# TEXAS FORENSIC SCIENCE COMMISSION

Justice Through Science

FINAL REPORT ON COMPLAINT BY LISA GEFRIDES AGAINST THE HOUSTON FORENSIC SCIENCE CENTER

HALL

July 20, 2018

11.11

# **REPORT OF THE TEXAS FORENSIC SCIENCE COMMISSION**

Complaint by Lisa Gefrides re: Houston Forensic Science Center (HFSC) Forensic Biology

> [Approved at Quarterly Meeting] July 20, 2018 Austin, Texas

# **Table of Exhibits**

Exhibit A	Gefrides complaint and exhibits
Exhibit B	Dr. Bruce Budowle curriculum vitae
Exhibit C	Dr. Sheree Hughes-Stamm curriculum vitae
Exhibit D	D. Jody Koehler, M.S. curriculum vitae
Exhibit E	Internal Contamination Memo 2016
Exhibit F	CAR 2017-075

This report contains observations and recommendations regarding the complaint filed by Lisa Gefrides on January 20, 2017 (*See* Gefrides Complaint and Exhibits at **Exhibit A**).

# 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 79<sup>th</sup> 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.<sup>1</sup> 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.<sup>2</sup>

The Commission has nine members appointed by the Governor of Texas.<sup>3</sup> 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).<sup>4</sup> 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:<sup>5</sup>

<sup>&</sup>lt;sup>1</sup> See Act of May 30, 2005, 79th Leg., R.S., ch. 1224, § 1, 2005.

<sup>&</sup>lt;sup>2</sup> See e.g., Acts 2013, 83<sup>rd</sup> Leg., ch. 782 (S.B.1238), §§ 1 to 4, eff. June 14, 2013; Acts 2015, 84<sup>th</sup> 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).

 $<sup>^3</sup>$  Tex. Code CRIM. Proc. art. 38.01 § 3.

<sup>&</sup>lt;sup>4</sup> Id.

<sup>&</sup>lt;sup>5</sup> Until the 84<sup>th</sup> Legislative Session, the accreditation program was under the authority of the Department of Public Safety ("DPS").

"...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."<sup>6</sup>

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.<sup>7</sup>

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.<sup>8</sup>

The forensic discipline discussed in this report is DNA analysis, which must be accredited

by the Commission in order for the analysis and related testimony to be admissible in a criminal

action.<sup>9</sup> The laboratory that is the subject of this report, Houston Forensic Science Center

("HFSC") 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."<sup>11</sup> The Act also requires the Commission to: (1) implement a reporting system through which accredited

<sup>&</sup>lt;sup>6</sup> TEX. CODE CRIM. PROC. art. 38.35 § (a)(4).

<sup>&</sup>lt;sup>7</sup> *Id.* at § (a)(4).

<sup>&</sup>lt;sup>8</sup> *Id.* at § (d)(1).

<sup>&</sup>lt;sup>9</sup> *Id at* (a)(4).

<sup>&</sup>lt;sup>10</sup> See <u>http://www.txcourts.gov/fsc/accreditation/</u> for a list of accredited laboratories.

<sup>&</sup>lt;sup>11</sup> TEX. CODE CRIM. PROC. art. 38.01 § 4(a)(3).

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.<sup>12</sup>

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.<sup>13</sup>

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.<sup>14</sup>

## **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.<sup>15</sup> The Commission's written reports are not admissible in civil or criminal actions.<sup>16</sup> The Commission has no authority to subpoen 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

<sup>&</sup>lt;sup>12</sup> *Id.* at § 4(a)(1)-(2).

<sup>&</sup>lt;sup>13</sup> *Id.* at § 4-d(b-1).

<sup>&</sup>lt;sup>14</sup> *Id.* at § 4-d(b-2).

<sup>&</sup>lt;sup>15</sup> *Id.* at § 4(g).

<sup>&</sup>lt;sup>16</sup> *Id*. at § 11.

Federal Rules of Evidence (*e.g.*, against the admission of hearsay) or was subjected to crossexamination under a judge's supervision.

## **II. SUMMARY OF THE COMPLAINT**

The complaint alleges recurring non-conformities in the HFSC DNA laboratory including issues with contamination, proficiency testing and inadequate root cause analysis. The complainant also alleges the laboratory recognized the non-conformities had occurred yet did not take sufficient action to successfully remediate the non-conformities.

Requirements for corrective action in response to non-conforming work product are addressed by the ISO/IEC 17025:2005 General Requirements for the Competence of Testing and Calibration Standards under which crime laboratories are accredited. After a non-conformity is identified, these standards require root cause analysis, implementation and selection of corrective actions, and monitoring the results to ensure that the corrective actions implemented have been effective.

The Federal Bureau of Investigation Quality Assurance Standards ("FBI QAS") also require DNA laboratories to identify the root cause of non-conformities and implement corrective and preventative actions, as necessary.

### **III. INVESTIGATIVE PROCESS**

The Commission assembled a review panel including Commissioners Dr. Bruce Budowle and Dr. Sheree Hughes-Stamm and Jody Koehler, the Commission's Senior Scientific Advisor (*See* Budowle CV at **Exhibit B**; *See* Hughes-Stamm CV at **Exhibit C**; and Koehler CV at **Exhibit D**.)

### A. Documents Reviewed

The Commission's staff reviewed approximately 100 quality incidents (e.g. corrective actions) ranging from 2012 through 2017. Other documents reviewed included: FBI QAS audits (internal and external) from 2014 to 2017, management system reviews from 2015-2017, the forensic biology decontamination experimental study plan, the PrepFiler Hamilton Validation, and the AB robotics validation. The laboratory was very responsive in providing documents during this process. The laboratory also has an external website that provides final quality system documentation for non-conformities, standard operating procedures for all disciplines, and the laboratory's quality manual. The website is accessible the following at link: https://records.hfscdiscovery.org.

### **B.** Staff Interviews

During staff interviews, Dr. Budowle and Ms. Koehler interviewed 12 analysts (from a total of 33 FTE's in the DNA section). The primary concern voiced by the group was a need for improvement in the internal training program. Comments included the perception that the section lacks a defined training program, there is no designated training coordinator, and training/competency sets do not mimic actual casework. The need for improvement in the training program was also identified in the 2017 internal DNA audit. Some analysts also expressed a perception that "quantity" of casework was more important than "quality" of casework, others expressed their belief that the quality of the work environment needs to be improved. One analyst described internal training on DNA mixtures as lacking sufficient structure and direction. Some analysts noted high turnover in the section, with 17 people having left the DNA section since 2016. Other analysts expressed a perception that upper management does not fully appreciate the analysts' concerns with respect to these issues.

## **IV. OBSERVATIONS**

## A. Assessment of Professional Negligence/Misconduct

Article 38.01 of the Texas Code of Criminal Procedures requires the Commission to describe whether professional negligence or misconduct occurred for complaints filed involving accredited laboratories and accredited forensic disciplines. Neither "professional negligence" nor "professional misconduct" is defined in the statute. The Commission has defined both terms in its policies and procedures and published rules.<sup>17</sup> The term "professional negligence" is defined as follows:

"<u>Professional Negligence</u>" means the actor, through a material act or omission, negligently failed to follow the standard of practice generally accepted at the time of the forensic analysis that an ordinary forensic professional or entity would have exercised, and the negligent act or omission would substantially affect the integrity of the results of a forensic analysis. An act or omission was negligent if the actor should have been but was not aware of an accepted standard of practice required for a forensic analysis.

The term "professional misconduct" is defined as follows:

"<u>Professional Misconduct</u>" means the actor, through a material act or omission, deliberately failed to follow the standard of practice generally accepted at the time of the forensic analysis that an ordinary forensic professional or entity would have exercised, and the deliberate act or omission would substantially affect the integrity of the results of a forensic analysis. An act or omission was deliberate if the actor was aware of and consciously disregarded an accepted standard of practice required for a forensic analysis.

The complainant did not allege any intentional wrongdoing, and the Commission found no

evidence of misconduct. The Commission also did not find sufficient support to issue a finding of professional negligence against the laboratory, because staff made multiple good faith efforts to address the nonconformities described by the complainant. However, the Commission agrees with the complainant's observations that those efforts still resulted in inadequate root cause analysis,

<sup>&</sup>lt;sup>17</sup> The Commission's policies and procedures have been developed into administrative rules and will ultimately be published in 37 TEX. ADMIN. CODE §15.

inadequate corrective action, and inadequate evaluation of corrective actions. While it is not uncommon for forensic laboratories to struggle with effective root cause analysis, shortcomings in this area may have serious implications for the effectiveness of the overall quality system of the laboratory as described in further detail below.

### **B.** Complaint Substance vs Review Panel Observations

## 1. Inadequate Root Cause Analysis

The laboratory did an excellent job summarizing quality events in the DNA section but did not conduct a sufficient inquiry to determine the true root cause of the events. The review panel observed several quality incidents where root cause analysis was attempted but fell short of identifying the baseline cause. While there was an effort to reduce contamination by improved use of personal protective equipment (PPE) and cleaning of instruments and workspace, there did not appear to be a further effort to assess to what extent internal processes, (e.g., analyst training), may have been responsible for weaknesses in the system.

One example was a series of events in which the DNA section detected contamination in blanks (reagent blanks and/or controls) processed with the samples. Analysts detected the contamination, however, neither the DNA section nor the quality assurance staff attempted to identify whether sample to sample contamination may have occurred. Examples of action by the laboratory are included in the internal contamination memo dated November 4, 2016 that attempted to address increases in contamination events in 2016. (*See* Internal Contamination Memo 2016 at **Exhibit E**). Another increase in contamination occurred in 2017 indicating that the true root cause may not have been adequately addressed (*See* CAR 2017-075 at **Exhibit F**). Interviews with staff led Dr. Budowle and Ms. Koehler to the conclusion that inadequacy of the

training program was the true root cause for the contamination that occurred with relative frequency and was not addressed effectively in CAR 2017-075.

Many of the contamination incidents were attributable to newer analysts, and the staff interviewed understood overall training weaknesses to be the root cause. However, this observation was not reflected in the documents generated by the quality system. Specific weaknesses in the training program included: (1) training assignments did not mimic actual casework; (2) the training process was "rushed"; (3) there was a lack of consistency due to the fact that different senior analysts provided training to new analysts depending on scheduling availability; and (4) some training was substantively inadequate. These shortcomings, which can lead to weaknesses in essential skills among analysts, could easily lead to contamination incidents regardless of how many times the laboratory emphasized the importance of using PPE and cleaning instruments and workspaces.

# 2. Inadequate corrective action

While the laboratory has been proactive in taking corrective action to address nonconformities in the DNA section, because the true root cause was not identified, the corrective actions that followed were inadequate to prevent recurrence. An example is proficiency tests (CTS 14-574 and CTS 14-575) where the laboratory detected semen yet according the proficiency test provider, the test was comprised of female-only bodily fluids. An outside laboratory (Bode Cellmark Forensics) examined the slides HFSC had examined and concluded initially that no spermatozoa were detected. Once HFSC contacted Bode and told them HFSC had observed spermatozoa, Bode examined the slides again and stated they also observed spermatozoa on two of the three slides. The presence of spermatozoa on a test that ostensibly contained female-only body fluids should have raised a red flag regarding the possibility of contamination not only in the proficiency test sample but also in other samples that may not have been as easily detected.

In response to the proficiency test discrepancy, the DNA section held a section-wide meeting to discuss transfer of contact DNA in the laboratory. The laboratory then moved to a DNA-based male screening technique which eliminated the need for analysts to identify spermatozoa. However, this change in analytical approach does not address whether similar potential contamination issues may have occurred in casework that was processed before moving to the DNA-based male screening technique. Finally, the internal contamination memo from November 4, 2016 and CAR 2017-075 show many similarities in the corrective actions taken. If the corrective actions taken in 2016 had been adequate there may have been significant improvement in 2017, instead of repetition of similar issues.

## 3. Inadequate evaluation of implemented corrective actions

When corrective actions are implemented, it is imperative to evaluate their effectiveness to ensure quality issues do not recur. More effective follow-up by the HFSC DNA and quality sections after the rise in contamination events from 2016 should have reduced the contamination events in 2017. The effect of corrective action should have been monitored with follow up especially given that some of the corrective actions were substantively the same as in 2016. Other examples unrelated to contamination events include proficiency tests being submitted to the test provider with clerical errors (e.g., incorrect or omitted results) and samples from different cases being given the same unique identifiers. The proficiency test issues occurred four separate times from 2014-2016. The duplication of sample identifiers occurred five separate times in 2015. While the laboratory attempted some follow-up to evaluate the effectiveness of the corrective actions, because they did not identify the true root case, the events recurred.

# V. CORRECTIVE ACTIONS AND RECOMMENDATIONS

The Commission commends Robin Guidry, DNA Technical Leader, and Peter Stout, Chief Executive Officer of HFSC, for providing their full support and commitment to the review process since the original complaint was filed. The DNA analysts interviewed were also forthcoming, cooperative and eager to participate in positive training initiatives and discussions with the review panel. The following areas of improvement were identified by the review panel:

- 1. Improve DNA training program, update the training manual and ensure consistent implementation, including the following:
  - a. Hire a dedicated training coordinator who has subject matter expertise and can be readily informed regarding new technologies utilized by the laboratory;
  - b. Identify and utilize personnel who are good instructors;
  - c. Perform evaluation of trainers by trainees and management; and
  - d. Ensure practice/competency sets are consistent with the magnitude and complexity of samples encountered during casework.
- 2. Assess the quality assurance (QA) program to ensure QA personnel are effective and have the authority to perform their job proactively;
- 3. Evaluate the extent to which shortcomings in root cause analysis may exist in other forensic disciplines outside of DNA;<sup>18</sup>
- 4. Ensure performance of adequate root cause analysis for quality events;
- 5. Ensure adequate evaluation of the effectiveness of implemented corrective actions;
- 6. Due to observations regarding the possibility of carryover contamination, in collaboration with Dr. Budowle and Ms. Koehler, develop a plan to review of a body of cases for which carryover risk may be present.
- 7. Due to observatonis regarding inadequacies in the training program particularly with respect to interpretation of DNA mixtures, review a representative sample of DNA mixture casework for newly qualified analysts to ensure protocols are being applied appropriately.

<sup>&</sup>lt;sup>18</sup> See e.g., Report of Texas Forensic Science Commission dated January 23, 2014 noting inadequacies in the quality system with respect to a blood alcohol analysis nonconformity.

HFSC has implemented important and significant changes in the last few months, including the following:

- 1. Retained ANAB expert to provide Root Cause Analysis Training for all division managers and supervisors on May 29, 2018;
- 2. Hired FBIO Training Coordinator who starts July 23, 2018;
- 3. Hired Assistant CODIS Administrator who started June 18, 2018;
- 4. Posted CODIS Liaison position, laboratory is currently evaluating resumes;
- 5. Purchased Small Pond for contamination detection with a target implementation date of summer 2018;
- 6. Conducted round tables with all Forensic Biology staff to enhance training programs for screening, analytical procedures, and DNA data analysis; and
- 7. Completed procurement process to outsource DNA analysis to Bode Cellmark Forensics for at least 10 months, which will enable the laboratory to focus on intensive training and improve internal training processes.

HFSC should continue the action items outlined above and address any Commission

recommendations that have not yet been addressed. Finally, the Commission requests that HFSC

provide Commission staff with quarterly updates regarding the progress made on the items

outlined above until such time as all items on the list have been addressed.

# TEXAS FORENSIC SCIENCE COMMISSION • COMPLAINT FORM (Cont.)

# **1.** Person Completing This Form

Name:	Lisa Gefrides, MS
Address	: 16806 Glenshannon Dr
City:	Houston
State: 7	exas Zip Code: 77059
Home	Phone: 7137035472
Work P	'hone: 7137035472
Email A	ddress (if any): LISA.GEFRIDES@GMAIL.COM

# 2. SUBJECT OF COMPLAINT

List the full name, address of the laboratory, facility or individual that is the subject of this disclosure:

Individual/Laboratory:	Houston	Forensic	Science	Center
------------------------	---------	----------	---------	--------

Address:	1301 Fannir	n St, Ste. 170
City:	Houston	
State: Te	exas	Zip Code: 77002
Date of I	Examination, Ar	alysis, or Report:
Type of f	orensic analysis:	Forensic Biology
Laborato	ry Case Numb	er (if known):

Is the forensic analysis associated with any law enforcement investigation, prosecution or criminal litigation? Yes No

\* If you answered "Yes" above, provide the following information *(if possible):* 

\* Name of Defendant:

- \* Case Number/Cause Number: (if unknown, leave blank)
- \* Nature of Case: (e.g burglary, murder, etc.)
- \* The county where case was investigated, prosecuted or filed:

\*The Court:

\* The Outcome of Case:

\* Names of attorneys in case on both sides (*if known*):

### Your relationship with the defendant:

Self	Family Member	
Parent	Friend Attorney	
None	Other (please specify):	

If you are not the defendant, please provide us with the following information regarding the defendant: Name:

Address (if known):

Home Phone:

Work Phone:

# 3. WITNESSES

Provide the following about any person with factual knowledge or expertise regarding the facts of the disclosure. Attach separate sheet(s), if necessary.

First Witness (if any):
Name:
Address:
Daytime Phone:
Evening Phone:
Fax:
Email Address:
Second Witness <i>(if any):</i>
Name:
Address:
Daytime Phone:
Evening Phone:
Fax:
Email Address:
Third Witness <i>(if any):</i>
Name:
Address:
Daytime Phone:
Evening Phone:
Fax:
Email Address:

# TEXAS FORENSIC SCIENCE COMMISSION • COMPLAINT FORM (Cont.)

# 4. DESCRIPTION OF COMPLAINT

Please write a brief statement of the event(s), acts or omissions that are the subject of the disclosure.

The Houston Forensic Science Center's Biology Laboratory's quality assurance program is not adequately identifying and controlling errors associated with the testing of biological evidence.

Naturally, when humans are involved in a process, mistakes will occur. Laboratory personnel are no exception. A good laboratory will have safeguards in place to detect errors and ensure they are contained. When a laboratory error occurs, the laboratory must determine the source of the error (root cause), determine whether other cases/samples are affected (quantify the scope of the error and whether steps to contain it are needed), correct the error (corrective action), and take steps to prevent the error from repeating (preventive action).

The Houston Forensic Science Center's Biology Laboratory is not taking adequate steps to diagnose the source of lab errors, to determine whether other cases/samples may be affected, and to prevent recurrence. Because of this, it is likely that cases have been reported with incorrect results.

-Issue 1: Proficiency test results-

-On three proficiency tests used to evaluate the effectiveness of personnel and procedures to perform casework, the HFSC detected semen on samples that were female bleed (only). This incorrect positive result likely is attributed to cross-contamination during slide making or misidentification of cellular material as sperm cells. There is no documentation that the -laboratory reviewed actual case files to determine whether similar mistakes were made in easework.

-Issue 2: Contaminati

-Between 2012-2014, the HFSC laboratory reported nine contamination events over a three-year period. Since 2015, the laboratory has reported six additional-contamination events withanother twenty still under investigation (at least twenty-six in less than two years).

In every instance, the laboratory failed to review additional cases to determine whether non-blank samples processed concurrently or similarly were affected. Not only has the laboratory failed to make process improvements to reduce occurrence, it has not processed additional control samples to better identify and quantify sample errors.

#### Issue 3: Repeated quality issues

The Houston Forensic Science Center's Biology Laboratory is not taking adequate steps to control the source of lab errors, as the repetitive nature of its quality incidents suggests:

Four corrective action reports involve proficiency tests where the laboratory submitted incorrect (or omitted) results due to clerical errors. (2014-014, 2015-003, 2016-004, 2016-083)
 Five separate times in 2015, samples from different cases were given the same unique identifiers (sample names), (2015-006, 2015-007, 2015-010, 2015-018, 2015-022)
 At least 26 contamination events have occurred since 2015.

Issue 4: 2016 Internal Audit

The Houston Forensic Science Center's Biology Laboratory is not taking adequate steps to diagnose the source of lab errors. The laboratory's mindset is likely the basis for this failure as evidence by the laboratory's response to their own internal audit findings:

For each of the 9 audit findings on their 2016 Internal Audit (2016-IA-10 through 2016-IA-18), the laboratory concluded the following:

"This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology...) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's [sic] issued through internal audits."

The root cause of all quality issues should be addressed to better understand system failures.

In conclusion, these issues indicate a quality system that is not functioning in a manner to prevent compromised results. A thorough review of the Biology Division's quality system and case work should be undertaken to guarantee the validity of its findings. Based on the outcome of the review, a laboratory-wide quality review may be necessary.

# TEXAS FORENSIC SCIENCE COMMISSION • COMPLAINT FORM (Cont.)

# **5.** EXHIBITS AND ATTACHMENT(S)

Whenever possible, disclosures should be accompanied by readable copies (NO ORIGINALS) of any laboratory reports, relevant witness testimony, affidavits of experts about the forensic analysis, or other documents related to your disclosure. Please list and attach any documents that might assist the Commission in evaluating the complaint. Documents provided will **NOT** be returned. List of attachments:

The following Corrective and Incident Reports can be located online at http://www.hfscdiscovery.org/:

Issue 1: Proficiency Test (2015-001)

-Issue 2: Contamination (2014-010, 2014-013, 2014-027, 2015-024, 2016-005, 2016-032, 2016--049, 2016-050)

Issue 3: Proficiency tests (2014-014, 2015-003, 2016-004, 2016-083), Mislabeling (2015-006, 2015-007, 2015-010, 2015-018, 2015-022), Contamination (2014-010, 2014-013, 2014-027, 2015-024, 2016-005, 2016-032, 2016-049, 2016-050)

Issue 4: 2016-IA-10 through 2016-IA-18

The following Corrective and Incident Reports are attached (3):

1. 2012-005 to 017 contains information for Issues 2 and 3: Contamination (2012-007, 2012-008, 2012-014, 2012-017)

-2. 2013-011 to 2014-015 contains information for Issues 2 and 3: Contamination (2013-018, 2014--004, 2014-009)

3. Email regarding 20 contamination events that are not yet closed.

4. My CV		
1		

# 6. YOUR SIGNATURE AND VERIFICATION

By signing below, I certify that the statements made by me in this disclosure are true. I also certify that any documents or exhibits attached are true and correct copies, to the best of my knowledge.

