboratory being audited:
Laboratory being audited: NMS Labs As of [date] 06/19/13
Technologies currently in use: STR, Y-STR
Platforms currently in use: Organic, EZ1, RT-PCR, PCR amplification, CE
Validations needing to be memorialized: Qiagen Investigator Quantiplex HYres Validation, Powerplex Fusion Amplification Kit Validation, Identifiler Plus Amplification Kit Validation, and EZ1 Robotic Extraction Validation
Outsourcing agreements in place or in process: None
The laboratory being audited may request documentation for the information reported in Section 2 below.

Section 2 – to be completed by the auditor who will sign the attestation statement below the questions and (a) for external audits, return to the laboratory prior to the scheduled audit date; or (b) for internal audits, maintain in the laboratory's files.
Auditor Qualifications:
Name of Auditor: Gina Pineda
Auditor's Employer: GMP Forensic Consultants
Auditor's Title or Position: President/DNA Consultant
Qualified Auditor[2]: Yes No (Circle One)
Year Completed FBI DNA Auditor Class: 2003, 2007 (refresher) & 2009 (refresher)
Current or Previously Qualified DNA Analyst: Yes No (Circle One)
Current or Previously Qualified in Casework, Database Analysis, or Both[3]:
Casework Database Both (Circle One)
Technologies Currently or Previously Qualified In (e.g., STR, mtDNA) (Please List):
STR, Y-STR, mtDNA, Mini-STR
Platforms Currently or Previously Qualified In (e.g., Gel based/CE)
(Please List): Gel & capillary electrophoresis, real-time PCR

I verify that:

I understand the requirements of Standard 15.2[4]; and
I have no conflicts of interest with the laboratory being audited; and
The information contained in Section 2 above is correct.

Signed By _____ **Date** 6/19/13

[2] A Qualified Auditor is a current or previously qualified DNA analyst who has successfully completed the FBI DNA Auditor training course.
[3] If the laboratory being audited performs both casework and database analyses, then the audit team or auditor must be qualified in both casework and database analyses.
[4] Standard 15.2 requires that "at least once every two years, an external audit shall be conducted by an audit team comprised of qualified auditors from a second agency(ies) and having at least one team member who is or has been previously qualified in the laboratory's current DNA technologies and platform."

Appendix E: Approved Validations

This form may be used to document the evaluation and approval of validations by the external audit team according to Standard 8; this documentation to be maintained by the audited laboratory to comply with Standard 15.2.2.

To be completed by the audit team:

List of validations, if any, evaluated and approved during this audit:

EZ1 Advanced XL Biorobot (validation approved by TL on 5/14/13)

Qiagen Investigator Quantiplex HY res Kit (validation approved by TL on 8/21/12)

Powerplex Fusion Amplification Kit (validation approved by TL on 6/19/13) –
APPROVAL PENDING REMEDIATION OF FINDING UNDER STANDARD 8.3.1

Identifiler Plus Amplification Kit (Full scale and reduced scale reaction volumes) (validation approved by TL on 6/19/13)
APPROVAL PENDING REMEDIATION OF FINDING UNDER STANDARD 8.3.1

The following internal validations were not reviewed during this audit. However, they have been reviewed by previous audit teams as indicated below. Findings were identified by previous audit teams that precluded the validations from being listed as Approved Validations in Appendix E of the audit documents. The current audit reviewed the corrective actions implemented as remediation for the findings identified in the previous audits. Therefore, the following validation studies were fully reviewed by prior audit teams, and related corrective actions reviewed during this audit, and are being captured on this document as approved:

Identifiler (approved 7/1/2004 and 8/1/2011 and reviewed in the 2009 QAS audit)

Yfiler (approved 4/29/2010 and reviewed in the 2011 QAS audit)

Powerplex Y (approved on 7/19/2004 and reviewed in the 2011 QAS audit)

Powerplex 16 Hot Start (approved on 1/18/2010 and reviewed in the 2011 QAS audit)

Appendix C – Auditor Self-Certification for QAS Audits

Section 1 – to be completed by the laboratory being audited (use additional blank sheets if necessary):
Laboratory being audited: NMS Labs Forensic Biology As of [date] 03/05 - 04/05/2015
Technologies currently in use: PowerPlex 16/16 HS, QuantiPlex HyRes
Platforms currently in use: 7500, 3130, 310
Validations needing to be memorialized: NA
Outsourcing agreements in place or in process: NA
The laboratory being audited may request documentation for the information reported in Section 2 below.

Section 2 – to be completed by the auditor who will sign the attestation statement below the questions and (a) for external audits, return to the laboratory prior to the scheduled audit date; or (b) for internal audits, maintain in the laboratory's files.
Auditor Qualifications:
Name of Auditor: Allison Yvonne Eastman
Auditor's Employer: Contracted by ASCLD/LAB / University at Albany, SUNY
Auditor's Title or Position: Private Contractor / Associate Professor
Qualified Auditor[2]: Yes No (Circle One)
Year Completed FBI DNA Auditor Class: 2009
Current or Previously Qualified DNA Analyst: Yes No (Circle One)
Current or Previously Qualified in Casework, Database Analysis, or Both[3]:
Casework Database Both (Circle One)
Technologies Currently or Previously Qualified In (e.g., STR, mtDNA) (Please List):
STR, qPCR, Serology (body fluid identification), reverse dot blot
Platforms Currently or Previously Qualified In (e.g., Gel based/CE) (Please List): Capillary electrophoresis, qPCR

I verify that:
I understand the requirements of Standard 15.2[4] ; and
I have no conflicts of interest with the laboratory being audited; and
The information contained in Section 2 above is correct.
Signed By _____ **Date** 04/06/2015

---

[2] A Qualified Auditor is a current or previously qualified DNA analyst who has successfully completed the FBI DNA Auditor training course.

[3] If the laboratory being audited performs both casework and database analyses, then the audit team or auditor must be qualified in both casework and database analyses.

[4] Standard 15.2 requires that "at least once every two years, an external audit shall be conducted by an audit team comprised of qualified auditors from a second agency(ies) and having at least one team member who is or has been previously qualified in the laboratory's current DNA technologies and platform."

EXECUTIVE SUMMARY

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Lynn Robitaille Garcia, Esq.
General Counsel
Texas Forensic Science Commission
1700 North Congress, Suite 445
Austin, TX 78701

Date: 08/10/2017
Re: NMS Labs testing in *United States of America v. Cardell Torney*

Dear Ms. Garcia:

On July 27th, 2017, NMS Labs received an inquiry from the Texas Forensic Science Commission (FSC) in regard to claims made by Mr. Michael Ambrosino (U.S. Attorney's Office, Washington DC) in a recent presentation to the National Association of Attorneys General in which he included a discussion of *US v. Torney.* NMS Labs disputes the claims of Mr. Ambrosino; the findings of the court and the factual content of the order. NMS Labs stands by the scientific and forensic defensibility of its results in that case, and the validity of the analytical procedures in place at the time, and in place today. This document provides a summary of NMS Labs' response to the salient points raised by the FSC.

- *NMS Labs has demonstrated to ASCLD/LAB and other assessors, on multiple occasions, its compliance with the appropriate accreditation standards, prior to, during, and after the Torney matter. NMS Labs has received written notices that we are fully compliant with the method validation requirements and the underlying standards recommendations of the forensic community.*

- *NMS Labs validated and adhered to the relevant SOP for the Qiagen Investigator® Quantiplex HYres assay, including documentation of relevant controls and technical review. All performance parameters and results were found to comport with the expected values observed in internal and developmental validation studies. Accordingly, there is no objective evidence that the Investigator® Quantiplex HYres assay was improperly used by NMS or that the results obtained were unreliable.*

- *NMS Labs validated and adhered to the relevant SOP for the Promega PowerPlex® 16HS assay, including documentation of relevant controls and technical review. The mathematical accuracy of all the reactions was confirmed. Accordingly, there is no objective evidence that the STR amplification reactions were improperly prepared or analyzed by NMS Labs.*

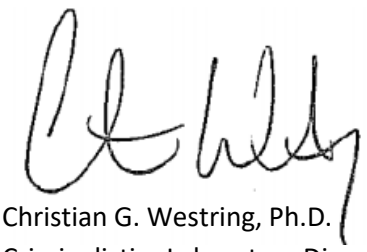
- *The DNA profile developed and interpreted by NMS Labs was not "overblown". The sample performed within the validated parameters of the Promega PowerPlex® 16HS assay on the Applied Biosystems Prism 3130 Genetic analyzer. Based on the genetic information available, the laboratory reported that no inculpatory conclusions were appropriate for the minor profile.*

- *NMS Labs adhered to the laboratory's DNA Interpretation Guidelines and Policies which are founded on the recommendations of several professional groups in the relevant scientific community. All of the results, interpretations, and opinions were subject to technical and administrative review by a competent and qualified expert in accordance with laboratory SOP.*

- *Representatives from ASCLD/LAB also conducted a "Special Assessment" upon my request, including all the data obtained through internal validation, including quantitation assays and STR profiles, SOPs, and NMS Labs' reporting guidelines as referenced in the Judge Dixon's order. NMS Labs passed the audit without findings, and the audit report was approved by the ASCLD/LAB Board of Directors.*

- *NMS Labs has an impeccable record for providing forensic testing services that meet the highest quality standards, including key casework contributions to the state of Texas. We stand by our core principles that NMS Labs is committed to the continued delivery of scientific excellence. Our position in this matter – which is grounded in hard science – does not waver*.

Respectfully,



Christian G. Westring, Ph.D.
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Lynn Robitaille Garcia, Esq.
General Counsel
Texas Forensic Science Commission
1700 North Congress, Suite 445
Austin, Texas 78701

Date: 08/10/2017
Re: NMS Labs testing in *United States of America v. Cardell Torney*
NMS Labs WO#13001065

Dear Ms. Garcia:

On July 27th, 2017, NMS Labs received an inquiry from the Texas Forensic Science Commission (FSC) regarding claims made by Mr. Michael Ambrosino (U.S. Attorney's Office, Washington DC) in a recent presentation to the National Association of Attorneys General in which he included a discussion of *US v. Torney*. Judge Dixon's ruling in that case suppressed the results of DNA testing performed in 2013 by NMS Labs on the grounds that NMS Labs had failed to comport with accepted scientific principles in the generation and interpretation of laboratory test data. Specifically, Mr. Ambrosino and Judge Dixon have asserted that:

- The methodologies employed by NMS Labs for use of the PowerPlex® 16HS kit were not in accordance with accepted scientific practices
- The protocols employed by NMS Labs for interpreting DNA test results were not grounded in validation data

The inquiry by the FSC specifically referenced three particular areas of interest (notation 1-3 below). Furthermore, on August 2nd, 2017, the Commission requested additional documentation as summarized below (notations 4-5 below). They are as follows:

(1) According to the attached, the analyst did not perform the quantitation assay properly, resulting in too much DNA being used during the amplification process. This resulted in an "overblown" data. Can you please explain your understanding of this issue, what root-cause analysis was performed, and what corrective action was taken to ensure this does not occur again in other cases? Please provide any QA documentation related to the issue. Please also provide an assessment of whether any Texas cases could have been similarly affected by an error in performance of the quantitation assay, whether any testimony could have been provided regarding similarly overblown data, and what corrective action was taken in these cases.

(2) According to the Judge's findings, a representative from Promega maintained the kit (PowerPlex® 16HS) used in this case was misused by NMS. Can you please explain your understanding of this conclusion and what corrective action was taken by the laboratory? Please provide any QA documentation related to the issue.

(3) A former analyst and tech reviewer appears to have raised concerns regarding the analytical steps and related interpretation in this case. Please provide any information regarding NMS' vetting of the analyst's concerns and related documentation. Please provide any QA documentation regarding the resolution of disagreement between the analyst and tech reviewer.

(4) Were the ASCLD/LAB assessors referenced in the attached letter provided a copy of the Judge's findings in Torney? Were the ASCLD/LAB assessors provided the specific validation data/studies in the Torney order? Please provide documentation in support.

(5) Please provide a copy of the NMS Lab's laboratory report(s) in the Torney case including any amendment(s) or revisions to the report(s).

Having no legal standing to challenge the opinion on matters of law, NMS Labs took immediate action with our accrediting body, ASCLD/LAB[1], and requested an immediate audit. We sought independent verification that our validation studies, analytical procedures and interpretation guidelines in this matter were grounded in reliable scientific data and comported with the highest international standards of the forensic science community.

NMS Labs has repeatedly demonstrated to ASCLD/LAB and other auditors our compliance with the appropriate accreditation standards (June 2013; December 2014; March 2015; November 2015; December 2016). NMS Labs has received written notices that we are fully compliant with the method validation requirements, and the underlying standards and recommendations of the forensic community. This includes the Federal Bureau of Investigation's (FBI's) Quality Assurance Standards for Forensic DNA Testing Laboratories; the Scientific Working Group on DNA Analysis Methods (SWGDAM); and the International Society for Forensic Genetics (ISFG).

NMS Labs disputes the claims of Mr. Ambrosino; the findings of the court and the factual content of the order. NMS Labs stands by the scientific and forensic defensibility of its results in that case, and the validity of the analytical procedures in place at the time, and in place today. Given the serious nature of the claims made by Mr. Ambrosino, which are reflected in Judge Dixon's ruling, I fully understand your cause for concern. I appreciate, therefore, that you have contacted NMS Labs directly and I am happy to answer your questions and to address the issues raised in this case.

(1) Performance, Reliability and Validation of the DNA Quantitation Assay; Autosomal STR Profiling and Data Interpretation

DNA Quantitation by the Investigator® Quantiplex HYres Kit **-** A careful review of the case file and associated documentation for *US v. Torney* was conducted by NMS Labs' Criminalistics Laboratory Director

[1], DNA Technical Leader[2] and Science Advisor[3] to verify that the DNA quantitation assay was executed in accordance with the relevant laboratory SOP and to verify that the performance of the assay was in accordance with the validated quality parameters. This review confirmed that in accordance with FBI QAS Standard 9.2[4], all reagents used were of good quality and were used prior to their expiration/discard date[5]. The reagent volumes used for the preparation of the Reaction Mix FQ and Primer Mix IC YQ and the volume dispensed to each reaction well were in accordance with the relevant laboratory SOP[6] as required by FBI QAS Standard 9.1.1 [7]. The results obtained in regard to *US v. Torney* [8] comported with performance parameters based on both internal[9] and developmental validation studies[10]. Because the reliability of the human DNA quantitation assay has been raised as a potential concern, it is necessary to review the results obtained by NMS Labs in greater detail.

First, DNA quantification standards are critical for accurate analyses. As recommended by the manufacturer, a dilution series of control human DNA (20.00 ng to 0.00488 ng in triplicate) was used to generate a standard curve. This curve was then used to estimate the concentration of DNA in questioned samples. The standard curve obtained had an R^2 of 0.996 demonstrating that the dilution series had near perfect linearity and that the replicates yielded results with near perfect precision (CV=0.13 to 1.97%). While the standard curve was generated using commercially prepared control DNA of known concentration, the accuracy of the DNA quantities used was also independently confirmed. This was achieved by comparing the C_T values obtained for each dilution to those obtained for the corresponding dilutions in NMS Labs' internal validation studies and the manufacturer's developmental validation studies (Table 1).

Second, the Investigator® Quantiplex HYres kit includes an internal positive control (IC) to detect chemistry or instrument failure, errors in assay setup and/or sample inhibition. The Investigator® Quantiplex HYres Handbook states that:

> *"Positive amplification of the IC system will generate a C_T value of approximately 31.* A variation of ±1 in the C_T values of the IC system for the standard curve samples can be*

---

[1] Christian G. Westring, PhD

[2] Britton Morin, M.Sc.

[3] Phillip B. Danielson, PhD

[4] Federal Bureau of Investigation, "Quality Assurance Standards for Forensic DNA Testing Laboratories" (Effective 09/01/2011).

[5] STANDARD 9.2 The laboratory shall use reagents that are suitable for the methods employed. The quality and quantities of regents used are provided in "Forensic DNA Analysis Cover & Controls Sheet" (Code 20130311CA) dated 03/12/13 and signed by analyst Jillian Fesolovich and analyst Laura Cronin; and "RT PCR Quantitation Worksheet: Investigator® Quantiplex HYres Kit" dated 03/11/13 and signed by analyst Jillian Fesolovich.

[6] NMS #CR-914 RT Quantitation ASSAY BY QIAGEN SOP is based on the manufacturer-recommended protocol contained in the "Investigator® Quantiplex Handbook" and internal validation studies for reduced-scale reactions.

[7] STANDARD 9.1.1 The laboratory shall have and follow a standard operating procedure for each analytical method used by the laboratory. The procedures shall specify reagents, sample preparation, extraction methods (to include differential extraction of nuclear DNA samples with adequate amount of sperm), equipment, and controls which are standard for DNA analysis and data interpretation. "Quality Assurance Standards for Forensic DNA Testing Laboratories" (Effective 09/01/2011).

[8] Results of the Investigator® Quantiplex HYres assay are presented in file Qiagen HYres_031113_JF.sds

[9] NMS Labs' Validation Report on the Investigator® Quantiplex HYres kit

[10] QIAGEN Validation Report: Developmental validation of the Investigator® Quantiplex HYres Kit, Qiagen Corporation (11/2012).

expected. Using large amounts of human DNA (>150 ng/reaction) can give a higher C_T value for the IC system."

The IC C_T obtained for the standard curve in *US v. Torney* was 31.19±1.09 ($\bar{x}$±SD). The IC C_T obtained for the four questioned samples ranged from 30.85 to 32.74, *i.e.*, the C_T values were stable and within the expected range of variability relative to the standard curve. It is recognized by the manufacturer that very high concentrations of DNA may interfere with the amplification of the IC resulting in elevated C_T values[11]. The manufacturer's developmental validation studies addressed this concern by demonstrating that the IC C_T value was stable even at concentrations above the standard curve. The stable C_T values observed for all questioned samples in the *US v. Torney* case support the conclusion that the assay performed as validated.

Table 1: Comparison of Standard Curve CT values from WO#13001065 to Validation Studies

DNA Standard Concentration (ng/µ)	WO#13001065 (C_T)	NMS Internal Validation (C_T)	Qiagen Developmental Validation (C_T)†
20 ng/µ	20.08	19.83	20.69
5 ng/µ	22.29	22.01	22.71
1.25 ng/µ	24.20	24.02	24.74
0.313 ng/µ	26.08	25.81	26.77
0.0781 ng/µ	28.07	27.88	28.79
0.0195 ng/µ	29.99	29.87	30.82
0.00488 ng/µ	32.48	32.02	32.84

†Calculated from the linear equation (y = -3.365x + 25.066) for the human target standard curve reported in the manufacturer's developmental validation report.

Third, all other controls run in accordance with manufacturer's protocol; the guidelines of the Scientific Working Group on DNA Analysis Methods[12] (SWGDAM) and FBI QAS Standard 9.5[13] (*i.e.*, positive controls, no template controls, reagent blank controls and extraction controls), all yielded the expected results.

Summary: *In regard to NMS Labs' analyses in US v. Torney, adherence to the laboratory's relevant SOP for the Investigator® Quantiplex HYres kit was documented (J.* Fesolovich*) and reviewed (L. Cronin). All performance parameters and the results from all control samples comported with expected values observed in internal and developmental validation studies. Accordingly, there is no objective evidence that the Investigator® Quantiplex HYres kit was improperly used by NMS Labs or that the results obtained were unreliable.*

Dilution of the DNA Extracts and STR Profiling by Promega PowerPlex® 16HS Kit - A careful review of the case file and associated documentation for *US v. Torney* was conducted by NMS Labs' Criminalistics Laboratory Director, DNA Technical Leader and Science Advisor to verify that the PowerPlex® 16HS amplification reaction (including the dilution of DNA extracts for questioned samples) was executed in

[11] QIAGEN Validation Report: Developmental validation of the Investigator® Quantiplex HYres Kit, Qiagen Corporation (11/2012).

[12] SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories. APPROVED 1/14/10.

[13] STANDARD 9.5 The laboratory shall monitor the analytical procedures using the following controls and standards. "Quality Assurance Standards for Forensic DNA Testing Laboratories" (Effective 09/01/2011).

accordance with the laboratory's relevant SOP. This review confirmed that all reagents used were of good quality and were used prior to their expiration/discard date[14]. The reagent volumes used for the preparation of the PCR Reaction Mix, STR Primer Mix and *Taq* Polymerase and the volume dispensed to each reaction well were in accordance with the relevant laboratory SOPs[15]. The accuracy of all mathematical calculations performed to determine the DNA extract volume required to achieve a target DNA input of 1 ng were confirmed. Review of the GeneMapper ID files generated in the course of analyzing all control and questioned samples associated wit*h* NMS Labs' analyses in *US v. Torney* confirmed that the instrument protocol, analytical method, STR panel, size standard and instrument type were correctly set.

Summary: *In regard to NMS Labs' analyses in US v. Torney, adherence to the laboratory's relevant SOP for set up of the PowerPlex® 16HS amplification reactions was documented (J. Fesolovich) and reviewed (L. Cronin). The accuracy of all associated mathematical calculations was confirmed. Accordingly, there is no objective evidence that the STR amplification reactions were improperly prepared or analyzed by NMS Labs.*

***Limit of Linearity Validation and Interpretation of* DN*A Profiles* -** A careful review of the case file and associated documentation for *US v. Torney* was conducted by NMS Labs Criminalistics Laboratory Director, DNA Technical Leader and Science Advisor. This included item EX02.2-1A (referenced in the Dixon order) as well as the results of NMS Labs' internal validation studies for both the PowerPlex® 16HS chemistry and the ABI Prism 3130 Genetic Analyzer. This review was conducted to confirm that NMS Labs' DNA Interpretation Guidelines and Policies SOP[16] were supported by the results of our internal validations and were consistent with the recommendations of the scientific community. Because it was claimed that NMS Lab analysts interpreted DNA profiles that exceeded the limit of linearity (*i.e.*, "overblown"), it is necessary to review the results obtained, the interpretation guidelines employed; and the supporting validation data in greater detail.

First, NMS Labs recognizes that forensic specimens are samples of unknown composition. Such samples may contain environmental contaminants that can result in the inhibition, enhancement or other deviations of target allele amplification from expected norms. Furthermore, while substantial improvements have been made to the accuracy and precision of DNA quantization assays, the manufacturers themselves emphasize that the assays are not designed to ensure flawless profiles but rather the more modest objective of confirming, "…whether a sample contains sufficient DNA to enable DNA fingerprinting analysis (such as STR, DIP, or SNP analysis)[17]". Accordingly, even when DNA quantization results are used to estimate DNA input for amplification reactions, analysts must confirm

[14] The quality and quantities of regents used are provided in "Forensic DNA Analysis Cover & Controls Sheet" (Code 20130311CA) dated 03/12/13 and signed by analysts Jillian Fesolovich and analyst Laura Cronin and "PCR Amplification Worksheet: PowerPlex® Y & PowerPlex® 16" dated 03/11/13 and signed by analyst Jillian Fesolovich.

[15] NMS #CR-320 "DNA Amplification by Polymerase Chain Reaction" SOP is based on the manufacturer-recommended protocol contained in the "Technical Manual: PowerPlex® 16HS System, Instructions for Use of Products DC2100 and DC2101 (Revised 10/2011)" and internal validation studies for reduced-scale reactions. NMS #CR-337 "3130 Capillary Electrophoresis Preparation" and NMS #CR-338 "GeneMapper Analysis for 3130" are additional relevant SOPs.

[16] NMS # CR-915 "DNA Interpretation Guidelines and Policies"

[17] Qiagen Corporation "Investigator® Quantiplex Handbook For quantification of human and male DNA in forensic samples", Germantown, MD.

that the resulting DNA profiles are within the validated limits of linearity (40-7559 RFU in the analyzed data) and thus are suitable for interpretation.

The critical concerns associated with exceeding the limit of linearity for the instrument are clearly described in the PowerPlex® 16HS System Technical manual[18] which states:

> "***Notes:***
>
> 1. *Peak heights outside the linear range of the instrument may generate artifact peaks due to instrument saturation (i.e., overloading the sample). Bleedthrough (pull-ups) from one color to another may be observed. Saturated signal also may appear as two peaks (split peak).*
> 2. *If peak heights are not within the linear range of detection of the instrument, the ratio of stutter peaks to real allele peaks increases, and allele designations become difficult to interpret. The balance of peak heights also may appear less uniform.*
> 3. *There can be variation between instruments regarding the relative fluorescence levels detected using the same sample. Furthermore, different instruments vary in the relative efficiency of color detection, affecting the dye color-to-dye color balance."*

Promega Corporation has published specific guidance on the internal validation of the limit of linearity for STR systems, recommending that DNA input be plotted against the average peak height in a profile. The limit of linearity is then defined as the mass of DNA that results in saturation of the detector such that a further increase in template mass no longer result in a linear increase in fluorescent signal[19].

NMS Labs conducted rigorous internal validation studies of the PowerPlex® 16HS chemistry on the Prism 3130 instrument. The studies encompassed a 9-point dilution series with total DNA inputs ranging from a low of 15.63 pg to a high of 4000 pg. All samples were prepared and amplified in pentuplicate and injected at 1, 5 and 10 seconds on two different Prism 3130 genetic analyzers. The results of these validation studies showed near perfect linearity ($R^2 = 0.9998$) in the performance of the PowerPlex® 16HS kit up to 4000 pg of input DNA (the highest input quantity tested).

Concerns in regard to the generation of artifact peaks or the reliability of stutter ratios, however, are a function of signal saturation and thus the linear range of detection of the instrument (*e.g.*, the Prism 3130 genetic analyzer). NMS Labs' validation studies addressed this issue in two ways. First, the Promega approach of plotting the average peak height across a profile against DNA input was used. This demonstrated near perfect linearity ($R^2 = 0.9993$) of signal detector response in RFU (Relative Fluorescence Units) such that an increase in DNA produces a corresponding linear increase in detected signal. This linearity was maintained up to an average peak height across the entire profile of at least 4686 RFU. The highest average peak height for any of the profiles interpreted in regard to NMS Labs' analyses

[18] Promega Corporation "Technical Manual: PowerPlex® 16HS System, Instructions for Use of Products DC2100 and DC2101 (Revised 10/2011)"Madison, WI.