Signature:	
Date Signed: January 20, 2017 - 1:04am	

# LISA A. GEFRIDES, MS

Forensic Serology/DNA Consultant

### PROFESSIONAL EXPERIENCE

2013-current	Consultant Forensic Biology & DNA
2009-2013	<u>Co-founder</u> & Member Forensic Test Preparation, LLC/ABCTestprep.com
2005-2011	DNA Technical Assessor (Auditor) Consultant National Forensic Science Technology Center (NFSTC)
2004- 2011	DNA Analyst I – Compliance/R&D Manager Harris County Institute of Forensic Sciences Forensic Genetics Laboratory Joseph A. Jachimcyzk Forensic Center, Houston, TX
	DNA Compliance/R&D Manager; supervised a staff of 5-8 DNA Analysts; responsible for training of new laboratory analysts; section QA/QC Liaison; responsible for validation and implementation of new technologies; serology casework, STR-DNA casework (ABI-3130XL), expert testimony (Harris & Montgomery Counties)
2000- 2004	DNA Analyst II Harris County Medical Examiner's Office DNA Laboratory Joseph A. Jachimcyzk Forensic Center, Houston, TX
	MtDNA casework (ABI 377), serology casework, STR-DNA casework (ABI 310, ABI 3100-Avant), CODIS, Trace evidence collection from homicide victims, expert testimony (Harris & Montgomery Counties)
1999- 2000	<u>Research Assistant II</u> Bluebird Developmental Neurogenetics Laboratory Department of Neurology Baylor College of Medicine, Houston, TX
	<u>Predoctoral Fellow</u> , EPA Training Grant USA-EPA, NHEERL, Research Triangle Park, NC Curriculum of Toxicology, UNC-Chapel Hill
1995- 1998	<u>Research Assistant</u> Birth Defects Research Laboratory Texas A&M University, College Station, TX
OTHER EXPERIENCE	
1995- 1998	<u>Teaching Assistant</u> Department of Biochemistry and Biophysics

Texas A&M University, College Station, TX Advanced Human Genetics (1 semester) Introduction to Genetics Laboratory (5 semesters)

# **EDUCATION**

January 2015	Certificate of Biblical and Theological Studies (CBTS) Dallas Theological Seminary
December 1998	M.S. Genetics Department of Veterinary Anatomy and Public Health Texas A&M University GPA 4.0
December 1994	B.A. Anthropology/ Genetics minor Texas A&M University <i>Cum Laude</i> (GPA 3.6)

## **CONTINUING EDUCATION & MEETINGS**

January 2001	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX) Topics included mtDNA extraction from difficult samples
February 2001	Training at the FBI DNAUII (Washington, DC) on mtDNA analysis
July 23-Aug. 3, 2001	Two-week training course at the FBI Academy on Forensic Mitochondrial DNA Sequencing and Analysis (Quantico, VA)
September 9, 2002	CODISmt 5.2W Usability Review at SAIC—8 hour training/evaluation on new CODIS software for mtDNA focusing on Missing Person Database (SAIC facility)
January 9-10, 2003	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX) Topics included Crime Scene Investigation, Animal DNA Forensics, Ethics, and Identification of non-standard bodily fluids
March 18-19, 2003	DNA-VIEW software and statistics training—6 hour training by software developer
May 5-6, 2003	DNA Auditor Training, Austin, TX 16 hour course presented by the FBI
July 31-Aug. 1, 2003	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX)
November 17-21, 2003	Grant Writing Class (40 hours) Northeast Counterdrug Training Center, Fort Indiantown Gap, PA
January 15-16, 2004	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX)
November 15-17, 2004	10th Annual National CODIS Conference (Crystal City, VA)
January 20-21, 2005	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX)
September 12-13, 2005	"Forensic DNA Statistics" presented by Dr. George Carmody (16 hours).

March 20-21, 2006	"Bloodstain Pattern Recognition and Examination of Bloodstained Clothing Workshop" (16 hours) presented by Michael J. VanStratton and Kevin R. Winer
October 23-24, 2006	12th Annual National CODIS Conference (Crystal City, VA)
June 7-8, 2007	Grant Progress Assessment (GPA) Program: FBI DNA Audit Refresher Training & Annual Training for GPA Assessors (Washington, DC)
July 10, 2007	Future Trends in Forensic DNA Technology (ABI) (Austin, TX)
July 23-25, 2007	DNA Grantees Meeting (NIJ) (Arlington, VA)
October 2-4, 2007	18th International Symposium on Human Identification (Hollywood, CA)
August 7-8, 2008	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX)
December 9, 2008	Mixture Interpretation Workshop (8 hours) presented by Gary Shutler, PhD and Phil Hodge, MS from the Washington State Highway Patrol.
January 13, 2009	Ethics Seminar "Is there a science to right and wrong? Responsibilities of forensic scientists in today's crime laboratories" (2 hour)
January 27, 2009	Forensic DNA Training Workshop (8 hours) by John Butler, PhD from NIST
February 18-21, 2009	American Academy of Forensic Science 61st Annual Meeting (Denver, CO)
March 13, 2009	Introduction to Uncertainty in Forensic Chemistry (On-demand portion), NIJ/RTI International on-line course worth 1 contact hour
November 3-4, 2009	DNA Auditor Training, Houston, TX 16 hour course presented by the FBI
January 28-29, 2010	Association of Forensic DNA Analysts and Administrators (AFDAA) meeting (Austin, TX)
Jan/Feb 2010	Ethics in Forensic Science, West Virginia University Extended Learning (online)

## MANAGEMENT TRAINING

January 25, 2005	"Supervising and Motivating Difficult People" (4 hours)		
May 30, 2007	Understanding and Implementing the Fair Labor Standards Act, the Americans with Disabilities Act and the Family and Medical Leave Act. Eileen C. Begle (3.5 hours)		
December 5, 2007	Building Organizational Excellence. Walter Natemeyer. (4 hours)		
December 11, 2007	Preventive Counseling. Jay Aldis (3 hours)		
March 20, 2008	Hiring, Lawful Documentation, and Evaluations and Counseling. (3.5 hours)		
November 19, 2008	Coaching for Continuous Improvement (4 hours)		
January 15, 2009	Performance Management Part 2: Conducting Successful Conversations. Deedee Ostfeld. (4 hours)		

December 14, 2009 Achieving Communication Effectiveness (1.5 hours). Vital Learning on-line.

May 24, 2010 Communicating Up (1.5 hours). Vital Learning on-line course. **PUBLICATIONS** 

Lisa A. Gefrides and Katherine E. Welch. 2011. Forensic Biology: Serology and DNA. In <u>The Forensic</u> <u>Laboratory Handbook Procedures and Practice</u>, 2<sup>nd</sup> edition. A. Mozayani and C. Noziglia eds. Humana Press (Springer Science+Business Media). pp. 15-50.

L.A. Gefrides, et al., UV irradiation and autoclave treatment for elimination of contaminating DNA from laboratory consumables, Forensic Science International: Genetics 4 (2010) 89–94.

Lisa A. Gefrides and Katherine E. Welch. 2005. Serology and DNA. In <u>The Forensic Laboratory</u> <u>Handbook: Procedures and Practice</u>. A. Mozayani and C. Noziglia eds. Humana Press. pgs. 1-30.

Mayra Mori, Daniel L. Burgess, Lisa A. Gefrides, Perry J. Foreman, Joseph T. Opferman, Stanley J. Korsmeyer, Esper Abrao Cavalheiro, Maria da Graca Naffah-Mazzacoratti, Jeffrey L. Noebels. 2004. Expression of apoptosis inhibitor protein Mc11 linked to neuroprotection in CNS Neurons. <u>Cell Death and Differentiation</u>. 2004 Nov;11(11):1223-33.

Lisa A. Gefrides, Gregory D. Bennett, and Richard H. Finnell. 2002. The effects of folate supplementation on the risk of spontaneous and induced neural tube defects in Splotch mice. <u>Teratology</u> 65:63-69.

Daniel L. Burgess, Lisa A. Gefrides, P. Jay Foreman, and Jeffrey L. Noebels. 2001. A Cluster of Three Novel Ca<sup>2+</sup> Channel  $\gamma$  Subunit Genes on Chromosome 19q13.4: Evolution and Expression Profile of the  $\gamma$  Subunit Gene Family. <u>Genomics</u> 71 (3):339-350.

Daniel L. Burgess, Caleb F. Davis, Lisa A. Gefrides, and Jeffrey L. Noebels. 1999. Identification of three novel Ca(2+) channel gamma subunit genes reveals molecular diversification by tandem and chromosome duplication. <u>Genome Research</u> 9(12):1204-13.

Gregory D. Bennett, Jie An, Johanna C. Craig, Lisa A. Gefrides, Jim A. Calvin, and Richard H. Finnell. 1998. Neurulation abnormalities secondary to altered gene expression in neural tube defect susceptible Splotch embryos. <u>Teratology</u> 57:17-29.

### ABSTRACTS

Katherine Welch, MSFS\*, Tiffany Best, BS, Anna Timanova, PhD, <u>Lisa A.Gefrides, MS</u>, and Roger Kahn, PhD. "An Efficient, Systematic Approach to Serology Screening of Sexual Assault Evidence." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 38.

Rhonda C. Williams, PhD\*, <u>Lisa Gefrides, MS</u>, and Roger Kahn, PhD. "Characterizing DNA Contamination on the Outer Packaging of Forensic Biology Evidence." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 42.

Nikia S. Redmond, MSFS\*, Katherine Welch, MSFS, <u>Lisa Gefrides, MS</u>, and Roger Kahn, PhD. "Touch DNAFrom Property Crimes – CODIS Success Stories." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 42.

Michal L. Pierce, MS, Diana Gonzalez, MS, <u>Lisa Gefrides, MS</u>, Jennifer Sycalik, BS, and Roger Kahn, PhD. "The Effectiveness of Bleach for Eliminating Contaminating DNA on Laboratory Surfaces." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 47.

Kevin J. MacMillan, MS\*, Cindi L. Klein, MS, and <u>Lisa Gefrides, MS</u>, and Roger Kahn, PhD. "Validating the Use of a Human and Male Specific Quantitation Kit to Establish Minimum Amplifiable Quantities for Autosomal and Y-STRs." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 59.

Anna Timanova, PhD\*, Kailin Len, MS, Tiffany Best, BS, Katherine Welch, MSFS, <u>Lisa Gefrides, MS</u>, and Roger Kahn, PhD. "Development and Implementation of a Custom Paperless LIMS Serology Module." *Proceedings of the American Academy of Forensic Sciences* (2010) XVI: 123.

Jennifer Stipanovic, B.S., F-ABC, Kimberly Kerlec, B.S., Cindy Klein, M.S., Wendi Phelps, M.S., Sapana Prajapati, B.S., MB(ASCP), Dennis Yip, M.S., F-ABC, Mark Powell, M.S., F-ABC, Lisa Gefrides, M.S., <u>F-ABC</u>, Roger Kahn, Ph.D., F-ABC. "Validation of the Tecan Evo 150 for use in forensic casework." *Genetic Identity Conference Proceedings*, 21st International Symposium on Human Identification (2010): <u>http://www.promega.com/geneticidproc/ussymp21proc/abstracts/poster 2.pdf</u> [accessed 3/11/11).

Tammy Taylor, MS, Jennifer Stipanovich, BS, Sapana Prajapati, BS, Mike Donley, MS, Kim Kerlec, BS, Mark Powell, MS, <u>Lisa Gefrides, MS</u>, Roger Kahn, PhD. "Casework validation of the QIAsymphony automated extraction system." *Genetic Identity Conference Proceedings*, 21st International Symposium on Human Identification (2010):

http://www.promega.com/geneticidproc/ussymp21proc/abstracts/poster\_4.pdf [accessed 3/11/11].

Kevin MacMillan, MS, F-ABC, Dennis Yip, MS, F-ABC, Mark Powell, MS, F-ABC, <u>Lisa Gefrides, MS</u>, <u>F-ABC</u>, and Roger Kahn, PhD, F-ABC. "Applying a minimum amplifiable DNA threshold to sexual assault samples." *Genetic Identity Conference Proceedings*, 21st International Symposium on Human Identification (2010): <u>http://www.promega.com/geneticidproc/ussymp21proc/abstracts/poster\_12.pdf</u> [accessed 3/11/11).

Abby Burg, BS, F-ABC; Cindi Klein, MS; <u>Lisa Gefrides, MS, F-ABC</u>, and Roger Kahn, PhD, F-ABC. "A comprehensive sample barcoding program to automate witness steps for forensic DNA casework." *Genetic Identity Conference Proceedings*, 21st International Symposium on Human Identification (2010): <u>http://www.promega.com/geneticidproc/ussymp21proc/abstracts/poster\_46.pdf</u> [accessed 3/11/11).

Lisa Gefrides, MS, F-ABC, Michael Donley, MS, Kevin MacMillan, MS, F-ABC, Cindi Klein, MS, and Roger Kahn, PhD, F-ABC. "Identifiler Plus validation for forensic casework and implications for quantification of inhibited samples." *Genetic Identity Conference Proceedings*, 21st International Symposium on Human Identification (2010): http://www.promega.com/geneticidproc/ussymp21proc/abstracts/poster 93.pdf [accessed 3/11/11).

Jennifer Petrash, MS, Shahida Flores, BS, Dustin Foley, MS, <u>Lisa Gefrides, MS</u>, Alex John, MD, Dwayne A. Wolf, PhD, and Roger Kahn, PhD. "Evaluation of Deparaffinization Techniques and DNA Extraction Methods for Formalin-Fixed Paraffin-Embedded Tissue." *Proceedings of the American Academy of Forensic Sciences* (2011) XVII: 122.

Michael A. Donley, MS\*, Dustin Foley, MS, and Mark Powell, MS, <u>Lisa Gefrides, MS</u>, Roger Kahn, PhD. "Using the Autoclave for DNA Decontamination of Consumables for Use in Low Template DNA Testing. "Proceedings of the American Academy of Forensic Sciences (2011) XVII: 125.

Alex John, MD\*, Dwayne A. Wolf, PhD, Jennifer Petrash, MS, Shahida Flores, BS, Dustin Foley, MS, Lisa Gefrides, MS, and Roger Kahn, PhD. "DNA Extraction From Paraffin Blocks: Organ Selection and Pre-Embedding Fixation Times – Practical Implications for Forensic Pathologists." *Proceedings of the American Academy of Forensic Sciences* (2011) XVII: 265.

### PRESENTATIONS

Speaker. Validating the use of Quantifiler Duo to Establish Minimum Amplifiable Quantities for Autosomal and Y-STRs. Presented at AFDAA January 28, 2010.

Speaker. Sexual Assault Kit Processing. Presented to the SANE/ Forensic Nursing Course at the HCHD Administration Building on May 20, 2009.

Speaker. Sexual Assault Kit Processing. Presented to the Sexual Assault Response Regional Group at the Houston Area Women's Center, 1010 Waugh, Houston, Texas 77019 on April 30, 2009.

Speaker. A Y-STR Mixture Calculator for Forensic Casework. Presented at AAFS on February 20, 2009.

Speaker. Y-STR Mixture Database. Presented at AFDAA August 7, 2008.

Poster Presentation. The Effective Detection and Treatment of Consumable Contamination. 18<sup>th</sup> International Symposium on Human Identification. October 2, 2007.

Speaker. Understanding New Toxicology and DNA Testing. Harris County District Attorney's Office, October 6, 2005.

Speaker. Forensic Biology: Serology & DNA. Leadership Houston Justice Day 2005. April 14, 2005.

Speaker. ABI 3100-Avant Validation for Forensic Casework. Presented at AFDAA January 20, 2005. Austin, TX.

Speaker. DNA & Serology (Collection and Preservation of DNA evidence). For Harris County Sheriff's Office Intermediate Crime Scene Class. Dec. 8, 2004.

Speaker. DNA & Serology (Collection and Preservation of DNA evidence). For Harris County Sheriff's Office Intermediate Crime Scene Class. Sept. 1, 2004.

Speaker. DNA & Serology (Collection and Preservation of DNA evidence). For HPD Intermediate Crime Scene Class. December 11, 2003.

Poster. LA Gefrides, K. Welch, J. Mathew, and A. Mozayani. Mitochondrial DNA Casework at the Harris County Medical Examiner's Office: Impressions from the First Two Years. Forensic Science International. September 2003. 136(S1): 61.

Speaker. Mitochondrial DNA Casework Experience. Presented at AFDAA July 31, 2003. Austin, TX.

Speaker. DNA and Serology. For Sexual Assault Family Violence Investigators Course (SAFVIC), April 3, 2003. Tomball, TX.

Poster. LA Gefrides, K Welch. J Mathew and A Mozayani. First Mitochondrial DNA Case at Harris County Medical Examiner Uncovers Novel Mutation. <u>AAFS</u> February 2002, Atlanta, GA.

Poster. LA Gefrides, K Kohl, DA Wideman, B Moore, J Mathew, and A Mozayani. Validation of the QIAamp DNA Mini Kit for Use in Mitochondrial DNA Casework. <u>SWAFS</u> November 2001, San Antonio, TX.

### **PROFESSIONAL ORGANIZATIONS & APPOINTMENTS**

2001-2011	Association of Forensic DNA Analysts and Administrators (AFDAA)
2003-2011	<u>Clinical Instructor</u> Voluntary Faculty Department of Pathology Baylor College of Medicine, Houston, TX
2005-2011	NDIS Audit Review Panel Member
2007-2012	Fellow, American Board of Criminalistics
2010-2011	American Society of Crime Laboratory Directors



From the Desk of Robin D. Guidry Criminalist Specialist Crime Laboratory Tuesday, February 14, 2012

# Subject: Failure to Complete the DNA Monthly Clean-Up Tasks

It was discovered well into January, 2012, that the monthly clean-up check-list for the DNA section had not been completed for December, 2011. Jennifer Clay and Kirbie Watson were the assigned analysts for the month.

The applicable maintenance tasks had been completed (e.g., 7500 monthly maintenance, 3130 spectral), but the weekly tasks of replenishing reagents and pipette tips, replacing expired reagents, and cleaning up work areas was not performed and thusly not documented.

Efforts to minimize this type of oversight, such as administrative email alerts at the beginning of one's clean-up month, will be explored. This issue was also addressed at the DNA sectional meeting that occurred on January 25, 2012.

cc: Irma Rios, Laboratory Director - Hullm 2/15/2012 cc: Lori Wilson, Quality Assurance Manager

Robinwe need a vesponse from Jemniter Clary & Kirbie Watson as to why they did NOT complete assyred Watson as to why they did NOT complete assyred tasks. What will be done if this recurs? What will be done to prevail this fun Rive 2-15-12



From the Desk of Robin D. Guidry Criminalist Specialist Crime Laboratory Monday, February 20, 2012

# Subject: Follow-Up to Re-analysis of Samples with PBS Buffer

To ensure the accuracy of analysis conducted at this laboratory, semen-detection cases processed from December 1, 2011 through December 21, 2011 were re-evaluated to ensure that potential staining problems did not interfere with the accuracy of reported results. Casework observations suggested that the use of SERATEC® PSA-SEMIQUANT Cassette Tests kit buffer in lieu of PBS buffer interfered with the ability of sperm to either fix to slides for microscopic reading or to properly absorb the dyes included in Seri's XMAS TREE STAIN for microscopic analysis.

- Fifty-seven cases that were processed between December 1, 2011 and December 21, 2011 were reevaluated.
- Of the 57 cases, 36 (63.2 %) warranted the issuance of a supplemental report, as the initial reports had already been issued by the analyst. The supplemental reports note the retesting and whether the initial results were confirmed or not.
- Of the 57 cases, retention and not retesting was the chosen course of action due to extremely limited sample sizes for two cases (Inc #s 032304806 and 067443506).
- Of the 57 cases, retesting with PBS buffer resulted in 4 cases (7.0%) having different results. For the following cases, the initial screening results were negative for semen. However, the following changes were observed:
  - Inc #156376311: Item 1.1 was microscopically positive when PBS buffer was used, but had
    previously been microscopically negative when the SERATEC® kit buffer was used
  - Inc # 152898311: Items 1.2 and 1.3 were microscopically positive when PBS buffer was
    used, but had previously been microscopically negative when the SERATEC® kit buffer was
    used
  - Inc #082140711: Item 1.8 was microscopically positive when PBS buffer was used, but had
    previously been microscopically negative when the SERATEC® kit buffer was used
  - Inc #074288109: Item 1.8 was positive for p30 when PBS buffer was used, but had
    previously been p30 negative when the SERATEC® kit buffer was used

While the reported results of the vast majority of the cases were unchanged when retested using PBS buffer, a few cases yielded different results, making this effort well worth the extra time and expense. For the 4 cases with different results, DNA analysis is now warranted, where it previously would not have been. Had retesting not taken place, potentially probative evidence may have never been uncovered.