[19] Promega Corporation "Reference Manual: Internal Validation of STR Systems (Revised 9/06)" Part# GE053. Madison, WI.

in *US v. Torney* was for EX02.2-1A (referenced in the Dixon order) which had an average peak height of 4414 RFU, *i.e.,* within the validated linear range of the instrument.

A second approach used by NMS Labs, recognized that the use of average peak heights across a profile does not adequately address the risk that stutter ratios may be artificially elevated when the signal from the source/parent peak saturates the instrument detector. This is because stutter ratios are not determined – and stutter filters are not applied – on the basis of the average peak height of a profile. Rather, these are based on the height of the individual source/parent peak. NMS Labs, therefore, also validated the linearity of individual allelic peaks on the 3130 instrument up to the theoretical detector maximum of 8192 RFU[20]. This was achieved by plotting the height of single allele peaks at individual loci across all three dye channels against DNA input. These studies validated the near perfect linearity of the instrument regardless of locus or dye channel (R^2 = 0.978 to >0.999) up to a signal intensity of 7559 RFU. Within this range, we have validated that an increase in DNA quantity correlates tightly with a corresponding linear increase in the detected signal. The highest peaks for any of the profiles interpreted in regard to NMS Labs' analyses in *US v. Torney* was in the profile for EX02.2-1A (referenced in the Dixon order) which had a peak height of 7490 RFU at D8S1179, *i.e.,* within the validated linear range of the instrument (Table 2).

Table 2: Validated Linearity Limits for PowerPlex® 16HS on Prism 3130 Genetic Analyzer

Linearity Parameter	NMS Labs' Validation Studies	PowerPlex® 16HS Technical Manual	Item EX02.2-1A (*US v. Torney*)
Average Peak Height Across Profile (RFU)	4686	ND*	4414
Individual Peak Upper Limit of Linearity (RFU)	7559	ND*	7490
Analytical Threshold (RFU)	40	50–150RFU†	40

† Per Promega Corporation's "Technical Manual: PowerPlex® 16HS System (Revised 10/2011)", individual laboratories should determine peak amplitude thresholds from internal validation studies."

* ND = Not Determined. No manufacturer recommendations provided for this parameter.

When profiles are found not to lie within the 40-7559 RFU limits of linearity, NMS Labs "DNA Interpretation Guidelines and Policies" instruct the analyst that:

> *"In such cases, the following actions may be taken to resolve the issue:*
>
> 1. *The amplified sample may be reinjected at a decreased injection time.*
> 2. *The amplified sample may be diluted and reinjected (add 0.5µL of amplified PCR product to 10.5 µL of formamide/size standard).*
> 3. *The original DNA extract may be diluted and re-amplified."*

[20] Butler, JM (2014) Advanced Topics in Forensic DNA Typing: Interpretation. Academic Press, San Diego CA.

In *US v. Torney*, where the initial DNA profile for item EX02.2-1A (referenced in the Dixon order) exceeded the 7559 RFU upper limit of linearity, the analyst chose to reinject the sample at a decreased injection time. Doing so produced a DNA profile that was within the limits of linearity.

We also confirmed that peaks near the instrument's validated upper limit of linearity were not generating artifact peaks by artificially elevating the stutter ratios. This was achieved by validating the consistency of stutter ratios for known stutter peaks up to the limit of linearity. This validated the reliability of stutter filters to correctly identify potential stutter regardless of the height of the source/parent peak. This was demonstrated by plotting the ratio (as a percentage) of peaks in both positive and negative stutter positions against the height of the source/parent peak. These data were collected from across the entire validated linear range of the instrument (*i.e.*, 40-7559 RFU). The results of these studies validated that stutter ratios do not change as a function of the height of a source/parent peak (*i.e.*, stutter ratios are stable and thus stutter filters remain reliable up to the limit of linearity (Figure 1).

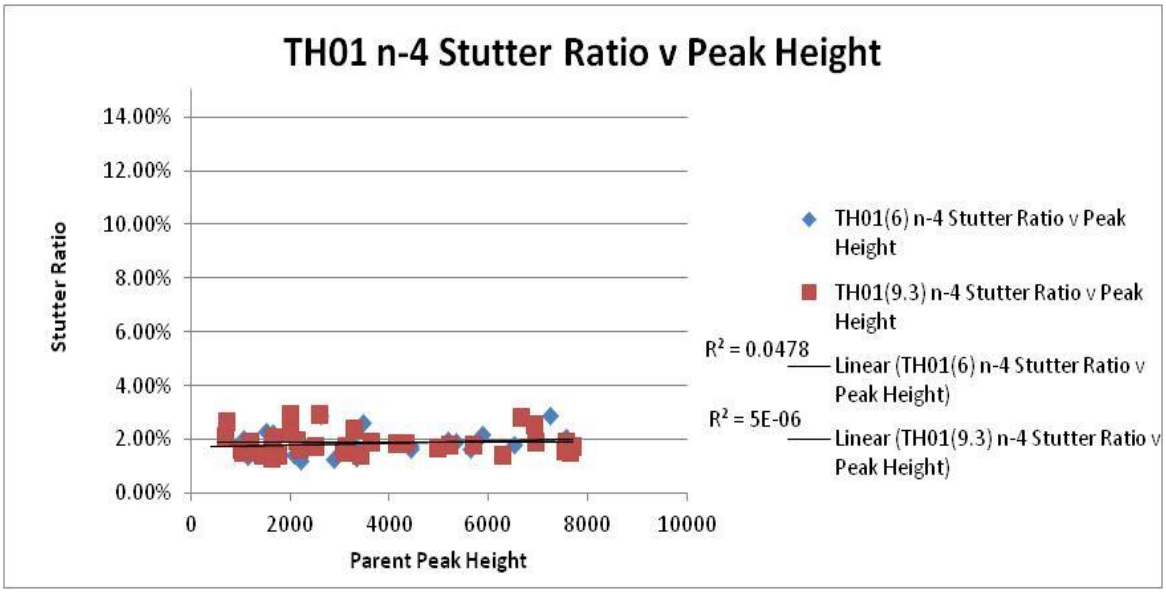


Figure 1: Plot of the PowerPlex® 16HS stutter ratios for two N-4 stutter positions at the TH01 locus as a function of the height of the source/parent peak. Stutter ratios are stable across the full dynamic range of the Prism 3130 Genetic Analyzer.

An additional caveat to this is the importance of assessing the morphology of peaks near the 7559 RFU upper limit of linearity to ensure that they are suitable for interpretation. As peaks become increasingly saturated, their morphology is often characterized by the presence of a split at the crest of peak. The depth of the split is correlated with the degree of detector saturation. NMS validation data demonstrate that minor saturation may cause peaks to deviate slightly from an ideal morphology. Such morphological deviations are detectible before any quantifiable impact on profile interpretation parameters such as stutter ratios. Moderate to excessive saturation, however, results in deeper splits in the allelic peak. Saturation at this level can complicate the accurate quantitative interpretation of DNA profiles[21]. Only a minority of peaks for any of the profiles interpreted in connection with NMS Labs' analyses in *US v. Torney*

[21] McKiernan H.E. and Danielson, P.B. (2016) Molecular Diagnostic Applications in Forensic Science. In: Molecular Diagnostics 3rd Edition (Patrinos G., Ansorge W. and Danielson, P.B. Eds.). Academic Press.

were near the upper limit of linearity. All of these peaks, however, were determined to have morphologies that made them acceptable for interpretation.

Uncertainty in Minor Contributor Interpretation **-** The recognition of uncertainty is fundamental to good science. In the realm of forensic DNA analyses, this is especially true for the interpretation of mixtures particularly where a major contributor may mask the alleles of a minor contributor or where potential stutter peaks are similar in size to peaks of a minor contributor in non-stutter positions and where artifacts may have peak heights similar to true alleles. In all of these examples, there is an unavoidable degree of uncertainty. This has been recognized by the scientific community and multiple guidelines for the interpretation of uncertain peaks in stutter positions have been published for adoption by forensic laboratories.

Referencing the 2010 SGWDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories, Guideline *3.5.8. Interpretation of Potential Stutter Peaks in a Mixed Sample* states as follows:

> ***"3.5.8.1.*** *For mixtures in which minor contributors are determined to be present, a peak in stutter position (generally n-4) may be determined to be 1) a stutter peak, 2) an allelic peak, or 3) indistinguishable as being either an allelic or stutter peak. This determination is based principally on the height of the peak in the stutter position and its relationship to the stutter percentage expectations established by the laboratory.*
>
> ***3.5.8.2.*** *Generally, when the height of a peak in the stutter position exceeds the laboratory's stutter expectation for a given locus, that peak is consistent with being of allelic origin and should be designated as an allele.*
>
> ***3.5.8.3.*** *If a peak is at or below this expectation, it is generally designated as a stutter peak. However, it should also be considered as a possible allelic peak, particularly if the peak height of the potential stutter peak(s) is consistent with (or greater than) the heights observed for any allelic peaks that are conclusively attributed (i.e., peaks in non-stutter positions) to the minor contributor(s)."*

Referencing the 2006 Recommendations by the DNA Commission of the International Society of Forensic Genetics on the Interpretation of Mixtures[22], Recommendation 6 on the treatment of stutter states as follows:

> ***"Recommendation 6:*** *If the crime profile is a major/minor mixture, where minor alleles are the same size (height or area) as stutters of major alleles, then stutters and minor alleles are indistinguishable. Under these circumstances alleles in stutter positions that do not support Hp should be included in the assessment."*

NMS Labs follows these guidelines and has incorporated the SWGDAM language verbatim into our DNA Interpretation Guidelines and Policies SOP. We remain firm that when interpreting mixed profiles with minor contributors, the peaks detected in stutter positions may either be a) of true human origin, or b)

[22] DNA Commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures, June 2006

elevated stutter. In accordance with the recommendations from the scientific community, therefore, NMS Labs treats peaks in stutter positions in mixtures as potential alleles.

Discrimination between potential allelic peaks and artifacts of similar size also involves uncertainty. This is an area of concern that NMS Labs has carefully considered in the course of our validation studies. As demonstrated through our internal validation studies, an increase in total DNA quantity does not appear to correlate with an increase the amplification of non-target PCR artifacts. Rather, such artifacts are readily identified across a wide range of DNA concentrations and are highly reproducible regardless of DNA input. This is demonstrated by the observation that the same artifact peaks seen in high DNA input reactions can also be detected in low DNA input reactions with increased injection times. These artifacts are generally characterized by off ladder positioning and/or poor peak morphology. As emphasized in the laboratory's DNA interpretation guidelines, therefore, care should be taken by analysts to assess peak morphology and positioning when evaluating potential minor contributor peaks. The alternative of increasing the analytical threshold for the purpose of avoiding the labeling of potential artifacts would have contravened SWGDAM Guideline 3.1.1.2. which warns that:

> *"The analytical threshold should not be established for purposes of avoiding artifact labeling as such may result in the potential loss of allelic data."*

Therefore, NMS Labs correctly employed the laboratory's DNA Interpretation Guidelines and the recommendations of the relevant scientific community on how to address artifacts and the uncertainty associated with stutter and peaks in mixed DNA profiles. The notion that a peak should be eliminated from consideration, simply because it is indistinguishable as either an allele or stutter, is unfounded and lacks support in the relevant scientific community.

Quality Audit for the State of Texas – A careful review of all forensic DNA casework that stems from the state of Texas has been conducted by the NMS Labs Criminalistics Laboratory Director. *In toto*¸ NMS Labs performed DNA testing using the PowerPlex® 16HS kit on eight cases between 2012 and 2014[23]. None of those cases contained DNA profiles with comparable peak height amplitude(s) as those observed in the *Torney* case. In 2015, the PowerPlex® 16HS kit was replaced by the Applied Biosystems AmpF*l*STR® Identifiler Plus kit. No cases with the same peak height amplitude as previously referenced have been observed since the implementation of Identifiler Plus kit. DNA profiles exhibiting complexities similar to those observed in the *US v. Torney* case are rare. NMS Labs' SOPs are designed such to target optimal quantities of input DNA such that the vast majority of profiles occur near the center of the dynamic range. Profiles outside of the dynamic range are reinjected for a shorter period of time, diluted or reamplified in accordance with the laboratory's SOP. Caution must be exercised, however, when minor contributors are present because over dilution or excessive reduction in the injection time can artificially eliminate the detection of a minor contributor. Further dilution of the profile detected in the US v. *Torney* case would have resulted in the loss of potential minor alleles. In order to avoid bias during the DNA interpretation process, NMS Labs' analysts are not permitted to view DNA profiles from known contributors until the interpretation of unknown samples is complete and documented per SWGDAM and ISFG recommendations. In accordance with the laboratory's SOP, NMS analysts in the *US v. Torney* case completed their interpretation without *a priori* knowledge of Mr. Torney's profile, and thus did not know

[23] Zero (0) cases in 2012, five (5) cases in 2013, and three (3) in 2014, respectively.

if the minor peaks detected matched him or not. Such interpretations are based solely on the data available, and do not rely on any other factors other than those defined in the laboratory's DNA Interpretation Guidelines and Policies.

Summary: *NMS Labs conducted rigorous internal validation studies of the PowerPlex® 16HS chemistry on the Prism 3130 instrument. The established limits, developed through internal validation, define the limits of linearity and consistency of stutter ratios. These were correctly applied to the interpretation of all questioned samples in US v. Torney. The results of the audit conducted by NMS Labs on cases from the state of Texas revealed that no cases contained complex DNA profiles similar to those seen in the US v. Torney case. A review of casework on a national scale indicates the same finding, thus, this has been isolated to a single event.*

(2) Assertion by Margaret Ewing that NMS Misused the PowerPlex® 16HS Kit

NMS Labs refutes the allegations made by Ms. Ewing that the PowerPlex® 16HS kit was misused and not validated appropriately. Ms. Ewing did not testify in the case, nor was an affidavit she prepared, and which was relied on by Mr. Ambrosino in his argument, ever provided to NMS Labs.

Referencing the Promega "Internal Validation of STR Systems reference manual"[24]:

> *"In addition to the validation studies described above, each laboratory is required to perform an internal validation study with the STR typing system it intends to implement"*.

In accordance with this guidance, NMS Labs developed a detailed validation protocol to assess the performance of the PowerPlex® 16HS kit prior to the use of this technology in forensic casework. These carefully designed studies were based on the published and generally accepted guidelines of SWGDAM[25] and the European Network of Forensic Science Institutes (ENFSI) for the validation of DNA analysis methods[26]. These studies were designed to evaluate specified performance parameters relevant to forensic laboratories. These included the use of known and non-probative evidence samples or mock evidence samples; studies of sensitivity, stochastic effects, dynamic range, optimal DNA input and signal-to-noise ratios for the determination of limit(s) of detection and the analysis of mixtures. Also included were studies of the limits of quantitation, precision and accuracy, linearity, heterozygote peak balance, stutter variation (n-4 and n+4) and other factors which impact the accurate and reliable interpretation of data.

The results of these validation studies, including the rigorous evaluation of the data generated, are the foundation of the methods and DNA interpretation guidelines employed by NMS Labs. These studies/methods have been subject to repeated peer review during five routine external audits by our accrediting body ASCLD/LAB and other auditors since 2012. These audits included verification of compliance with the FBI Quality Assurance Standards. In order to comport with the evolving recommendations of the scientific community NMS Labs conduct comprehensive revalidations of the technologies that we employ. Despite her opinion, Ms. Ewing has never reviewed the extensive validation

[24] Promega REFERENCE MANUAL – Internal Validation of STR Systems, Revised 9/06

[25] SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories. APPROVED 1/14/10

[26] Recommended Minimum Criteria for the Validation of Various Aspects of the DNA Profiling Process, ENFSI, November 2010

studies that were conducted by NMS Labs on either the Investigator® Quantiplex HYres kit or the PowerPlex® 16HS kit. Nor at any point in time did Ms. Ewing contact NMS Labs regarding the testing done in the *US v. Torney* matter to discuss our procedures or the scientific basis by which NMS had interpreted the data. It is particularly noteworthy that if Ms. Ewing felt that the PowerPlex® 16HS kit had not been properly validated or had been incorrectly used, that she made no effort before, during or after the *US v. Torney* matter to review these materials with NMS Labs. On the contrary, NMS Labs validation studies were the focus of a Special Assessment by ASCLD/LAB in April 2015 that verified the appropriate use of the PowerPlex® 16HS kit and the scientific grounding of our interpretation guidelines and policies (see Section 6 for additional details). It is inconceivable that if NMS Labs had misused the PowerPlex® 16HS kit as alleged by Ms. Ewing, that the Promega Corporation would continue to serve as a key supplier of DNA profiling chemistries to NMS Labs as well as a source of forensic applications trainings and technical support for our analysts.

Therefore, NMS Labs rejects the assertion that the PowerPlex® 16HS kit was "misused". Furthermore, NMS provides the following responses to the major points attributed to Ms. Ewing in Judge Dixon's order:

- NMS Labs did not interpret data (measured in RFU) outside of the linear range of the instrument. The validations studies conducted by NMS Labs clearly demonstrate the data were within the validated linear range of 40 to 7559 RFU (Table 2).

- The characteristics of the electropherograms (e.g., the presence and preponderance of non-specific amplification products and other uncharacterized artifacts and background instrument noise) cannot be used to assess proper DNA quantity for amplification, particularly when working with forensic casework samples. Forensic samples are of unknown origin, and may contain a multitude of unknown substances including PCR inhibitors/enhancers, chemical and/or environmental insults, and/or other factors which impact the efficiency of PCR amplification. While total DNA quantity can and will impact peak height amplitude (measured in RFUs), other factors may also contribute to profile variation. Furthermore, increases in total DNA quantity do not appear produce an increase in the amplification of non-target PCR artifacts. Rather, the same artifacts are reproducibly generated across a wide range of DNA concentrations.

- As demonstrated through our internal validation studies, stutter ratios are not artificially elevated by increases in the height of the source/parent peak within the linear range of the instrument. Since the source/parent peaks in the *US v. Torney* case did not exceed the upper bound limit of linearity, the validated stutter filters served as reliable means of assessing stutter artifacts for all loci.

- As demonstrated through our internal validation studies, the data in the *US v. Torney* matter remained below the validated upper limit of linearity as described in the laboratory's DNA interpretation guidelines (*i.e.*, 8100RFU in the raw data, or 7559 RFU in the processed data).

- As demonstrated through our internal validation studies, total DNA quantity does not appear to increase the amplification of non-target PCR products and other artifacts. Rather, these non-target amplification products and other peak-like artifacts are reproducible; readily identified across a wide range of DNA concentrations and generally characterized by peaks

that are off ladder and/or have poor morphology. As referenced in the laboratory's DNA interpretation guidelines, particular care should be taken to assess peak morphology and positioning when evaluating potential minor contributor peaks.

- While not published prior to the preliminary hearing, the difference between major and minor split peaks has in fact been published[27]. This phenomenon, which was recognized in the internal validation studies conducted by NMS Labs, was considered by NMS labs with regards to the interpretation of the questioned profile in the *US v. Torney* matter. The level of spectral correction noted near (but not above) the upper limit of linearity was not associated with a quantifiable increase in the stutter ratio.

- Given the nature of an unknown forensic sample which may include the presence of one or more contributors (male or female), the failure of the Investigator® Quantiplex HYres kit to indicate the potential presence of a low-level male contributor does not (and cannot) confirm the absence of a male donor. The Investigator® Quantiplex HYres kit is not without limits. As demonstrated by our internal validation studies on mock casework samples known to contain male DNA, the presence of high quantities of female DNA can result in a failure to detect low-level male DNA. It is not uncommon with sexual assault type samples for analysts to obtain interpretable profiles matching suspects even though the results of the quantitation assay failed to detect male DNA. The subsequent detection of a Y allele at the Amelogenin locus in the PowerPlex® 16HS data generated by NMS Labs supports the potential presence of one (or more) low level male contributor(s).

Summary: *NMS Labs has conducted extensive validation studies of the PowerPlex® 16HS kit. These studies were founded on the generally accepted recommendations of several professional groups in the relevant scientific community. These studies, the SOPs for the PowerPlex® 16HS kit and NMS Lab's DNA interpretation guidelines have undergone multiple external audits and were found to be in compliance with highest quality standards. NMS Labs adherence to the relevant SOP for set up of PowerPlex® 16HS amplification reactions was documented and reviewed. All performance parameters and the results from all control samples were found to comport with expected values observed during our internal validation studies. Accordingly, the assertion that NMS Labs "misused" the PowerPlex® 16HS is unfounded and lacks scientific merit.*

(3) Assertion that Laura Cronin Disagreed with NMS Interpretation of Data

NMS Labs rejects the notion that Ms. Cronin raised any concerns regarding the analyses conducted by the laboratory, or the subsequent interpretation of the data developed during the course of testing. Ms. Cronin did not testify in the case, nor was an affidavit she prepared, and which was relied on by Mr. Ambrosino in his argument, ever provided to NMS Labs. As an ASCLD/LAB-*International* accredited laboratory, NMS Labs recognizes the critical importance of impartial and independent review of all analytical results associated with forensic casework. Referencing the ISO 17025 standard, it reads as follows:

"4.1.5 The laboratory shall

[27] Molecular Diagnostics 3rd E 2017 Chpt 21 Molecular Diagnostic Applications in Forensic Science, page 383

b) have arrangements to ensure that its management and personnel are free from any undue internal and external commercial, financial, and other pressures and influences that may adversely affect the quality of their work;

d) have policies and procedures to avoid involvement in any activities that would diminish confidence in its competence, impartiality, judgement or operations integrity;"

NMS Labs maintains such procedures[28] to address disagreements between an analyst and a technical reviewer without undue influence. While such conflicts are rare, these procedures provide the requisite support necessary to ensure that any technical/scientific disparities can be resolved without repercussion. Ultimately, the identification and resolution of such concerns is documented within the bench notes for future reference and proper procedural continuity. In the event that the reviewer does not agree with the resolution, the case record is transferred to the DNA Technical leader and often to another qualified reviewer. In the *US v. Torney* case, Ms. Cronin was the technical reviewer of all of the analytical case records (*i.e.*, Forensic DNA Analysis Cover & Controls Sheets, STR Interpretation Worksheets, and Autosomal STR Results: PowerPlex® 16HS Worksheet). Furthermore, she was also the technical and administrative reviewer of the entire case record (*i.e.*, Case Folder Contents and Review Sheet A and B)[29] and the final report[30]. As indicated by her signature on these documents, Ms. Cronin was in agreement with the analyst of record in this case, including the conclusions contained within the report dated 03/18/13. Had Ms. Cronin disagreed with the interpretation of the profile in question, Ms. Cronin could have readily removed herself as the reviewer without repercussion. Ms. Cronin's signature on these case records, and the absence of any clarifying notes in the case file, refutes the allegation that Ms. Cronin didn't agree with the interpretation rendered.

Summary: *NMS Labs rejects the notion that Ms. Cronin raised any concerns regarding the analyses conducted by the laboratory, or the subsequent interpretation of the data developed during the course of testing. In accordance with ISO 17025 standard 4.1.5, NMS Labs maintains procedures to address disagreements between an analyst and a technical reviewer without undue influence or repercussions. Ms. Cronin's signature on all case records, and the absence of any clarifying notes in the case file, refutes the allegation that Ms. Cronin didn't agree with the interpretation rendered.*

(4) Judge Dixon's Order and Documentation Provided to ASCLD/LAB:

Upon receipt of Judge Dixon's order in 2015, NMS Labs took immediate action with our accrediting body, ASCLD/LAB, and requested an immediate audit by a qualified DNA expert. NMS Labs' analytical procedures, interpretation guidelines, internal validation studies, and data analysis referenced in the order by Judge Dixon were subject to review. These files were provided to ASCLD/LAB, along with all other records requested during the course of the audit. The files were transferred to ASCLD/LAB via DropBox, and the Criminalistics Laboratory Director was made available to answer questions via email and

[28] NMS Labs SOP 09-022, "Forensic Biology Procedure Manual", Section 5.9 Assuring the quality of test results; NMS Labs SOP 09-035 "Case Documentation and Review Practices", Section D. Case Review, subsection 1e; and NMS Labs SOP 09-055 "Quality Assurance Policy Manual", Section 4.1, subheading "NMS Labs Criminalistics Department Functional Responsibilities"

[29] NMS Labs supporting documentation of Technical and Administrative review of WO# 13001065

[30] NMS Labs Forensic Biology Report, dated 03/18/13, bearing the signature of Ms. Laura M. Cronin.

telephonically. ASCLD/LAB, including the Board of Directors, were in possession of Judge Dixon's order, and used it in their evaluation of the final audit report. The assessor selected by ASCLD/LAB (Allison Y. Eastman, PhD) has more than 20 years of forensic DNA experience and has served on multiple SWGDAM subcommittees including the DNA Mixture Interpretation Subcommittee. She also serves as a member of the New York State Commission on Forensic Science DNA Subcommittee and the National DNA Indexing System (NDIS) Audit Review Panel. The results of the Special Assessment that she conducted, including reference to validations, methods, and SOPs reviewed, are documented in full within ASCLD/LAB Special Assessment Report provided[31].

Summary: *Upon receipt of Judge Dixon's order in 2015, NMS Labs took immediate action with our accrediting body, ASCLD/LAB, and requested an immediate audit of NMS Labs' analytical procedures, interpretation guidelines, internal validation studies, data analysis by a qualified DNA expert. The results of the Special Assessment that she conducted, including reference to validations, methods, and SOPs reviewed, are documented in full within ASCLD/LAB Special Assessment Report provided.*

(5) Reports, Including Amended Report Issued by NMS Labs:

NMS Labs' recognizes the uncertainty associated with the interpretation of mixtures and peaks in stutter positions. Our DNA Interpretation Guidelines and Policies on this matter are clear that, in the context of a mixture, a peak in a stutter position may be a stutter peak; a true allelic peak; or indistinguishable as either a stutter or an allelic peak. Judge Dixon, however, expressed some confusion during the *in limine* hearing with regard to the uncertainty associated with the interpretation of challenging samples, statements of exclusion and the reflection of that uncertainty in the reporting language used by NMS labs. In an effort to address these concerns, NMS Labs elected to issue an amended report which emphasized the possibility for multiple hypotheses as to the number of potential contributors to this sample and the inherent limitations of statements of exclusion.

The first report[32] was issued on 3/18/13 and the amended report[33], which supersedes the original report, was later issued on 07/03/14. The changes between the original and amended reports were isolated to the sections for Item 2.2 Anorectal swab. In brief, the language in the report was changed from "*The sample produced a DNA profile presenting a mixture of a least three contributors*" to "*The sampled produced a mixed DNA profile consistent with one major and one or more minor contributor(s)*". A second section was changed from "[redacted] *and Cardell Torney is/are excluded as a minor-source contributor(s) to this mixed profile*" to "*Based on the available genetic information, no inculpatory statements regarding the minor component can be made at this time*" followed by "*No further conclusions should be drawn at this time*".

Summary: *Judge Dixon expressed some confusion during the in limine hearing with regard to the uncertainty associated with the interpretation of challenging samples, statements of exclusion and the reporting language used by NMS labs. In an effort to address these concerns, NMS Labs elected to issue an amended report which sought to highlight the inherent limitations of statements of exclusion and the fact that multiple hypotheses could exist with respect to the number of potential contributors.*

[31] ASCLD/LAB *International,* Special Assessment Report, NMS Labs Criminalistics Laboratory, 04/06/2015
[32] NMS Labs Forensic Biology Report, dated 03/18/13
[33] NMS Labs Forensic Biology Amended Report, dated 07/03/14

(6) Additional Independent Special Assessment by ASCLD/LAB:

NMS Labs' has a well-documented history of providing forensic testing services that meet the highest of quality standards. It is, therefore, important to us demonstrate the principle that we are fully committed to the consistent delivery of scientific excellence. It is for this reason that in addition to an internal quality review in this matter, the Director of Criminalistics also asked ASCLD/LAB to perform an independent audit to the auditable standards of the FBI's 2011 Quality Assurance Standards for DNA Testing Laboratories as well as the recommendations of both SWGDAM[34] and ENFSI[35]. ASCLD/LAB was requested to assess the following methods and/or procedures employed by NMS Labs that were raised in Judge Dixon's order. Specifically, these were to:

- Review and assess the internal validation studies in support of the SOPs used by NMS Labs for the Investigator® Quantiplex HYres kit.
- Review and assess the internal validation studies conducted by NMS Labs of the Investigator® Quantiplex HYres kit including known and non-probative casework type/mock evidence samples, reproducibility and precision, sensitivity studies, mixture studies, and contamination audit – including documentation and summary reports.
- Review and assess the internal validation studies in support of the SOPs used by NMS Labs for the PowerPlex® 16HS chemistry.
- Review and assess the validation studies conducted by NMS Labs for the PowerPlex® 16HS chemistry including known and non-probative casework type/mock evidence samples, reproducibility and precision, sensitivity and thresholds (analytical and stochastic), signal detection linearity and DNA input linearity, dynamic range for peak interpretation, stutter thresholds within the interpretable detection range, mixture studies, and contamination assessments – including documentation and summary reports.
- Review and assess the procedure for DNA interpretation[36] employed by NMS Labs for the PowerPlex® 16HS kit, reflecting the data obtained through internal validation prior to use in forensic casework. Specifically, this includes valid procedures to address stutter interpretation in mixed DNA profiles – particularly in the cases where minor contributors may be present; handling of off-scale data; reporting language to address uncertainty of conclusions, especially exclusions (to include associated addendum notes in reporting).

The validation studies, interpretation guidelines, and analytical procedures – including those in place at the time of the testing referenced in Judge Dixon's order – were found to meet the highest international standards for forensic science. The conclusion section of the Special Assessment report, which summarizes the salient findings of the assessor, states:

> *"The Laboratory's validation studies were well planned and summarized, and the summaries were traceable back to the original data. The studies were well thought out and carefully*

[34] Scientific Working Group on DNA Analysis Methods (http://www.swgdam.org/)
[35] European Network of Forensic Science Institutes (http://www.enfsi.eu/)
[36] NMS CR-916 "DNA INTERPRETATION GUIDELINES AND POLICIES" SOP

evaluated, particularly the more detailed and complex studies conducted on PowerPlex® 16HS kit including linearity, stochastic behavior, heterozygote peak balance, and stutter variation. These and other studies conducted by the lab provided a foundation for developing a sound protocol for interpreting mixed DNA profiles and establishing limits to conclusions that can be drawn from the data. It was clear that trends observed in the validation studies translated to improvements and/or adjustments to the laboratory SOPs. The validation studies and laboratory SOPs follow guidelines recommended by experts from the forensic community, were (and continue to be) subjected to external review by qualified auditors/assessors, and conform to all standards and requirements for accreditation by ASCLD/LAB-International."

These conclusions, which summarize over eight pages of detailed audit results, underscore our position that NMS Labs was, at the time of testing in the *US v. Torney* matter, and continues today to be fully compliant with the highest quality performance standards of the forensic science community. Our staff members are actively involved in the quality community and serve on some of the forensic science community's highest standards organizations.

Scope of the Special Assessment by ASCLD/LAB – After obtaining a copy of the order issued by Judge Dixon, the Criminalistics Laboratory Director contacted Director John Neuner with ASCLD/LAB to discuss the findings of the court and my desire for an independent audit. In accordance with this discussion, emphasis was placed on the auditable standards which apply to the critical points raised in the order, and the suitability of these methods for forensic DNA casework. A copy of the original letter requesting an audit by ASCLD/LAB is attached to the *ASCLD/LAB Special Assessment Report*. While ASCLD/LAB used Judge Dixon's order to evaluate the suitability of the audit, ASCLD/LAB did not audit any casework. All of the validation studies, methods and procedures, and reporting practices employed by NMS Labs were reviewed and found to comport with the applicable standards for forensic DNA testing. We have always maintained that NMS Labs adhered to the validated and approved protocols which were referenced in Judge Dixon's order, and that those SOPs comport to the highest quality standards.

NMS Labs stands by the scientific and forensic defensibility of its results in *US v. Torney*, and the validity of the analytical procedures in place at the time, and in place today. Our track record with ASCLD/LAB, including the *Special Assessment* we requested from our accrediting body support this position. At the request of the Texas Forensic Science Commission, NMS Labs would welcome the opportunity for an independent qualified expert to audit the case record, including the interpretation of data and test reports, to the SOPs employed by NMS Labs. This, of course, includes all of the validation studies, data analysis, and summary reports used in the development of those SOPs.

Audit History Prior to Special Assessment by ASCLD/LAB and Dissemination of Results – The Forensic Biology department at NMS Labs was subject to a full audit by ASCLD/LAB to the FBI Quality Assurance Standards for Forensic Testing Laboratories (QAS) in December of 2014. The results of that audit, which includes the review of forensic casework, supported the suitability of the methods and SOPs employed before, during, and after the testing in the *US v. Torney* matter.

NMS Labs is routinely audited by representatives from the National DNA Index System (NDIS) participating laboratories for the purpose of uploading profiles generated by NMS Labs into the Combined DNA Index System (CODIS). NMS Labs has participated in those types of audits since 2013. Following the *Special Assessment* by ASCLD/LAB in March 2015, the Forensic Biology department was subject to a required QAS

audit by a representative from the Texas Department of Public Safety (TXDPS). The scope of that audit was specific to Standard 17 of the QAS document. The TXDPS audit was to assess the suitability of the validation studies, methods, and SOPs employed by NMS Labs in forensic DNA casework for the upload of profiles into CODIS by TXDPS. Given the specific scope of the audit conducted by TXDPS, the only pertinent documentation that was subject to review was the full QAS audit conducted in December of 2014 (or similar audits conducted previously or as requested by the TXDPS auditor). Similar to other auditing functions conducted by ASCLD/LAB (*i.e.* serology or reference to non-auditable guidelines like those published by SWGDAM and ISFG which are considered best practices by those organizations), the Special Assessment we requested would not have been subject to review. Should the Commission desire, NMS Labs would be pleased to furnish the results of those audits/reviews to the TXDPS.

Summary: *NMS Labs' has a well-documented history of providing forensic testing services that meet the highest of quality standards. It is for this reason ASCLD/LAB was asked to perform an independent audit to the auditable standards of the FBI's 2011 Quality Assurance Standards for DNA Testing Laboratories. The validation studies, interpretation guidelines, and analytical procedures – including those in place at the time of the testing referenced in Judge Dixon's order – were found to meet the highest international standards for forensic science. NMS Labs stands by the scientific and forensic defensibility of its results in US v. Torney, and the validity of the analytical procedures in place at the time, and in place today. Our track record with ASCLD/LAB, including the Special Assessment we requested from our accrediting body support this position.*

(7) NMS Labs' Position on Quality in Forensic Science:

For more than 40 years, NMS Labs has demonstrated an unwavering commitment to providing our clients with the highest quality of laboratory testing and expert services. We do this with integrity, accuracy, and a keen awareness of the continuous advances in forensic science and the evolving legal and scientific standards that govern this field. It is for this reason, that NMS Labs rejects as scientifically unfounded the opinions contained in Judge Dixon's order rendered in connection with DNA analyses performed by NMS Labs in 2013.

True to our history, NMS Labs employs internationally recognized scientific experts and board-certified forensic practitioners to ensure that our test methods, interpretations, and laboratory reports are driven by science and grounded in rigorous validation. Our work is fully compliant with the most current recommendations of the forensic community, including SWGDAM, ENFSI, ISFG and the Federal Bureau of Investigation's Quality Assurance Standards for Forensic DNA Testing Laboratories. For this reason, NMS Lab's test results are routinely admitted as evidence without challenge in criminal proceedings across the United States and around the world.

NMS Labs has a long history of participation in voluntary laboratory accreditation and licensure programs to ensure that our laboratory consistently meets or exceeds the highest standards of excellence in forensic testing. In support of these claims, we note the following:

- NMS Labs is the only independent forensic facility in the nation to be certified by both ASCLD/LAB-*International* (American Society of Crime Laboratory Directors/Laboratory Accreditation Board) and the ABFT (American Board of Forensic Toxicology). NMS Labs has diligently maintained these certifications in good standing since 2003 and 2005, respectively.

- NMS Labs is assessed annually by trained experts from recognized accreditation bodies including ABFT, ASCLD/LAB, and ANSI FQS. Our successful performance in these audits and continuous accreditation underscore the scientific rigor employed in our methods and reporting.

- NMS Labs has successfully completed five external audits to the FBI Quality Assurance Standards for DNA Testing Laboratories since 2009. These rigorous and thorough inspections were conducted by laboratory technical leaders, independent forensic scientists and forensic examiners from the FBI. This openness to external review and scrutiny demonstrates our sustained commitment to quality and scientific rigor.

- NMS Labs has successfully completed six external audits to the FBI Quality Assurance Standards for the purposes of Combined DNA Index System (CODIS) entry since 2013. These inspections were conducted by experts from National DNA Index System (NDIS) participating laboratories.

- The methods employed by NMS Labs Forensic Biology Department have undergone thorough internal validations that meet or exceed the 2011 FBI Quality Assurance Standards for DNA Testing Laboratories; the 2012 SWGDAM Validation Guidelines for DNA Analysis Methods, and the recommendations of the 2010 ENFSI DNA Working Group.

- The validations of all fourteen of the DNA analysis chemistries employed by NMS Labs for human identity testing fully adhere to the recognized standards of the scientific community. Repeated external reviews by forensic experts and the aforementioned auditors found NMS Labs' methods to be scientifically sound and reliable. In fact, multiple auditors have complemented the scientific rigor of our validation work.

- In accordance with ASCLD/LAB accreditation standards, NMS methods are subject to annual review. Since 2012, the NMS Forensic Biology "DNA Interpretation Guidelines and Policies" have been updated to comport with evolving standards in the scientific community and data from internal validation.

- NMS Labs participates in semi-annual proficiency testing through the Collaborative Testing Services (CTS) forensic proficiency test program. Since 2012, NMS Labs' Forensic Biology scientists have participated in more than 30 external proficiency tests with a perfect track record for quality.

- NMS Labs actively contributes to advancing forensic science. The Forensic Biology staff at NMS Labs have authored ten papers in internationally recognized peer-reviewed forensic journals and; presented more than 70 posters/presentations on training, method development, validation, and data interpretation at national/international meetings.

- As the former DNA Technical Leader, Britton Morin is a recognized forensic geneticist with more than ten years of case working experience. Ms. Morin came to NMS Labs after having served as a case working analyst at the New York Office of the Chief Medical Examiner's (OCME). Ms Morin has presented her findings in local, state, and federal Courts, and has never been disqualified as an expert in any court. As a DNA expert, Ms. Morin is also an active contributor to the quality community and has served as a DNA Technical Assessor for ASCLD/LAB.

- As science advisor, Dr. Phillip Danielson is an internationally recognized scientist with 25 years of experience in molecular and forensic biology. He is a member in good standing of the Biology/DNA Scientific Area Committee within the Organization of Scientific Area Committees (OSAC). The OSAC is a joint initiative of the National Institute of Standards and Technology and the U.S. Department of Justice that supports the development of national forensic science standards and guidelines. Dr. Danielson focuses on standards related to forensic laboratory DNA analysis methods and DNA profile interpretation. Dr. Danielson also served as science advisor to the National Law Enforcement and Corrections Technology Center-Rocky Mountain and as a National Institute of Justice reviewer for the Forensic DNA Research and Development program; the Applied Research and Development in Forensic Science for Criminal Justice Purposes program; the Solving Cold Cases with DNA program; the Forensic Science Technology Center of Excellence program and; the Coverdell Laboratory Improvement program. Dr. Danielson is routinely called on to present his expert opinion on complex forensic testing in court proceedings, and has never been disqualified as an expert in any court.

- As Laboratory Director, Dr. Christian G. Westring is an internationally recognized forensic geneticist with over 14 years of experience in forensic and molecular biology. Dr. Westring has held multiple positions throughout his career from bench scientist to Laboratory Director. As the former DNA Technical Leader in multiple laboratories, Dr. Westring has a broad understanding of the science behind human identity testing. He has presented his findings in local, state, and federal Courts, and has never been disqualified or disallowed as an expert in any court. Dr. Westring is an active contributor to the forensic community. He serves on the ASCLD Board of Directors where he has served as the Chair for the Ethics and Bylaws Committee and currently serves as the Chair of the International Committee. Dr. Westring has also served as a DNA Technical Assessor with ASCLD/LAB. He is also a member in good standing with the NIST OSAC DNA Analysis 2 Subcommittee (DNA Interpretation). Dr. Westring's specific focus is on developing standards and guidelines related to forensic laboratory DNA interpretation, including terminology, mixture analysis, and acceptable practices for calculating the weight of DNA evidence. He currently serves as Chair of the Thresholds Task Group where his focus is on developing standards, guidelines and best practices for the application of analytical and stochastic thresholds to DNA interpretation.

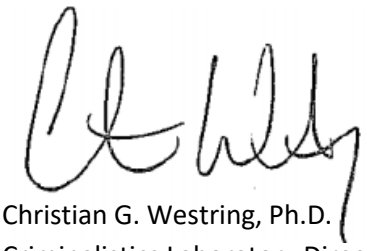
- As Vice President of Forensic Science Services at NMS Labs, Dr. Barry K. Logan is an American Board of Forensic Toxicologists (ABFT) Certified forensic toxicologist with more than 30 years of experience, and over 100 peer reviewed publications in the field of alcohol and drug impaired driving, and death investigation toxicology. Dr. Logan has had the unique privilege of serving as the President of the American Academy of Forensic Sciences (AAFS) in 2014, and has previously served as one of sixteen members of the NIST Forensic Science Standards Board (FSSB) which oversees the entire OSAC process. In addition to his service to the Academy, Dr. Logan is a member of several professional organizations in forensic science including the Society of Forensic Toxicologists, The American Society of Crime Laboratory Directors, The International Council on Alcohol, Drugs and Traffic Safety, and the Canadian Society of Forensic Sciences, and currently serves on the Transportation Research Board of the National Academies.

Given our well-documented history of providing forensic testing services that meet the highest quality standards, including key casework contributions to the courts of the state of Texas, and the recognized

experts which we employ, we want to emphasize that NMS Labs is committed to the continued delivery of scientific excellence. Our position – which is grounded in hard science – does not waver. Although we have no legal standing to appeal Judge Dixon's rulings in the *US v. Torney* case, we completely dispute the alleged scientific basis of that ruling. The results of the Special Assessment conducted by ASCLD/LAB in April of 2015, and those prior to and afterwards support this position.

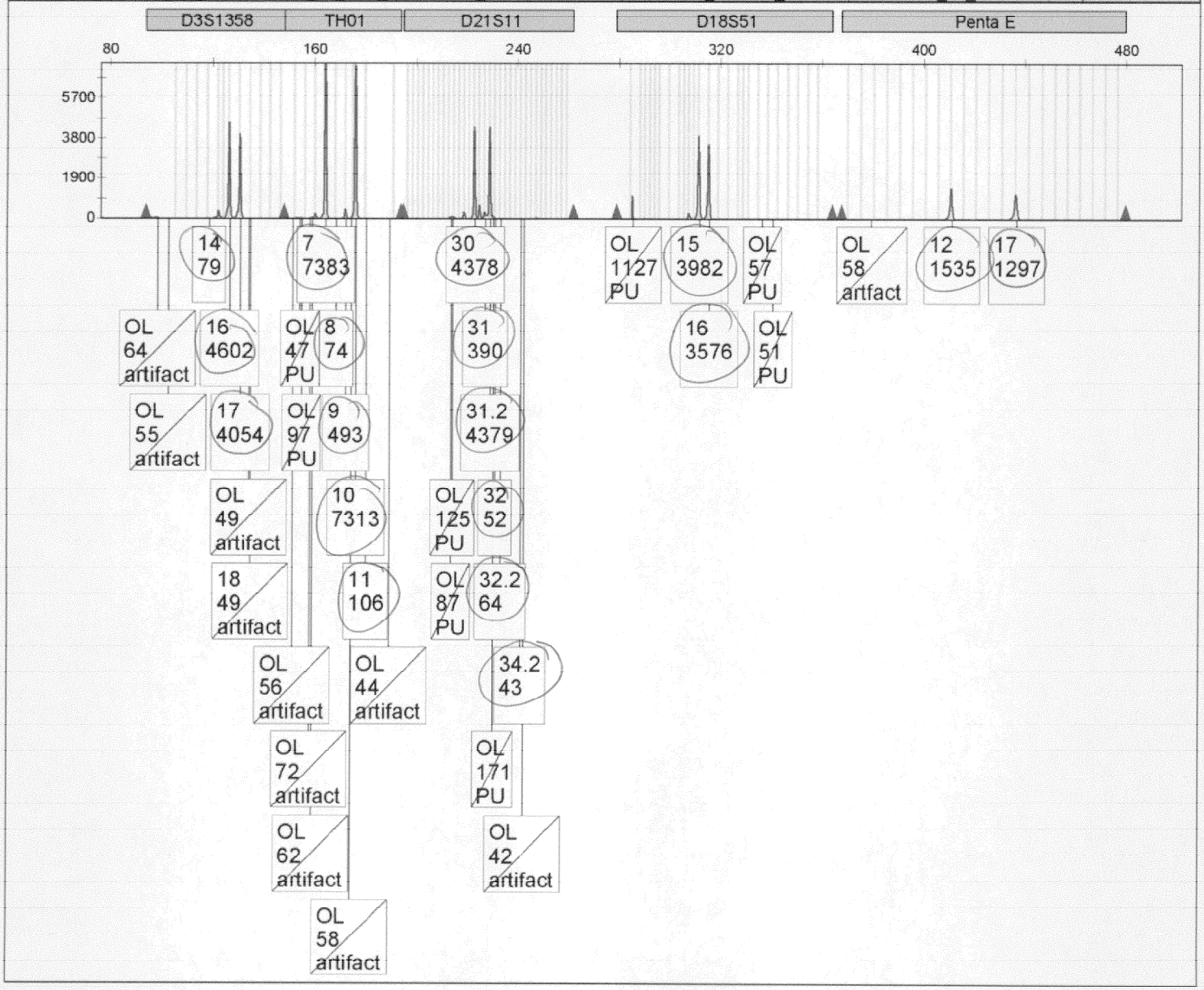
We have an unwavering commitment to the scientific integrity of our work and an objective, unbiased approach to forensic biology casework, serving the prosecution and defense alike. If you require additional information or if I can be of further assistance, please do not hesitate to ask.

Respectfully,



Christian G. Westring, Ph.D.
Criminalistics Laboratory Director
christian.westring@NMSLABS.COM

Sample File	Sample Name	Panel	SQO	SQ
13001065_02.2-1A_HS_20130312CA_JF_C03_2013-03-12_09-17-25.fsa	13001065_02.2-1A_HS	PowerPlex_16_v2.0	X	



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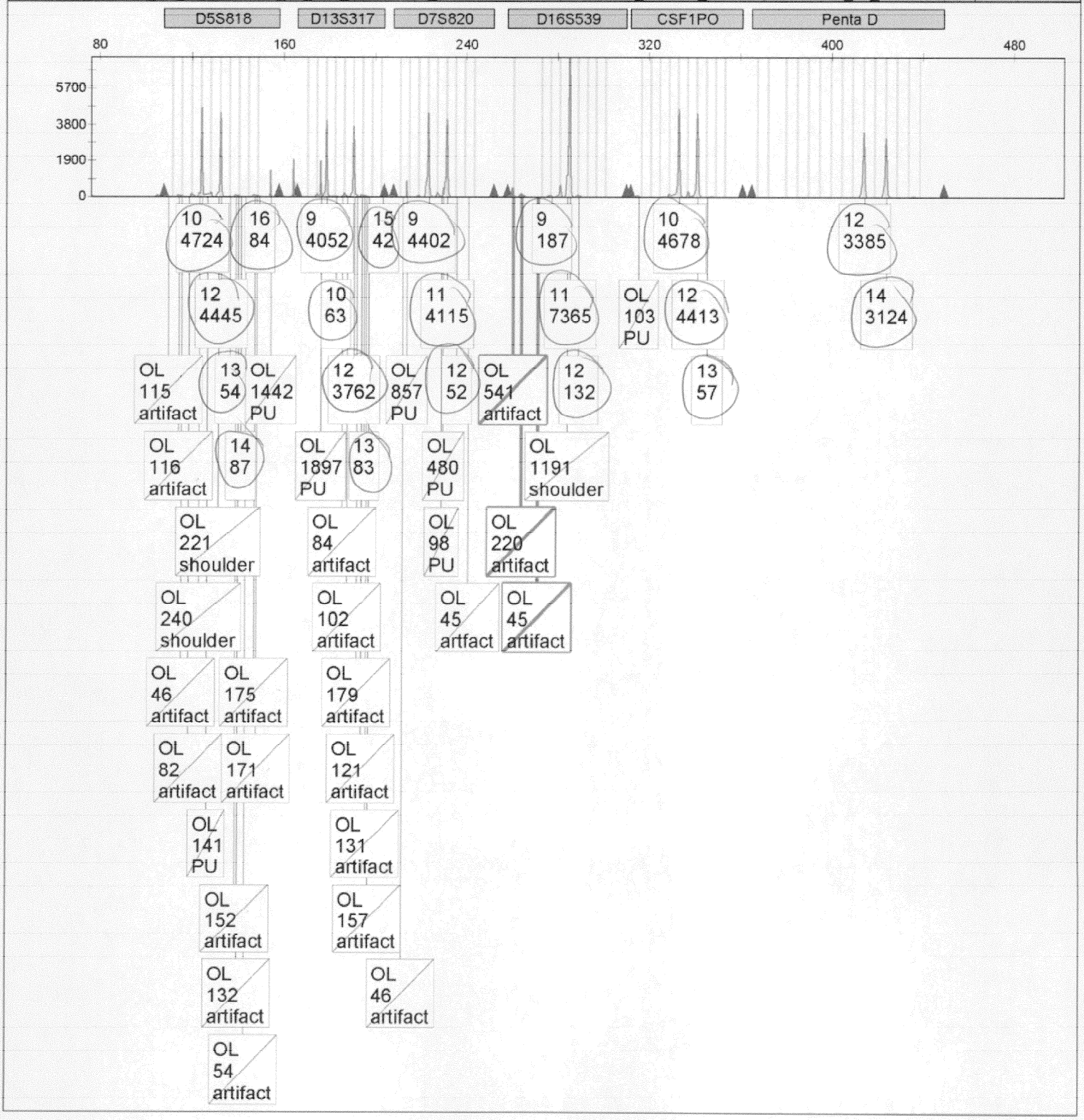
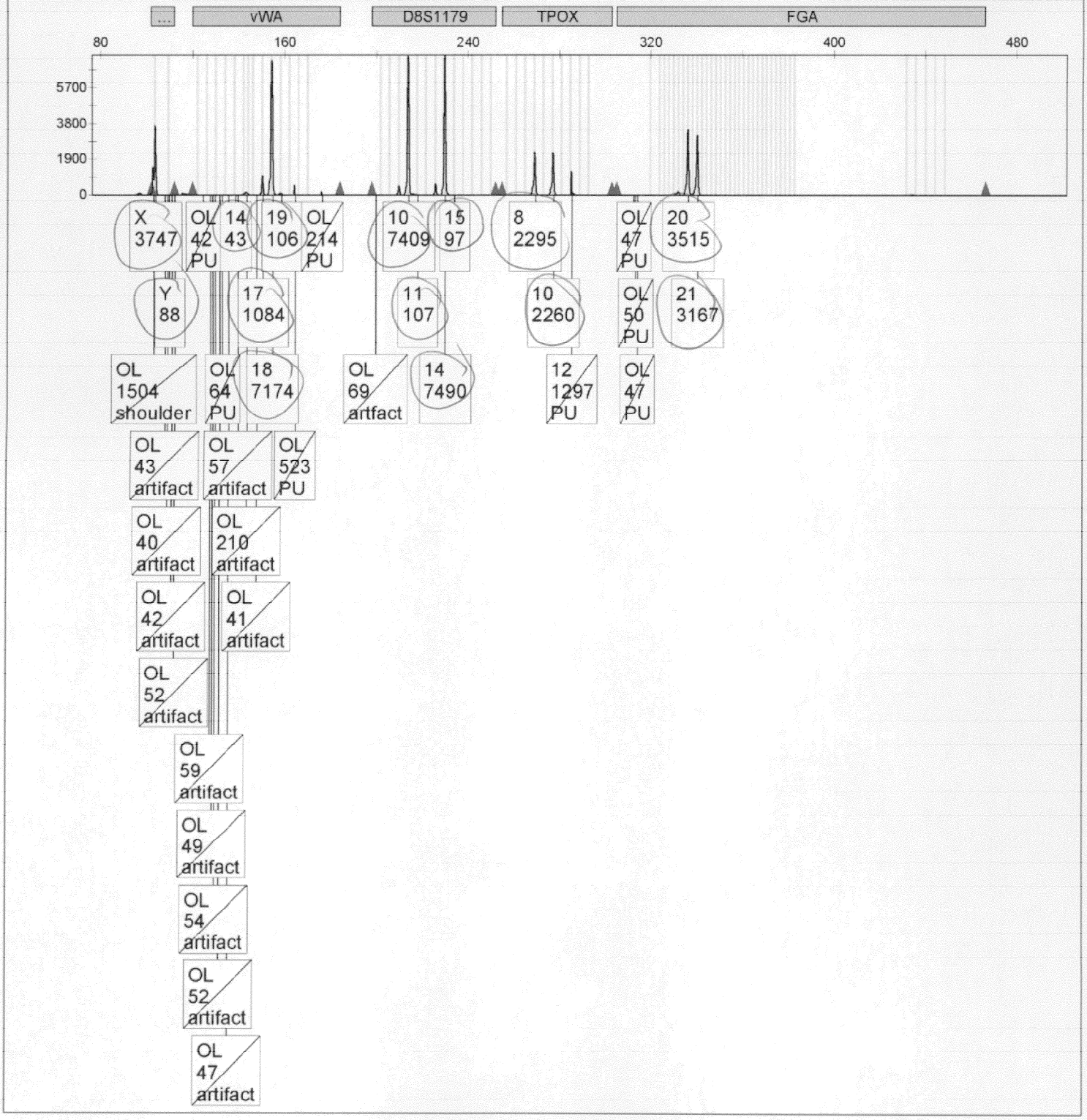
20130113