Robin D. Guidry

Criminalist Specialist (Acting Technical Leader)

Jun Kin 2.27-12

Tracking Number	2012-007			
Incident Number	033876811,	119632711, 103113611, 070988107, <del>09591</del>		11,109146111 \$ 031247
Reported On	April 9,2012			
Reported By	Jennifer Clay	(PR#123898)	7	
Description of Issu	ie	Peaks observed below threshold in reag	ent blank 274KG12 (RE	3K031912KG).
Description of Root Cause		Unable to determine root cause. After a reagent blank 274KG12 (RBK031912KG)	re-amplification all sar was clean.	mples yielded expected results and
Description of Acti Prevent Recurrenc	on Taken to e	All clean work environment techniques a	as outlined in our SOP 1	will continue to be used.
Attach	evidence t	hat corrective action has been cor	npleted successfu	lly (if applicable).
ction Completed	Ву	Jape (Illij	on_	4/30/12
eviewed by Lab M	lanager	1.	on _	4-30-12
eviewed by Qualit	y Manager	- Fathalilim	on	5/1/2012
dditional Action T f applicable)	<sup>r</sup> aken	On April 9, 2012, i noticed possible peaks 274KG12 (RBK031912KG). The reagent bl same day. Acting Technical Leader Robin on project SS041012. No more peaks wer expected results. At the request of Robin up and run on project SS041112. One peak several more observed below threshold. amplification. The original an plification p amplification of the samples vas set up m	below our interpretation ank as well as all related Guidry was notified as e observed in the reage Guidry, the originally a ak was observed above The contamination app plate was set up using t anually by analyst Shar	on threshold in reagent blank d samples were re-amplified on the well. All samples were then run ent blank and all samples yielded implified reagent blank was reset our interpretation threshold and bears to have been introduced at the Tecan robot. The re- una Schoonover.
				88 \$4

king Number	2012-0	08		
	1012.0			
dent Number	058851589			
orted On	May 7, 2012			
orted By	Clay Davis			
scription of Issu	le	Allele being called below threshold for reblank is a combination of two reagent bl (RBK032612KG1). The first injection of th 50-100RFU, a re-set up and second inject below 50RFU. There is only one peak bu determine if this is true DNA activity or s threshold of 100 RFUs.	eagent blank 283KG12 lanks 240KG12 (RBK03 is reagent blank produ- tion still produced the t it happens to be at a purious activity. Eithe	2 (RBK032612KG1). This reagent 1312KG) and 283KG12 uced a peak at D195433 between peak visually but the peak was now smaller locus, so it is difficult to r way, it is below the analytical
scription of Root Cause		The root cause of this possible allele being result of a myriad of causes, such as, but not changed throughout the extraction extraction and loading of samples. Becau profile, the sample and reagent blank wi not be re-amplified to determine wheth amplification, we cannot be certain the from carry over from the amplification s	ow threshold is difficu not limited to, carry o and loading process, o use the sample (131KC ill not be used for inte- er this activity is repro reagent blank extract i et up or loading proce	It to determine. It could be the ver from the original sample, gloves or tubes not properly sealed during 512RE2) did not produce a viable rpretation. This reagent blank will ducible. Without the re- is producing the peak or If this is ss.
scription of Action Taken to vent Recurrence		The analyst Karen Gincoo will continue t and traffic within areas where samples a often during the extraction, amplificatio tubes are closed during handling and co continuous cleaning, before, during, and	o practice sterile labo re being processed. Ti n, and loading process ontinue to promote a I d after sample-handlin	ratory procedures and limit talking he analyst(s) should change gloves ses. She will continue to ensure that DNA-free environment with
Attach	evidence th	at corrective action has been con	npleted successf	ully (if applicable).
ion Completed	і Ву	Cay Davis	on	5.7.12
riewed by Lab Manager		- fi	on	5-7-12
riewed by Qual	ity Manager	How Frither	dichin on	5/7/2012
ditional Action applicable)	Taken	Non Ami 51.	1/12-	
The chilig	Galy- 1	No Further action tak	eri at this	time 5/7/2012

king Number	2012-009
dent Number	76495910
orted On	lay 15, 2012
orted By	bin Guidry
cription of Issue	<ul> <li>While preparing samples for an overnight digestion, DNA Technician Karen Gincoo discovered that she did not have enough of Proteinase K lot # 139313083 to add to reagent blank sample #295KG12, when she already added it to her evidentiary samples (#5 293KG12 &amp; 294KG12). She proceeded to add a different lot of Proteinase K (lot #136266121) to her reagent blank to ensure that all reagents added to the above samples were also added to her reagent blank. That same day, she inquired about this solution with Acting Technical Leader R. Guidry, who indicated this was not acceptable because the same lot # needed to be used on both the samples and the reagent blank. It was discovered that a sufficient volume of the initial lot # of Proteinase K (lot #139313083) was available for use on reagent blank sample #295KG12. As a result, the evidentiary reagent blank from 3/29/12 had two separate lots of Proteinase K added (lot #139313083 and #136266121). While this was not ideal, it would satisfy the need to demonstrate that all reagents applied to a sample were proven to be free of contaminating DNA prior to use.</li> <li>However, in trying to understand how she ran out of reagent mid-extraction, R. Guidry realized Karen not only processed the case reference sample just prior to handling the associated evidence sample (for which she had sufficient Proteinase K), but had also set the samples up beside one another on the same heat block for overnight incubation. The samples were essentially being processed side-by-side.</li> <li>This was a huge concern, given the anticipated high level DNA concentration of the known and what was expected to be low level DNA concentration of the evidence and the reference DNA profiles were different, contamination was not a likely occurrence. However, if the samples yielded the same DNA profile, it would be impossible to rule out contamination as the cause. If the evidence sample sylelded the same DNA profile, it would be moved to a abundance of caution, they would be re-extracted and the</li></ul>
cription of Root (	Lause It was immediately made clear to K. Gincoo by R. Guidry why her actions were unacceptable and she understood. Karen believes that her haste resulted in this oversight.
cription of Action vent Recurrence	<ul> <li>Taken to</li> <li>The DNA profile from the Initial evidentlary extraction did in fact match that of the reference sample with which it was extracted. For this reason, the evidence samples were re-extracted at a later time, to help ensure that the profile obtained originated from the samples themselves, and not possible contamination from the higher level reference sample. The results of the re-extraction were concordant with the initial extraction results, suggesting that contamination was not the cause of the matching DNA profiles.</li> <li>On the morning after the initial discovery, a meeting was held with DNA analysts C. Davis and P. Hill, along with Karen, to explain the situation and prepare them for the potential re-extraction. There was a concern that the evidentiary samples were in limited supply and re-extraction may warrant written consumption permission; the DNA analysts were instructed, should they be the one to review the case file, to closely review the quantification data for guidance in deciding how much sample could be consumed in the potential re-extraction.</li> </ul>

Furthermore, the DNA SOPs were updated to specify the need to extract evidentiary samples in a separate time and/or location from reference samples. Previously it was common practice, but now the policy dictates this separation.

on 5/17/2012

Attach evidence that corrective action has been completed successfully (if applicable).

on Completed By

on 5-15-12

ewed by Lab Manager

Dee above R. Guidry, 71 stal on

ewed by Quality Manager

0

pplicable) Kan Ami 5.15.17 Uniconstrond of Jeconducal Jeach on Mary 14. Sectemenan as unan of folicy & proceasive. The further action takin at the Unre - Ami

A-CAPA- 2010.1

effective 01-04-2011



From the Desk of Robin D. Guidry Police Administrator Crime Laboratory 2012-010

Sunday, June 10, 2012

# Subject: October 2011 Monthly Maintenance Not Performed on the 7500 Real Time PCR System

On Friday, June 8, 2012, it was discovered that the monthly maintenance had not been performed on the 7500 Real Time PCR System in October, 2011, even though the 7500 was used on casework, starting in October, 2011. For each month since October, 2011, the appropriate maintenance has been performed on this instrument.

The DNA Monthly Clean-Up schedule was updated in February, 2012, to include the 7500, in addition to the 7000 Sequence Detection System, for documentation of the appropriate maintenance.

cc:

Lori Wilson, Quality Assurance Manager, Crime Laboratory JULMON 6/11/2012 Irma Rios, Laboratory Director, Crime Laboratory

Page 1 of 1

	·		
cking Number	2012-0	12	
ident Number	077165311 and	071177311	
ported On	May 21, 2012		
ported By	Diana Crossan (	PR# 136431), Criminalist	
scription of Issu	ue I	On 05/21/12 the following samples we	re extracted by differential extraction:
		Sample 369DC12 - Item 1.2.1 - Portion Sample 370DC12 - Item 1.2.1 - Portion Sample 371DC12 - Item 1.2.1 - Portion Sample 372DC12 - RBS052112DC Sample 373DC12 - Item 1.2.1 - Portion Sample 374DC12 - Item 1.2.1 - Portion Sample 375DC12 - Item 9.1.1 - Portion Sample 376DC12 - RBE052112DC The differential extraction procedure I 13-15. After the initial digestion, analy had expired, which is a deviation from expiration date of 05/20/12.	of vaginal swabs – SF from INC# 077165311 of vaginal swabs – SF from INC# 071177311 of stain from panties - SF from INC# 071177311 of vaginal swabs – EF from INC# 077165311 of vaginal swabs – EF from INC# 071177311 of stain from panties – EF from INC# 071177311 s documented in the DNA SOP under section 7.6 pages st Diana Crossan realized that the TNE used for the digestior of the SOP. The lot number of this TNE was 062411DC with an
escription of Root Cause		The samples had already been put on informed Technical Leader, Robin Gui from attending a meeting. Robin Guid DNA Analyst who would be writing th the samples would have to be re-extra Crossan with a new reagent blank eac and 392DC12 respectively. All of the s blanks. The report will reflect results c	the block for digestion and so analyst Diana Crossan dry, PR# 136530, of the Incident once she became available fry stated that a CAPA needed to be generated and that the se case should be informed of the event. She also said that acted. All of the above samples were re-extracted by D. th for the sperm and epithelial fractions labeled as 391DC12 amples yielded expected results, including the reagent obtained from the re-extraction.
escription of Action Taken to revent Recurrence		In order to prevent this kind of mistak that not only should the analyst be pa and QC dates, but they should record then have the information verified by even started. As of right now, analysts later time on the extraction sheet after reoccurring, it may be recommended Robin Guldry dld discuss the idea of h before an extraction at the next DNA the reagent's information should be verification could be done anytime d	te from happening again in the future, it is recommended aying close attention In noting lot numbers, expiration dates all of the reagent Information on the extraction sheet and another analyst to catch a mistake before the extraction is swill record reagent information and have it verified at a er the extraction has started. In order to prevent this from that the verification be done prior to starting the extraction having the reagent's information recorded and verified meeting held on 05/25/12, it was discussed and decided that recorded prior to starting the extraction, but that the uring the extraction.
Atta	ch evidence th	at corrective action has been o	completed successfully (if applicable).
ction Complete	ed By	Desire Crosser	on 24 7/2/12
eviewed by Lab	Manager	4	on 7-9-12
eviewed by Qu	ality Manager	Falletin	on <u>7/13/2012</u>
Additional Actio	n Taken		

king Number	2012-013
dent Number	097200511, 045131011, and 122026111
orted On	Jun 11, 2012
orted By	Diana (Crossan) Donley (PR# 136431), Criminalist
cription of Issu	e Sample Switch Criminalist Diana (Crossan) Donley (PR# 136431) extracted evidentiary samples in Inc#s 097200511, 045131011, and 122026111. The following are the corresponding sample numbers, incident numbers, and items extracted in the batch:
	Sample #, Incident # and item Descriptions:
	377DC12       097200511 – 4.2.1 – Portion of "SW #2 right ankle" swabs - SF         378DC12       045131011 – 1.2.1 – Portion of vaginal swabs - SF         379DC12       045131011 – 1.3.1 – Portion of vaginal swabs - SF         380DC12       122026111 – 2.3.1 – Portion of "labia minora" swabs - SF         381DC12       122026111 – 2.5.1 – Portion of anal swabs - SF         382DC12       122026111 – 2.7.2.1 – Portion of stain from panties – SF         383DC12       RBS052212DC
	384DC12       097200511 – 4.2.1 – Portion of "SW #2 right ankle" swabs – EF         385DC12       045131011 – 1.2.1 – Portion of vaginal swabs – EF         386DC12       045131011 – 1.3.1 – Portion of vaginal swabs – EF         387DC12       122026111 – 2.3.1 – Portion of "labia minora" swabs – EF         388DC12       122026111 – 2.5.1 – Portion of anal swabs – EF         389DC12       122026111 – 2.7.2.1 – Portion of stain from panties – EF         390DC12       RBE052212DC
	Timeline of Events
	May 22, 2012: Samples extracted by Criminalist Donley May 29, 2012: Samples quantified by Criminalist M. Bryan Davis (PR #141059) Results: 389DC12: Undet. 390DC12: 149.97 ng/uL June 4, 2012: Dilution of 390DC12 re-quanted by Criminalist Davis, given it exceeded 50.0 ng/uL
	Results: 390DC12 (1:20): 7.40 ng/uL June 6, 2012: Samples amplified and prepped for CE load by Criminalist Davis June 11, 2012: Criminalist Davis notified Criminalist Donley of the potential for a sample switch, given the high quant value of a sample for which DNA was not expected; Criminalist Donley immediately notified the Technical Leader, Robin Guidry (PR #136530); TL Guidry asked Criminalist Donley to examine the data to try to determine where the profile in the RB may have come from; TL Guidry also indicated that the samples would need to be re-extracted.
scription of Roc	Criminalist Donley analyzed the run data from the original extraction on June 11, 2012 and noted that the same DNA profile was observed in samples 387DC12, 388DC12, and 390DC12, while sample 389DC12 had no interpretable result. This suggests that samples 389DC12 and 390DC12 were switched during extraction of the samples, since the reagent blank should not have yielded a DNA profile. Criminalist Davis made the dilution for re-quatitation from the neat tube labeled 390DC12 and again obtained a detectable amount of DNA consistent with the initial quantification data, suggesting the switch occurred prior to the initial quantitation.

Criminalist Donley acknowledges that she could have caused this sample switch by mislabeling the final tubes for samples 389DC12 and 390DC12 or by switching the sample tubes after removal from the centrifuge just prior to the final tube transfer of the samples.

All of the associated samples were re-extracted by Criminalist Donley. The reagent blanks of the re-extraction yielded no DNA, thus permitted the use of this new data. Data from the initial extraction will not be used for interpretation and the associated DNA reports will reflect results obtained from the re-extraction.

scription of Action Taken to vent Recurrence

For future extractions, Criminalist Donley will work at a slower pace and will pay more careful attention when transferring samples between tubes and when removing sample tubes from the centrifuge to ensure they are in the proper order, so as to minimize the potential for this incident to occur again.

Attach evidence that corrective action has been completed successfully (if applicable).

ion Completed By

lewed by Lab Manager

iewed by Quality Manager

**ditional** Action Taken pplicable)

on 7-16-12 on 7/17/2012

A-CAPA- 2010.1

effective 01-04-2011

king Number	2012-0	14	]	
dent Number	184934607			
orted On	Jul 30, 2012			
orted By	Clay Davis (PR#	125253)		
cription of Issu	le	The first injection of sample 190BC12 on p below threshold. A request dated 7-19-12 (BC) to re-inject for 20 seconds to bring up BC071912 produced no data for sample 1 requested on 7-20-12 for this sample. The BC072312 produced a full male profile the MBDBC061412. The profile developed in 1 developed from samples 180BC12, 182BC	project MBDBC06141 was made to DNA Te palleles below thresh 90BC12. A complete re-set up and injection at was different than the re-set up injection (12 & 183BC12.	2 produced a mixture with alleles echnician Ben Cambridge (141062) hold. The re-injection on project re-set up of the 3130 plate was on of sample 190BC12 on project the original sample data on project n is consistent with the profiles
cription of Roc	ot Cause	The incident was discussed with fellow ar Guidry (136530) and it was decided to re- associated with this case and compare th MBDBC061412. Diana Donley and I sat do the correct well number for sample 190B and well numbers were correct. The re- project BC072412. Both newly amplified s the original samples injected and will be meeting was called on 7-24-12 with Ben C and Clay Davis to discuss how the sample mis-read of the sample name 190BC12 ve error occurred when viewing the second were 190BC12(well 1F - amp plate 05301: association of sample 190BC12 with well male that was seen in the second re-injec So either a misread of the sample ID or th could have produced the male DNA profi	analyst Diana Donley (1 amplify both evidence ose results with the o own and confirmed the C12 and that the sam nplified samples were samples (190BC12RA used in the interpreta Cambridge, Robin Gu es could have been sw ersus 180BC12. Anoth re-injection workshee 2BC) and 185DC12 (w 1A instead of 1F wou tion request; sample e wrong association le observed in the see	136431) (DD) and Tech Lead Robin te samples (190BC12 & 191BC12) riginal injection on project tat the re-injection worksheets had ple names were correct. All names a requested on 7-24-12 and ran on & 191BC12RA) are consistent with thion and results for this case. A idry, Michael Bryan Davis (141059) witched. Ben suggested a simple er possible explanation is that the et, where the two samples listed rell 1A - amp plate 061112BC). An Id have produced the unknown 1A on this plate is sample 180BC12. with sample name and well number cond injection.
scription of Action Taken to vent Recurrence		During the meeting held on 7-24-12 with Bryan Davis suggestions were made to he discussed getting ideas and procedures f samples and how they keep the large vol was made to Ben C. to make a copy of pa into the amp room and circling or highlig upon the analysts' re-work request works being more diligent about double checki future.	Robin Guidry, Ben Ca elp prevent this from rom other DNA techn ume of samples that perwork (either grid o hting the samples ne heets (e.g., re-amp or ng sample names, we	ambridge, Clay Davis and Michael happening in the future. The group licians about how they process we process in order. A suggestion or TECAN printout) before going eded for that re-injection, based re-inject). Ben C. committed to ell locations and plate names in the
Attach	evidence th	at corrective action has been con	pleted successfu	ılly (if applicable).
ion Completed	Ву	Clay Waves	on	7.30.12
iewed by Lab N	Manager	<u>fr</u>	on	7-30-12
iewed by Quali	ity Manager	Inn Ris	on	8-6-12
ditional Action pplicable)	Taken	BC 7-30-12 B	2 2 2 12	Tellibre 8/6/2012 N
		MED 7/30/12		CLO

acking Number	2012-0	7/5		
cident Number	#075069710 ar	nd #178324410		
ported On	OCT 2, 2012			
eported By	Karen Gincoo and M. Bryan Davis			
escription of Issu	e	incident #075069710 was included in 1 and i (Karen Gincoo PR#129764) were discovered a discrepancy. While the o incident #075069710, the tubes conta #178324410 (see photos). The incider #178324410. The outer packaging, ho numbers on the tubes (3.1.1, 3.2.1, and #075069710.	Batch 35 for DNA analysi labeling sample tubes fo uter packaging indicate ined within were actually it number on the tubes i wever, was correct, #075 19.1) were consistent wi	is. While Bryan Davis (PR#141059) or this incident number, we d that the samples were from y labeled as being from incident abeled by the screener was 5069710 (see photos). The item th the evidence retained in incident
escription of Root Cause		Next, I retrieved the evidence retained observed that the date on the evidence #075069710, indicating that both sets freezer on the same day. The evidence was consistent with the items retained	for Incident #17832441 te tape matched the date of portions were packag e contained in the 6"x 9" d, per the screening repo	0 from the walk-in-freezer. i e on the evidence tape on Incident ged and placed into the walk-in- envelope for Incident #178324410 ort.
escription of Action Taken to revent Recurrence		The most likely explanation is this was Watson, when she was labeling her tu the Crime Lab, and therefore we are u in both cases, the item numbers on th report. Furthermore, there is no replic #s 3.1.1, 3.2.1, and 9.1 and incident #1	a transcriptional error n bes for portioning. The s nable to have her addres e tubes corresponded w ation of item numbers: In 78324410 includes item	hade by the screening analyst, Kirble screening analyst is no longer with ss what is likely improper labeling. With the items retained in each incident #075069710 includes item
Attach	evidence th	at corrective action has been c	ompleted successfu	ully (if applicable).
ction Completed	By	M By Dais	on	10/11/12
eviewed by Lab N	Manager	lp	on	10-11-12
eviewed by Quali	ity Manager	Flillim	on	10/12/2012
dditional Action f applicable)	Taken Ai	The portions in the incorrectly labeled have been tested and that reported re 3.2, and 9) will be recalled from the Pro- calist will fellow-up cloce current of complete Autom	tubes were tested, but t sults are completely accur operty Room for re-portion of the fight of re-	o ensure that the correct samples urate, the remaining samples (3.1, oning and subsequent DNA analysis.