Sample File	Sample Name	Panel	SQO	SQ
13001065_02.2-1A_HS_20130312CA_JF_C03_2013-03-12_09-17-25.fsa	13001065_02.2-1A_HS	PowerPlex_16_v2.0		



40

Sample File	Sample Name	Panel	SQO	SQ
13001065_02.2-1A_HS_20130312CA_JF_C03_2013-03-12_09-17-25.fsa	13001065_02.2-1A_HS	PowerPlex_16_v2.0		



41

Missing Alleles	Hand calculated stutter %	Manufacturer Stutter %
CSF - 1000PG_2_HS_HSVal_080612_CA_H03_2012-08-07_01-08-55.fsa	12%; 11 at 854; 12 at 7136	10%
CSF - 2000PG_1_HS_HSVal_080612_CA_B03_2012-08-06_22-57-44.fsa	19.6%, 11 at 1329; 12 at 6783	10%
D5 - 2000PG_1_HS_HSVal_080612_CA_B03_2012-08-06_22-57-44.fsa	13.7%, 11 at 974; 12 at 7108	11%
CSF - 2000PG_2_HS_HSVal_080612_CA_C03_2012-08-06_22-14-09.fsa	11%, 11 at 799; 12 at 7244	10%
CSF - 2000PG_2_HS_HSVal_080612_CA_C03_2012-08-06_22-57-44.fsa	22.6%, 11 at 1515; 12 at 6700	10%
D16 - 2000PG_2_HS_HSVal_080612_CA_C03_2012-08-06_22-57-44.fsa	14.2%, 12 at 1057; 13 at 7446	13%
D5 - 2000PG_2_HS_HSVal_080612_CA_C03_2012-08-06_22-57-44.fsa	13.8%, 11 at 985; 12 at 7129	11%
CSF - 2000PG_4_HS_HSVal_080612_CA_E03_2012-08-07_01-08-55.fsa	19%, 11 at 1300; 12 at 6722	10%
D16 - 2000PG_4_HS_HSVal_080612_CA_E03_2012-08-07_01-08-55.fsa	13.9%, 12 at 1005; 13 at 7230	13%
D5 - 2000PG_4_HS_HSVal_080612_CA_E03_2012-08-07_01-08-55.fsa	14.3%, 11 at 1003; 12 at 7011	11%

Missing Stutter Study Data

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Scott Taliaferro
Assistant District Attorney
Chief, Appellate Section
Travis County District Attorney's Office
P.O. Box 1748
Austin, TX 78767

Date: 08/03/2017
Re: NMS Labs testing in *United States of America v. Cardell Torney*
Cc: District Attorney Margaret Moore

Dear Mr. Taliaferro:

You have brought to our attention an order by Federal Judge Herbert B. Dixon in the District of Columbia, regarding the admissibility of results of DNA testing performed by NMS Labs' Forensic Biology Department. In the order, Judge Dixon suppressed the results of tests performed in 2013 by NMS labs, citing non-compliance with accreditation quality standards. Given the language in the order, we understand that you may have some concerns that merit further discussion. NMS labs had a similar response when we were first presented with the order, and as a result, took immediate action with our accrediting body in 2015. I am writing to provide you a summary of the results of the 2015 ASCLD/LAB[1] audit requested by NMS Labs in response to the ruling by Judge Dixon in the matter of the US v. Cardell Torney.

We requested that ASCLD-LAB perform an independent assessment of the methods, interpretation protocols and the validation data employed by NMS Labs (including those in place at the time of the testing in dispute before Judge Dixon) to FBI's Quality Assurance Standards for DNA Testing Laboratories. The audit was conducted between March 5, 2015 and April 5, 2015.

The validation studies, interpretation guidelines, and analytical procedures – including those in place at the time of the testing in dispute before Judge Dixon – were found to meet the highest international standards for forensic science, including the recommendations of both SWGDAM[2] and ENFSI[3].

The conclusion section of the audit report, which summarizes the salient findings of the auditor, states:

> *"The Laboratory's validation studies were well planned and summarized, and the summaries were traceable back to the original data. The studies were well thought out and carefully evaluated, particularly the more detailed and complex studies conducted on PowerPlex® 16 HS kit including linearity, stochastic behavior, heterozygote peak balance, and stutter variation. These and other*

[1] American Society of Crime Laboratory Directors / Laboratory Accreditation Board (http://www.ascld-lab.org/)
[2] Scientific Working Group on DNA Analysis Methods (http://www.swgdam.org/)
[3] European Network of Forensic Science Institutes (http://www.enfsi.eu/)

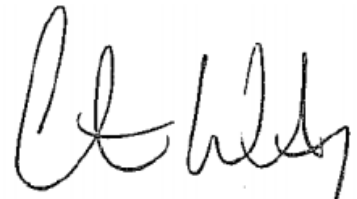
studies conducted by the lab provided a foundation for developing a sound protocol for interpreting mixed DNA profiles and establishing limits to conclusions that can be drawn from the data. It was clear that trends observed in the validation studies translated to improvements and/or adjustments to the laboratory SOPs. The validation studies and laboratory SOPs follow guidelines recommended by experts from the forensic community, were (and continue to be) subjected to external review by qualified auditors/assessors, and conform to all standards and requirements for accreditation by ASCLD/LAB-International."

These conclusions, which summarize over eight pages of detailed audit results, underscore our position that NMS Labs was and continues to be fully compliant with the highest quality performance standards of the forensic science community. The findings of the audit reflects our continued commitment quality. Our internationally recognized scientists are actively involved in both the quality and leadership community, and serve on some of the forensic science community's highest standards organizations.

We are commitment to the scientific integrity of our work. With more than a 15-year track record in DNA testing, our methods have been subject to repeated independent audits. Through this voluntary process, we have maintained compliance with the highest quality standards for forensic DNA analysis. NMS Labs Forensic Biology Department has been continuously accredited by ASCLD/LAB since 2003. On April 17, 2015, the ASCLD/LAB Board voted to reaccredit our laboratory to a new 4-year cycle under ASCLD/LAB *International* (ISO17025). NMS Labs has never had its accreditations suspended or revoked, and has never lost or failed to obtain any accreditation for which it has applied.

On behalf of NMS Labs, we look forward to furthering a productive relationship that benefits the criminal justice community and the citizens of Texas. We would welcome the opportunity to meet you and your staff to discuss the specifics of this matter.

Respectfully,



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Lynn Robitaille Garcia
General Counsel
Texas Forensic Science Commission
1700 North Congress, Suite 445
Austin, Texas 78701

Date: February 14th, 2018
Re: NMS Labs testing in *United States of America v. Cardell Torney*
NMS Labs WO#13001065

Dear Ms. Garcia:

I am writing with some additional information following on from the February 2nd, 2018 hearing of the Commission, based on our current understanding of the Commission's concerns, issues raised by stakeholders present at the hearing, and additional internal review with our consultant Dr. Charlotte Word.

In addition to the actions identified in our prior correspondence, I wanted to let you know of the scope of work I have developed with Dr. Word and to solicit any additional recommendations from the review panel as we move proactively to address the Commission's concerns. She and I will be meeting during the AAFS meeting next week to review this list and schedule the various reviews.

Our staff is currently identifying all DNA cases originating in Texas between 2010 and 2018 (the period of Dr. Westring's tenure with NMS Labs) for inclusion in the case reviews discussed below.

Dr. Word has been provided with a copy of all the materials previously provided to the Commission, including our correspondence with the Commission and recordings of the two Commission hearings, and has been actively reviewing these materials. She will participate in a three-day preliminary on-site visit at our Willow Grove facility scheduled for February 28th through March 2nd.

Dr. Word is currently tasked with the following tasks as part of her review:

- An independent root cause analysis on why the overblown *Torney* profile was interpreted, including any issues with NMS Labs' SOP's, training on interpretation of analytical data, and policies and practices around dilution and reinjection versus re-amplification and reanalysis.
- An independent review of NMS Labs' policies and training on resolving disputes between analysts and reviewers.
- An assessment of NMS Labs' recently amended SOP's related to the above issues.
- A review of the corrective action (CAPA) resulting from the *Torney* case performed by Dr. Westring and Ms. Aliece Watts, NMS Labs Quality Auditor, intended to address the above issues.
- A plan for the review of a representative number of NMS Labs DNA cases (to include all NMS Labs Texas cases involving DNA analysis) will be reviewed to determine whether the issues identified above (interpretation of overblown data or overruling of an analyst's opinion) have had any systematic impact on NMS Labs' DNA casework.
    - Oversee and perform review of these cases, with assistance from other reviewers as required.
- A plan for the independent review of NMS Labs SOP's on method validation, and review of selected validations and studies performed under those SOP's, including:
    - The NMS Labs "Stutter Study" identified by the Commission in which the panel raised concerns about the exclusion of certain data from the calculations.
    - The NMS Labs Promega HS16 validation studies (specifically the sensitivity and mixture studies with attention to the analytical threshold determination), with respect to the issues raised in the statement by Margaret Ewing of Promega in the *Torney* case.
    - Review of other NMS Labs validation studies as deemed appropriate.
    - Review of any calculations, calculators, or SOP's developed on behalf of NMS labs by external consultants.
- Additional training or retraining for staff as needed on any of the above issues, or other matters arising.

Dr. Word also has broad latitude to review or make recommendations on any other matters arising during her review.

As we are eager to address proactively the Commissions concerns as rapidly as possible, I would appreciate you bringing to my attention any other items not included in the above scope.

NMS Labs is committed to this open and transparent review and remediation of this complaint and welcomes further input from the Commission during this period of review.

Sincerely

Barry K Logan PhD, F-ABFT
Laboratory Director, NMS Labs Criminalistics/IFS
Senior Vice President, Forensic Science Initiatives, Chief Scientist
NMS Labs

Cc: Dr. Charlotte Word, Consultant
Ms. Aliece Watts, NMS Labs QA
Dr. Heather Degnan, NMS Labs Forensic Biology Supervisor
Ms. Kristen Smith, NMS Labs DNA Technical Leader

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Lynn Robitaille Garcia
General Counsel
Texas Forensic Science Commission
1700 North Congress, Suite 445
Austin, Texas 78701

Date: March 25th, 2018
Re: NMS Labs testing in *United States of America v. Cardell Torney*
NMS Labs WO#13001065

Dear Ms. Garcia:

I am writing with some additional follow up information for the Commission on progress on our review of the matter in the above referenced case, and to alert you to the disclosure of additional matters arising from that review.

Following my appearance at the Texas Forensic Science Commission meeting on February 2nd, 2018, NMS Labs initiated the process of review of the issues identified by the Commission in consultation with our retained expert Dr. Charlotte Word. Dr. Word spent three days onsite at NMS labs, had unlimited access to our staff, records and operating documents. She performed multiple areas of review referenced in our prior correspondence; the attachment to this letter represents a report of the status of those reviews, additional matters under review, and ongoing remediation of the associated findings. A return visit by Dr. Word is planned for April 23rd to 27th, 2018 to perform additional review, focusing on casework.

Various follow-up quality improvement initiatives, and investigations (corrective actions) have been initiated as a result of this process. These corrective actions indicated below are being submitted to the Commission as Laboratory self-disclosures using your required procedure.

CA 18-WLG-006	Investigation of inhibition in the Qiagen EZ1 DNA Tissue Kit.
CA 18-WLG-007	Investigation of the issues identified in the *Torney* case (overblown peaks and technical review). Was NMS Labs CAPA 29868; completed and attached.
CA 18-WLG-008	Investigation of artifacts included in the interpretation of Y-STR profiles.
2018-WLG-009	Investigation of missing stutter study data and other issues in the PowerPlex 16 HS validation.
CA 18-WLG-010	Investigation of management issues contributing to quality issues in forensic biology operations.

NMS reiterates its commitment to an open and transparent review and remediation of the above issues and welcomes further input from the Commission during this period of review.

Sincerely,

Barry K Logan PhD, F-ABFT
Laboratory Director, NMS Labs Criminalistics/IFS
Senior Vice President, Forensic Science Initiatives, Chief Scientist
NMS Labs

Cc: Dr. Charlotte Word, Consultant
Ms. Aliece Watts, NMS Labs QA
Dr. Heather Degnan, NMS Labs Forensic Biology Supervisor
Ms. Kristen Smith, NMS Labs DNA Technical Leader
Mr. Santosh Aravind, Scott, Douglass & McConnico
Ms. Anna Yoder, ANAB

NMS Labs Follow Up from the February 2nd 2018 Meeting of the Texas Forensic Science Commission

Issue	Status effective March 23rd, 2018
A. Commission Letter Item – Perform an independent root cause analysis on why the overblown *Torney* profile was interpreted, including any issues with NMS Labs' SOP's, training on interpretation of analytical data, and policies and practices around dilution and reinjection versus re-amplification and reanalysis.	Dr. Charlotte Word has performed a review of the original Torney casefile (13001065) and data, and a second associated case (13059644) run as part of the same batch. As a result, the corrective action report previously provided to the Commission (CAPA 29868, now CA 18-WLG-007 in our new LIMS cataloging of corrective actions) has been revised and is attached. Dr. Word is preparing a report on this case, with additional recommendations for process improvements.
B. Commission Letter Item- Perform an independent review of NMS Labs' policies and training on resolving disputes between analysts and reviewers.	As documented in the above CA 18-WLG-007, with input from Dr. Word, amendments have been proposed to SOPs CR-940, SOP-09-022, SOP-09-055 regarding dispute resolution. These proposed changes are being shared with staff in a training meeting scheduled for April 4th, 2018 to solicit feedback and clarifications, and will be finalized and approved following incorporation of that feedback.
C. Commission Letter Item – Perform an assessment of NMS Labs' SOP's related to interpretation of overblown data	As documented in the above CA 18-WLG-007, with input from Dr. Word, amendments have been proposed to SOPs CR-940, SOP-09-022, SOP-09-055 regarding data interpretation. These proposed changes are being shared with staff in a training meeting scheduled for April 4th, 2018.
D. Commission Letter Item – Develop a plan for the review of a representative number of NMS Labs DNA cases (to include all NMS Labs Texas cases involving DNA analysis between 2010 and 2018) to determine whether interpretation of overblown data, or overruling of an analyst's opinion have had any systematic impact on NMS Labs' DNA casework.	Between January 2010 and February 2018, NMS Labs performed analysis in approximately 1300 forensic biology cases, including forensic serology and forensic DNA cases. As of today 88 DNA cases from Texas have been identified. Dr. Word conducted an initial review of a few NMS Labs' case files and approved the following plan for review of NMS Labs data. She plans to review the 88 DNA cases from Texas initially. Based on observations from that review, additional cases, as needed, will be selected for review to address specific issues identified in the initial review. Dr. Word prepared a template for recording the results of case review to document: (i) evidence of overblown data, (ii) evidence of disputes between analysts and reviewers; and the following additional issues identified during the course of case review and discussed below: (iii) use of the Qiagen EZ1 DNA Tissue Kit in which inhibition of amplification has been identified, (iv) possible inappropriate combining of CPE/2P calculations for mixed DNA profiles, and (v) the

	presence of artifacts in Y-STR analysis which could have resulted in incorrect interpretation. (The latter issue was identified through NMS Labs own internal review.) NMS Labs has elected to perform and document the review of all (approximately 1,300) cases tested between January 2010, and February 2018 for the above issues. This review is in process. Dr. Word will provide additional re-review of selected cases at her discretion and at the request of the NMS Labs.
E. Commission Letter Item – Perform an independent review of NMS Labs method validations studies including the missing data from NMS Labs "Stutter Study" identified by the Commission in which the panel raised concerns about the exclusion of certain data from the calculations; and the NMS Labs Promega HS16 validation studies issues raised in the statement by Margaret Ewing of Promega in the *Torney* case.	A corrective action (2018-WLG-009) has been initiated on the issue of missing stutter study data in the PowerPlex 16 HS validation. A preliminary internal review of stochastic threshold (ST), analytical threshold (AT), peak height balances, linear range/saturation point for the kits listed below and applicable CE platforms have been reviewed and found to be acceptable by the DNA Assistant Technical Lead. A summary of the findings and any recommendations for corrective action will be provided upon completion of the review of the stutter data with Dr. Word. Validations, including new stutter studies, are being performed on selected kit chemistries currently in use in the laboratory, including Globalfiler, Fusion, Fusion 6C, and Y23, used in conjunction with the EZ1 Extraction procedures and the Quantifiler Trio quantitation kit. Dr. Word has preliminarily reviewed portions of the NMS Labs validation of the Promega PowerPlex 16HS amplification kit. Further review is in process. If necessary, Dr. Ewing's criticisms will be addressed through additional validation studies and appropriate modifications to the relevant SOPs.
F. Commission Letter Item – Perform review of any calculations, calculators, or SOP's developed on behalf of NMS labs by external consultants.	An internal review has been conducted of the in-house developed Excel-based statistical calculator "STRstats" to assess its accuracy and reliability. The statistical calculations evaluated included Random Match Probability (RMP), 2P, combined RMP-2P, Combined Probability of Exclusion (CPE), and paternity, maternity and uniparental parentage. A review of all formulas utilized in STRstats and manual checking of the calculations is being done to validate the spreadsheets' use of the formulae. An evaluation of the in-house Excel-based calculators for full-siblings, half-siblings and missing child calculations is planned. Due to the complexity of these statistical formulas, an additional external consultant will be utilized for this review.

G. Matters Arising – LR Mix calculation.	It has been noted that the NMS Labs LR Mix calculation used a value of 0 for θ, rather than 0.01 or 0.03, which is the more common practice. NMS Labs has retained Mr. Keith Inman to evaluate various aspects of the use of this calculation and its validation, and conversion to the use of LRMix Studio. This evaluation is scheduled for completion by April 6th, 2018.
H. Matters Arising – Qiagen EZ1 DNA Tissue Kit Issue.	An issue has been identified involving the Qiagen EZ1 DNA Tissue Kit. An inhibitor of the PCR amplification may be eluting in the extraction process resulting in failures to generate a DNA profile when large volumes of the extract are used in the PCR. A corrective action (CA 18-WLG-006) has been initiated on this issue. As part of its above case review, NMS Labs is identifying and reviewing cases processed using the Qiagen EZ1 DNA Tissue Kit, and where appropriate, contacting clients to propose retesting of those cases using a clean-up and reamplification of the affected DNA extracts. This may require issuance of amended reports.
I. Matters arising: Y-STR artifacts.	During an internal review of a Texas (Harris County) case, it has been noted that artifacts included in the interpretation of a Y-STR profile, led to an incorrect exclusion. Removal of the artifacts and reinterpretation changed the opinion from "excluded" to "cannot-be–excluded". The client has been notified. All cases included in the above described comprehensive casework review are being evaluated for impact of this issue. A corrective action (CA 18-WLG-008) has been initiated.
J. Matters arising: Management Review.	A corrective action (CA 18-WLG-010) has been initiated to examine the management issues that led to the above quality issues.

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CORRECTIVE ACTION
2018-WLG-007
March 26, 2018

Background

NMS Labs performed DNA analysis on case number 13001065 in March of 2013 at the request of the Washington DC Public Defender's Office. There was a pre-trial hearing on the case where questions arose regarding the interpretation of one sample, 02.2-1A (non-sperm fraction of anorectal swab). During the hearing, an amended report was issued to clarify the reporting language. No corrective action was initiated at the time for the amended report. The hearing was suspended prior Dr. Christian Westring's testimony. A ruling by Judge Dixon (that NMS became aware of in February, 2015) prohibited the use of the evidence and was critical of NMS' interpretation of the results. This case was brought to the attention of the Texas Forensic Science Commission in 2017, who requested information from NMS Labs regarding the incident. A preventive action (CAPA 29868) was initiated to address the concerns of the Commission. An investigation was opened by the Commission and a panel was convened by the Commission to review the data and validation studies. The issue was changed to a Corrective Action (CA 2018-WLG-007) as a result of the findings of the Commission's investigation and NMS' re-evaluation of the case file.

Statement of Problem

The PowerPlex 16HS electropherogram for 02.2-1A (non-sperm fraction of anorectal swab) at the 1 second injection showed many high peaks (some over 7,000 RFU) with multiple pink bars in GeneMapper ID indicating that the data are off-scale (i.e., "overblown" data) with many lower RFU peaks that required numerous edits. The products for this sample (1 second injection) were re-run after a 5 second injection. These data are consistent with far more DNA being amplified than the targeted amount of 1 ng. Due to the off-scale data, elevated baseline and the numerous lower RFU peaks, it is unclear if true alleles vs. artifacts can be appropriately edited. It is also unclear if the stutter filters would be sufficient to edit out stutter peaks. These conditions made the interpretation of any minor DNA contributor(s) extremely difficult, if not impossible, to evaluate.

Additional Comments

In the course of investigating this incident, it was learned that there had been an undocumented disagreement between the analyst, technical reviewer and the Technical Leader about the reporting of this sample. The proposed addition to the Forensic Biology Procedure Manual (09-022) will provide options (external to the DNA unit) to resolve disagreements.

Mandatory documentation of any unresolved or escalation of disagreements will also be added. The Quality Manual (09-055) will be amended to include language regarding technical disagreements.

Cause of the Problem:

The quantitation system used in this case was Qiagen's Investigator®Quantiplex HYres. The quantitation value for this sample was 223 ng/µl total human DNA, a value that is well above the range used for generating the standard curve for the quantitation system. The validation studies performed either by the laboratory or in developmental studies for the quantitation system do not provide supporting information for the adequacy of the extrapolation of the standards data at this concentration, as no samples with concentrations as high as 200-250 ng/µl were tested. Page 19 of Qiagen's Investigator®Quantiplex HYres Kit Validation Report indicates that the quantitation values are reliable over the full range tested, listing 100 ng as the highest amount tested. Clearly, the sample had a very high amount of total DNA, however the actual concentration is not known. For amplification, 1 µl of the DNA extract was diluted into 99 µl of TE^{-4} buffer, and 0.45 µl of the diluted sample was targeted for amplification with the PowerPlex 16 HS amplification kit without additional quantitation. It is possible that the amount of DNA was higher than the estimate used, and that the pipetting of the very small volumes for the dilution and amplification may have contributed to too much DNA being present during the PCR amplification step, resulting in the off-scale data on the two electropherograms when analyzed using standard procedures. No additional steps were taken to improve the quality of the data from this sample.

Review of a second case that had a sample processed alongside this case suggests that the high concentration of the DNA extract for the sample is the underlying issue since the electropherograms generated in the companion case and for the extraction controls (ECA and ECB) processed with this batch of samples all seem appropriate for the methods followed. These data suggest that the quantitation assay and subsequent amplification and electrophoresis steps performed correctly overall. A pipetting error for this one sample cannot be ruled out as a possible contributing factor based on these data.