racking Number	2012-0	17	
ncident Number	089098612, 03	حين ك 1022991, 078344011, 061428511, <del>16769761</del> الم	7697610, 149195410
eported On	Dec 20, 2012		
eported By	C. Davis (PR# 1	25253)	
escription of lssu	ie	On 12-20-12 while analyzing reagent blank 90 profile was seen above 50 RFU's in this reagen notified and a re-amplification was requested 906MBD12 revealed a complete profile; this pr employees as well as the DNA profiles from th discovered to be that of analyst M.B. Davis (PR Technical Leader R. Guldry were notified of the this issue. Analyst C.Davis (PR# 125253) notifie with the reagent blank and how it affects batch reviewing cases in this batch.	6MBD12 processed on run data SS121912, a partial t blank. Technical Leader R. Guidry (PR# 136530) was for this sample on the same day. Re-amplification of rofile was compared to the DNA profiles of the e extraction batch. The unknown DNA profile was # 141059). Analyst M.B. Davis (PR# 141059) and e issue and all three of us had a discussion regarding the fellow analyst A.Castillo (PR# 139273) of the issue th 45 due to C.Davis and A. Castillo both writing and
Description of Roo	ot Cause	The root cause of the contamination is difficul causes, such as, but not limited to, gloves not during the extraction batch, touching or hand of the evidence items. All samples associated consumption of any of the samples is needed Attorney. Note: The DNA profile from Analyst M.B. Davis training purposes in serology and DNA.	t to determine. It could be a result of a myrlad of changed during the extraction process, talking lling items not decontaminated during the analysis with this reagent blank will be re-extracted; if then a request will be made to the officer or District is used for the NIST traceable and has been used for
Description of Act Prevent Recurren	tion Taken to ce	A discussion between R. Guidry (Tech leader), possible explanations of how this issue could introduced into the tube through possible cou blank tube was introduced into the extraction sterile techniques which include minimize tall Gloves will be changed often and a no talking	C. Davis (analyst) and M.B. Davis (analyst) listed have occurred. M.B. Davis believes that his DNA was ntaminated gloves or talking when the reagent batch. Analyst M.B. Davis will continue to follow king in extraction, pre-amp and post-amp rooms. policy will be practiced by this analyst.
Attac	h evidence th	at corrective action has been comple	ted successfully (if applicable).
Action Completed	i By	Clay Davis	on <u>12.28.12</u>
Reviewed by Lab	Manager	fri	on 12-28-12
Reviewed by Qua	lity Manager	NO AL My Dasy Willing	on 12 114/2013
Additional Action (if applicable)	Taken	and a large state of the second state of the s	
	1	11. Azor V Dais 12/28/12	
)	Ly	10/38/12	
		CL-QA-CAPA- 2010.1	effective 01-04-2011
Fracking Number	2.013-	011	
---	----------------------------------	--	--
Incident Number	133691198		
Reported On	Jul 2, 2013		
Reported By	Shamika Kelley	,	
Description of Issu	le	A sample was processed and the data appeared dropout. Therefore, the sample was re-amplified single source sample. The sample was then re-a data was confirmed to be a single source sample	to be a mixture with low RFU and possible d. After re-amplification, the data appeared to be a mplified for a second time to confirm the data. The e.
Description of Roo	ot Cause	A plausible explanation would be that as the sai one sample was loaded twice into a well that al caused the data to appear as a mixture.	mple plate was being loaded during amplification, ready contained sample. This is what possibly
Description of Act Prevent Recurrent	tion Taken to ce	Since the incident, the analyst has developed a check that the correct sample goes into the coronce.	system during the loading process to double rect well and that the samples are only loaded
Attack	h evidence th	at corrective action has been complet	ed successfully (if applicable).
Action Completed	i By	Shamiles Seller	on 7/02/13
Reviewed by Lab	Manager	4	on_7/2/13
Reviewed by Quality Manager		Filleling	on_718/2013
Additional Action (if applicable)	Taken Bug Widlepel Macruce	eftig discute the sugar the percente samplie	From theing souded
lpon taking e to use an	the san	iples from the cooler -+ fl ack as well. As the sample	acing them into a rack, 1 m

e to use an empty rack as well. As the samples are loaded onto the sample te. they are moved from the full rack to the empty rack to indicate they've en loaded onto the sample plate. Simultaneously, the tips for the pipettes being used in the same order that the samples are loaded onto the sample te. For example, the tip located at the top left of the tip box will be used the sample located at Al on the sample plate. The next tip down will be used Bl and so on until all the samples are properly loaded. This method serves a second check that the samples were loaded in the correct sample wells. effective 01-04-2011

king Number	2013-0	12	
lent Number	121706893		
orted On	Jul 11, 2013		
orted By	Jisel Be	ailon	
ription of Issu	Je	On July 10, 2013 Jisel Ballon (PR #150997) notice #121706893 did not have correct documentati as being packaged with parent in LIMS; howev an inventory of Item 1 on June 26, 2013, she no July 10, 2013, Elizabeth Richey re-opened Item that Item 2.1.1 (not Item 2.1) was packaged with documentation that in fact Item 2.1.1 was pack correct documentation for the location of Item date of repackaging as April 23, 2013 by Rebect	ced that the chain of custody in LIMS for Incident on for the location of Item 2.1. Item 2.1 was noted er, while Elizabeth Richey (PR# 151453) was doing beted that Item 2.1 was packaged with Item 1. On 1 to confirm its inventory, and it was discovered th Item 1. Elizabeth Richey corrected the caged with Item 1; therefore, LIMS did not have 12.1.1. The evidence tape on the item indicates the ca Gonzales (PR #139392).
cription of Root Cause		item 2.1.1 was not documented correctly regar custody must include documentation of evide locations.	rding its location. Per Quality Manual, the chain of ence transferred to and from individuals/storage
cription of Ac vent Recurren	tion Taken to ice	The analyst will continue to be diligent when a location of this item will be changed in LIMS to 2013 by a LIMS administrator.	documenting the transfer of items of evidence. The o indicate that it was placed in item 1 on April 23,
Attac	h evidence th	at corrective action has been comple	ted successfully (if applicable).
on Complete	d By	fiBl=	on <u>1/12/13</u>
iewed by Lab Manager		flar h.	on 7/16(13
	lite : Manager	Falilm	on 7/19/2013
iewed by Qua	inty Manager		
iewed by Qua ditional Actior pplicable)	n Taken	Jensabeth Prates	7/12/13

icrify via LIMS that the chain has been corrected. Allelin thousa storm 2 1.1 be Pachaged of parent stim # or worth farent stim #2?

3.13, Hem 2.1.1 was taken out of Hem 1 + placed back into Hem 2 by Rebecca mates. - RG But 7/29/2013

acking Number	2013	-014	
cident Number	100655107	017	
cident Number	100855107		
ported On	June 13,2013		
ported By	J. Clay (PR# 123	3898)	
≥scription of issu	le	During the technical review of inc#10065. Clay (PR# 123898) by analyst Clay Davis (P \C9WW.3.1 had not been portioned accord the extraction worksheet. Analyst J. Clay of in order to determine what had happener portioned. According to LIMS as well as the C9WV\C9WW.3.1 were not portioned at sa- unable to determine if the evidence was a discarded. Since we were unable to locat the item was consumed without notifying Evidence Handling:	5107 It was brought to the attention of analyst Jennifer PR# 125253) that items C9WV\C9WW.2.1 and C9WV ding to the description in LIMS or the descriptions on contacted the technician Elizabeth Richey (PR# 151453) d. Elizabeth stated she received these two items already the paperwork within the file, items C9WV\C9WW.2.1 and creening by analyst Amy Castilio (PR #139273). We are actually consumed because the original packaging was a any remaining sample at this time, there is a possibility pappropriate personnel. Please see DNA SOP Section 4.4
		"Consumption of Evidence The evidence quality and quantity will be quality of the analyses. Whenever possible preserved for possible re-analysis. When t officer, prosecuting attorney, and/or defe evidence and permission to consume will first having documented permission, pref efforts should be made to limit the consum The DNA results of items C9WV\C9WW.2.1 complainant's reference profile. There are from all individuals who handled the case	preserved as much as possible without sacrificing the e, at least half of the evidence sample will be his is not possible, appropriate personnel (submitting nse attorney) will be notified prior to the consumption of be requested. Samples will not be consumed without erably in writing. Furthermore, wherever possible, mption of DNA extracts." and C9WV/C9WW.3.1 are consistent with the e no indications of a second contributor. Statements are provided below.
escription of Roo	ot Cause	Analysts Elizabeth Richey (PR#151453), Ar and Kerry Todd (PR#141057) have provide Please see statements below: Statement provided by Elizabeth Richey: "items C9WV\C9WW.2.1 and C9WV\C9WW respectively) for incident 100655107 were extraction. Prior to receiving the evidence amounts sent to DNA. The notes stated th analysis. Therefore Elizabeth foresaw that done so, or she had to process them as lar envelope which contained these two Item (Item C9WV\C9WW.1). Elizabeth opened t swabs were already in microcentrifuge tul rather than two. Even though there were r that these were portions since the items w looked to be about half the amount that ti The outer envelope and the inner envelop were discarded, and the blood stain card w extracted the entirety of each of the swabs extraction sheet that she received one swa possibility of there being missing swabs car morgue kit (Item C9WV\C9WW) from the p	A.3.1 (swabs from the FNSC from the right and left hands, assigned to Elizabeth Richey (PR# 151453) for , she looked at the serologist notes to determine the at for both items, two swabs were retained for DNA she either had to portion the items, if not previously ge volume extractions. The items were enclosed in an is, plus a known blood stain card for Anthony Moore this envelope on 05-14-13, and she noticed that the bes and they looked to contain only ~one swab each, no portions made for these items in LIMS, she assumed ere In tubes that are used for portioning and the swabs he serologist stated to have retained for DNA analysis. es for items C9WV\C9WW.2.1 and C9WV\C9WW.3.1 was given to Benjamin Cambridge for portioning. She is contained in the tubes on 05-14-13, and noted on her ab for each item and took all for analysis. When the ime to our attention, Elizabeth requested the original property room on 06-13-13 and opened it to see if there

Pagutten 9"

were any swabs of the FNSC contained in the parent. No swabs were found, but the fingernal clippings, sticks, and clippers still remained for each of the two items in question."

#### Statement provided by Amy Castillo:

"Per the worksheet filled out on 12/9/10 I inventoried the morgue kit for this case, I also swabbed the fingernail scrapings and clippings with two swabs. The swabs taken were retained (unportioned), along with the unportioned blood stain card. Per the official chain of custody I packaged these three items together (Items C9WV\C9WW.1, C9WV\C9WW.1.2.1, C9WV \C9WW.1.3.1). Per my notes two swabs were taken and were not portioned, I do not remember the details of what I did in this case except by my notes therefore I would have expected there to be two unportioned swabs for both the left (C9WV\C9WW.1.3.1) and right (C9WV\C9WW.1.2.1) hand and an unportioned bloodstain card (C9WV\C9WW.1) in the sealed envelope stored in room temperature storage from 1/6/11 until recently."
Statement provided by Ben Cambridge: "On 05/14/2013 I received item C9WV\C9WW.1 (bloodstain card - Anthony Moore ML# 07-2273) in a sealed bloodstain card envelope. The item was transferred directly to me from E. Richey as detailed in the chain of custody in LIMS. I made two portions of the bloodstain card (items C9WV \C9WW.1.1 and C9WV\C9WW.1.2) and then sealed it in the bloodstain card envelope with evidence tape. Having noticed that the original outer envelope containing the item had been discarded in a biohazard waste container, I sealed the bloodstain card in a new yellow envelope and returned it to room temperature storage shelf B-RT-07D on 05/14/2013 as accurately reflected in the chain of custody."

#### Statement provided by Kerry Todd:

"I (Kerry Todd, Criminallst, PR#141057) received items BXFX\BXFY, BXG1\BXG2 and BXG3\BXG4 from case L07-3045/100655107 on April 2, 2013. After the analysis was complete on these items, I portioned item BXG1\BXG2.1 (swab from Band-Aid), item BXG1\BXG2.2 (stain from Band-Aid) and item BXG3\BXG4.2 ("From kitchen knife" swabs). The portions from the items were retained by taking approximately half of the total swab amount from each item and placing it in a serology tube. Once the portion is placed inside the serology tube, the tube is labeled with the incident number, my initials and item number. Typically, I repackage the portions in the tubes by placing them into individual small zip lock bags. i seal the top of the small zip lock bag containing the portion with evidence tape. I place the date and my initials on the evidence tape. After this occurs with each portion, i place all the evidence portions in a larger manila envelope with the appropriate barcodes on the front along with my initials. The manila envelope was sealed with evidence tape with the date and my initials on it. Lastly, the manila envelope containing the portions was placed in Freezer 13 on April 19, 2013."

#### scription of Action Taken to event Recurrence

This seems to be an isolated incident. In the future, should an analyst or technician notice a discrepancy between the description of the item (portion vs. non-portioned items) and the item actually received, a supervisor or other qualified individual should be notified. In our section meeting on June 27, 2013, the issue was discussed with all analysts to help prevent any future issues. Internal temporary packaging can be discarded only if all pre-portioned items contained within the packaging are consumed. in our current method of processing cases portions are usually made at screening. Sgt. M. Miller has been notified of the incident. Please see page C16 for email communication.

tion Completed By

viewed by Lab Manager

viewed by Quality Manager

**Iditional Action Taken** applicable)

Attach evidence that corrective action has been completed successfully (if applicable). on 7/29/2012

Inc# Indiction

page#C18 9-

QA-CAPA- 2010.1

effective 01-04-2011

Inc#100655107



# ncident Number Update Request



**Houston Police Forensic Services** 1200 Travis Houston, Texas **Harris County** 77002 Phone: 713-308-2600

**Current Date** 

7/19/13

yee Number:	139392	
yee Name:	Rebecca Gonzales	
	rebecca.gonzaies@houstonpolice.org	
:	713-308-2612	

#### **Describe The Problem in Detail:**

tem 2.1.1 is stated in LIMS to be packaged with parent. This item was found to be packaged with item 1 on 6/26/13. The evidence tape on the item has the date of repackaging as 04/23/13. This is the date the item was actually repackaged under item 1. Couid you go in LIMS and transfer item 2.1.1 into the custody of item 1 on 04/23/13?

#### Info

nt:

**/erified via OLO** 

121706893

es

Internal Use Only Action Taken:

Sample Parent Relationship has been changed to item # 1 a note has been added to the custody comments for this item.

al Signature

Rebecca Gonzales

al Signature Supervisor Robin D. Guidry

il : hector.sustaita@cityofhouston.net

#### Internal Use Only

	Hector
LIMS Administrator	Arjona-



Date

racking Number	2013-	017	20	13_017
ncident Number	PAR-B 2013			13-017
Reported On	Sept.19, 2013			
Reported By	Clay Davis (PR	125253)		
Description of Issu	le	During the analysis of project MBI 308PL13, well B2 of amplification request for re-injection of sample 8 other samples from two differer 308PL13 on project PL080613 pro- from project MBD080113. After an injection, it was determined that 1 the amplification plate MBD08011 sample was re-injected on project injection from project MBD080111.	D080113 by C. Davis (PR# 125 plate MBD080113, was found 308PL13 was sent to P. Lentz at plates, PL080113 and MBD0 oduced a profile that was not o halyzing and reviewing the Di the re-injection sample was fr 13. A re-injection request was t BC080613 with the results be 3.	53), the injection of sample to have excessive artifacts. A (PR# 151448) on 8-5-13 along with 080113. The re-injection of sample consistent with the initial injection NA profile produced in this re- om plate PL080113 and not from sent to P. Lentz on 8-6-13 and the eling consistent with the original
Description of Roc	ot Cause	Statement provided by Peter Lent and myself (P. Lentz) and it was de Instead of well B2 from plate MBD	tz: "The incident was discussed etermined that I had re-injecto 0080113."	d between C. Davis (PR#125253) ed well B2 from plate PL080113
Description of Acti Prevent Recurrence	ion Taken to :e	Peter Lentz will double check sam take more care in handling multip	ple names, wells, and plates o le plates.	on all runs in the future and will
Attach	evidence th	at corrective action has bee	en completed successfu	lly (if applicable).
oction Completed	Ву	Clay Davis	on_	10.4.13
leviewed by Lab N	lanager	1-	on _	10-4-13
leviewed by Quali	ty Manager	Sullan	on	10/4/2013
Additional Action If applicable)	Taken	Quelator	7	10-4-13

CL-QA-CAPA- 2010.1

effective 01-04-2011

king Number	2013	-018	
dent Number	080008113, 08	2259013, 112386312, 102925900, oy	5323313,071332513,072450813,
orted On	Sep 19, 2013		181795510,073558113,160892012
orted By	Clay Davis (Pr#	125253)	
cription of Issu	Je	During the analysis of Project BC0829 to have one peak above our analytica 50RFU's but consistent with true DNA evidentiary samples for Batch 26. A re with just the positive, negative and la labeled as BC082913C revealed the per configuration as mentioned in the ori immediate request for a re-amplificat On 9-3-13 the re-amplification plate ver reagent blanks in the set were clean a	13, the negative control labeled as NEG082813BC appeared I threshold of 50RFU at vWA and three locations below activity. This negative control is associated with the equest was made the same day for a re-set up of the plate dder being processed. An analysis of the re-set up plate eaks to be reproducible upon re-injection with the same ginal injection (1 peak > 50RFU's, 3 locations <50 RFU's). An ion of the entire plate of evidence samples was requested. was processed and the negative controls as well as all the and free of DNA.
cription of Root Cause		The root cause of this contamination negative control was compared to the 141062), who set up the amplification compared all DNA profiles from the e well as all lab staff DNA profiles to the none were consistent with this DNA p amplification reaction of the evidenti reference samples with controls label was done without prior knowledge o The positive control for the reference control being clean. All DNA profiles to level DNA profile of the contaminated	cannot be conclusively determined. The contaminated e positive control and to the analyst, Ben Cambridge (PR# n on 08-29-13. Analyst Jennifer Clay (PR # 123898) and I also vidence samples associated with this negative control as e low level DNA profile found in the negative control and profile. The TECAN EVO 150 was used to set up the ary samples first and then used to setup a plate of known led as POS082913PL and NEG082913PL. This second setup f the problem with the evidentiary amplification negative. plate produced the expected results with the negative from the known references were also compared to the low d amplification negative control and, none were consistent.
scription of Act vent Recurrence	tion Taken to ce	Analyst Ben Cambridge will continue for extraction, quantification, amplific routine flush is performed between e controls were clean the TECAN negat the incident.	to follow all sterile techniques as outlined in the DNA SOP cation and plate set-up. The TECAN is wiped down daily and a each reaction setup. Even though the subsequent negative five was replaced by analyst Ben Cambridge upon learning of
Attach	n evidence th	at corrective action has been o	completed successfully (if applicable).
ion Completed	Ву	day Dowis	on $\underline{q \cdot  q \cdot  3}$ .
riewed by Lab N	Manager	- Cul	on_9-20-13
viewed by Qual	ity Manager	Sulum	on 10/4/2013
ditional Action applicable)	Taken Out	Ceg 9/19/13	2013-018 /19/13
	July	CL-QA-CAPA- 2010.1	effective 01-04-2011

racking Number	2013-018 11 013-019		2013-019		
ncident Number 092787509		· · · · · · · · · · · · · · · · · · ·			
Reported On	Aug 6, 2013				
Reported By	Karen Gincoo				
Description of Issue		Criminalist Clay Davis received a call on complainant's reference sample in case DNA profile from Inc# 092787509 was us L09-12679. The ADA was confused beca Eligah Williams who is still alive. It shoul deceased complainant and daughter of listed as Eligah Williams in OLO for both since been changed to Undra Williams in 8/5/13 by Clay Davis for ADA Palmer's en It was discovered through that conversa containing the reference sample for the had been a mix up in the complainant's Eligah Williams is the complainant's figah Williams is the complainant's fath When this evidence was initially process complainant name used was verified us in OLO about the complainant. The com Williams to Undra Williams in OLO by th already printed out of OLO by lab perso complainant name. Property Room #003 was requested from Criminalist Juli Rehfuss re-inventoried t evidence did not have the complainant.	August 5, 2013 from ADA Rachel Palmer about the Inc#088322509/L09-12679 (cross-referenced case). The sed for comparison to evidence in Inc#088322509/ use the morgue evidence was described as being from Id have been identified as being from Undra Williams, the Eligah Williams. The complainant's name was initially Inc#088322509/L09-12679 and Inc# 092787509, but has in Inc #092787509. (see Correspondence Record dated xplanation) ation that Inc# 092787509 had the morgue evidence complainant. As ADA Palmer stated to Clay Davis, there name: Undra Williams is the actual complainant and her. sed in July 2011 by Criminalist Karen Gincoo, the sing the ML # on the morgue evidence and the information inplainant's name had been later changed from Eligah e investigating officer, but after the information was nnel. LIMS was also Inaccurate in the reported		
		Unknown" and " ML #09-2098".			
Description of Root	Cause	incorrect information in OLO and in LIM evidence, resulted in the improper iden case inc#088322509/L09-12679 also sho Williams. Furthermore, the bloodstain of profile given extreme degradation. As a available for verification.	S, coupled with no associated name on the morgue tification of morgue evidence. Also, the cross-referenced bwed Eligah Williams as the complainant instead of Undra card from the morgue evidence failed to yield a DNA a result, the gender of the complainant's known was not		
Description of Action Taken to Prevent Recurrence		This issue has been discussed via email in the event of an "unknown" name or r contact the investigator to confirm the information through the method descri morgue evidence will be described usin examination documentation and labora SOP revision.	and in sectional meetings with the entire Biology Section. name discrepancy on the morgue evidence, the analyst will complainant's name in writing instead of verifying this bed above. If written verification cannot be obtained, the g the ML # and as being from "unknown" in the atory reports. These points will be included in the next		
		Reports associated with this case will be	amended to reflect the correct complainant name.		

Action Completed By

Amica arec.

on \_\_\_\_

10/1/13

eviewed by Lab Manager

12 .F. TESSER

eviewed by Quality Manager

dditional Action Taken f applicable)

Abora 1.13

L-QA-CAPA- 2010.1

effective 01-04-2011

0 1

on <u>10-1-13</u> on <u>10/4/2013</u>

king Number	2013-	021				
dent Number	35987	805,056226712,01427 17113,054559312.	6213,06	391	85513,	
orted On 1	0/18/2013					
orted By	Maria A. Rumbl	le				
cription of Issue		Analyst upon removing amp plate from the was present due to a smaller volume than analyst accidentally did not remove the mint into the TECAN. The TECAN was told that Due to the upload of the csv file with the negative where a sample was supposed to one. This also caused an incorrect volume The samples located after the negative witvolumes.	ne 9700 discovere what was in the egative from the there was one m negative not omi o be. Samples ion to be amplified i ere manually re-a	ed that other v sample ore sar tted, th cated a for any mplifie	in the last wei vells. it was di e setup file tha nple than ther ne TECAN was fter the negati samples behir ed using the co	l, only master mix scovered that t was imported e actually was. told there was a ve were shifted up nd the negative. prrect template
cription of Root Cause		Analyst error and oversight is the root cau the negative was removed and that all we prepare the amp plate.	use. Analyst shou ells had the same	id have volum	e double check e after using ti	ed to make sure he TECAN to
cription of Actio vent Recurrence	on Taken to	Anaiysts will visually inspect that all wells volume and that the correct file is upload technical leader, the SOP will also be upd of the tubes coincide on the racks and in	of the quant or a led into the TECA ated requiring a the software.	mp pla N. Per witness	ate have the sa communications to verify the c	me amount of on with the order and identity
Attach e	evidence th	at corrective action has been con	npleted succe	ssfull	y (if applica	ble).
ion Completed B	By	Mahmon		on	11/15/1	3
iewed by Lab Ma	anager	1-	1	on	1-22-	13
iewed by Quality	y Manager	Sultan		on	12/2/	2013
ditional Action T applicable) Act	aken e attac	ched				

2013-021

A-CAPA- 2010.1

..

effective 01-04-2011

к, CC	DRRECTIVE & PREVENTIVE ACTION REPORT
king Number 2014-	<i>coz</i> 2014-002
lent Number nla	
orted On Jan 14, 2014	
orted By Robin D. Guide	у
ription of Issue	On 1/2/2014, Criminalist Vanessa Alvarez notified Criminalists Belinda Salinas and Diana Donley via email that her review of the records for the dry baths and thermomixers indicated that some of the units checked on October 21 and 22, 2013 were checked using expired NIST thermometers (NIST #3 and #4). Those units include dry baths #1 and #6 in the y-screening area and thermomixer #1 and dry bath #9 in the not-yet-on-line QiaCube laboratory. All blocks used for the extraction of DNA samples were calibrated using current NIST thermometers. During the investigation of this issue, it was also discovered that been subjected to a performance check in October, 2013. Additionally, NIST thermometers #3 and #4 were used to calibrate the DNA extraction heat blocks, despite being expired, on October 17, 2012.
cription of Root Cause	The cause is believed to be rooted in the lack of marking on the actual thermometers regarding their expiration and/or need for performance check. There is ample paper documentation of when the NIST thermometers expire and/or need a performance check, but this historically has not been transferred to the actual units. At the time of these checks in October, 2013, the NIST thermometers were stored in a single location, regardless of whether they are out of calibration and no longer in service.
cription of Action Taken to /ent Recurrence	Corrective Actions: 1. N ST #7 underwent a performance check on January 8, 2014. 2. Dry baths #1 and #6 in the y-screening area and the thermomiker #1 and dry bath #9 in the QIACube laboratory have been recalibrated using current NIST thermometers on January 8, 2014 and January 13, 2014, respectively. Preventative Actions: 1. Each current NIST thermometer has been transferred to a bag that is labeled with the expiration date. 2. Expired NIST thermometers have been stored separately from the current thermometers. 3. A single individual, Christine Konecny, has been tasked with maintaining the section's NIST thermometers. 4. The heat block calibration form has been updated to require the analyst to include not only the NIST thermometer used, but also its expiration date. 5. The DNA monthly checklist has been updated to require the monthly review of whether NIST thermometers are expired and/or in need of a performance check.
Attach evidence th	at corrective action has been completed successfully (if applicable).
on Completed By	on 1-14-14
iewed by Lab Manager	Bilindo U. Solunas on 1-14-14
iewed by Quality Manager	- Stullebar on 1115/2014
litional Action Taken pplicable) perufted wi the therefore straig	a Koncony that expose there or the are labeled as tally these many to used for the particular

A-CAPA- 2010.1

70

effective 01-04-2011

king Number	ing Number 2014-004			
dent Number	Batch 34 (see li	st of incident numbers below)		
orted On	Dec 30, 2013			
orted By	Lloyd Halsell III			
cription of Issu	le	On November 18, 2013, while analyzing ru threshold in the amplification negative co the load plate and re-inject this negative of from run BC111813. The peaks persisted a with this amplification negative control re run BC111913, the negative control displa	In BC111513 for Batch in BC111513 for Batch in Introl, NEG111513BC. A control. This data was a sand a decision was mach-amped. Upon re-amped. Upon re-amped no peaks.	34, I noticed two peaks below a request was made to re-set up inalyzed on November 18, 2013 de to have all samples associated lification on November 19, 2013;
scription of Root Cause		The root cause is difficult to determine sir it is clear that it did occur during or after a	ce the potential contai mplification setup.	nination was so minimal.
scription of Act	ion Taken to ce	On December 4, 2013, following the dete amplification negative controls, multiple to determine if it might be the source of t conical tube in Quant set up room, the tu Tecan, and the stock TE. No concerning a precaution all aliquots of TE in the Quant trough on the Tecan. The Tecan was wip Tecan in post-amp was wiped down as w	ction of other peaks be amplifications of the TE he peaks. Duplicate an be aliquot for the Tecar ctivity was detected in set up room were discar ed down with DNAway ell.	low threshold in separate currently in use was undertaken polifications were made from the n, the TE trough used on the any of the samples. As a arded and replaced, including the and ethanol. Additionally the
Attack	h evidence th	at corrective action has been con	pleted successful	ly (if applicable).
tion Completed	i By	-SA-	on	12-30-13
viewed by Lab i	Manager	L	on	1=15-18 Por 1-15-14.
viewed by Qual	lity Manager	Fullilin	on	1/22/2014
ditional Action Taken applicable)		Incident numbers: 002920113, 110399812, 127475513, 0540 178104010, 077734613, 057331113	54813, 092787509, 109	165313, 113684710, 066994213,
1.00. 10 -01 50, 1.0000 -1000	above 271 above 2 1/22/2014	ne, and yte al little	tha deing -	fullifield.

king Number 2014	- 004		
dent Number 121060012			
orted On Dec 30, 2013			
orted By Lloyd Halsell i	11		
cription of Issue	On December 4, 2013, while analyzing run the amplification negative control, NEG120 and re-inject this negative control. This da BC120413. The peak persisted and a decisi amplification negative control re-amped. BC120513, the negative control displayed	BC120313, one peak l 0313BC. A request was ata was analyzed on Da ion was made to have Upon re-amplification no peaks.	below threshold was detected in s made to re-set up the load plate ecember 4, 2013 from run all samples associated with this on December 4, 2013; run
cription of Root Cause	The root cause is difficult to determine sind it is clear that it did occur during or after an	ce the potential contar mplification setup.	nination was so minimal.
scription of Action Taken to vent Recurrence	On December 4, 2013, following the detect amplification negative controls, multiple a to determine if it might be the source of the conical tube in Quant set up room, the tube Tecan, and the stock TE. No concerning ac precaution all aliquots of TE in the Quant set trough on the Tecan. The Tecan was wipe Tecan in post-amp was wiped down as we	tion of other peaks be mplifications of the TE he peaks. Duplicate an be aliquot for the Tecar tivity was detected in set up room were disca d down with DNAway II.	low threshold in separate currently in use was undertaken aplifications were made from the any of the samples. As a rded and replaced, including the and ethanol. Additionally the
Attach evidence t	hat corrective action has been com	pleted successfull	y (if applicable).
ion Completed By	-SR-	on	12-30-12
iewed by Lab Manager	<u>(.</u>	on	1-15-14
iewed by Quality Manager	- Son Viulim	on	1/2 2/2014
ditional Action Taken			

racking Number	2014-	005	
icident Number	073173313		
eported On	Oct 8, 2013		
eported By	Peter Lentz		
escription of issue	e	During the process of combining prev the same sample, the extract of a cons another sample during the concentrat	iously extracted DNA with the remaining extracted DNA of sumed sample was mistakenly combined with the extract of tion step.
escript.on of Roo	t Cause	I had two samples that were to be cor Samples 548PL13 (Item 2.2, Inc #0731) extracted and set up under the hood it the tube rack with the old extracts, I n using so I moved all my samples and r move, I vortexed and spun down the mistakenly added the new extract from extract for 478BC13 (Item 6.1.1 INC# 0 sample remains for testing, these item this laboratory's quality assurance stat	hbined and concentrated to attempt a better DNA profile. 73313) and 550PL13 (Item 6.1, Inc #037002913) were for combination before being concentrated. As I arranged oticed there was not a 1000ul pipet in the hood that I was acks to another hood that I had just cleaned. After this old extracts and switched their places on the rack. I in sample 548PL13 (Item 2.2, Inc # 073173313) to the old 37002913). Because these samples were consumed and no is will be reported as inconclusive due to a failure to satisfy indards.
Pescription of Action Taken to revent Recurrence		In the future, if there is more than one proceeding. More care will be taken w the middle of setting up for analysis. extraction SOP will be updated to req	Microcon needed, I will do them individually before then combining samples and I will not change my plans in Furthermore, per Technical Leader R. Guidry, the DNA uire a witness when DNA extracts are to be combined.
Attach	evidence th	hat corrective action has been c	ompleted successfully (if applicable).
ction Completed	Ву	Redal when	on <u>1-14-14</u>
eviewed by Lab N	lanager	L	on_1-14-14
eviewed by Qualit	ty Manager	Sallilin	on 1/22/2014
dditional Action	Taken		

00

10

effective 01-04-2011

### **HOUSTON POLICE DEPARTMENT** CRIME LABORATORY

### **CORRECTIVE AND PREVENTIVE ACTION REPORT**

X CHECK IF ADDITIONAL PAGES ARE USED

	SECTION 1		
Date: Apr 14, 20	014	CAPA #:	2014-008
DESCRIPTION OF ISSUE/NON- CONFORMANCE	On 2/21/14, the Quality Assurance Manager and I were inform protocol when investigating possible contamination for a sar that he did not amplify the actual reagent blank sample when reproducible upon re-amplification. The "examination docur indicates that he did use the reagent blank sample for the re- measured the sample in question on 2/25/14 and the measur actually re-amplified the reagent blank sample. Peter was re- review with the internal Affairs Division began on 2/27/14.	ned that Peter Lentz alleg nple extracted 2/5-6/14 i n he was attempting to d mentation" produced by amplification, which con rement I obtained is cons moved from casework or	gedly did not follow proper n inc #155416912. It was alleged etermine if activity was Peter for this re-amplification tradicts the allegation. I istent with Peter not having 2/25/14 pending a review. A
CLASSINCATIO		61455 1	ACTION ONLY
PROPOSED The samples as amplification of of the aileged ASCLD/LAB an	CORRECTIVE ACTIONS/RECOMMENDATIONS TO ADDRESS THE associated with the reagent blank in question were already re-ex- of the reagent blank in question. However, given the allegation failure to follow protocol (along with the Texas Forensic Science d DPS) and provided with a list of all cases with which Peter wa	DEFICIENCY AND PREVE stracted on 2/17-18/14 dr the Harris County Distri the Commission and the la sinvolved. Retesting ha	NT RECURRENCE; ue to low-level activity in the re- ct Attorney's Office was notified boratory's accrediting bodies, s been requested and has
SECTION MANA		Date:	Apr 14, 2014
Fina Resolution	Review ingring at this time two	AND RESOLUTION	)
QUALITY MANA	AGER: Fruillicm	Date:	4/11/2014
LABORATORY	DIRECTOR: Dun Kevis	Date:	4-14-14
Con Issu	rective and Preventive Action Form ed By: Quality Manager	CL-1	QA -CAPA

Issue Date: February 1, 2014 Page 1 of 1

commenced on many cases by ADAs, while the lab has initiated retesting on cases for which Peter handled samples but reports had not yet been issued. Examples of unethical behavior and the potentially far-reaching consequences in a forensic laboratory were discussed at the most recent laboratory-wide meeting on 4/10/14. DNA protocol will be enhanced to require that steps taken to verify possible contamination will be performed by a third party within the lab.



# HOUSTON POLICE DEPARTMENT CRIME LABORATORY

# CORRECTIVE AND PREVENTIVE ACTION REPORT

K CHECK IF ADDITIONAL PAGES ARE USED

### **SECTION 1**

Date: Mar 4, 2014	CAPA #: 2	014-009
DESCRIPTION OF On 03/03/14 it was noted by Criminalist Diana Donley during ISSUE/NON- CONFORMANCE: being performed and this sample was a reference from a kin sample 76MR14Y be re-injected to confirm activity. On 03/0 confirmed. Criminalist Diana Donley then requested a re-an Leader R. Guldry of possible contamination in the sample. This is in regards to Policiency CTS-14-	g data analysis, that item 1.1 (po vity. This sample should have ha own female. Criminalist Diana D 4/14 76MR14Y was re-injected a hplification of sample 76MR14Y i 571-005555 C . 30	rtion of known blood from d no result, as YSTR's was onley requested that nd alielic activity was and informed Technical PREVENTIVE ACTION ONLY
CLASSIFICATION OF NONCONFORMATION and a second provident of the second provide	file was produced from the re-a e consistent with alleles found in in extracted next to 76MR14Y. It mple 77MR14Y during the extra nician Maria Rumble. Upon re-ex THE DEFICIENCY AND PREVENT R ces of contamination will continu- bes, i.e. changing gloves, using D	mplification of sample sample 77MR14Y, item 2.1 is suspected that the ction process. Sample straction, 76MR14REY, ECURRENCE:
handling samples. Great care will also be taken when manaling camples from tube to tube.	Date: Ma	ar 14, 2014
FINAL n/a		
QUALITY MANAGER: FUILUIN	. Date:	3/17/2014
LABORATORY DIRECTOR: Una Rida	Date:	3-17-14
Corrective and Preventive Action Form	CL-Q. Issue	A -CAPA Date: February 1, 2014 1 of 1

### HOUSTON FORENSIC SCIENCE CENTER CORRECTIVE AND PREVENTIVE ACTION REPORT **X CHECK IF ADDITIONAL PAGES ARE USED SECTION 1** CAPA #: 2014-015 Vate: 06/03/2014 ESCRIPTION OF On Monday May 12, 2014, while I, Kristina Blackmon, was reviewing the quant data for Batch 20-2014 samples, I SUE/NONnoticed that extract #440KB14 (inc#144712412 item 2.2 - Portion of known buccal swabs from Leaundrea Fields) ONFORMANCE: displayed a male quant value. Then I noticed the next extract #441KB14 (Inc#144712412 Item 3.2 - Portion of known buccal swabs from Marcellus Sampson) displayed a female quant value. I had extracted these samples on May 8, 2014. Both of these samples were being re-extracted due to the involvement of Peter Lentz in the initial testing; they had been tested in June, 2013 and reported in July, 2013. I verified that the extract tubes for these extract numbers corresponded with the labeling on the extraction sheet, meaning that if a switch was to have occurred, it occurred during the extraction and was not a tube misplacement at quant set-up. I notified DNA analyst Diana Donley of the C ACTION ONLY LASSIFICATION OF NONCONFORMANCE: see Quality Manual for description TT ROOT CAUSE Analyst error and oversight are believed to be the cause of this sample switch. I should have verified that the sample ANALYSIS tube containing the portion corresponded to the extraction worksheet as well as the Fitzco tube loaded onto the FZ1 instrument. PROPOSED CORRECTIVE ACTIONS/RECOMMENDATIONS TO ADDRESS THE DEFICIENCY AND PREVENT RECURRENCE: Both samples were re-extracted and only the results of my second extraction were reported. To prevent this situation from reoccurring, I will remain more conscientious of the samples I am extracting and constantly visually inspect that the correct samples are being extracted in the correct order. Date: 6-3-14 ECTION MANAGER: SECTION 2 (MANAGEMENT REVIEW AND RESOLUTION) FINAL No unpad do latoristoregriporto. Switch Mated during Ne-yetra ation (see 2014-008). No funther adress taken at the time-feel 4125/2014 6/23/2014 **QUALITY MANAGER:** Date: ABORATORY DIRECTOR: Date: Corrective and Preventive Action Form FAD-QA -CAPA Issued By: Quality Manager Issue Date: May 16. 2014 Kustime Blackmon 6/3/14 Page 1 of 1

#### Description of Issue:

On Monday May 12, 2014, while I, Kristina Blackmon, was reviewing the quant data for Batch 20-2014 samples, I noticed that extract #440KB14 (Inc#144712412 Item 2.2 - Portion of known buccal swabs from Leaundrea Fields) displayed a male quant value. Then I noticed the next extract #441KB14 (Inc#144712412 Item 3.2 – Portion of known buccal swabs from Marcellus Sampson) displayed a female quant value. I had extracted these samples on May 8, 2014. Both of these samples were being reextracted due to the involvement of Peter Lentz in the initial testing; they had been tested in June, 2013 and reported in July, 2013. I verified that the extract tubes for these extract numbers corresponded with the labeling on the extraction sheet, meaning that if a switch was to have occurred, it occurred during the extraction and was not a tube misplacement at quant set-up. i notified DNA analyst Diana Donley of the situation and she advised me to continue with amplification and capillary electrophoresis of my original extracts but to also take another portion of each sample and re-extract them. I took another portion of each sample and re-extracted them on May 12, 2014. Extract # 440KB14RE and 441KB14RE were quantified, amplified and loaded onto the 3130 for data analysis. On May 16, 2014, review of DNA electropherograms for samples 440KB14 and 441KB14 confirmed that a sample switch had occurred in my initial extraction. Extract 440KB14, which should have yielded a female DNA profile, was observed to be a male DNA profile. Extract 441KB14, which should have yielded a male DNA profile, was observed to be a female DNA profile. On May 23, 2014, all other samples that were extracted with 440KB14 and 441KB14 were checked as possibly having been switched. It was concluded that only 440KB14 and 441KB14 were switched because: 1) an extraction confirmation had been performed; or 2) the reference was not excluded from evidence associated with its case. In addition, a comparison of the results issued in July, 2013 with my initial extraction data showed that a switch had occurred. The results of my reextraction are concordant with the results initially reported in July, 2013; these results are also consistent with Leaundrea Fields being female and Marcellus Sampson being male.

#### **Root Cause Analysis:**

Analyst error and oversight are believed to be the cause of this sample switch. I should have verified that the sample tube containing the portion corresponded to the extraction worksheet as well as the Fitzco tube loaded onto the EZ1 instrument.

#### **Proposed Corrective Action:**

Both samples were re-extracted and only the results of my second extraction were reported.

To prevent this situation from reoccurring, I will remain more conscientious of the samples I am extracting and constantly visually inspect that the correct samples are being extracted in the correct order.

To: Aimee Grimaldi, M.S.; Callan M. Hundl; Robin Guidry, MS ABC-F; Jennifer O'Callaghan Cc: Peter Stout, Ph.D.; Ron Sandberg; Lloyd Halsell III, MS F-ABC; Elizabeth Richey, MS, F-ABC; Quality; Ashley Henry, MA Subject: Re: 39.14 Request for Documents (Miranda, Abel)

### PRIVILEGED AND CONFIDENTIAL ATTORNEY COMMUNICATION

Colleagues:

Aimee and I just spoke by phone. You explained that HFSC received the evidence on April 12, 2015, and completed the analysis (with written report) on March 11, 2016. Therefore, the window for records responsive to Category No. 12 is from October 12, 2014, to September 11, 2016. (I'm confident you guys already have made this calculation, but I'm stating it here for the sake of the team as a whole.)

I agree that HFSC should not provide IRs or CARs until the reports are closed. In light of the almost-two-year window, we're likely to be updating our response until Christmas or later. Fortunately, we can direct Olvera to our e-discovery website for these reports as they become available. We'll need to lay this out in our initial response to the request, and, again, I will plan on helping you with that language.

Let me know if you disagree with any of the above. Also, please keep Ashley Henry in the loop for the matter, since CS/CM will be responsible for HFSC's response. Onward.

Tom

From: Aimee Grimaldi, M.S. Sent: Monday, June 20, 2016 10:01 AM To: Tom P. Allen; Callan M. Hundl; Robin Guidry, MS ABC-F; Jennifer O'Callaghan Cc: Peter Stout, Ph.D.; Ron Sandberg; Lloyd Halsell III, MS F-ABC; Elizabeth Richey, MS, F-ABC; Quality Subject: Re: 39.14 Request for Documents (Miranda, Abel)

Hi Tom,

Quality has approximately 20 Biology Incidents or CARs regarding contamination events that are not yet closed. We have draft reports for these but Paula and I are still working on the root cause analysis. Since these are in draft stage we are not going to include these in this request. Please let us know your thoughts on this.