Recommended Corrective Action for the Case:

The DNA extract should be diluted at least 1:250, if not more, (e.g., 1-2 µl of DNA into 250-600 µl DNase-and DNA-free buffer, water, etc.) and the diluted sample quantitated and retained. The diluted sample would then be re-diluted if necessary for additional quantitation, or used for the amplification directly depending on the resulting DNA concentration and the appropriate volume needed to achieve the 1 ng target DNA amount.

The evidence and extracts have been returned to the client. The client does not wish to have additional testing performed, thus the corrective action cannot be completed at this time. In the absence of re-testing, the putative data from any minor contributor(s) is uninterpretable and thus, unsuitable for comparison (i.e., inconclusive). The laboratory issued an amended

report, dated 07/03/14, stating "no inculpatory statements regarding the minor component can be made at this time."

Preventative/Corrective Action for the Laboratory:

Quantitation Range Manufacturer literature, developmental and internal validation studies for the quantitation kit currently in use will be reviewed, and the range where appropriate estimates of the DNA concentration can be made will be established. This will be done for the Applied Biosystems Quantifiler™ Trio DNA Quantification Kit, as the Qiagen Investigator®Quantiplex HYres kit is no longer in use by the laboratory.

Pipette Accuracy Pipettes are available and calibrated down to a P2.5 pipette (range of .01 – 2.5 µl). Calibration certificates for all DNA pipettes from 2013 were reviewed and calibrations performed in January 2013 (good through July 2013) all passed. Samples in this case were processed in March of 2013. One pipette, with a range of 50 – 200 µl, failed calibration in July 2013. All pipettes continue to be calibrated twice a year and any failing pipettes are removed from casework use until they pass the calibration criteria.

StarLIMS Dilution Logic The laboratory moved to a LIMS system (StarLIMS) for case and sample processing and tracking in June 2017. The current quantitation and amplification logic in StarLIMS does not allow for pipetting at a volume lower than 1 µl. This will reduce the need to pipette extremely small volumes and thus improve pipetting accuracy. The current StarLIMS logic flags a sample as needing dilution and re-quantitation if the sample concentration exceeds 500ng/µl. This value will be reevaluated during the Quant Trio method validation review.

Method Modifications The DNA method CR-940 will be modified to include the criteria obtained from the above quantitation studies as well as clearer guidance for what to do when the estimated concentration values fall outside of the acceptable range.

Additionally, method CR-940 will be modified to more clearly define the limitations of the DNA testing processes and methodologies utilized. The DNA staff will be trained on the method changes and the processing of extracts, products and data when they fall outside of the acceptable range.

The Forensic Biology DNA Methods will also be updated to include improved criteria for editing artifacts.
Some of these method modifications necessitate additional and/or modified internal validation studies. The DNA method will be updated as soon as practicable following these additional studies and those results as well as the associated method changes will be conveyed to all DNA staff.

Validation Studies Single source and mixture validation studies conducted with samples having known genotypes at all loci across various levels of input DNA and mixture ratios will be

reviewed for chemistries currently in use to assess the optimal range for interpretation of the data and establish criteria for editing out artifacts and deciding where data may be of insufficient quality to interpret.

The Quant Trio quantitation kit validation will be reviewed to revise and possibly lower the upper limit of the assay.

A review of the stutter validation study for PowerPlex 16HS will be conducted to determine the accuracy of the conclusions.

Interpretation Disagreements SOP 09-022 Forensic Biology Procedure Manual and SOP 09-055 Quality Assurance Policy Manual will be edited to include revised guidelines more clearly addressing discrepancies that may arise between analyst(s) and technical reviewer(s).

Retrospective Review of Cases The Quality Assurance Director will oversee a retrospective review of NMS Labs' DNA casework, including all DNA cases submitted by agencies from Texas since 2010. Additional review of cases for off-scale data and correct use of statistics will be performed by our consultant, Dr. Charlotte Word.

Kristen Smith
E-signed 2018-03-26 12:39PM EDT
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Kristen Smith, DNA Technical Leader

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Heather H. Degnan (Mar 26, 2018)

Heather Degnan, PhD, DNA Assistant Laboratory Director

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CRIMINALISTICS

NMS

Corrective Action for Torney FINAL.PDF

Adobe Sign Document History 03/26/2018

Created:	03/26/2018
By:	Alexandria Shults (Alexandria.Shults@nmslabs.com)
Status:	Signed
Transaction ID:	CBJCHBCAABAAhACxA_9N7exfvXFyEZeDfkLhhvzTppAt

"Corrective Action for Torney FINAL.PDF" History

Document created by Alexandria Shults (Alexandria.Shults@nmslabs.com)
03/26/2018 - 9:22:32 AM PDT- IP address: 76.204.62.202

Document emailed to Kristen Smith (Kristen.Smith@nmslabs.com) for signature
03/26/2018 - 9:25:43 AM PDT

Document viewed by Kristen Smith (Kristen.Smith@nmslabs.com)
03/26/2018 - 9:39:19 AM PDT- IP address: 146.145.50.100

Document e-signed by Kristen Smith (Kristen.Smith@nmslabs.com)
Signature Date: 03/26/2018 - 9:39:41 AM PDT - Time Source: server- IP address: 146.145.50.100

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03/26/2018 - 9:42:40 AM PDT- IP address: 71.15.121.140

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03/26/2018 - 9:43:13 AM PDT

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03/26/2018 - 9:52:10 AM PDT- IP address: 146.145.50.100

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03/26/2018 - 9:55:45 AM PDT

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03/26/2018 - 10:03:39 AM PDT- IP address: 146.145.50.100

Document e-signed by Barry Logan (barry.logan@nmslabs.com)

Signature Date: 03/26/2018 - 10:04:02 AM PDT - Time Source: server- IP address: 146.145.50.100

Signed document emailed to Heather H. Degnan (heather.degnan@nmslabs.com), Aliece Watts (Aliece.Watts@nmslabs.com), Barry Logan (barry.logan@nmslabs.com), Kristen Smith (Kristen.Smith@nmslabs.com), and 1 more

03/26/2018 - 10:04:02 AM PDT

NMS Biology Training

Analyst/Technical Reviewer Discrepancy Resolution, Off-Scale Sample Data Interpretation and Y-STR Artifacts

April 4, 2018

Kristen Smith, DNA Technical Leader

US v Cardell Torney

- Washington, DC case; tested by NMS Labs in 2013
- Under review by Texas Forensic Science Commission beginning 2017
  - Specifically asked to address discrepancies between analyst(s)/technical reviewer(s)
  - Interpretation of off-scale/oversaturated STR typing data

Definitions

- Analyst – an employee or contract employee, that has successfully completed the laboratory's training requirements for casework sample analysis, passed a competency test, and has entered into a proficiency testing program according to these Standards. This individual conducts and/or directs the analysis of forensic samples, interprets data and reaches conclusions (*QAS 2011*)

- Technical Review – an evaluation of reports, notes, data, and other documents to ensure there is an appropriate and sufficient basis for the scientific conclusions (*QAS 2011*)

- Technical Review – Review of technical records, test reports and testimony to ensure the validity of test results, opinions and interpretations (*ANAB AR 3028*)

ANAB Guiding Principles

- Required to be reviewed annually *by* all staff and record of review retained

- *Clear Communications*
  - 17 – Support sound scientific techniques and practices and do not use their positions to pressure an examiner or technician to arrive at conclusions or results that are not supported by data
  - 18 – Testify to results obtained and conclusions reached only when they have confidence that the opinions are based on good scientific principles and methods. Opinions are to be stated so as to be clear in their meaning. Wording should not be such that inferences may be drawn which are not valid, or that slant the opinion to a particular direction.

Discrepancy – what to do

- As technician, analyst or technical reviewer must ensure you agree with what you are signing your name to
  - Extraction paperwork
  - Incident log/Corrective Action
  - Report/Technical Review
- If disagree, take to supervisor to get further clarification
  - If resolved, then ok to sign
  - If not, can escalate to ATL, TL and/or QM
  - Also able to escalate to Director or HR if feel response is not satisfactory

Discrepancy – what to do

- Email sent 01/12/18
  - (Q:\FORENSIC BIOLOGY FILES\Memos and Emails)

From: Smith, Kristen
Sent: Friday, January 12, 2018 8:31 PM
To: Degnan, Heather; Foley, Megan; Jardel, Danielle; McComsey, Laura; Sanders, Chenique; Sears, Jennifer; Seehousz, Jessica; Sgueglia, Joanne; Shaffer, Justin; Walsh, Thomas; Westring, Christian; 'Heather McKiernan'
Cc: Watts, Aliece
Subject: Data Interpretation Disagreement

All,
Should any questions and/or concerns arise through case write-up or technical review regarding interpretations, comparisons, protocols, etc., please address those with either the Tech Lead or Assistant Tech Lead. Routine questions and discussions regarding write-ups/interpretations/comparisons and review can be resolved between analyst and reviewer, but should additional discussion and/or disagreement develop, please do not address directly with the analyst and/or technical reviewer. These should be brought to the attention of either myself or Tommy.

Tommy and I will address the question or issue and attempt to resolve it. Should an agreement or resolution not be able to be reached, the matter will be brought to the attention of the Quality Director and the Quality Director will determine the final outcome. In these instances, documentation will be included within the applicable casefile(s) to indicate that a disagreement occurred and the discussion was forwarded onto the Tech Lead/Assistant Tech Lead and ultimately the Quality Director for final resolution.

This updated protocol is effective immediately and will be included in the next revision of SOP 09-055.

Please see Tommy, Christian, Aliece or myself if you have any questions.

Thank you,

NMS LABS

Kristen Smith
DNA Technical Leader
Phone: 215.366.1500
www.nmslabs.com

Discrepancy – what to do

- Must include clear documentation in casefile
  - Discrepancy/issue
  - Escalation pathway
  - Final resolution
- Incident log – must be able to query/identify/track
  - Entered by TL/ATL or QA
  - Noted by Category: "Other" and Type of Incident: "Escalation"
  - No specific details in general description
  - Attachments in Incident Log containing details will only be able to be seen by supervisory levels (QA, ALD and TL/ATL)

Proposed SOP Changes

- SOP 09-022 Forensic Biology Procedures and SOP 09-055 Quality Assurance Policy

Case Record Reviews:

Data, documentation, and reports must be reviewed by a second qualified individual. Prior to issuing a report, both individuals must agree on the interpretation of the data and the conclusions derived from the data. In the event of an unresolved disagreement between an analyst and a reviewer, the Technical Leader must be notified to assist in resolving the disagreement. If after consulting the Technical Leader a disagreement still exists, the matter will be brought to the attention of the Quality Director. The Quality Director will review the case/disagreement to ensure compliance with all SOP's and interpretation guidelines. Additionally, either party may seek additional assistance from a representative from Human Resources without undue influence or reprisal.

The nature of the disagreement and the subsequent resolution must be documented in sufficient detail to allow a third party to understand the disagreement as well as the final resolution. The analyst and/or reviewer may request, following authorization from the Technical Leader, that a sample be re-analyzed to potentially facilitate resolution. The DNA Technical Leader has the final authority on the interpretation(s) reported. Situations will be evaluated on a case-by-case basis to ensure all assumptions are considered and clearly stated, if utilized in the final reporting. Collectively, the combination of analyst(s), technical reviewer(s) and the Technical Leader must agree on the most appropriate and scientifically-defensible outcome to report. Generally, the most conservative result will be reported (usually "inconclusive" or "uninterpretable"), if no agreement can be reached. See SOP 09-055 and 09-035 for specifics for case record review.

Proposed SOP Changes

- Questions?
- Feedback?

Data Interpretation – Off-Scale

- When too much DNA is added to PCR reaction, can result in:
  - Fluorescence exceeding the linear dynamic range of detection ("Off-Scale" data)
    - Elevated stutter
    - Excessive pull-up
    - Inaccurate peak height assessment
  - Incomplete nucleotide addition (many -A peaks)

Back to the DNA Basics

- Non-Template Addition
  - Taq polymerase adds extra nucleotide (typically A) to 3'-end of a PCR product
  - This can be facilitated:
    - Final soak at 60°C or 72°C at end of PCR cycling
    - Having a G or specific sequence at 5'-end of reverse primer
      - Ensures DNA strands are all uniformly adenylated so not a mix of -A/+A forms of amp products
  - All commercial kits are in the +A form

Non-template Nucleotide Addition

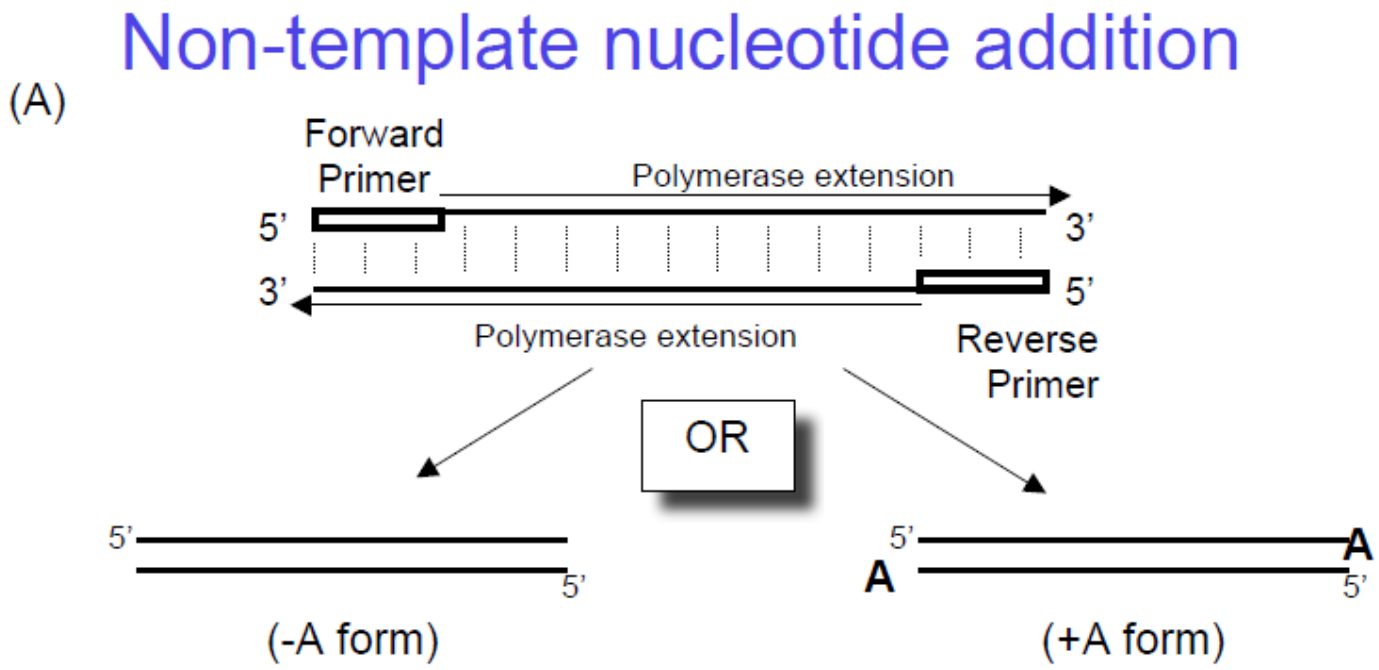


Figure 6.4, J.M. Butler (2005) *Forensic DNA Typing*, 2nd Edition © 2005 Elsevier Academic Press

Non-template Nucleotide Addition

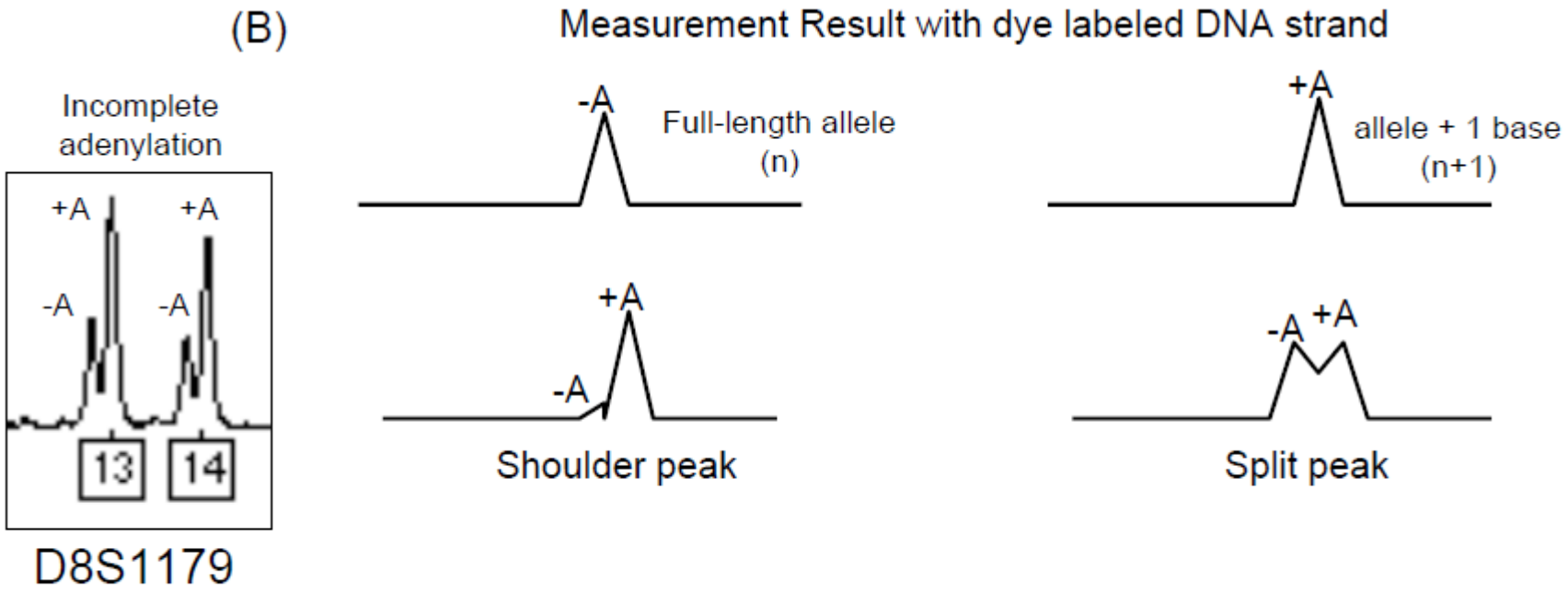


Figure 6.4, J.M. Butler (2005) *Forensic DNA Typing*, 2nd Edition © 2005 Elsevier Academic Press

Data Interpretation – Off-Scale

- High Levels of DNA Template

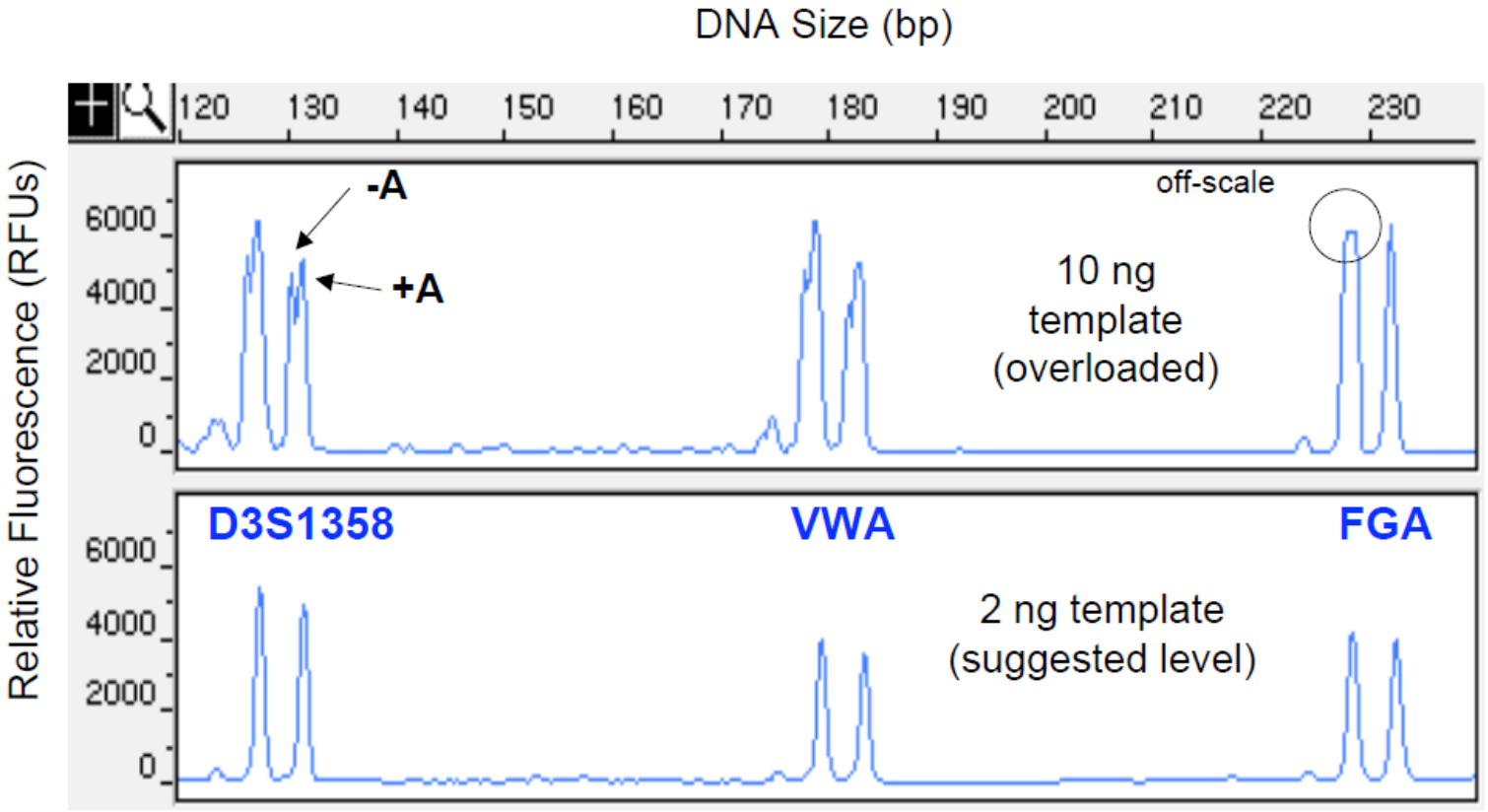


Figure 6.5, J.M. Butler (2005) *Forensic DNA Typing*, 2nd Edition © 2005 Elsevier Academic Press

Data Interpretation – Off-Scale

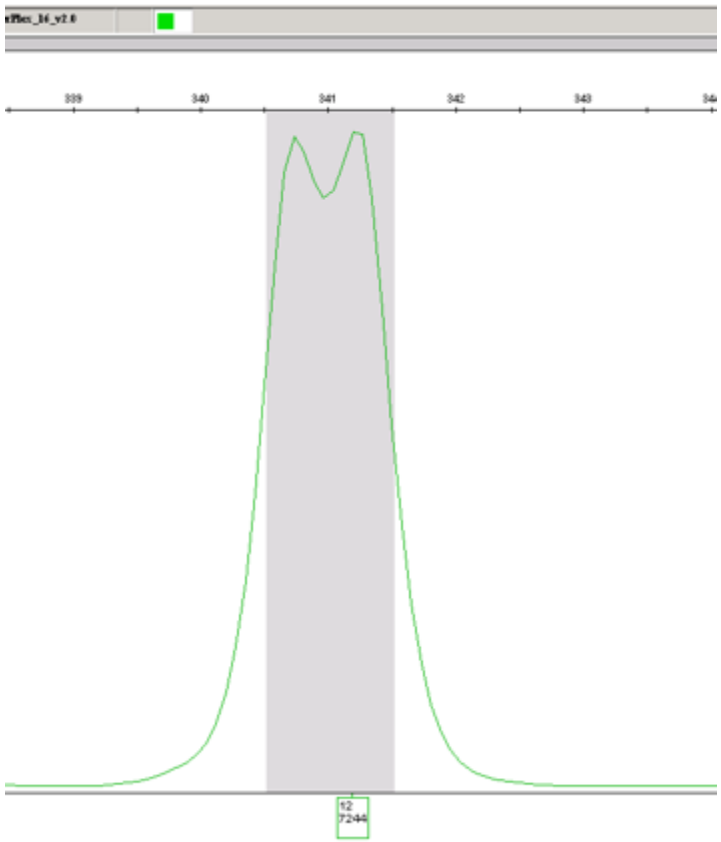
- Why is off-scale data problematic?
  - Peak height and area of off-scale peaks is not accurate
    - Mixture deconvolution inaccurate
  - Corresponding stutter peak may appear higher in relative intensity
  - Multicomponent analysis of off-scale data is not accurate
    - Poor spectral separation (pull-up; matrix oversubtraction)

Off-Scale Data: Characteristics

- Flat-topped Peaks
- Matrix Oversubtraction
- Split Peaks
- Excessive/elevated stutter
- Excessive pull-up
- Excessive -A peaks/shoulders

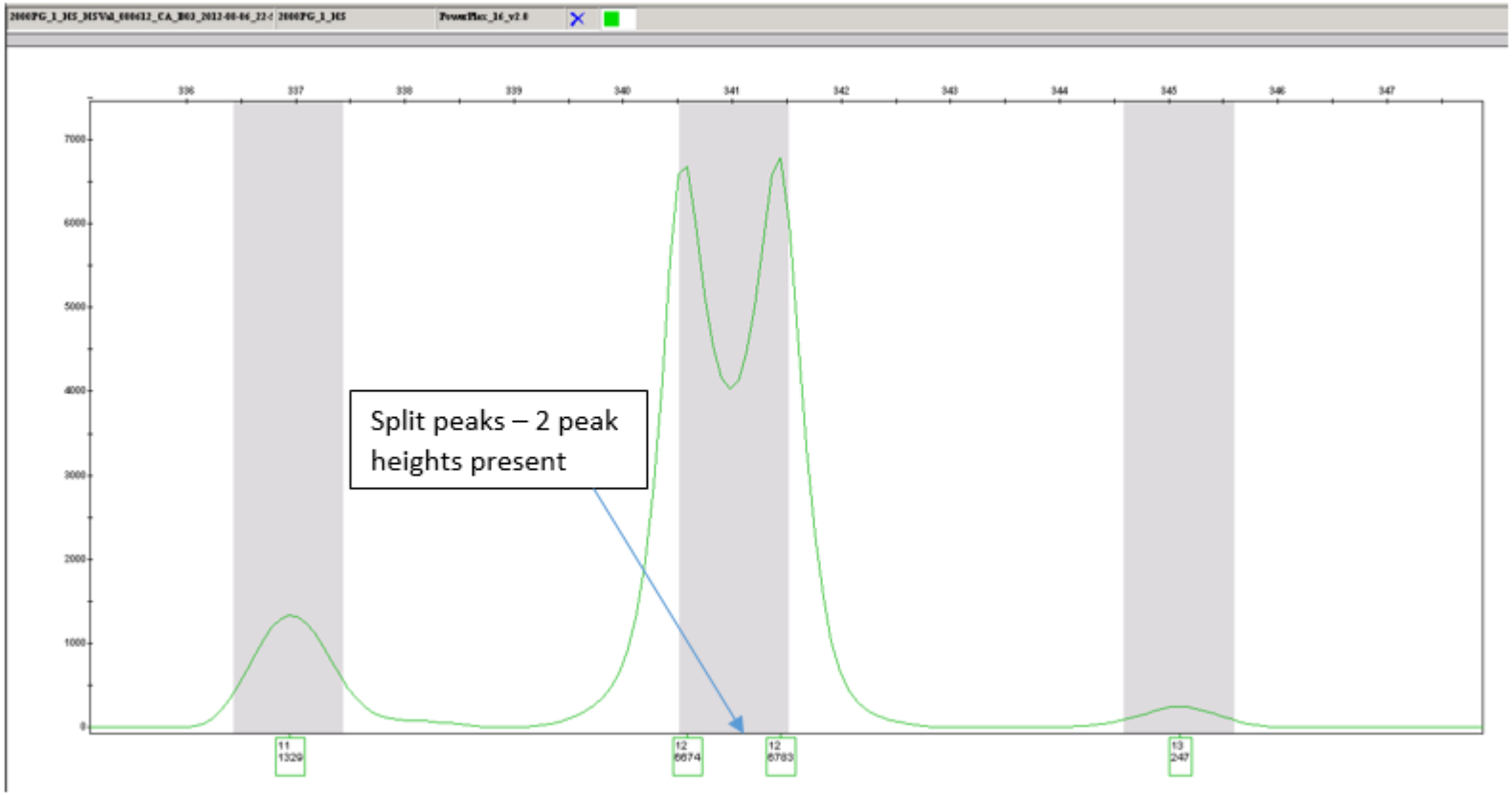
Data Interpretation – Off-Scale

- Input of 2ng of DNA at amp (PP 16HS on 3130)

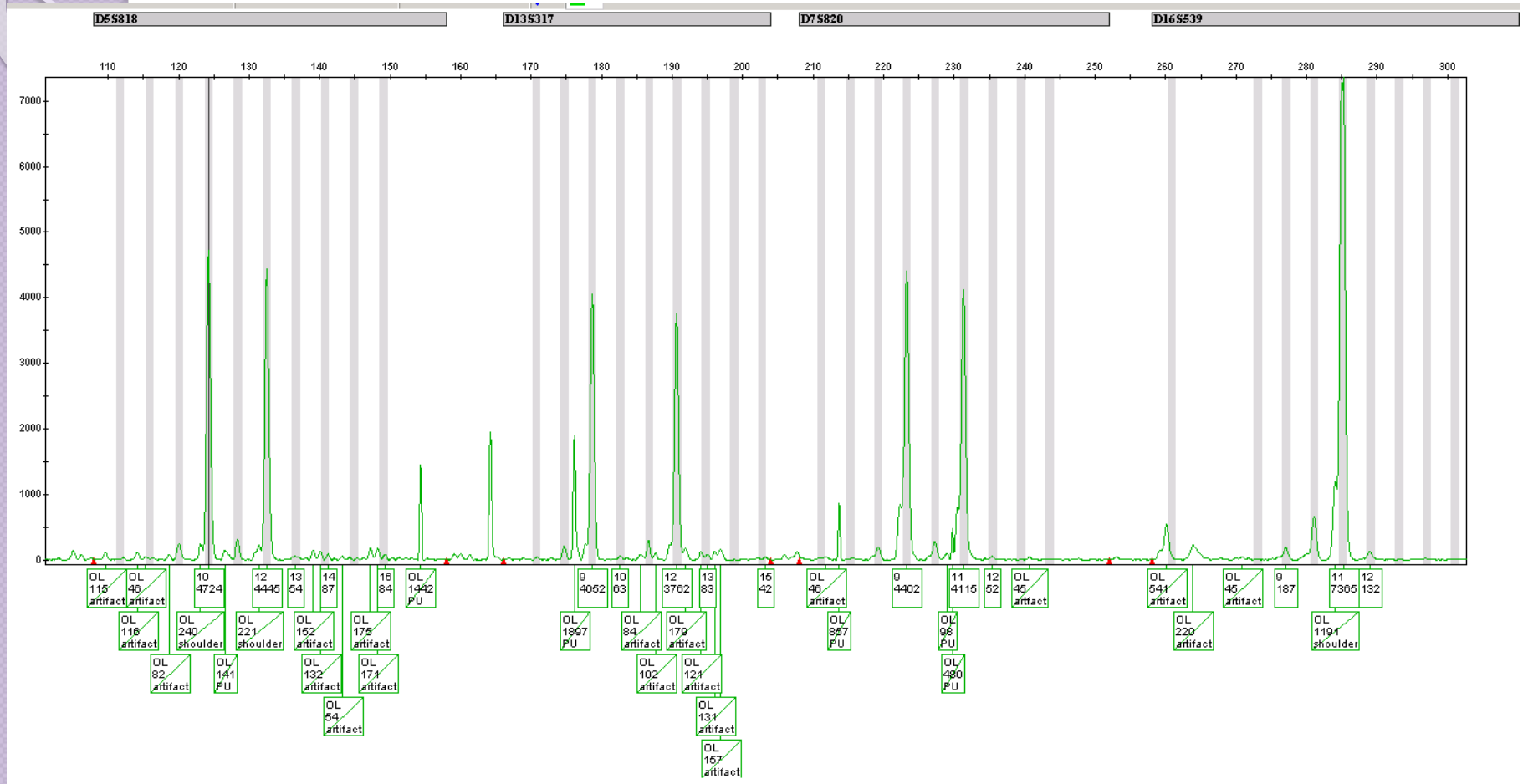


Data Interpretation – Off-Scale

- Input of 2ng of DNA at amp (PP 16HS on 3130)

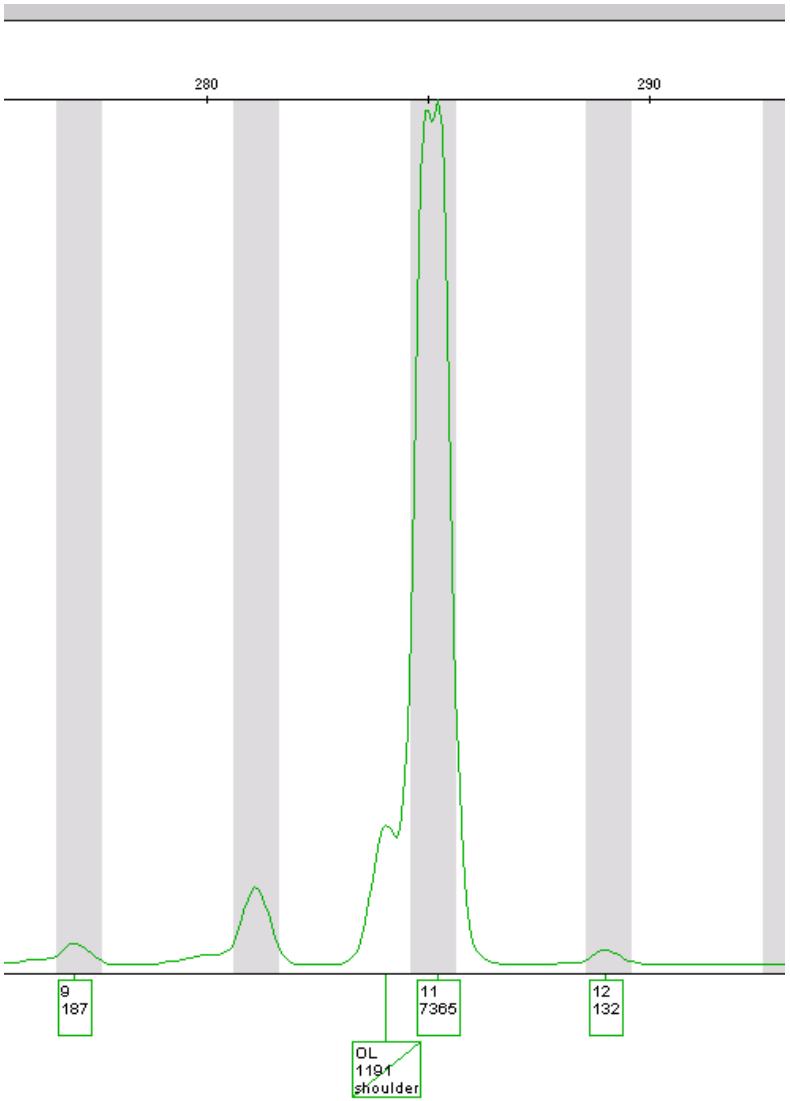


Data Interpretation – Off-Scale



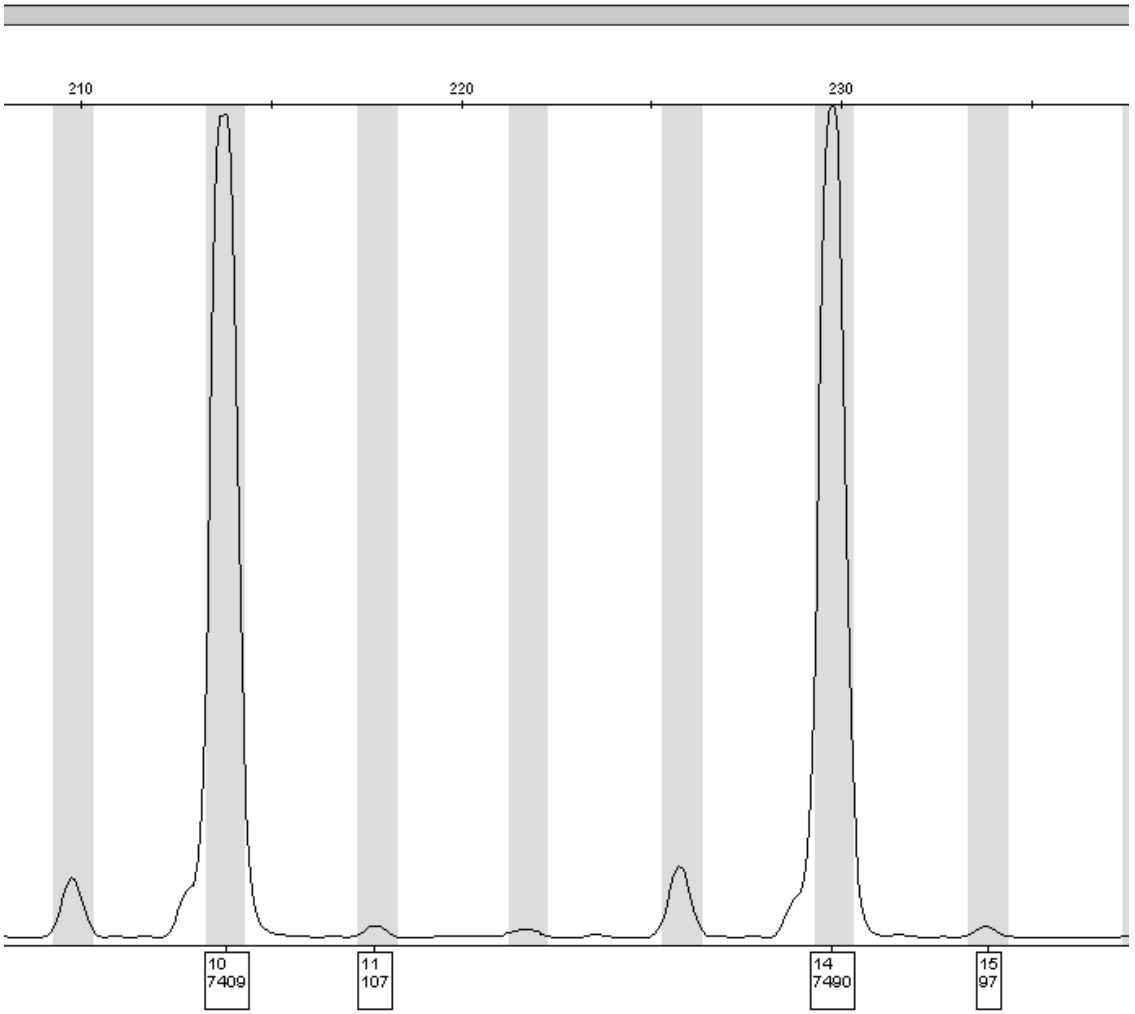
Data Interpretation – Off-Scale

- D16S539



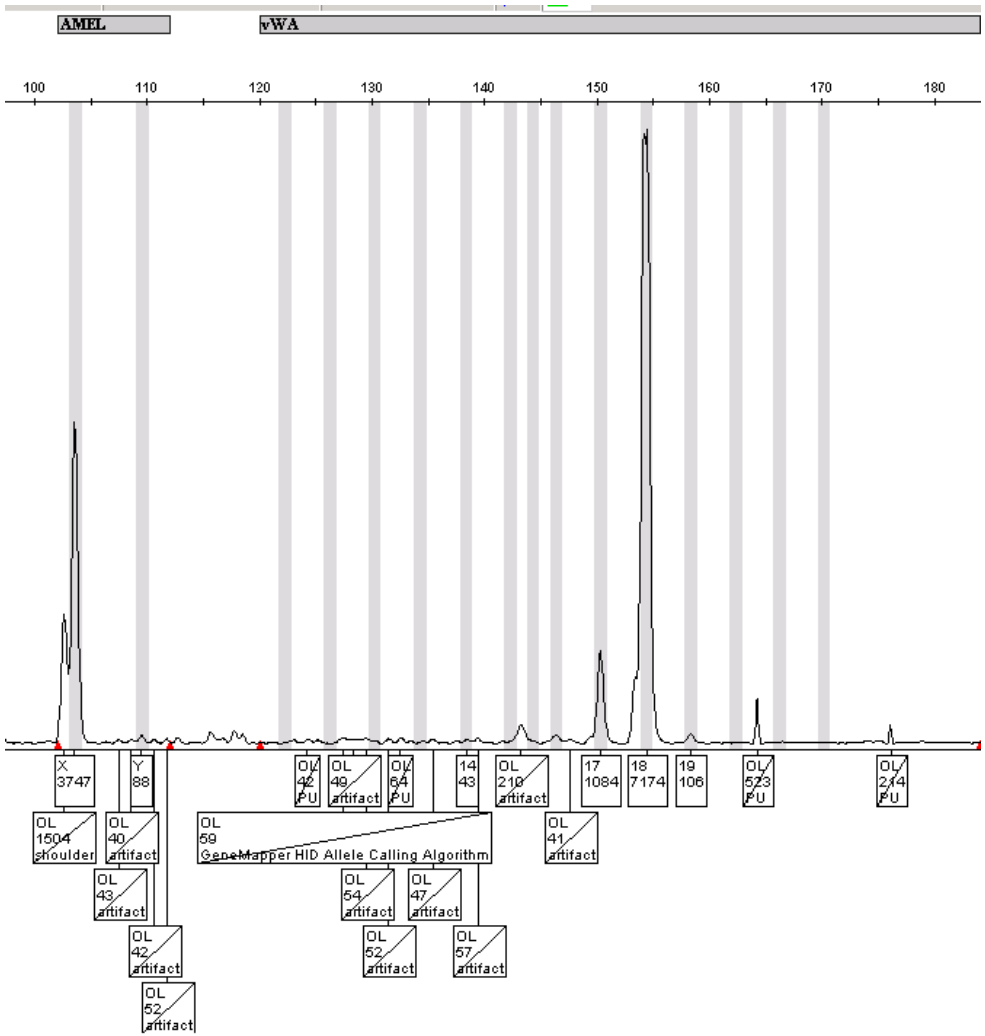
Data Interpretation – Off-Scale

- D8S1179



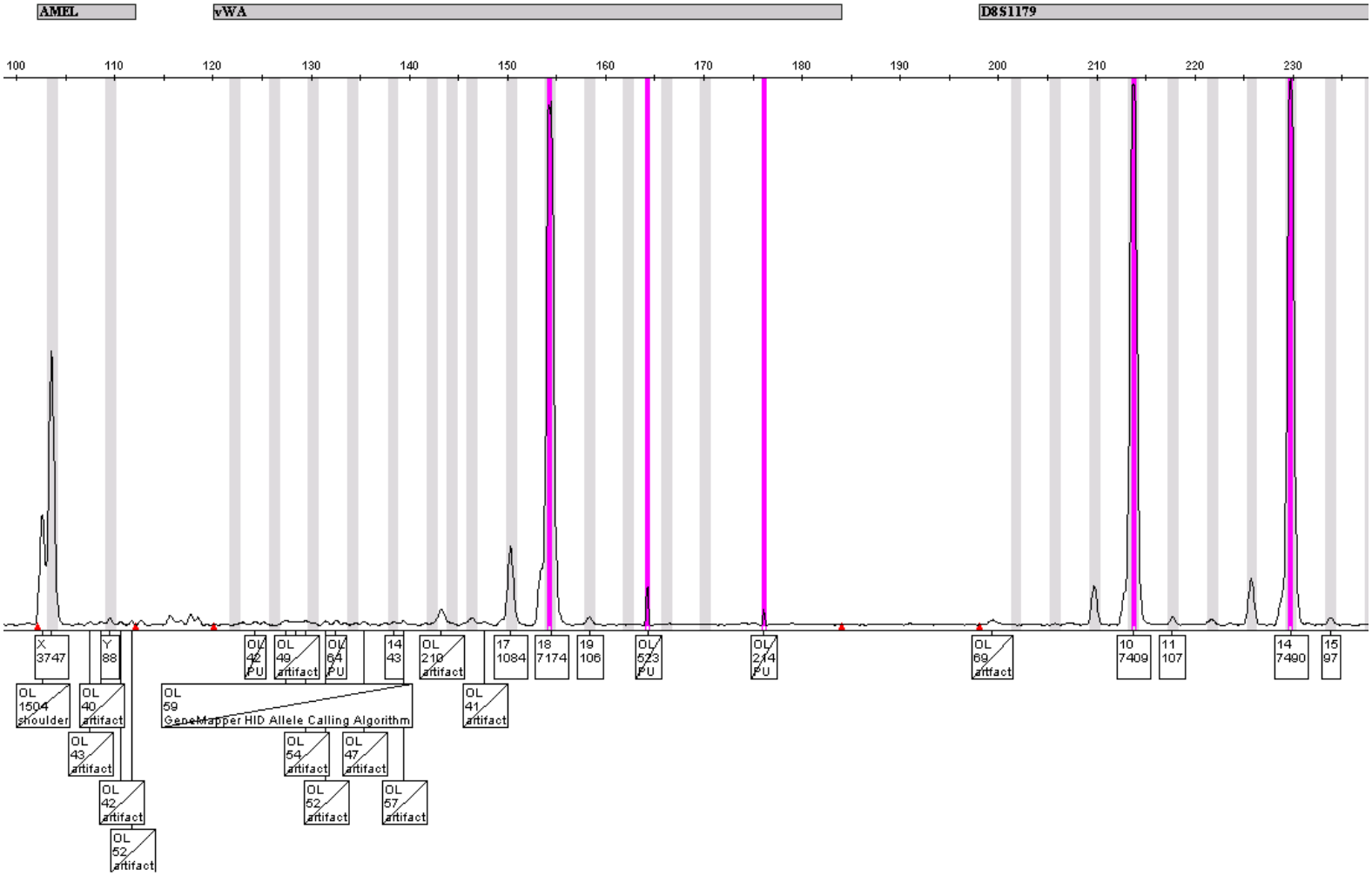
Data Interpretation – Off-Scale

- Amelogenin and vWA



Data Interpretation – Off-Scale

- Amelogenin, vWA and D8S1179 (Off-Scale Peak Indicator on)



Off-Scale Data: Remediation

- Run at lower injection time
  - Will not correct amp-related issues/excessive off-scale data
- Dilute amp product and re-run on CE
  - CE issues only
- Re-amplify with lower input of DNA
  - Decrease input amount
  - Dilute extract
- Evaluate quant data!
  - If beyond linear range of standard curve, quant value may be inaccurate
  - Check prior to re-work; may need a re-quant

Off-Scale Data: Remediation

- Quant Data
  - Trio standard curve: 50ng/ul to 0.005ng/ul
    - Per Trio manual, curve is linear 5pg/ul to 100ng/ul
  - Current NMS LIMS quant logic
    - Flags sample for dilution and re-quant if at amp the Small Autosomal (SA) target is >500ng/ul
    - "DILUTE+REQUANT" in Recommended Action
  - Samples with high quant values should be evaluated for possible dilution and re-quant

Quantitation Data – Trio Notes

- Detects DNA <5pg/ul but variation will be greater
- At high DNA concentrations (>100ng/ul) increase in the IPC C_T value may be seen
  - Increase in IPC value due to competition within the reaction among targets
  - Observed more often >50ng/ul
- Future evaluation to include linear range of quant curve
  - Establish upper cutoff for acceptable quant value?
  - Evaluate extended linearity of standard curve?

Proposed Method Changes

- Changes to method addressing quantitation (CR-940)
  - To be evaluated as additional/new validation data is obtained
  - Develop/define better parameters for use of Quant Trio data
    - M:F ratio
    - Inhibition
    - Degradation
    - Upper and lower limits of detection

Proposed Method Changes

- Changes to method addressing typing data (CR-940)
  - To be evaluated as additional/new validation data is obtained
    - Thresholds
    - Overblown/off-scale saturation point
    - Stutter percentages
    - Clearer guidelines in STR analysis/review section pertaining to artifacts and editing of profiles and troubleshooting/remediation

CA 18-WLG-008 (Y-STR's)

- Corrective Action pertaining to Y-STR artifacts and profile interpretation

- Amended report issued for case [redacted]
  - Original report was exclusion
  - Amended to cannot be excluded
  - Y-STR artifacts present in high amount of female DNA

Y-STR Artifacts: Refresher

- TW Journal Club presentation 01/04/17

(Q:\FORENSIC BIOLOGY FILES\Meeting Minutes\2017\2017 Journal Clubs\TW_Jan 04)

Forensic Science International: Genetics 24 (2016) 44–50

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Short communication

Description of artefacts in the PowerPlex Y23® system associated with excessive quantities of background female DNA

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ARTICLE INFO

Article history:
Received 21 December 2015
Received in revised form 6 May 2016
Accepted 14 May 2016
Available online 19 May 2016

Keywords:
Y23
DNA artefacts
Sexual assault
Y-STR

ABSTRACT

Male on female sexual assault cases that involve azoospermic individuals, those where the male has penetrated but failed to ejaculate, those where there has been an extended interval between the sexual assault and sample collection or where there has been only digital penetration are often difficult to investigate by employing traditional autosomal STR testing. Such cases often involve minimal amounts of male DNA either being deposited initially or remaining after the passage of time. These cases are often further complicated by the presence of large amounts of female DNA compared to the relatively small amounts of male DNA on the intimate samples taken. Y-STR kits provide a solution that allows targeting of male DNA in a mixed male/female sample. However, large quantities of excess female DNA have the potential to generate non-specific artefact peaks. Here we characterise a number of previously reported artefacts observed in the PowerPlex® Y23 system. We demonstrate that some of these artefacts can impact on profile interpretation and that they are highly dependent on the levels of female DNA present. These artefacts have been characterised to assist practitioners with the interpretation of such samples.