4R-



# HOUSTON FORENSIC SCIENCE CENTER QUALITY DIVISION CORRECTIVE ACTION REPORT

Quality CAR #	2015-001		Date Su	bmitted:	4/29/2015
.evel/Type of Discre Non-Conformance	pancy/ II		Dat	e Closed:	516/2015 JBW
Date of this Report:	4/28/2015	Division:	FAD	FCN:	(If applicable)
Date of Incident:	2/6/2015	Section:	Forensic Biology		
Description of Discrep	ancy/Non-conforman	ce:			
visualization, but CTS of the second se	consensus results and t ee the attached memo	the CTS explan os dated 2/6/1	nation on sample prepa 5 for additional inform	ation.	ed these items as
Root Cause of Discrep	ancy/ Non-conforman	nce:			-
IT BACCIAIO TA PLATA					
n two of three slides.	the identification of sp	permatozoa wa	as corroborated by a pr	ivate laborato	ory. It is unclear at this
In two of three slides, time if the sperm iden	the identification of sp tification is the result of	permatozoa wa of sample prep	as corroborated by a proparation by CTS or from	rivate laborato slide prepara	ory. It is unclear at this tion here in the lab.
In two of three slides, time if the sperm iden T + S M u(d be)	the identification of sp tification is the result of Norco that Bud	oermatozoa wa of sample prep le ini finiliy	as corroborated by a proparation by CTS or from	ivate laborato slide prepara การคกับร คร	ory. It is unclear at this tion here in the lab.
In two of three slides, time if the sperm iden If not discovered at th	the identification of sp tification is the result of NoteD that Bud his point, where else in	ermatozoa wa of sample prep او زیرز (شهر/( the process v	as corroborated by a proparation by CTS or from <i>version by CTS or from</i> <i>version sliges</i> would this incident hav	ivate laborato slide prepara ארק איזער אג ve been discov	ory. It is unclear at this tion here in the lab. <i>per Report duren 3-</i> <i>pered:</i>
In two of three slides, time if the sperm iden Tt should be If not discovered at th This issue was identified discrepant results from results.	the identification of sp tification is the result of worch the Ar Bud nis point, where else in ed by the laboratory du n test participants with	bermatozoa wa of sample prep <b>ve jui (شمار)</b> <b>the process v</b> uring the testin hin this lab. W	as corroborated by a proparation by CTS or from would this incident hav ng and CTS was contact 'hen issued to this lab,	ivate laborato slide prepara איץ הועד 25 ve been discov ted to make th CTS reports in	bry. It is unclear at this tion here in the lab. <b>prr Report dures 3-</b> <b>rered:</b> hem aware of dicated the discrepant
In two of three slides, time if the sperm iden Tt should be If not discovered at th This issue was identified discrepant results from results. Actions Taken:	the identification of sp tification is the result of Norch Mar Bud nis point, where else in ed by the laboratory du n test participants with	bermatozoa wa of sample prep الا نبذ (شمال the process w uring the testin hin this lab. W	as corroborated by a proparation by CTS or from baration by CTS or from <b>would this incident hav</b> ng and CTS was contact then issued to this lab,	ivate laborato slide prepara איץ הועד 25 ve been discov ted to make th CTS reports in	bry. It is unclear at this tion here in the lab. Arr Report dates 3- rered: hem aware of dicated the discrepant
In two of three slides, time if the sperm iden <b>T+ shard be</b> <b>If not discovered at th</b> This issue was identified discrepant results from results. <b>Actions Taken:</b> 1. Instead of test treated more are negative.	the identification of sp tification is the result of worco the Bod is point, where else in ed by the laboratory du n test participants with sting each proficiency se like casework. Sampl This approach was ta	the process will not neck	as corroborated by a pro- paration by CTS or from would this incident hav ing and CTS was contact then issued to this lab, the available screening to cessarily proceed to min- tests 15-571 and 15-57.	rivate laborato a slide prepara <b>Mrg mive as</b> <b>re been discov</b> ted to make th CTS reports in est, moving fo croscopy if aci 2 this year.	bry. It is unclear at this tion here in the lab. Are Report dures 3- rered: mem aware of dicated the discrepant brward, samples will be d phosphatase results
In two of three slides, time if the sperm iden T+ should be If not discovered at th This issue was identified discrepant results from results. Actions Taken: 1. Instead of test treated more are negative. 2. Starting on C has replaced sexual assaul	the identification of sp tification is the result of <i>NoteO M A Bud</i> <b>his point, where else in</b> ed by the laboratory du in test participants with sting each proficiency se like casework. Sampl . This approach was ta TS test 15-571, fewer se conventional serologic t kits for semen.	sample for each ken with CTS to screening analysis of the state of the second s	as corroborated by a pro- paration by CTS or from would this incident hav ing and CTS was contact then issued to this lab, the available screening to cessarily proceed to min- tests 15-571 and 15-57 ysts will maintain profi- uch as microscopy, as to	ivate laborato slide prepara איז איז איז ve been discov ted to make th CTS reports in est, moving fo croscopy if aci 2 this year. ciency on micr the primary mo	bry. It is unclear at this tion here in the lab. per Report dures 3- rered: hem aware of dicated the discrepant brward, samples will be d phosphatase results roscopy, given qPCR ethod for screening
n two of three slides, time if the sperm iden T+ should be if not discovered at th This issue was identified discrepant results from results. Actions Taken: 1. Instead of test treated more are negative. 2. Starting on C has replaced sexual assaul 3. The Biology S spermatozoa	the identification of sp tification is the result of worco where else in a by the laboratory du n test participants with sting each proficiency se like casework. Sampl This approach was ta TS test 15-571, fewer se conventional serologic it kits for semen. SOP for semen identific is observed:	bermatozoa wa of sample prep الا زير (مرارع the process w uring the testin hin this lab. W sample for eac les will not nec ken with CTS t screening anal- cal methods, si cation has been	as corroborated by a pro- paration by CTS or from would this incident hav ng and CTS was contact then issued to this lab, then issued to this lab, the available screening to cessarily proceed to mi- cests 15-571 and 15-57. ysts will maintain profi- uch as microscopy, as to n updated to address in	rivate laborato a slide prepara <b>Proprive a s</b> <b>re been discov</b> ted to make the CTS reports in est, moving fo croscopy if aci 2 this year. ciency on micr the primary me nstances wher	bry. It is unclear at this tion here in the lab. Arr Report dates 3- rered: them aware of dicated the discrepant orward, samples will be d phosphatase results roscopy, given qPCR ethod for screening the only one
In two of three slides, time if the sperm iden <b>T</b> † <b>Shauld be</b> <b>If not discovered at th</b> This issue was identified discrepant results from results. <b>Actions Taken:</b> 1. Instead of test treated more are negative. 2. Starting on C has replaced sexual assaul 3. The Biology S spermatozoa a. the s docu	the identification of sp tification is the result of <b>Norco Mar Bud</b> <b>is point, where else in</b> ed by the laboratory du n test participants with sting each proficiency se like casework. Sampl This approach was ta TS test 15-571, fewer se conventional serologic t kits for semen. SOP for semen identific is observed: lide must be verified b imentation	ermatozoa wa of sample prep in i ki kinii in the process v uring the testin hin this lab. W sample for eac es will not nec ken with CTS t screening anal- cal methods, si cation has been	as corroborated by a proparation by CTS or from overation by CTS or from overation by CTS or from overation of slides of would this incident hav mg and CTS was contact then issued to this lab, then issued to the islab, then issued to address in alified analyst who must	rivate laborato a slide prepara <b>Proprive a s</b> <b>re been discov</b> ted to make the CTS reports in est, moving fo croscopy if aci 2 this year. ciency on micr the primary me nstances wher st initial and di	bry. It is unclear at this tion here in the lab. Arr Report dates 3- rered: mem aware of dicated the discrepant orward, samples will be d phosphatase results roscopy, given qPCR ethod for screening monly one ate the examination
In two of three slides, time if the sperm iden <b>T</b> + <b>S</b> AUCE <b>be</b> <b>If not discovered at th</b> This issue was identified discrepant results from results. <b>Actions Taken:</b> 1. Instead of test treated more are negative. 2. Starting on CC has replaced sexual assaul 3. The Biology S spermatozoa a. the s docu b. a sec	the identification of sp tification is the result of <b>NoteO MAT Bod</b> <b>his point, where else in</b> ed by the laboratory due in test participants with sting each proficiency se e like casework. Sampl This approach was ta TS test 15-571, fewer se conventional serologic It kits for semen. SOP for semen identific is observed: lide must be verified be mentation cond slide must be created	the process with the process with the process with the process with the testime in this lab. We sample for each es will not need ken with CTS the process will not need ken with CTS the process will not need ken with the proces will not need ken with the proces	as corroborated by a proparation by CTS or from would this incident hav ing and CTS was contact then issued to this lab, then issued to this lab, the available screening to tests 15-571 and 15-57. ysts will maintain profi uch as microscopy, as to n updated to address in alified analyst who mus- ed using the same supe	rivate laborato a slide prepara <b>Proprint a s</b> <b>Je been discov</b> ted to make th CTS reports in est, moving fo croscopy if aci 2 this year. ciency on micr the primary mon stances wher st initial and dis ernatant, wher	bry. It is unclear at this tion here in the lab. Are Report dates 3- rered: them aware of dicated the discrepant orward, samples will be d phosphatase results roscopy, given qPCR ethod for screening the only one ate the examination the possible.

Corrective Action Report Issued by: Quality Director

hece

HFSC-QDiv-CAR Issue Date: March 02, 2015 Page 1 of 3



K

## HOUSTON FORENSIC SCIENCE CENTER QUALITY DIVISION CORRECTIVE ACTION REPORT

presence of spermatozoa. If the second slide is negative for the presence of spermatozoa, the sample shall be reported as inconclusive for the presence of spermatozoa.

- 4. On Friday, March 13, 2015, all members of the Forensic Biology section attended a section-wide meeting, with the following exceptions: Brittany Beyer (absent), Clay Davis (absent), Shamika Kelley (maternity leave), and Katherine Morgan (absent). One of the journal club articles presented related to possible contamination within the lab. Below is an excerpt from my meeting notes that I discussed after this particular article's presentation by Zoraya Reyes:
- Transfer of contact DNA in the lab:
  - Secondary and tertiary transfers are very possible; we cannot avoid what happens prior to receipt in lab but we can prevent further transfer when in our possession; we would never know if we contaminated within the lab, as we have no expectation of what DNA is on what item; but, by employing extremely careful and deliberate lab techniques, we can minimize the possibility of transfer and more confidently respond as to why we do not think transfer occurred in the lab (e.g., on the stand)
  - Assume everything is dirty (swab sticks are NOT clean, evidence packaging is NOT clean)
  - o How to pull gloves from box and put on; do not handle fingers or palms with your bare hands
  - o Clean hand, dirty hand method
  - Change gloves anytime evidence is handled; do NOT touch reagents or supplies without new gloves!!!
  - Gloves must be clean when accessing reagents or tubes
  - Reagents should not be in close proximity to evidence
  - o Folders and exam documents should not be in close proximity to evidence, or treated as clean
  - Do not go "into" bags of tubes; pour out # of tubes needed, discard extras (do not return extra to bag)
  - Do not handle evidence and packaging without changing gloves in between; packaging has been handled by countless folks before arriving in lab and we know gloves, much less clean gloves, were not used in each of those events
  - Be aware of what you touch before touching evidence or reagents (e.g., mask, ear buds, chair, freezer door handle, etc.)
  - Do not treat paper or labels you grabbed from your desk area as clean

5. The three slides in question were submitted to Bode Technologies, a private and independent accredited laboratory, for a 2<sup>nd</sup> read on 1/6/2015. Initially, all slides were reported by Bode as negative for spermatozoa (report dated March 6, 2015). In an email dated March 16, 2015, after having reviewed the case file/examination documents, I inquired with Bode on the likelihood of whether examination documents would reflect if "sperm-like" objects were observed. I noted in that email that we did observe spermatozoa on each of the 3 slides. On March 19, 2015, Bode notified this lab that upon additional review, they did observe sperm on 2 of the 3 slides. See attached email.

6. The Biology SOP will be edited further to require that only one sample is loaded onto a slide for microscopic examination. The microscopic slides used in the lab are designed to enable the loading of 3 individual stains per slide. To rule out the theoretical possibility of a transfer of spermatozoa from one stain area to another, only one sample will be loaded on a slide (e.g., if a bubble in the liquid sample pops, could it possibly cause a spermatozoa to be propelled from one area on the slide to another?).

Technical Personnel:	Date:
Corrective Action Report Issued by: Quality Director It should be Noted that the Technica did NOT Notify Bude that the proticiency pr aid NOT identify Sperm, cur 5-6-15	HFSC-QDiv-CAR Issue Date: March 02, 2015 Page 2 of 3 Ovider that



### HOUSTON FORENSIC SCIENCE CENTER QUALITY DIVISION CORRECTIVE ACTION REPORT

Immediate Supervisor:	
Section Manager:	li,
	10 11 und

CODIS Administrator: Cleve Webt (If applicable)

Date:	
Date:	4/29/15
Date:	4/29/15

Additional Information/ Follow Up (If applicable):

Quality Director: Juluhm

**Division Director:** 

Date: 5/6/2015

Date:

identer Sevel II determined breause sperm was also identified by consultant Latriatory 516/2015

Corrective Action Report Issued by: Quality Director HFSC-QDiv-CAR Issue Date: March 02, 2015 Page 3 of 3

lob



### Houston Forensic Science Center

### INTEROFFICE MEMO

То:	Irma Rios, Director of Forensic Analysis Division
From:	Robin Guidry, Manager – Forensic Biology fol
Cc:	Lori Wilson, Quality Director Sulling 5/6/2915 Courtney Head, Supervisor – Forensic Biology
Date:	February 6, 2015
Re:	CTS Proficiency Test Number 14-575: Positive (Non-Consensus) Semen Results: EPDAJR(U2588D)

Item #4 was reported to CTS as "positive" for the presence of semen. Please see the table below for screening results. This is inconsistent with the majority of results submitted to CTS, according to the CTS Summary Report, as well as the CTS manufacturer's statement on how the samples were prepared.

When all screening results were complete and the cases were being batched for DNA processing, I noticed the discrepant results and reached out to CTS to notify them of the inconsistencies amongst the cases processed in this lab. Of eight cases, six yielded a negative semen result for item #4, one yielded an inconclusive result (due to presumptively positive results for PSA), and one yielded positive results (due to the observation of one spermatozoon). Please see the attached email. CTS was not aware of any issues regarding this particular test at the time of my email communication.

The spermatozoon was verified by a second qualified analyst. The analyst who screened EPDAJR/U2588D and obtained a positive result for item #4 also screened TMFHRE/U2588B and obtained a negative result for item #4.

A review of the CTS Summary Report for Test Number 14-575 dated January 7, 2015 showed that only this lab reported item #4 as positive for semen. Something to consider is that many of the labs included in the summary only tested for semen on item #4 using an alternate light source and acid phosphatase (they did not test for spermatozoa). Had this laboratory discontinued testing after negative alternate light source and acid phosphatase reactions, there would be no non-consensus spermatozoa results to be reported. It has been this lab's practice to employ all tests for which an analyst is competent, so that proficiency can be demonstrated for each test. Moving forward, however, proficiency samples will be treated more like casework in that testing will be discontinued on non-intimate samples that are negative for alternate light source and acid phosphatase, as is done in casework. Furthermore, only those analysts who use microscopy regularly and on casework will continue to perform

Reep of -1-15

microscopy on proficiency tests. Given the laboratory has moved to using qPCR in the vast majority of sexual assault cases, microscopy is no longer a primary screening tool for case work samples.

The analyst's interpretation and reporting as "positive" are compliant with the results and therefore laboratory protocol. However, in an effort to better understand the issue, the laboratory has submitted the slide produced for microscopy in this proficiency test to an accredited private laboratory for review. A follow-up memo will be issued with those results, which are anticipated by the end of February, 2015.

In addition to an external review of the slide in question, the following protocol changes have been made to Biology SOP #7 (Semen Detection):

- 1. When only one spermatozoon is observed:
  - a. the slide must be verified by a second qualified analyst who must initial and date the examination documentation
  - b. a second slide must be created and stained using the same supernatant, when possible.
  - c. if a spermatozoon is again observed, the slide must be verified by a second qualified analyst who must initial and date the examination documentation; this sample may be reported as positive for the presence of spermatozoa. If the second slide is negative for the presence of spermatozoa, the sample shall be reported as inconclusive for the presence of spermatozoa.

Semen Detection Screening Results

Case # and Sample #	ALS Screening Results	Acid Phosphatase Screening Results	Microscopic Screening Results	PSA Screening Results
EPDAJR/U2588D, item #4	Negative	Negative	1 sperm observed*	Negative

\*Verified by a second qualified analyst

Given the positive semen detection results, this item was subjected to a differential DNA extraction. No DNA results were obtained in the sperm cell fraction of this item, which is consistent with the screening results obtained for this item.

enu

# HOUSTON POLICE DEPARTMENT CRIME LABORATORY

## CORRECTIVE AND PREVENTIVE ACTION REPORT

CHECK IF ADDITIONAL PAGES ARE USED

### **SECTION 1**

Date: Apr 8, 2014	CAPA #: 2014-010
DESCRIPTION OF Contamination was detected in a reagent blank (11) ISSUE/NON- peaks appear to be from the samples (sperm fraction CONFORMANCE:	MS14 – RBS012714MS) for HPD Case #116874113. The observed ns) positioned before the reagent blank.
CLASSIFICATION OF NONCONFORMANCE: see Quality Manual for de	scription TT PREVENTIVE ACTION ONLY
ROOT CAUSE Mary Symonds performed the differential extraction ANALYSIS: analysis, re-amplification and genetic analysis of the Lentz. The reagent blank was re-injected and then r were present after re-amp; however they remained reproducibility of the contamination indicates that i during the set up for guant or amp. Either way, the PROPOSED CORRECTIVE ACTIONS/RECOMMENDATIONS TO ADD	<ul> <li>Benjamin Cambridge performed the quantification, genetic re-amp. Amplification and re-injection were performed by Peter e-amplified to confirm the presence of the alleles. Fewer alleles consistent with the DNA profile from the preceding samples. The t could have occurred from sample-to-sample during extraction or associated samples cannot be used for interpretation.</li> <li>RESS THE DEFICIENCY AND PREVENT RECURRENCE:</li> </ul>
All associated samples were re-extracted and all associated reagent poured new aliquots of reagents before re-extracting the affected sa Cambridge will continue to exercise extreme caution while handling	blanks yielded acceptable data. DNA Analyst Mary Symonds amples. DNA Analyst Mary Symonds and DNA Technician Benjamin g samples in the laboratory.
SECTION MANAGER:	Date: 4/14/14
SECTION 2 (MANAGEMENT RE	VIEW AND RESOLUTION)
FINAL Sie Tech Leader email dated 4. RESOLUTION: reported SINCE Jan. 2013) No.	123/2014(a total of 3 contanination events for ther action tak on a this time the star
QUALITY MANAGER: - Studim	Date: 4/28/2014
LABORATORY DIRECTOR: Lun Rios	Date: 5-6-14
Corrective and Preventive Action Form Issued By: Quality Manager	CL-QA -CAPA Issue Date: February 1, 2014 Page 1 of 1

### Wilson, Lori

From: Sent: To: Cc: Subject: Guidry, RobinD Friday, May 09, 2014 6:06 PM Wilson, Lori Rios, Irma Extraction contamination

Lori,

As you know, the Biology/DNA Unit of the Houston Forensic Science Center documents issues, such as DNA contamination, via the Corrective And Preventative Action (CAPA) form. This allows the detection of possible trends and presents any preventative measures that the lab may elect to employ.

In 2011, there were 18 CAPA-worthy events, 6 of which involved extraction contamination (33.3%). In 2012, there were 11 CAPA-worthy events, 3 of which involved extraction contamination (27.3%). In 2013, there were 18 CAPA-worthy events, 1 of which was associated with contamination at amplification in a negative PCR control (5.6%). In 2014 todate, there have been 8 CAPA-worthy events, 3 of which involved contamination (38%). Of those 3, 1 (12.5%) was associated with amplification contamination, while the other 2 (25%) were associated with extraction (1 reagent blank and 1 sample, both with low-level contamination). Please note that many of the CAPAs generated in 2013 and 2014 are associated with the massive outsourcing project of almost 10,000 cases and involve chain of custody documentation.

For perspective, the DNA lab has experienced a significant increase in production and therefore extractions. As the number of extractions increases, so does the potential for a contamiantion event.

- 472 DNA reports were issued in 2011
- 887 DNA reports were issued in 2012
- 1078 DNA reports were issued in 2013
- 330 DNA reports have been issued in 2014 (YTD)

The reduction in extraction contamination from 2011 to 2013 appears significant, and I suspect there is less due to an increased use of automation and a decreased use of manual extractions. 2014 has observed a percentage-wise increase of issues related to contamination, but year-to-date, is as high as 2012 and one half of 2011. One of the 2 extraction contaminations in 2014 was detected in a differential extraction, which is still a fully manual process; we are transitioning to an automated differential extraction at this time. The contamination events do not appear to be analyst-specific.

This lab continues to strive to completely avoid contamination through the use of good laboratory practices but also relies on mechanisms such as the extraction reagent blank to detect it when it is present. We will continue to employ good lab practices and will continue to document events and their corrective and preventative measures taken via the CAPA form. We will also continue to monitor contamination events for any trends and take action when necessary.