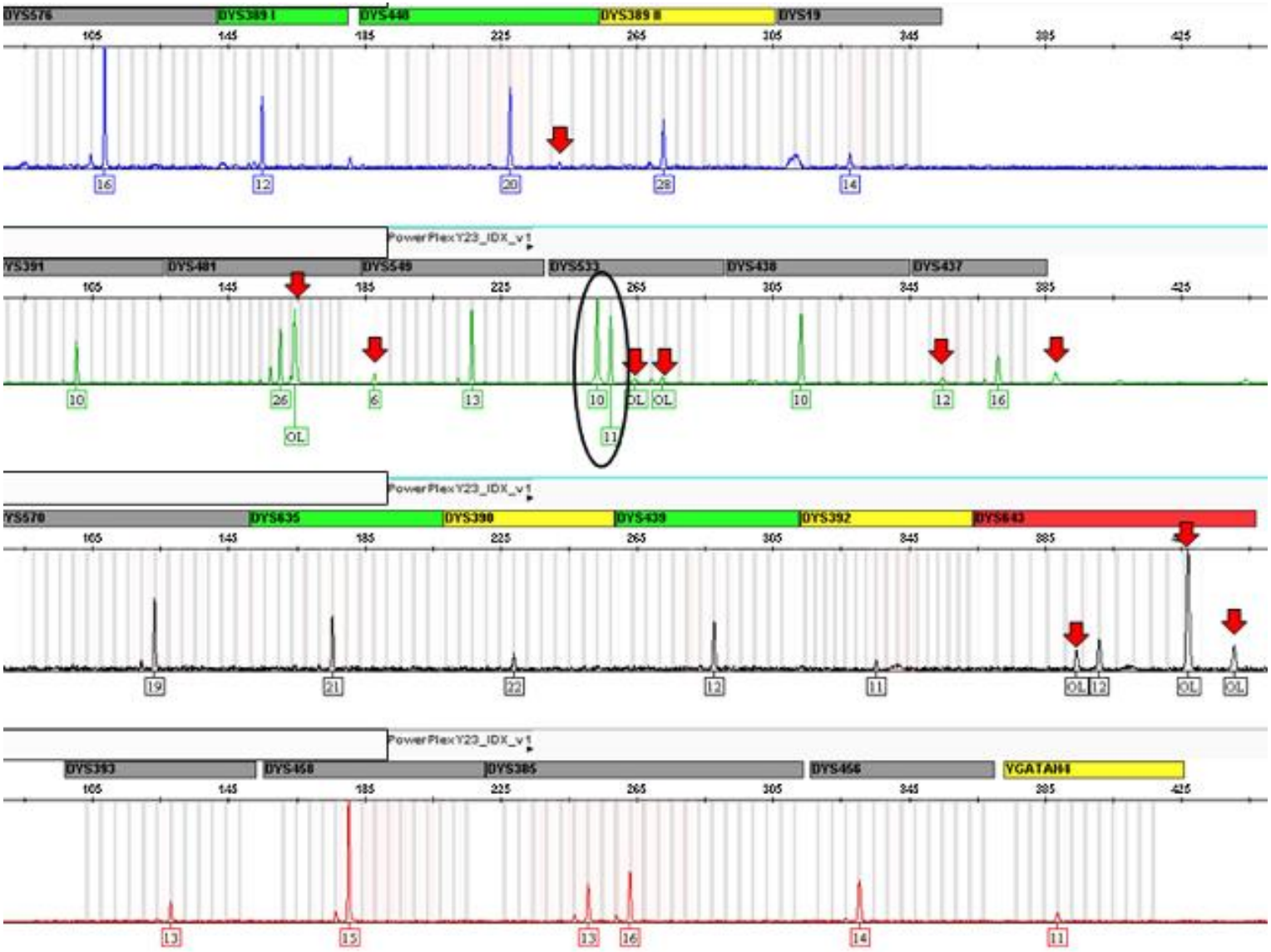
Y-STR Artifacts: Refresher

- Same as autosomal typing, artifacts commonly seen include:
  - Stutter
  - Dye blob's
  - Pull-up
- Also see artifacts specific to the presence of female DNA
  - Generally when Y-STR typing is used (high female/low male)

Y-STR Artifacts: Refresher

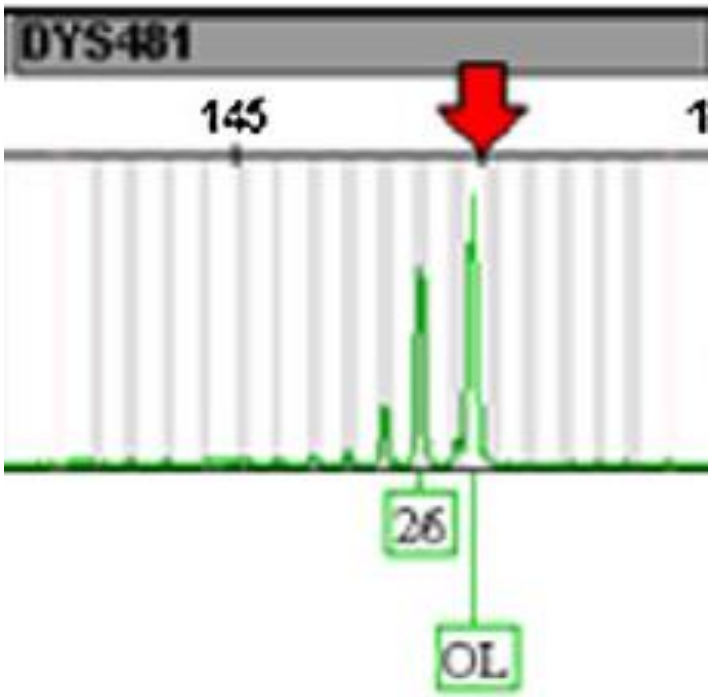
- PowerPlex Y23® Validation
  - Excess Female DNA Study
    - Ratios from 200:1 to 3200:1 (Female:Male)
    - No impact on Y-STR profile in presence of up to 100ng of female DNA
  - Casework Sample Study (more accurate evaluation)
    - 6 of 10 samples generated unusual peaks
      - On bin as well as OL peaks
      - Reproducible
      - Good peak morphology

Y-STR Artifacts: Refresher



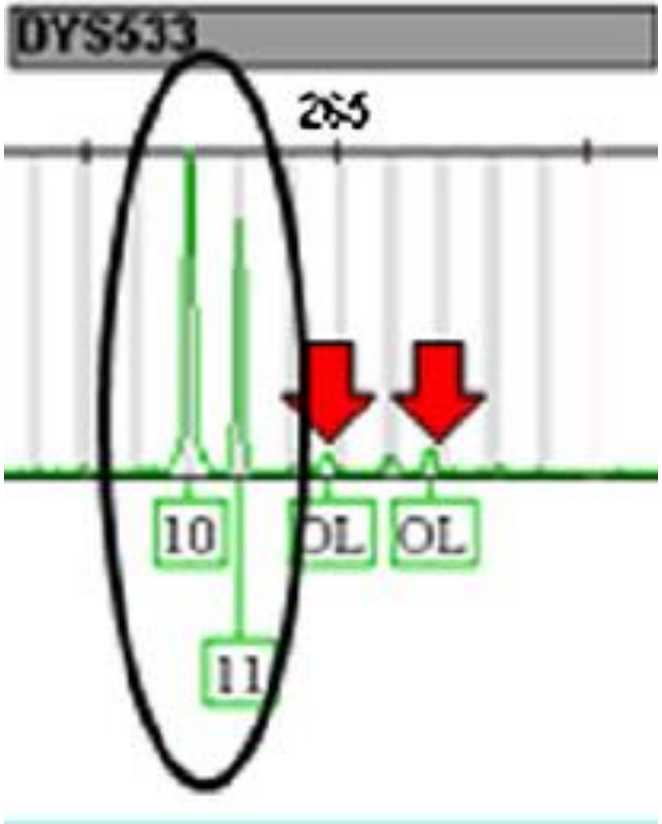
Y-STR Artifacts: Refresher

- DYS481 and OL peaks



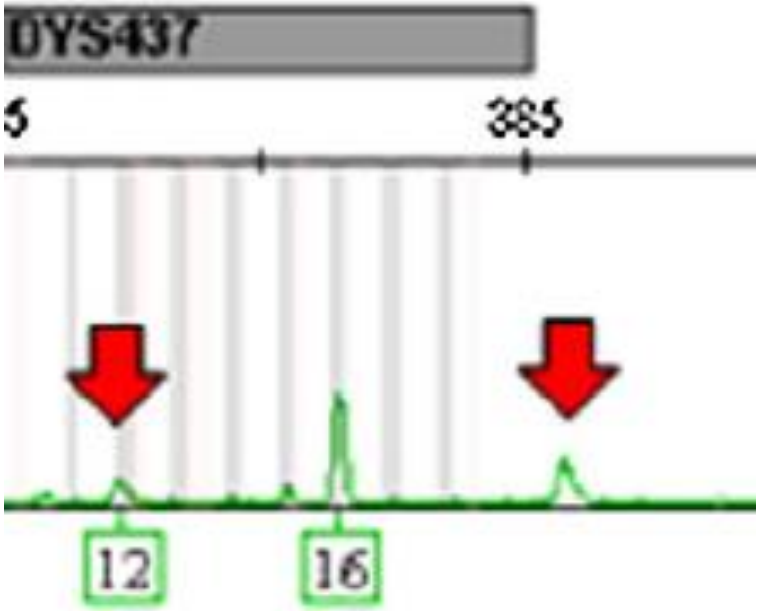
Y-STR Artifacts: Refresher

- DYS533 – 10, 11 and OL peaks



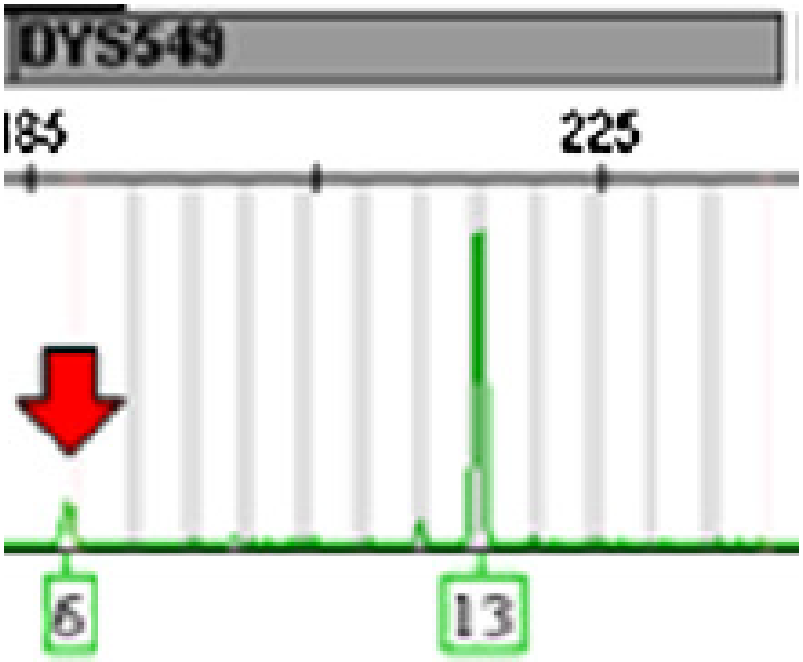
Y-STR Artifacts: Refresher

- DYS437 – 12, 16 and OL peaks



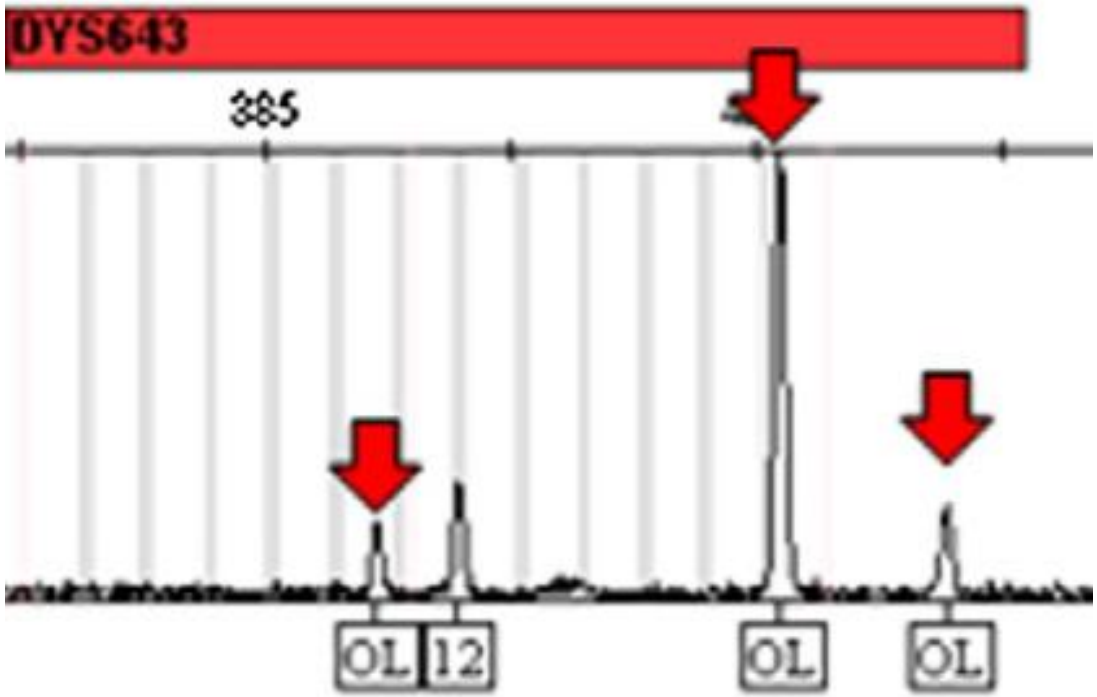
Y-STR Artifacts: Refresher

- DYS549 – 6 and 13 peaks



Y-STR Artifacts: Refresher

- DYS643 – 12 and multiple OL peaks



Y-STR Artifacts: Refresher

- All 6 samples where seen had very high excess of female DNA to male DNA
- Additional peaks exclusively found in samples with male DNA concentrations <0.0286ng/ul and total DNA concentrations of >40ng/ul (1,400:1 ratio female:male)
- Over 700ng of female DNA was added to PCR reaction

- Due to excess female and not mixture or duplication events

Y-STR Artifacts: Refresher

- DNA Concentrations

Table 1
Summary of DNA concentrations, DNA input amounts and larger artefacts observed in casework samples.

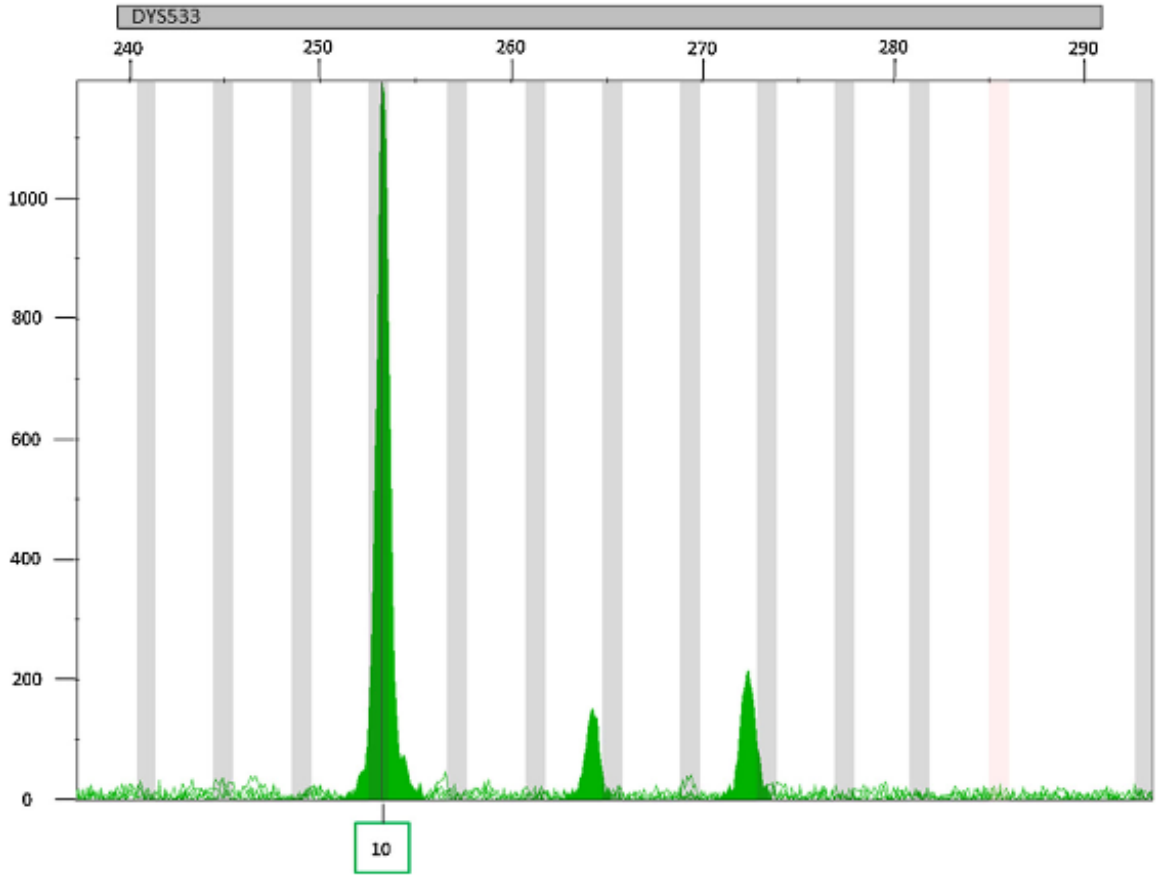
	Case circumstances	Autosomal DNA Conc. (ng/μl)	Male (Y) DNA Conc (ng/μl)	Approx. female: male ratio	Genomic DNA added in 17.5 μl (ng)	Amount of male DNA added in 17.5 μl (pg)	Additional Peaks (Height, rfu)			
							Green 164.5 bp peak, at the DYS481 27.1 allele position	Green 253.2 bp peak, at the DYS533 10 allele position	Yellow 440.5 bp peak	Yellow 426.75 bp peak
Sample 1	Oral intercourse by male on female (vaginal swab)	41	0.00022	186363	717	3.85	146	129	103	50
Sample 2	Suspected azoospermic semen (stain on underwear)	58	0.0017	34117	1015	29.75	107	200	378	264
Sample 3	Digitial penetration (vaginal swab)	60	0.0004	149999	1050	7	150	146	287	75
Sample 4	Penile penetration—no ejaculation (vaginal swab)	110	0.001	109999	1925	17.5	225	187	184	244
Sample 5	Penile penetration—no ejaculation (vaginal swab)	320	0.0021	152380	5600	36.75	792	586	235	204
Sample 6	Digitial penetration (vaginal swab)	500	0.0039	128204	8750	68.25	1235	1431	143	736

Y-STR Artifacts: Refresher

- Additional Study
  - 5 female donor samples with male quant values <0.0005ng/ul
  - Added between 1pg and 8pg of male DNA to PCR reaction
  - Saw artifact peaks in nearly all samples
    - Most likely due to excess female DNA

Y-STR Artifacts: Refresher

- DYS533: 10 peak present in 4 of 5 samples containing >500ng female DNA



Y-STR Artifacts: Refresher

- Observed artifacts: paper

Table 3
Summary table of all artefact peaks identified in this investigation and within the PowerPlex® Y23 technical manual [12]. Artefact peaks highlighted in bold indicate those that were observed in allele positions and/or were observed at peak heights greater than 300rfu.

Additional Peaks				
Dye	Approx. Size (bp)	Nearest Locus/Allele association	Height	Comments
Blue	143–147	DYS389 I	<100 rfu	Poor morphology; possible dye blob
Blue	152.5	DYS389 I	Input dependant; up to 100 rfu with 5 μg of DNA	
Blue	242	DYS448	Input dependant; up to 100 rfu with 5 μg of DNA	
Blue	308–315	DYS19	<100 rfu	Poor morphology; possible dye blob
Green	**164.5**	**DYS481: 27.1 allele position**	**Input dependant; up to 1200rfu with 5 μg of DNA**	**Peak height correlates strongly with green 253.2 bp peak. Detailed in PowerPlex® Y23 user manual**
Green	187.5	DYS549	Input dependant; up to 150 rfu with 5 μg of DNA	Detailed in PowerPlex® Y23 user manual
Green	**253.2**	**DYS533: 10 allele position**	**Input dependant; up to 1200 rfu with 5 μg of DNA**	**Peak height correlates strongly with green 164.5 bp peak, generally off-centre in bin. Detailed in PowerPlex® Y23 user manual**
Green	264.25	DYS533	Input dependant; up to 160 rfu with 5 μg of DNA	
Green	272.5	DYS533	Input dependant; up to 220 rfu with 5 μg of DNA	Detailed in PowerPlex® Y23 user manual
Green	**354.75**	**DYS437: 12 allele position**	**Input dependant; up to 100 rfu with 5 μg of DNA**	**Peak off-centre in bin**
Green	387.75	DYS437	Input dependant; up to 150 rfu with 5 μg of DNA	Outside marker range
Yellow	160	DYS635	Detailed in PowerPlex® Y23 user manual, not observed in internal investigation	
Yellow	**283**	**DYS439: 11 allele position**	**Input dependant; up to 160 rfu with 5 μg of DNA**	**Peak off-centre in bin**
Yellow	394	DYS643	Input dependant; up to 150 rfu with 5 μg of DNA	
Yellow	413–419	DYS643	<100 rfu	Poor morphology; possible dye blob
Yellow	**426.75**	DYS643	**Input dependant; up to 400 rfu with 5 μg of DNA**	**Detailed in PowerPlex® Y23 user manual**
Yellow	**440.5**	DYS643	**Input dependant; up to 1200 rfu with 5 μg of DNA**	**Detailed in PowerPlex® Y23 user manual**
Red	201	DYS458	Detailed in PowerPlex® Y23 user manual, not observed in internal investigation	

Y-STR Artifacts: Refresher

- Observed artifacts: Promega Y23 Manual

Table 4. DNA-Dependent Artifacts Observed with the PowerPlex® Y23 System.

Dye	Artifact
Fluorescein	DYS448 n–9 to n–15[1,2] DYS19 n–2; n+2[3]
JOE	163 bases[4] 187 bases[4] 253 bases[4] 272 bases[4]
TMR	159 bases[4] 428 bases[4] 441 bases[4]
CXR	201 bases[4]

[1]These variably sized peaks on the Applied Biosystems® 3130 and 3500 Genetic Analyzers may represent double-stranded DNA derived from the DYS448 amplicon. (Double-stranded DNA is known to migrate faster than single-stranded DNA on capillary electrophoresis [CE] instruments.)

[2]The low-level, DNA-dependent artifact is noticeable only with high input template amounts and allele peak heights.

[3]Two bases below and above the true allele peak, respectively.

[4]Artifact is observed more often with samples that contain relatively higher levels of female DNA.

Y-STR Artifacts: Refresher

- Additional artifacts: Promega Y23 Manual
  - Storage-related artifacts

Table 5. DNA-Independent Artifacts Observed with the PowerPlex® Y23 System.

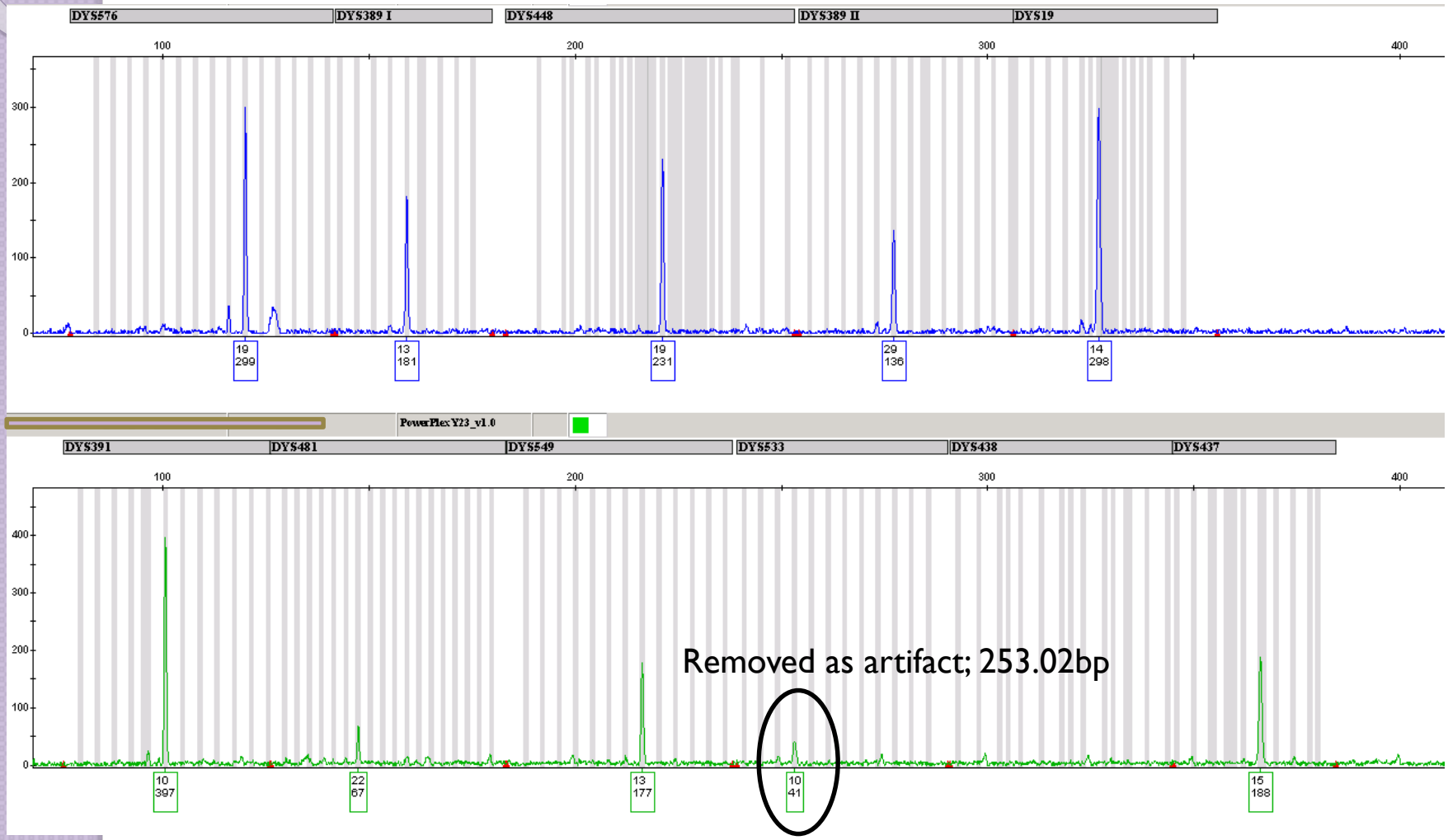
Dye	Artifact
Fluorescein	61–65 bases[1] 58–63 bases[1] 136–144 bases[2]
JOE	136–144 bases[2]

[1]The signal strength of these artifacts increases with storage of the amplification plate at 4°C, sometimes in as short a time period as overnight but more commonly when plates are left at 4°C for a few days. We recommend storing amplification products at –20°C.

[2]Artifact may appear as a dye blob or a peak in sample reaction and negative control reaction.