Thank you, Robin

Robin D. Guidry, M.S., F-ABC Police Administrator Houston Forensic Science Center Phone: 713-308-2620 Fax: 713-308-2645 Email: <u>robind.guidry@houstonpolice.org</u>

2014-13



# Houston Forensic Science Center

Inter-Office Correspondence

June 13, 2014

MEMORANDUM FOR:

SUBJECT: Root Cause Analysis of an Erroneous Identification made by

#### BACKGROUND SUMMARY:

- 1. The training procedure implemented by the Houston Forensic Science Center's Latent Print Unit requires all newly hired latent print examiners to be thoroughly competency tested prior to entering into any dependent supervised casework. Based on the documentation of qualifications and background experience the five (5) newly hired Certified Latent Print Examiners provided, a modified training program was implemented to test their knowledge and abilities in the area of Latent Prints. The competency testing program developed for the examiners was a two part test. A written competency test was developed consisting of 50 questions that would test the examiner's knowledge of the biology, history, processing techniques, various chemical development mediums, and the methodology if the science of friction skin identification. The second phase of the final competency testing consisted of a comparison examination developed from a three year old proficiency test from the testing agency CTS. The test was CTS Latent Print Test #11-517. The original test was scanned into Adobe Photoshop CS4 with the unknown latent images scanned at 2400 ppi resolution and the record finger and palm print cards scanned at 1000 ppi resolution. All information indicating which CTS version of the test was removed or redacted from the image. The scanned images were then printed using an Epson Stylus Pro 4900 high resolution ink jet printer. Four copies of the comparison competency test were made. The answer sheet was scanned as an Adobe PDF document with all extraneous information associated with the original CTS test cropped out.
- 2. On the cover of the final comparison competency test, the directions were as follows:

"Instructions: This is an assessment of your ability to identify or exclude latent prints when compared against known records. The test consists of twelve (12) latent images and four (4) records consisting of ten print and palm prints. You will have 8 hours to complete this assessment. No copies or scratch paper are allowed to leave the testing area. Please use a blue or black ink pen and write legibly on the answer sheet provided. You ARE allowed the use of your PC, scanner, and Photoshop software or your fingerprint loupe while in the process of completing this assessment. All work must be conducted independently."

- 3. The comparison test was administered to
  - Association for Identification. All of the above examiners successfully passed the examination.
- 4. On June 5,2014, **Example 1** was given the test with the above directions. Upon grading the test using the CTS answer key, it was discovered that he had erroneously identified Latent Image 5H. Todd was informed of this in the afternoon and advised that a resolution would be provided soon.
- 5. Per the Code of Ethics for Certified International Association for Identification Latent Print Examiners and the IAI Certification Manual Section X; subsection B under Technical Errors, the Secretary of the Certification Board, **Example 1** was notified on June 6, 2014 of the erroneous identification. Upon presentation of the facts, **Example 1** determined that since no report involving actual casework was issued and the erroneous identification was discovered in competency testing, it was unnecessary for **Example 1** to lose his status as a CLPE and in-house remedial assessments would be appropriate.

#### CAUSE ANALYSIS:

- 1. **Example 1** was instructed on June 6, 2014 to scan the latent identified and also the erroneous finger into Adobe Photoshop and chart what he saw during his analysis and comparison of the latent to known to better understand the thought process and determine possible causes. He was also instructed to provide a summary of possible factors as to why he erroneously identified the latent print. **Example** provided me with a summary of what he found and possible causes for the misidentification. (See Attached Summary from **Example**).
- 2. Upon analyzing the documentation and speaking with Todd, the following possible factors were likely contributors to the erroneous identification decision:
  - A. **Exercise the second second**
  - B. Although the directions stated a computer, scanner, and Photoshop software could be used, used a comparison loupe. He advised he was not aware he could have asked for access and his previous experience with comparing latent prints were conducted on the computer.
  - C. The location was taking his test was in the common area with many people walking and communicating around him.
  - D. **Example** started with the HFSC Latent Print unit on June 2, 2014 and was started with his competency testing within a few days. A summary of his explanations indicated that he also has external stressors that may have contributed to the erroneous identification.

#### CORRECTIVE ACTION PLAN

- 1. All further competency testing will be conducted in an environment that is free from extraneous noise and distractions.
- 2. Notifications will be posted that testing is in progress and to not disturb the person(s) taking the tests.
- 3. **Second and a series** will be administered a series of new competency tests to determine his skills and abilities further. This will consist of no less than four (4) additional comparison competency tests. These tests will be conducted using Photoshop software and he will be required to chart his conclusions so there will be a documented visual representation of the process. Once competency has been established and no errors have been noted, a new final comparison test will be issued. Upon successful completion of the re-testing phase, **Beneficient Proceed** will proceed into the dependent supervised casework portion of the HFSC Latent Print Training Program.
- 4. If further erroneous identifications are made during the re-evaluation phase, a re-evaluation of **Exercision** will need to be conducted to determine if he can remain in a Latent Print Examiner position with the Houston Forensic Science Center.

Timothy Schmahl, CLPE Latent Print Unit Manager To: Aimee Grimaldi, M.S.; Callan M. Hundl; Robin Guidry, MS ABC-F; Jennifer O'Callaghan Cc: Peter Stout, Ph.D.; Ron Sandberg; Lloyd Halsell III, MS F-ABC; Elizabeth Richey, MS, F-ABC; Quality; Ashley Henry, MA Subject: Re: 39.14 Request for Documents (Miranda, Abel)

### PRIVILEGED AND CONFIDENTIAL ATTORNEY COMMUNICATION

Colleagues:

Aimee and I just spoke by phone. You explained that HFSC received the evidence on April 12, 2015, and completed the analysis (with written report) on March 11, 2016. Therefore, the window for records responsive to Category No. 12 is from October 12, 2014, to September 11, 2016. (I'm confident you guys already have made this calculation, but I'm stating it here for the sake of the team as a whole.)

I agree that HFSC should not provide IRs or CARs until the reports are closed. In light of the almost-two-year window, we're likely to be updating our response until Christmas or later. Fortunately, we can direct Olvera to our e-discovery website for these reports as they become available. We'll need to lay this out in our initial response to the request, and, again, I will plan on helping you with that language.

Let me know if you disagree with any of the above. Also, please keep Ashley Henry in the loop for the matter, since CS/CM will be responsible for HFSC's response. Onward.

Tom

From: Aimee Grimaldi, M.S.	
Sent: Monday, June 20, 2016 10:01 AM	
To: Tom P. Allen; Callan M. Hundl; Robin Guidry, MS ABC-F; Jenn	ifer O'Callaghan
Cc: Peter Stout, Ph.D.; Ron Sandberg; Lloyd Halsell III, MS F-ABC;	Elizabeth Richey, MS, F-ABC; Quality
Subject: Re: 39.14 Request for Documents (Miranda, Abel)	

Hi Tom,

Quality has approximately 20 Biology Incidents or CARs regarding contamination events that are not yet closed. We have draft reports for these but Paula and I are still working on the root cause analysis. Since these are in draft stage we are not going to include these in this request. Please let us know your thoughts on this.

4R

# HOUSTON FORENSIC SCIENCE CENTER

Print Form

INCI	DENT	REP	ORT
------	------	-----	-----

Corrective	Preventiv					
A			imentation Only	Inc. Report #:	2014-027	
Date: Oct 31, 2014						
DESCRIPTION OF DISCREPANCY/ NON/CONFORMANCI	On 9/11/14, DNA / Reagent blank san reagent blank was consistent with the and loaded this rea contamination wa	Analyst Clay Davis observed alle nple 682MR14 was re-injected t re-amplified by a second techr e known DNA profile of DNA Te agent blank and its associated s s confirmed.	elic activity in a re he same day and ician and the ac chnician Maria R samples. The Tec	eagent blank during h I the activity was repli tivity was again repro umble who extracted chnical Leader was no	is review of the data. cated. On 9/12/14, the duced. This activity was , quantified, amplified tified as soon as the	
Date: Sep 11, 2014						
CAUSE OF DISCREPANCY/ NON-CONFORMANCE (if possible to determine)	When notified of the contamination. All the same preventa the analyst recalls f DNA was introduce When unusual circu handling), analysts explanation should and does not recall process, but rather can be very difficult DNA testing proces	ne contamination, the analyst e extractions by this technician tive measures that she routinel ollowing good laboratory pract and to the reagent blank tube. Instances occur during an extr are asked to make a note on ex data and/or controls exhibit un the need to do so. Because cor only once samples have been o to identify the exact cause of t s.	valuated her acti since this event h y incorporates in tices, at some po action (e.g., a tul amination docu nusual activity la tamination is ge juantified, ampli he contaminatio	ions and was unable t have been acceptable; to her laboratory prod int prior to amplification pe is dropped onto the mentation for easier to ter. The analyst did no merally not detected i fied, and subjected to n event, especially give	o pinpoint a cause for the she believes she is using cedures. Even though ion, it appears her own e bench top during roubleshooting or ot make any such notes mmediately in the fragment separation, it ven the sensitivity of the	
LEVEL/TYPE OF DISCREPANCY/NON-CONFORMANCE (see Quality Manual for description): CLASS II						
EFFECT OF DISCREPANCY/ NON-CONFORMANCE: (if possible to determine)	Because a reagent be interpretation. Sam re-extraction of the case due to limited a INC#024911686/L86 2014-14668. Consu Investigator is seekin This is the 682nd sar section-wide Forens	plank was found to be unaccept ples will need to be re-extracte associated samples. Consumpt sample remaining for each item i-3529/2014-13476, INC# 14104 mption has been granted for al ing input from the prosecuting a mple extracted by Maria this ye- ic Biology meeting held Senter	able, the data of d. Additional tin ion orders have n. Three cases are 4213, and INC# ( l but INC#02491 attorney. ar and this is the obse 26, 2014, th	the associated sample ne and resources will l been requested from e associated with this 074776514/ 1686/L86-3529/2014- first contaminated rea	es may not be used for be used to complete the case officers for each reagent blank: 13476; the case agent blank. At the	
	reminded to exercise things such as chair	e extreme caution and awarene s, face, face masks, etc. with glo	ess when handlin ved hands and t	g samples during extr o change gloves as fre	and analysts were raction by not touching	
lf no	ot discovered at this	point, where else in the proces	would this incid	lent have been discov	rered?	
Because the review of a technical review of dat the technical review of that controls are accep	all examination docu a, this issue, if not ca this case. The DNA r table.	imentation and controls, includ ught when it was during the ar eview checklist requires the rep	ling reagent blan alyst's initial rev porting analyst a	iks, is a required step i iew of the data, would nd the technical review	n data analysis and the I have been caught in wer to acknowledge	
Corrective Actions/Preventive Measures Taken (if applicable):						
Per laboratory protocol, given the unacceptable reagent blank control, re-testing has commenced for INC# 141044213 and INC# 074776514/2014-14668. Re-extraction is pending consumption permission for INC#024911686/L86-3529/2014-13476.						

Corrective and Preventive Action Form Issued By: Quality Director

41

4

HFSC -QDiv -CAPA Issue Date: August 19, 2014 Page 1 of 2
# HOUSTON FORENSIC SCIENCE CENTER

Print Form

#### INCIDENT REPORT

Corrective	Sper Preventive	Tracking/Doc	umentation Only	Inc. Repo	ort #: 201	14-027
ANALYST:	Alumer	MARIA	A RUMPLE	Date:	10 31	14
SECTION MANAGER:	hi	ROBIN	D. GUDKY	Date:	10/31/10	+
CODIS ADMINISTRATOR (if applicable):	Cleve West	Cler	IR WEST	Date:	10/31/1	14
ADDITIONAL INFORMATIC FOLLOW UP (if applicab	DN provide tollow	vp once a	Ill cases have	ve be	en reu	WV4ca
	,					
QUALITY DIRECTOR	Sulum	0		Date:	11/5/20	14
LABORATORY DIRECTOR	clunk	ios	1	Date:	17-7-1	14
	Da	te Closed: III	12/22/201	suser.	email d	atud 12/11/14
	CI	ay Davi	is da	ykar	ris_	10.31.14

Corrective and Preventive Action Form Issued By: Quality Director

4

ŧ.

HESC -QDiv -CAPA Issue Date: August 19, 2014 Page 2 of 2



	Qual	ity Divisi	on use	only	2	118/2016
Quality Tracking #	2015-024			Date Subm	itted: 4	12/2016 JBN
				Date Cl	osed: 📑	118/2016 FBW
Date of this Report:	12/11/2015	Division:	FAD		FCN:	2013-20123 / 073206213
Date of Incident:	2/27/2015	Section:	DNA			(If applicable)
In this space, record de instructed by the Section A request for YSTR and	tails of the incident, in on Manager or Divisio lysis was made on 2-16	nclude dates. n Director(s): 6-15 for case	<b>Do not in</b> 07320621	<b>clude analysts n</b> 3 (2013-20123) f	ames unle	ess otherwise ns associated with
tissue/fluid from a fetu Davis. Analysis of the a was DNA from tissue/fl	s (Items 1.5, 1.6, 1.7 & mplified items was per uid from a fetus, a mix	1.8). The fou formed and a ture of YSTR's	ir items w mixture v s in this ite	ere amplified wit vas observed in I em was not antic	th YSTRs of tem 1.5. S ipated.	n 2-20-15 by M. Bryan ince this sample type
A comparison of the st consistent with the "ex	aff YSTR database reve tra" alleles present in I	ealed that the tem 1.5.	analyst th	at amplified the	evidence	with YSTRs was
A re-amplification was source profile with no i	requested on 5-28-15 f ndications of a second	for Item 1.5; t contributor.	he second	I YSTR DNA profi	le produce	ed a partial single-
The extra alleles observent setup and not in the or consisted of a major co the DNA profile develop Bryan Davis. Therefore reporting purposes.	ed in the original YSTR iginal extraction of the mponent consistent w ped on other portions of the re-amplification r	amplification item. This th ith the biolog of the fetal tis results for Iten	n were mo leory is su ical mothe ssue/fluid. n 1.5 are	ost likely introduc pported by the fa er and 2 minor al These 2 minor a deemed accepta	ced at the act that the leles that a lleles are i ble and wi	YSTR amplification e autosomal profile are consistent with not consistent with M. Il be used for
Quality Division Use O	nly	able)				
The Quality Division re	equested associated ele	ectropherogra	ams.			
Algred Anader	it Form rear	ta 2/18/10	ly J	Webm. 4	adina	turell
Is Alanged.	until Amel	ine rai	ited 1	o allagla	supple	ung so and the
See timilin	e dated by T	Wilson ,	n 3/18	12016.		
	DION	CP NOCE V	list th	uplie was	6	

Incident Tracking Report

Issued by: Quality Director Compiles by TL Halsell. Issue Date: March 02, 2015

**HFSC-QDiv-INCR** Page 1 of 2



Technical Personnel: Boyce Davis No longes employed Date: 2.4.14 Section Manager: Dup Company by 14Psc Date: 2/8/14 Division Director: Curr Rubs 1-2010 Date: 2-16-16 Quality Director: Fullin

Technical Leader: SHALSELL CONTS admin. ! Clux What 2/16/16

Date: 3/18/2016

2-16-16 Resolving Quality Incident 2015-024 was a bit lengthy. Review as instituted for this mindenfunsers' I monogens were reminded of process in FAD meeting held 2-15-16. Process map was provide A. china Rivs 2-16-16

10 Willim rec'd 2/18/16

**Incident Tracking Report** Issued by: Quality Director

Time line to address delayed reporting of CAR 2015-024 regarding Incident number 073206213 to the **Quality Division** 

- 2-20-15: Item 1.5 (3225MR14) is amplified with YSTR
- 2-27-15: Item 1.5 (3225MR14) is run on CE
- 5-28-15: Item 1.5 (3225MR14) is requested for re-amplification and re-amplified
- 5-29-15: Item 1.5 (3225MR14) re-amplification is run for CE
- 12-14-15: DNA report is issued with results for Item 1.5

During the time that this case was identified and processed for YSTR analysis there was not a set schedule for the routine processing of YSTR requests. In February of 2015 two large YSTR amplifications were performed that consisted of most of the open requests. One reason for such a large run was that only two technicians were competent in processing YSTR samples. These samples were not part of an active batch and the cases were to be written by the few analysts that could issue YSTR reports. The analyst would work on these cases between their ongoing batches when they had time.

The data was initially reviewed in February 2015, but that analysis was not case specific. The first analysis was meant to check the controls and overall profiles as compared to amplified target and therefore the contamination was not detected at this time. The case was reviewed by the reporting analyst in May 2015. During the review conducted by the reporting analyst the contamination was detected.

After the re-amplification results were obtained it is possible that the complexity of the case and the Timeline prepareta by Cloyos Ithe sell Rule. (1) 03/29/16 UR 3.30-16 case type extended the completion date. This case request was a paternity testing case in which statistical analysis for paternity calculations was necessary. Due to the complexity of the case, many discussions and consultations occurred as to how it should be reported.



### HOUSTON FORENSIC SCIENCE CENTER CORRECTIVE ACTION REPORT

		QUALITY DIVIS	ION USE ONLY		
Quality CAR # 2	016-005		Date Subm	itted:	3/1/2016
Non-Conformance	Level CLASS I		Date C	losed:	6/14/2016
Date of this Report	5/23/2016	Division:	FAD	FCN :	2014- 19609/120012514 & 2014- 22128/136106214
Date of Incider	at: 3/11/2015	Section:	Forensic Biology/DNA		(If applicable)

#### Description of Discrepancy/Non-conformance:

The epithelial fraction reagent blank, RBE031115IH-1 (266IH15), was extracted on 3-11-15 on Batch 21. The extraction batch contained two cases, 2014-19609 (Incident # 120012514) and 2014-22128 (Incident # 136106214). The reagent blank was quantified on 3-12-15 and had a value of 0.0006 ng/ $\mu$ l. Amplification occurred on 4-3-15, with CE following on 4-6-15. The reagent blank contained a single peak above threshold with additional peaks that were distinguishable from background below analytical threshold.

The data was initially reviewed on 4-13-15, however this was not a case specific review. The reporting analyst did not review the CE run until 7-20-15 and the technical reviewer until 10-2-15.

#### Actions Taken:

Re-injection was requested on 7-27-15 and occurred on 8-5-15. The peaks persisted so the reagent blank was requested for re-amplification on 8-6-15 and occurred on 8-12-15, with CE following on 8-12-15. The peaks persisted after re-amplification.

The extraction batch and employee profile list were examined for possible sources, none were identified.

All samples from case 2014-22128 had been initially amplified. All samples with case 2014-19609 were either male negative or inconclusive, so no samples were amplified. To troubleshoot the source of the contamination, the sample immediately adjacent to the reagent blank, 265IH15, was requested for amplification on 9-3-15 and set up on 9-10-15. This profile was not consistent with the reagent blank.

All other samples from case 2014-19609 were requested for amplification on 9-15-15 and set up on 9-16-15. Several did not generate a DNA profile and those that did generate results were all consistent with the same female profile and not consistent with the contaminant.

Since no ADA was assigned to these cases to issue permission to consume, re-extraction did not occur. The acceptable sperm fractions were reported out and the associated epithelial fractions were reported as not meeting quality assurance standards.

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed

HFSC-QDiv-CAR Issue Date: October 30, 2015 Page 1 of 2



## HOUSTON FORENSIC SCIENCE CENTER CORRECTIVE ACTION REPORT

If not discovered at this point, where else in the process would this incident have been discovered? The DNA review checklist requires the reporting analyst and the technical reviewer to acknowledge that controls are acceptable. This incident would have been discovered during review.

$\bigcirc$	
Technical Personnel:	Date: 06-10-100
Immediate Supervisor: Shiputhe July	Date: 6/13/16
Section Manager: Jup C	Date: (3)16
CODIS Administrator (if applicable):	Date: (0/3/14
Division Director: Chuna Rus	Date: 6/3/16
Trich Lend: Stat	5-2476

#### Summary of Root Cause Analysis:

In this particular case the contamination was reproduced after re-amplification which suggests that the contaminant was most likely introduced to the extract at either the extraction or quantification steps. A likely root cause of this particular contamination event could be attributed to poor sample handling at either of these processes. Because the source of this contaminant is not a sample processed on Batch 21 nor an employee, extraneous DNA could have been deposited into the laboratory and introduced to this reagent blank during processing.

#### Additional Information/Follow-Up:

The Forensic Biology Section will be performing lab decontamination on a routine basis. Additional PPE requirements have also been implemented to prevent contamination issues. Lab coat, gloves, hair coverings and face masks are now required during screening, extraction, quantification, and amplification. In the post-amplification laboratory, gloves and a lab coat are required. This PPE is not optional and anyone entering the areas where these procedures are performed must abide by these requirements.

Quality Director: Sou William

Date: 6/14/2016

relieved for signatures 5/24/10 tiles.

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed

HFSC-QDiv-CAR Issue Date: October 30, 2015 Page 2 of 2 This time line addresses the delayed reporting of CAR 2016-005 regarding Incident numbers 2014-22128 (136106214) and 2014-19609 (120012514) to the Quality Division.

RBE031115IH-1 (266IH15) was extracted as part of SAK batch 2015-21.

- 3-11-15 Extraction
- 3-12-15 Quantification
- 4-3-15 Amplification
- 4-6-15 CE
- 4-13-15 Initial review for poor injections
- 7-20-15 Review by report writer
- 7-27-15 Requested for reinjection
- 8-5-15 CE of reinjection
- 8-6-15 Requested for reamplification
- 8-12-15 Reamplification
- 8-12-15 CE of reamplification
- 9-1-15 Email to Tech Lead asking how to report since there was no ADA assigned. Tech lead
  responds to report acceptable fractions and others as inconclusive and an incident report will be
  necessary. TL asks about other samples being amplified. Clearly a conversation was had in
  person based on the tone of the emails.
- 9-3-15 Sample 265IH15 requested for amplification as part of troubleshooting
- 9-10-15 Amplification of 265IH15
- 9-10-15 CE of 265IH15
- 9-15-15 Additional samples requested for amplification for trouble shooting
- 9-16-15 Amplification of additional samples
- 9-16-15 CE of additional samples
- 11-30-2015- 2014-22128 reported
- 12-21-15 2014-19609 reported

The cause of the delayed reporting of this corrective action to the Quality Division it not known. However, in October 2015 a re-organization of Biology section management occurred in which an Alternate Technical Leader was designated. This restructure could have contributed to reporting delay. The TL designated at the time of this event was involved in the troubleshooting of this contamination event and investigated the event thoroughly.