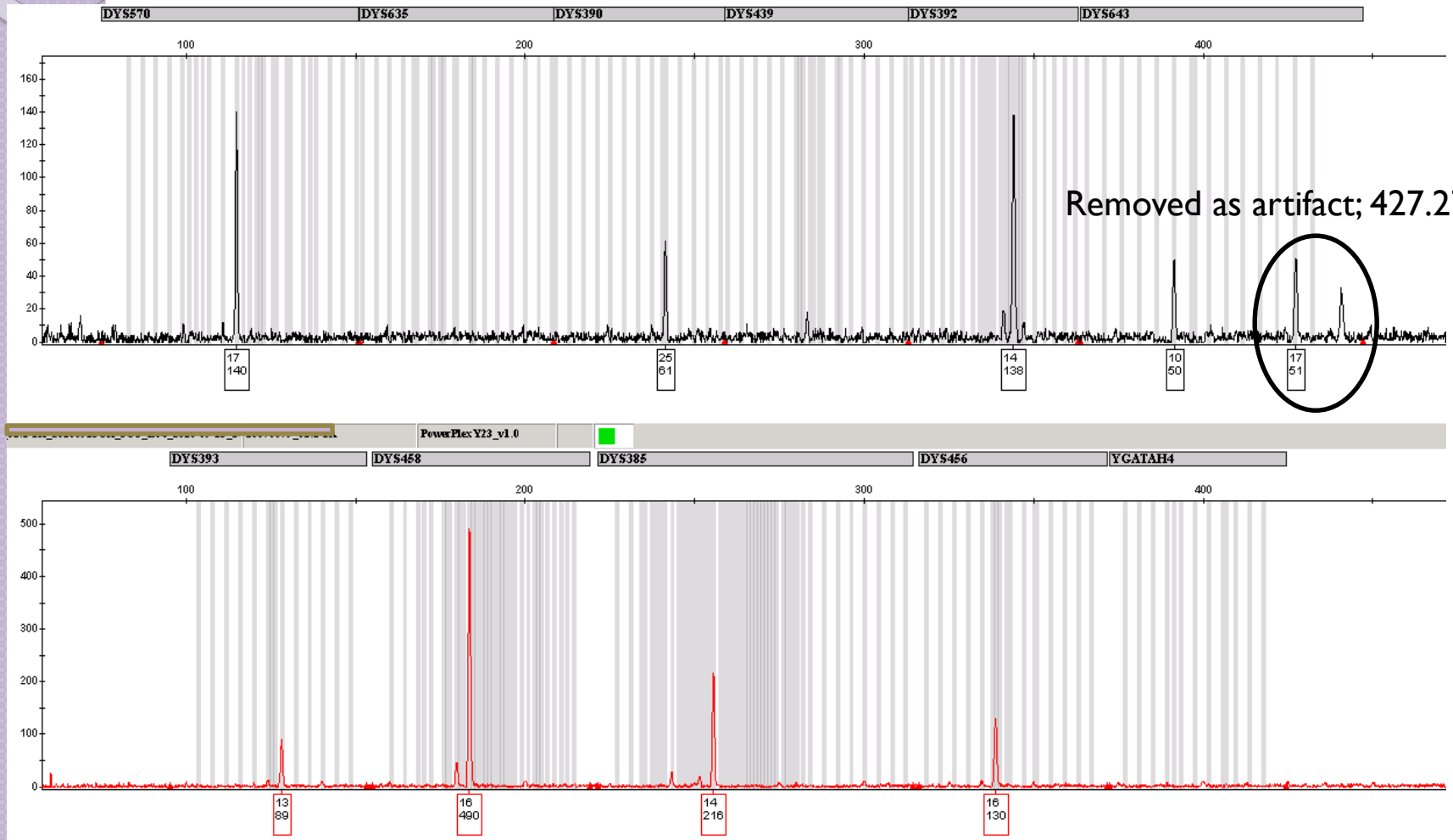
Y-STR Artifacts: Refresher

- NMS Example:



Y-STR Artifacts: Refresher

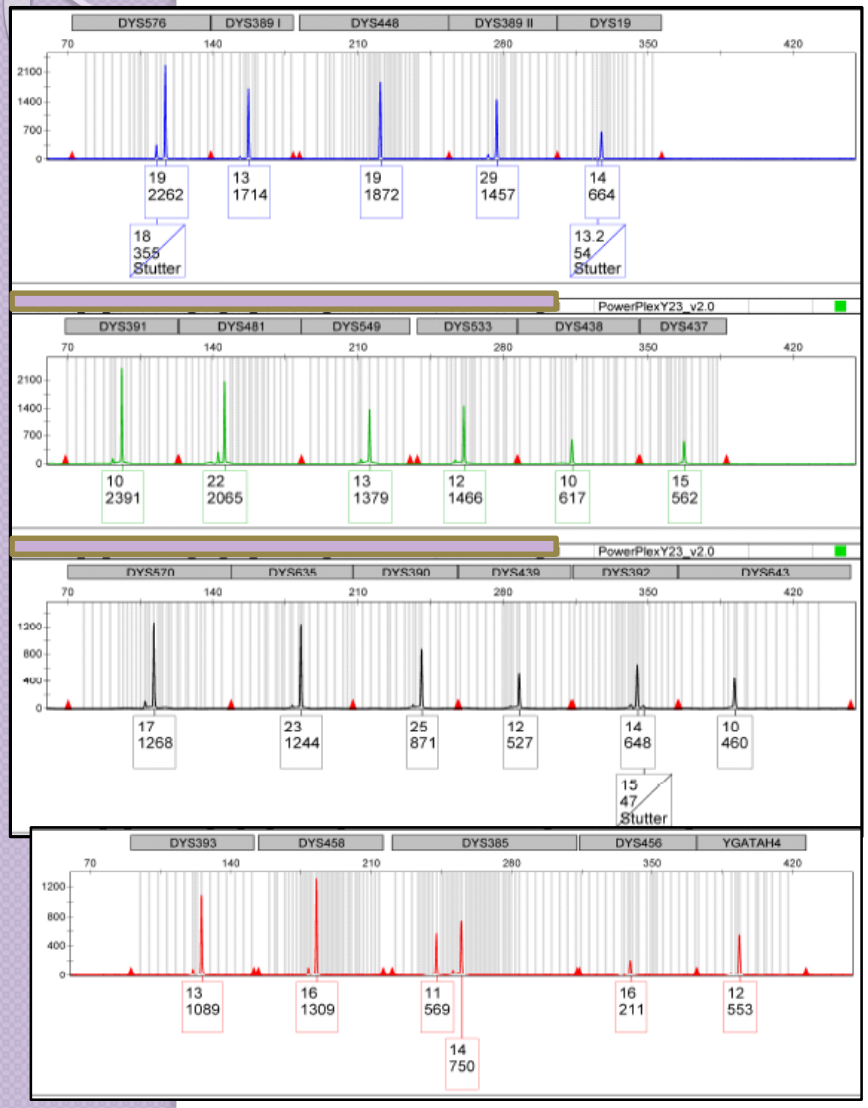
- NMS Example:

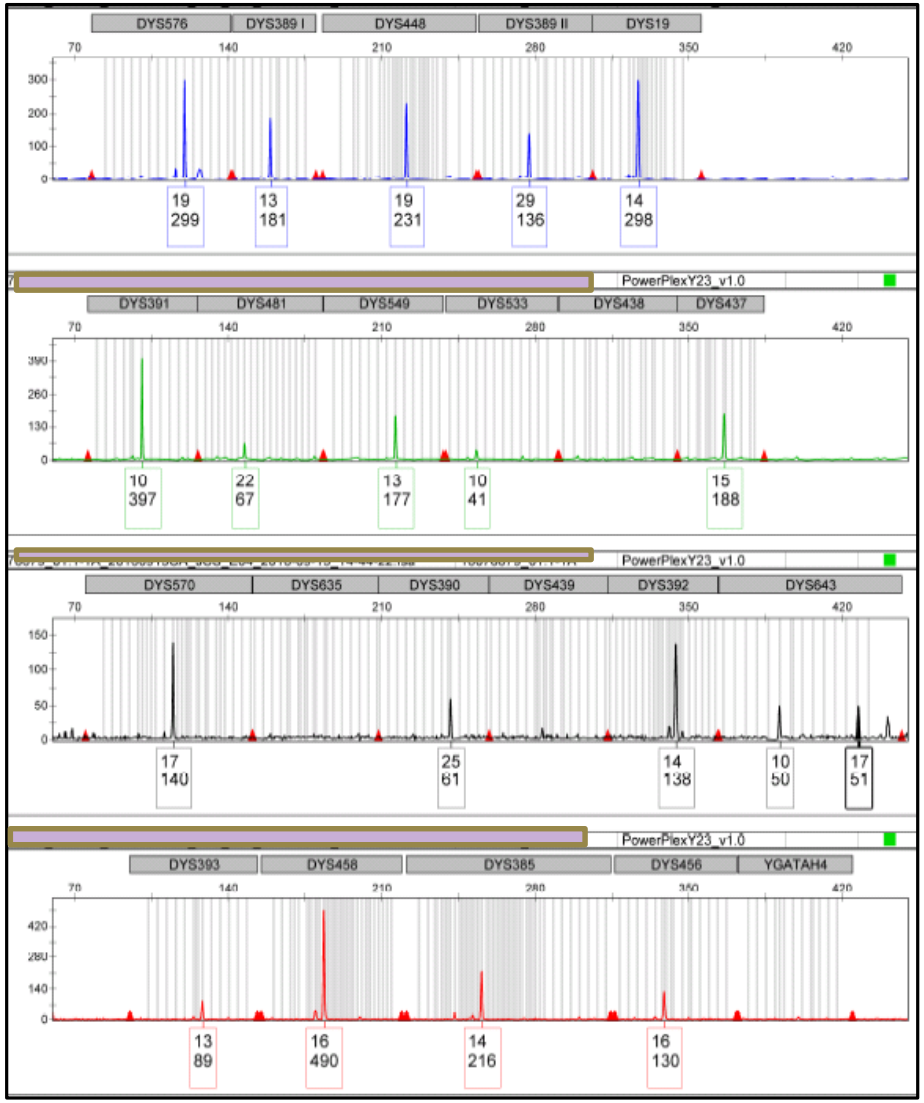


Removed as artifact; 427.27bp

Y-STR Artifacts: Refresher

→ SA=11.4183ng/ul Y=0.0020ng/ul (~5,700:1; 200ng female DNA)





Y-STR Artifacts: Refresher and Future

- Training for all staff (April 2018)
- Modifications to SOP
  - Will include more specifics on these artifacts/edits in STR analysis/review and data interpretation sections
- **Reference Y23 technical manual when analyzing/editing Y-STR data and writing/reviewing Y-STR profiles**
  - Copy is located: Q:\FORENSIC BIOLOGY FILES\Training\Reading Assignments\Amplification\Powerplex Y23 System Protocol_April 2017.pdf
- See Journal Club presentation PowerPoint from TW for additional NMS example data

Questions

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April 30, 2019

Dr. Barry K. Logan
National Medical Services, Inc.
3701 Welsh Road
Willow Grove, PA 19090

RE: Consultation in *United States v Torney*

Dear Dr. Logan:

In reference to the DNA testing performed by NMS Labs in the above-referenced case and the Final Report from the Texas Forensic Science Commission I was requested by you to review several sets of materials and documents and provide feedback to you regarding those reviews. I have completed the requested reviews and provide here a summary of the work performed to date under headers for each of the requested reviews.

Review of *US v Torney* case

Testing Summary

A portion of each of the two half swabs labelled “perianal/buttocks” received by the laboratory was removed for testing (NMS item # 01.2-1). A portion of each of the 1-1/2 swabs labelled “anorectal” received by the laboratory was removed for testing (NMS item #02.2-1). A positive extraction control sample (NMS item EC) was also tested. The samples were extracted using the laboratory differential organic extraction procedure (generating “A” and “B” fractions) and quantitated using the Qiagen Investigator Quantiplex HYres quantitation assay. Approximately 1 ng of DNA from each extract was targeted for amplification with the PowerPlex® 16 HS System amplification kit after dilution of the “A” fraction for each of the samples based on the estimated concentration values obtained. The amplified products were injected on a 3130 Genetic Analyzer for 5 seconds, and the 02.2-1A products were also injected for 1 second. The data were analyzed using GeneMapper ID software using an analytical threshold of 40 RFU. One sample from another case was tested at the same time using the same reagents and following the same procedures.

Data Analysis

The electropherograms for 01.2-1A and 01.2-1B, and 02.2-1B all seem appropriate for the amplification and run conditions stated in the case file and the peak heights for each are fairly similar. The extraction positive control (ECA and ECB) as well as the extraction negative control (RCA and RCB) and the positive and negative amplification controls (PC-031113 and NC-031113) performed as expected. In addition, the electropherograms from the sample from the other case tested at the same time as the

samples from the Torney case all gave appropriate profiles based on the testing performed.

The electropherogram for the 5 second injection of 02.2-1A was analyzed in GeneMapper but was not edited or interpreted by the laboratory. The electropherogram for the 1 second injection had one or two high RFU peak alleles at each locus, with six of the alleles having peak heights greater than 7,000 RFU. When set to label off-scale peaks, each of the six peaks was highlighted with a pink bar in GeneMapper ID, indicating they were off-scale. Three of the high peaks showed either a flat-top or a split "U-shaped" peak morphology, consistent with over-saturation of the CCD camera. The data strongly indicate that more than 1 ng of DNA was amplified for this sample. The high peaks are consistent with being from a single-source female contributor and are consistent with the individual from whom the swabs were collected. In addition, there are many lower RFU peaks above the analytical threshold, especially in the left half of the electropherogram. Many of the low RFU peaks, which are mostly labelled as "OL" (off-ladder) by GeneMapper, were edited out as artifacts, "PU" (pull up), or "shoulder" (probably –A peaks) as can be observed on the printed electropherogram in the case file, and are also indicative of the amplification of far greater than 1 ng of DNA. Overall the baseline/background levels are fairly high and quite jagged for the left half of the electropherogram. A low RFU peak (88 RFU) is present at the amelogenin locus and labelled as a Y allele with an X allele at 3747 RFU; however, the Y labelled peak is present in a series of approximately six peaks having peaks heights of 40-52 RFU making it impossible to draw a definitive conclusion regarding the presence of DNA from a minor male contributor. The jagged baseline on the left side of the electropherogram and the presence of many of the "OL" peaks may be the result of the products electrophoresing at a lower than optimal temperature causing re-annealed products to accumulate to the left side of the major allele peaks. All stutter peaks in the N-1 position to the major allele(s) at each locus were filtered out by GeneMapper using the programmed stutter filters, with the exception of the 9 peak at the TH01 locus, which is only 0.7% above the stutter filter value.

Explanation for Off-Scale Data

Since all of the profiles generated for this case, including all of the extraction and amplification control samples, and the sample from the other case file batched with this case seemed consistent and appropriate for amplification of approximately 1 ng of DNA, it seems unlikely that there was any systemic technical problem during the testing process. Furthermore, the data strongly suggest that the quantitation kit used, the amplification kit used and all other reagents performed appropriately.

The estimated concentration of the DNA for item 02.2-1A was 223 ng/µl, which is outside of the range of the DNA standards used for approximating the concentration. The likely explanations for the off-scale data observed include: a) pipetting error resulting in too much DNA being introduced into the PCR amplification tube and/or too much product in the set up tube for electrophoresis; b) using data outside of the acceptable range of extrapolation of the DNA standards during the quantitation assay without appropriate dilution and quantitation of the diluted extract prior to amplification; or c) a combination of both. According to the laboratory, they had pipettors in use during the time of this testing that were capable of accurately pipetting the correct volumes, and the pipettors had passed calibration tests only 2 months before according to the QA/QC documentation. Similar volumes of DNA were pipetted for amplification of the sample A and B fractions in the other case, supporting that the pipettors were working appropriately at the time of

testing. Without the ability to dilute the original DNA extract and assess the reliability of the DNA concentration previously determined for the extract or to quantitate the dilution made and used for the amplification, it is not possible to determine the specific event(s) that resulted in the off-scale data.

Due to the off-scale data and the numerous lower RFU peaks, it is unclear if true alleles vs. artifacts can be appropriately detected and edited for this electropherogram. This makes the interpretation of any potential data from one or more minor contributors extremely difficult, if not impossible, to evaluate. It is my opinion that the DNA for item 02.2-1A should have been diluted and re-quantitated until a value within the validated linear range for quantitation was obtained, and then the appropriate amount of DNA amplified. The final interpretation, comparison and conclusions should have been reported using data from a second amplification rather than from the initial electropherogram.

Texas Case Review

Between April 4, 2018, and January 21, 2019, a modified technical review was performed on all of the 100 cases submitted from clients in Texas with reports of DNA testing issued from February 2010 to July 30, 2018. An additional case from outside of Texas tested at the same time as the Torney case was also reviewed along with the Torney case for a total of 102 cases reviewed. The cases reviewed covered a variety of types of evidence submitted, amplification of DNA using all of the amplification kits available for use at NMS Labs during the time frame, and multiple staff members who signed reports as analysts and/or technical reviewers. The primary goal of the Texas case review was to address issues related to those observed in the Torney case and included identifying: 1) electropherograms from other samples in other cases with the characteristics of the profile in the Torney case (i.e., other examples of “overblown” data) that were edited and reported without additional testing; and 2) any other cases where there was a discrepancy or dispute regarding the interpretation and/or reporting of the results.

Additional goals of the review included: a) evaluating the calculations done to determine the volume of extract (and thus amount of DNA) to be used in the amplification based on the quantitation results; b) comparing the expected DNA results based on the amount of DNA amplified to the profile generated to identify possible issues/errors in calculations and/or pipetting that may result in profiles similar to the profile in the Torney case; c) evaluating the data generated and reported for consistency and appropriateness; d) providing suggestions and/or recommendations regarding improved documentation, report wording, interpretation or statement of conclusions based on the review of the documentation in the case files, and the data interpretations and conclusions in the reports generated by the laboratory; e) verification that correct and appropriate controls were used with all testing; and f) assessment of the general quality of the work performed in the laboratory with attention to quality issues that had not been addressed previously (e.g., contamination, missing or inaccurate documentation).

Primary Goal #1 and additional goals a) and b):

No other samples in any other cases were identified with “overblown” data that were not appropriately amplified again with a smaller amount of DNA at the time of the initial testing and prior to issuing of the report. Out of the other 101 cases reviewed, I recall only 1 or 2 instances where the sample needed to be re-amplified with less DNA due to an excess of DNA in the initial amplification. In general, all samples gave appropriate

profiles based on the quantitation data and the amount of DNA amplified (typically 0.5 ng of input DNA, when available) with consideration for degradation that was common to many of the types of samples tested in the laboratory. There were no calculation errors detected and no apparent incidences of pipetting errors. Notice was made of any samples with low amounts of DNA extracted using the Qiagen EZ1 Tissue Kit that may have been inhibited during amplification as previously identified by the NMS Labs staff, and which was under investigation and remediation when I started the reviews.

Primary Goal #2:
There was no documentation noted in any of the cases reviewed of discrepancies between any staff members in the interpretation and/or conclusions made from comparison of DNA profiles to known reference profiles. It is unclear whether no discrepancies occurred in any of the cases reviewed or if any that occurred were simply not recorded in the case file as it was not previously a policy in the laboratory to record any discrepancies. Thus it was not possible to evaluate this goal via case file review. However, based on discussions with current analysts, it should be noted that differences in interpretation and conclusions between analysts and technical reviewers are rare events that have all been resolved through discussions. None of the current analysts in the laboratory recall any incidence of a discrepancy that was not resolved through direct discussions of the analyst with the technical reviewer and required any escalation to additional members of the staff for resolution. The NMS Labs manuals were updated in 2018 specifying the process for resolution of and the requirement for the documentation of any discrepancies.

These 102 cases comprise a broad range of the total cases tested in the laboratory over the past 8 years (approximately 8%). Based on this review, it is my opinion that there is no immediate need to initiate any additional review of non-Texas cases to address the issues outlined by the Texas Forensic Science Commission. Based on any of the observations and recommendations that arose from the review of these cases and/or any of the other ongoing corrective actions identified by the laboratory, subsets of cases may be selected by the laboratory for additional review to address specific issues.

Additional goals and General Comments:
Overall the laboratory seems generally to be performing quality work based on the documentation available. Controls, including the laboratory required extraction control, were appropriately used in all cases, contamination was very rarely observed (and suitably addressed in the few instances), the very few errors in testing were appropriately detected and corrected, and the documentation overall was generally quite good so it was fairly straightforward to evaluate the cases and the work performed. The laboratory follows their excellent policy of always testing unknown evidence samples separately and independently from all known reference samples throughout the entire testing process. No significant issues were noted. Some suggestions were made regarding some possible overall improvements to documentation in the case file and report wording as well as in a few specific cases. A recommendation was made for the laboratory to consider first concentrating some samples in certain cases with low quantitation values prior to amplification to perhaps increase the data obtained. For the majority of the cases, I agreed with the interpretation and reporting of the results and conclusions. Some reports are being re-evaluated in light of the laboratory's current assessment of past and current validation studies particularly in regard to the interpretation of low template DNA samples and mixed DNA samples; some amended reports may be issued in a limited number of cases following the laboratory's internal

evaluation of my comments. A very few cases were found to have statistical calculations issued where RMP and CPI values were inappropriately combined. These cases are being evaluated and amended reports will be issued as needed, although it is anticipated that the change in the statistical values reported will not be drastically different from what has already been reported in the cases from Texas. The laboratory was already investigating the reporting of likelihood ratios using LRMix software. I simply flagged those cases and samples for the laboratory where likelihood ratios were provided and occasionally made a recommendation for considering an additional calculation (e.g., changing the number of contributors or adding another conditioned profile).

Because I was working from printed electropherograms and not the actual analyzed data, it was not always possible for me to evaluate peaks/alleles with low RFU values for quality, presence of artifacts and appropriate editing of artifacts by the analyst. All reporting of data, interpretation and conclusions were based on the assumption that this was appropriately performed. A recommendation to include printouts with a shortened range on the Y and/or X axes to better show minor alleles and the justification for editing out artifacts was made. Following additional training by the technical leader, Kristen Smith, I meet with all of the analysts in the laboratory, including very recent hires, in a group setting to discuss all of the artifacts that can occur in DNA testing. They individually described how the artifact arises and during which step of the DNA testing process, the biological/biochemical basis for the presence of the artifact, the characteristic/diagnostic appearance of the artifact in an electropherogram, and what additional testing procedures may be needed to address the artifacts. All of the staff were quite knowledgeable regarding artifacts and were very comfortable discussing all aspects of artifacts. A future competency assessment may be conducted for the laboratory staff to further evaluate the detection of artifacts and the appropriate follow-up actions.

I was able to verify correct data entry for all RMP and CPI calculations, but was not able to for any likelihood ratio calculations or biological relationship testing statistical calculations since the printouts available in the file do not show all of the data.

Possible Technical Issue Causing Some of the Artifact Peaks Observed in the Torney Case

During my review of the data in the Torney case and other cases worked in a similar time frame, the appearance of extra peaks in the internal lane standard of some of the electropherograms suggested that there may be a sporadic problem with re-annealing products generated during electrophoresis of the amplified products. When I brought this to the attention of the laboratory staff, they had noticed that the location of one of the Genetic Analyzers near the thermostat was causing the temperature in the room to be lower than desired. The Genetic Analyzer was immediately moved to another location. The laboratory is aware of this possible issue and is monitoring it closely during their current validation studies to ensure reannealing products will not be the cause of artifact peaks in future casework.

Corrective Actions in the Laboratory

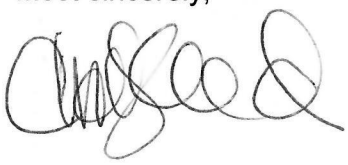
I was consulted regarding the corrective actions initiated in the laboratory in response to the Torney case and understand that they have been completed or are continuing to be appropriately addressed by the laboratory staff. In addition, there are several other corrective actions underway due to other issues identified within the laboratory around

the same time that I was retained as a consultant. I have provided some recommendations and opinions regarding the other areas being addressed, but have not been directly involved with those corrective actions. I am available to the laboratory to consult regarding any of those issues as requested in the future.

Evaluation of Missing Stutter Data from PowerPlex 16 HS Validation Studies
I have reviewed the report from Thomas Walsh regarding the stutter peaks that were deleted from the stutter percentage calculations during the laboratory's evaluation of the manufacturer's recommended stutter peak filter percentages for use with the PowerPlex 16 HS kit prior to introduction of the manufacturer's recommended values for use on casework. It is my understanding that some peaks in the stutter position were deleted from the calculations in this study for three primary reasons: 1) overlapping/compounded stutter peaks located between two alleles separated by two repeats (i.e., in both the N+1 and N-1 stutter position to the two alleles); 2) saturated split peaks with the "U-shaped" morphology; and 3) pull-up artifacts. I agree that for the purposes of this study, the values for these peaks were appropriately removed from the calculations by the laboratory. In response to the comments from the Texas Forensic Science Commission, the stutter peak percentages were re-calculated with the inclusion of the peaks that had been removed. These values are provided in the report from Mr. Walsh and indicate that there is no substantial change in the values obtained. It is my understanding that the laboratory chose to use only the manufacturer's recommended values for stutter filter cutoffs for all casework. It should be noted that the minus stutter peaks adjacent to all of the peaks from the major contributor profile for the 1 second injection for item 02.2-1A in the Torney case were removed by the stutter filter during analysis with GeneMapper ID software with the exception of the 9 peak at the TH01 locus, which was 0.7% above the stutter filter value. It is unclear if the 9 is a true allele or simply a stutter peak that was not filtered out due to the off-scale 10 allele.

Please let me know if you have any questions regarding any information provided in this summary or if there are any other areas that I still need to address. I look forward to an ongoing relationship with your laboratory and will be happy to assist you wherever possible.

Most sincerely,



Charlotte J. Word, Ph.D.