The ATL notified the Quality Division that a corrective action was necessary in February 2016. Since February 2016, the Quality Division and the ATL have worked together to close this corrective action report.

Time line provided by Lloyd Halsell III, Acting Technical Leader



	Qua	lity Divisi	ion use only		
Quality Tracking #	2016-032		Date	Submitted: 3	/29/2016
		Marina Marina (Marina Marina (Marina) Marina (Marina (Marina (Marina (Marina (Marina (Marina (Marina (Marina (M	D	ate Closed: 5	110/16
Date of this Report:	3/29/2016	Division:	FAD	FCN:	2016-02382/154.14115 2015-12890/13 12134231 2015-07396/018032416 (If applicable)
Date of Incident:	3/14/2016	Section:	Biology		
In this space, record de instructed by the Section Reagent blank 1343LS1 of 0.01274ng/µL. This is ZR031516). The reagen concordant with the sa 1342LS16, to verify qua results were N/A, sugges blank's DNA result of no accentable	etails of the incident, on Manager or Division 6 for Extraction Batch reagent blank was am it blank produced a clear imple's quant value, the antitation results. After esting that no DNA was o DNA activity presen	include dates on Director(s) 28-2016 was plified on 03/ ean profile wit his reagent bla er the re-quan ts present. Th t. Therefore,	Do not include ana originally quanted of 15/16 and then it wa th no DNA activity. S ank was then re-quantification, the reage e re-quantification r this reagent blank a	n 03/14/16 and as loaded on 03/ ince this DNA re nted along with nt blank and adj result correspon- nd the associate	ess otherwise yielded a quant value 15/16 (project sult was not an adjacent sample, acent sample's quant ded with the reagent d data are deemed

#### **Quality Division Use Only**

Additional Information/ Follow Up (If applicable):

It is unclear how extraneous DNA was deposited in the original quantification of the reagent blank yielding a result of 0.01274 ng/µl. A thorough laboratory clean was performed on 3/28/2016 to decontaminate the work areas of any extraneous DNA that may have been deposited. In addition, the section plans to perform this lab clean on a routine basis. As of 4/8/2016 additional PPE requirements have also been implemented as a preventive measure to prevent contamination. The required PPE in the pre-amplification areas include a lab coat, gloves, face masks, and head coverings.

Technical Personnel:	Date: 5-10-16
Section Manager:	Date: 5/6/16
Division Director: Sun fice	Date: 5/9/16
Quality Director:	Date: 5/10/2016
Tech led : SM it restell Incident Tracking Report Issued by: Quality Director released for signatures glzoji w tra	S-G-76 HFSC-QDiv-INCR Issue Date: March 02, 2015 Clunc Wood 5710/16 Page 1 of 1



	Qu	ality Division u	se only	
Quality Tracking #	2016-049		Date Subm	itted: 4/21/2016
			Date Cl	osed: 4/26/2016
ate of this Report:	4/4/2016	Division: FAD		FCN: 2014-15820
Date of Incident:	3/22/2016	Section: Fore	nsic Biology	OP7225614
basket during the extr	action procedure t	he DNA technician notic	ed that there was a	a strand of apparent hair on the
basket during the extr swab in the tube. The remained with the sw The technician record record.	action procedure to technician continu ab. The technician ed this informatior	the DNA technician notic retained the spin basket non a laboratory informa	ed that there was a into the spin baske with the apparent ation worksheet tha	a strand of apparent hair on the t making sure the apparent hair hair and placed it into Freezer 1. at was included as part of the case

#### **Quality Division Use Only**

#### Additional Information/ Follow Up (If applicable):

Three technicians were interviewed to determine the procedure for portioning an evidence swab with an apparent hair attached. All three screeners stated that if a hair was observed during the portioning process that it would be noted in their case notes. In addition, standard procedure is to portion one half of an evidence swab for extraction. During the portioning procedure, the technician would portion the area of the swab that did not contain the apparent hair. It is unclear if the apparent hair was present during the screening procedure and overlooked or if it was introduced during processing. Hair coverings have since been implemented as a required PPE in the screening, extraction, and pre-amplification areas of the laboratory.

Incident Tracking Report Issued by: Quality Director



Technical Personnel: In Mark Section Manager: Division Director: Quality Director: 71/

Tuh Leus: SAT HAUSEIL Marine Li

CODIS admin : Cleve West

Date:	041-25-16
Date:	4/21/16
Date:	4.26-16
Date:	4/26/2016

4-25-16

4/26/16

4/24/16

The swab was in the process of analysis when the hair was first sted. Since analysis had already begun, the sample, including the ssible nair, proceeded through the analytical process. Based upm I DNA results obtained, the nair did not impact the results and irefore, the results where deemed acceptable. Ron 4/20/10 SON

**Incident Tracking Report** Issued by: Quality Director

	2015-10459		0133	41215 5/31/2	016
	Qual	ity Divisi	on use or	nly	
Quality Tracking # 201	16-050			Date Submitted	: 4/22/2016
				Date Closed	5/31/2016
Date of this Report: 4/	/22/2016	Division:	FAD	F	CN: 2016-05328 2015-01631 2015-10459
Data of Incidents 4	/12/2016	Castions	Dielesu		(If applicable
Date of incluent. 4/	/13/2010	Section:	ыоюду		
allele below analytical three contamination. Re-injectio good morphology. Upon re reagent blank was then re- Upon re-amplification the p	eshold. This reagent b on of this reagent b re-injection the allel -amplified to deterr possible allele was	traction batch t blank yielded lank was requ le was reprod mine if this po not present a	a 39, RBE04131 d a quant value lested since th uced and now ssible allele wa nd therefore t	6LS-1 (1825LS16) of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. the amplification prod and the associated dat
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable.	eshold. This reagent b on of this reagent b re-injection the allel -amplified to deterr possible allele was	traction batch t blank yielded lank was requ le was reprod mine if this po not present a	a 39, RBE04131 d a quant value lested since th uced and now ossible allele wand therefore t	6LS-1 (1825LS16) e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. the amplification prod and the associated dat
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable.	eshold. This reagent b re-injection the allel -amplified to deterr possible allele was	traction batch t blank yielded lank was requ le was reprod mine if this po not present a	a 39, RBE04131 d a quant value lested since th uced and now ssible allele wind therefore t	6LS-1 (1825LS16) e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. the amplification prod and the associated dat
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo	ollow Up (If application of expension of the second	traction batch t blank yielded lank was requ le was reprod mine if this po not present a able): ensic Biology S	a 39, RBE04131 d a quant value lested since th uced and now ssible allele wind therefore the nd therefore the Section will be	e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank performing lab de	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. T the amplification prod and the associated dat
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo In response to contamination routine basis. Additional Pl gloves, hair coverings and f amplification. In the post-a anyone entering the areas of	ollow Up (If application of exemplified to deterring on of this reagent bre-injection the allel -amplified to deterring possible allele was only the state of the second state of the seco	traction batch t blank yielded lank was required was reproding mine if this point not present a able): ensic Biology S ave also been viequired dur atory, gloves a	a 39, RBE04131 d a quant value lested since th uced and now issible allele with nd therefore the Section will be implemented ing screening, and a lab coat a formed must a	e of 0.0ng/µl and s e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank performing lab de to prevent contar extraction, quant are required. This bide by these req	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. the amplification prod and the associated dat econtamination on a nination issues. Lab co ification, and PPE is not optional an uirements.
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo In response to contamination routine basis. Additional Pl gloves, hair coverings and f amplification. In the post-a anyone entering the areas of Technical Personnel:	ollow Up (If application of exemplified to deterring possible allele was on events, the Fore PE requirements has face masks are now amplification laboration where these procession of the proce	traction batch t blank yielded lank was required was reproding mine if this point not present a <b>able):</b> ensic Biology S ave also been viequired dura atory, gloves a dures are per	a 39, RBE04131 d a quant value lested since th uced and now issible allele with nd therefore the Section will be implemented ing screening, and a lab coat a formed must a	blocks-1 (1825LS16) e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank performing lab de to prevent contar extraction, quant are required. This bide by these req O5-24 Date:	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. the amplification prod and the associated dat econtamination on a nination issues. Lab co ification, and PPE is not optional an uirements. t- 2016
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo In response to contamination routine basis. Additional Pl gloves, hair coverings and fa amplification. In the post-a anyone entering the areas of Technical Personnel: Section Manager:	ollow Up (If application of examplified to deterr possible allele was on events, the Fore PE requirements has face masks are now amplification laboration where these procession of this reagent	traction batch t blank yielded lank was required was reproding mine if this point not present a <b>able):</b> ensic Biology S ave also been y required dure atory, gloves a dures are per	a 39, RBE04131 d a quant value lested since th uced and now issible allele with nd therefore the Section will be implemented ing screening, and a lab coat a formed must a	blocks-1 (1825LS16) e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank performing lab de to prevent contar extraction, quant are required. This bide by these req 05-04 Date: Date: 5/25	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. T the amplification prod and the associated dat econtamination on a nination issues. Lab co ification, and PPE is not optional an uirements. t- >01 (p
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo In response to contamination routine basis. Additional Pl gloves, hair coverings and fa amplification. In the post- anyone entering the areas of Technical Personnel: Section Manager: Division Director:	ollow Up (If application of examplified to deterr possible allele was on events, the Fore PE requirements has face masks are now amplification laboration where these procession of this reagent of the server of th	traction batch t blank yielded lank was required was reproding this point not present a able): ensic Biology S ave also been virequired dur atory, gloves a dures are per	a 39, RBE04131 d a quant value lested since th uced and now ssible allele wand therefore the observed the simplemented ing screening, and a lab coat a formed must a	bls-1 (1825LS16) e of 0.0ng/µl and s e possible allele w above analytical t as reproducible at his reagent blank performing lab de to prevent contar extraction, quant are required. This bide by these req 05-24 Date: Date: $5/25$ Date: $5/2$	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. T the amplification prod and the associated dat econtamination on a mination issues. Lab co ification, and PPE is not optional an uirements. $t - 301 \beta$
allele below analytical three contamination. Re-injectio good morphology. Upon re- reagent blank was then re- Upon re-amplification the p were deemed acceptable. Quality Division Use Only Additional Information/ Fo In response to contamination routine basis. Additional Pl gloves, hair coverings and f amplification. In the post- anyone entering the areas Technical Personnel: Section Manager: Division Director: Quality Director:	ollow Up (If application of examplified to deterr possible allele was on of this reagent b re-injection the allel -amplified to deterr possible allele was of the possible allele was of the possible allele was per requirements has face masks are now amplification laboration where these process of the possible of the possible allele was of the p	traction batch t blank yielded lank was required was reproding not present a able): ensic Biology S ave also been y required dur atory, gloves a dures are per	a 39, RBE04131 d a quant value lested since th uced and now ssible allele with nd therefore the bection will be implemented ing screening, and a lab coat a formed must a	$\frac{1825LS16}{c} = of 0.0 ng/\mu l and s$ $\frac{1}{c} = of 0.0 ng/\mu$	, produced a possible showed no other signs vas in a locus bin and h hreshold at 58 RFUs. T the amplification pro- and the associated dat econtamination on a mination issues. Lab co ification, and s PPE is not optional an uirements. t- >01 p   L .5/10   L016

### 21.5 HOUSTON FORENSIC SCIENCE CENTER CORRECTIVE AND PREVENTIVE ACTION REPORT CHECK IF ADDITIONAL PAGES ARE USED SECTION 1 CAPA #: 2014-014 Date: Jul 16, 2014 DESCRIPTION OF The Quality Manager submitted incomplete data sheets for CTS tests 14-572-U2588A, B and G. The sheets submitted contained only screening results rather than screening and DNA results. This is a violation of QAS 13.1 because the ISSUE/NON-CONFORMANCE: DNA results were not submitted to the proficiency test provider in order to be included in the provider's published external summary report. PREVENTIVE CLASSIFICATION OF NONCONFORMANCE: see Quality Manual for description CLASS III ACTION ONLY ROOT CAUSE Handwritten data sheets were completed by screeners and typed data sheets were completed by DNA analysts upon ANALYSIS: completion of all analysis. Because the Quality Manager did not review the sheets as closely as warranted, the forms with only screening results were submitted. PROPOSED CORRECTIVE ACTIONS/RECOMMENDATIONS TO ADDRESS THE DEFICIENCY AND PREVENT RECURRENCE: Screeners will no longer complete data sheets. Only one set of typed and complete forms will remain in each proficiency case record. DNA results will be reported as internal results only. The PRC (through the ASCLD/LAB Proficiency Program Manager) will be preemptively notified since the DNA results were not submitted to the test provider as required by QAS standards. see attached 7-24-14 Date: SECTION MANAGER: SECTION 2 (MANAGEMENT REVIEW AND RESOLUTION) nticipated revenen to SOP; additional unfo will be provided of the RESOLUTION QUALITY MANAGER: LOri Wilson Digitally signed by Lor. Wilson Discretion Wilson, art PD, ou email-lori wilson: Shoutsappoli Jul 24, 2014 Date: Date: 2014.07.16.07:24:40.05'00 Date: LABORATORY DIRECTOR: FAD-QA -CAPA Issue Date: May 16, 2014 Page 1 of 1

#### CAPA 2014-014 continued

10

Proposed Corrective Actions/Recommendations to Address the Deficiency and Prevent Recurrence: continued

Note: the DNA results that were not submitted were reviewed by the DNA Technical Leader and found to be concordant with CTS published data. The involved technicians and DNA analysts performed the tests properly.

#### May 28, 2014

Patti Williams, Proficiency Program Manager 139 J Technology Drive Garner, NC 27529

Re: CTS Test Number 14–571, 9RBUJE Houston Police Department Crime Laboratory/Houston Forensic Science Center ASCLD/LAB Certificate #317

#### Dear Ms. Williams:

I am writing to notify you of a potential non-consensus for CTS test #14-571 (9RBUJE). The results reported for this case include data that this above our analytical threshold (50 RFUs) but below our stochastic threshold (200 RFUs) for the Identifiler Plus PCR Amplification Kit. The analyst followed laboratory protocol by reporting the data in sample #2 and sample #4 with the appropriate indications of data being below our stochastic threshold.

In sample # 2, a reference sample, the loci with activity below the stochastic threshold (D5S818, Amelogenin, and FGA) all exist as heterozygous loci, meaning DNA data is not missing, assuming it is a single-source sample. This assumption is clearly stated in the "results and interpretations" section of the associated DNA report. Further, given this is a reference sample, statistics will not ever be performed on this item and therefore whether allelic activity exceeds the stochastic threshold is not as significant.

In sample #4, an evidence sample, there is data at D19S433 that is above the analytical threshold but below the stochastic threshold. Like item #2, this sample is assumed to be single-source, as is indicated in the "results and interpretations" section of the associated DNA report and in the legend of the allele chart of the associated DNA report. Unlike item #2, statistics may be applied, if warranted because this is an evidentiary item. Per laboratory protocol, which is influenced by the 2010 SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories, "a presumed single-source locus with two alleles may be used for comparison and statistical analysis, should one or both of the alleles not exceed the stochastic threshold."

It is also laboratory protocol to include defined symbols where appropriate. "Proficiency work is to follow as closely as possible that of normal casework. In doing so, DNA results reported to CTS (or other approved external proficiency test provider) should not vary from DNA results included within the case file, as established by the DNA SOPs. For example, notations to distinguish major and minor components in a mixture should be included in results submitted to the test provider, if applicable. If symbols are used in the reporting of data to the proficiency testing agency, they must be defined in the results submission form."

The analyst's interpretation and reporting is compliant with laboratory protocol and will therefore impact casework as well as proficiency tests. There are no planned corrective actions for this potential non-consensus, as the results reported by this analyst are concordant with the CTS consensus data.

Please do not hesitate to contact me, should you require any additional information.

Sincerely,

Robin D. Guidry, Technical Leader Houston Forensic Science Center

rdg:rdg



HOUSTON FORENSIC SCIENCE CENTER 1200 Travis St., 20th Floor Houston, TX 77002 (713) 929-6760

chin his

# HOUSTON FORENSIC SCIENCE CENTER

Print Form

		INCIDENT REPORT	
Corrective	Preventive	Tracking/Documentation Only	Inc. Report #: 2015-003
Date: Feb 3, 2015			
DESCRIPTION OF DISCREPANCY/ NON/CONFORMANCE:	See attached memo	dated 2/3/15 pertaining to a proficiency test da	ata entry transcription error for PAR-C 2014.
Date: Jan 26, 2015			
CAUSE OF DISCREPANCY/ NON-CONFORMANCE: (if possible to determine)	Human error and po	ssible computer glitch with the CAP system.	
LEVEL/TYPE OF DISCRE	PANCY/NON-CONFO	RMANCE (see Quality Manual for description):	CLASS III
EFFECT OF DISCREPANCY/ NON-CONFORMANCE: (if possible to determine)	The information repo comparison of paper reported incorrectly.	orted by examiners was correct. This was verifie data sheets and expected results. However, th	ed by the Quality Director through a le CAP system shows that one allele was
lf no	ot discovered at this p	point, where else in the process would this incid	lent have been discovered?
n/a			
	Correc	tive Actions/Preventive Measures Taken (if app	olicable):
No action can be taken entry. The HFSC did no Quality Division will end will review the data a fi	at this point. The test t order any CAP tests courage analysts to c nal time. This should	st was completed successfully by the examiners s for calendar year 2015. If online entry become complete online data entry, the reviewer will rev l prevent a recurrence.	5. The error occurred during on-line data es required for other providers (i.e. CTS), the view the data entry, and the Quality Division
ANALYST	Paula Evans	und seguer faine faine. Here and the second second second second second second S	Date: Feb 10, 2015
SECTION MANAGER	Robin Guidry	rathy signed by Rober Guidhy Can-Bold Guidhy, e. cu. An-abold guidhy gail cuickle a ang. («U)) 2012 12 11 (16) 41 (2) cu Cuic	Date: Feb 11, 2015
CODIS ADMINISTRATOF (if applicable)	Chur What	Ł	Date: Jeb. 11,2015
ADDITIONAL INFORMAT FOLLOW UP (if applica	FION/Although this is able): correct the data documentation consulted with	s reported by the Quality Division as a Level III t a entry. The proficiency test was deemed succe n. The Quality Division made this error and also the Biology Section Manager during the review	ranscription error, no action can be taken to essful based upon examination investigated this error. The Quality Director v of this incident.

Corrective and Preventive Action Form Issued By: Quality Director

, e <sup>· · ·</sup>

HESC -QDiv -CAPA Issue Date August 19, 2014 Page 1 of 2

# HOUSTON FORENSIC SCIENCE CENTER

### **INCIDENT REPORT**

Corrective	Preventive	Tracking/Documentation Only	Inc. Report #: 2015-003
QUALITY DIRECTOR	Lori Wilson	illy signed by Lon Wilson n Lan Wilson, d=Kluston Forensic Science n. an-Quality Dinson, WilkompH scutted formicScience org. <=US 2015/02/11 06:52:14:-06:50	Date: Feb 11, 2015
LABORATORY DIRECTOR	Im Riv	2	Date: 2-11-15
	C	Date Closed: Feb 11, 2015	
It is my of be entered person veri	ocommendalesi on-lin by by the dat	the QA Division to while it is be	is going to that a 2rd into
the CAPE	website	- Ruis 2.11-15	

Corrective and Preventive Action Form Issued By: Quality Director

. . . .

Print Form



# Houston Forensic Science Center

### **INTEROFFICE MEMO**

To:	Case Record for Proficiency Test PAR-C 2014
Cc:	Robin Guidry & Irma Rios
From:	Quality Division
Date:	February 13, 2015
Re:	UPDATE: Proficiency Test Transcription Error on PAR-C 2014

The Quality Division inquired with the College of American Pathologists (CAP) to see if any other customers had problems while submitting online proficiency tests. The following issues with the CAP website were discussed:

- 1. Difficultly logging onto the CAP website. The Quality Division had to login multiple times over an extended time period to gain access to the site. It seemed that the site was down many times that we tried to login.
- 2. During data entry, the same page was frequently reloaded when the "Next Page" button was selected.

The CAP representative, Tammy, informed the Quality Division that the glitch may have been an issue with an outdated internet browser. She explained that an outdated browser may not communicate with Adobe correctly and that could be why technical issues were experienced during data entry. On November 10, 2014, the day when the data entry, administrative review, and submission occurred, the Quality Division was using the outdated internet explorer browser version 9, the default version on all computers using the HPD network. The Quality Division will ensure that browsers are up to date and compatible with all CAP website features before entering and submitting proficiency test data in the future. The CAP phone conversation with Tammy was recorded and reference number 1677596 was assigned for future inquires.

Lori	Aller's specific and an a children in the second former in the second second second former in the second	
Wilson	the stand to react the stand to be stand t	



### Houston Forensic Science Center

### **INTEROFFICE MEMO**

To:	Case Record for Pre-	oficiency Test	PAR-C 2014
From:	Quality Division	Lori	Dig taky signed by Lan Wikon DN Envillen Wikon orthoustan Formsis Science Center, aur Quality Division, emailer Withoustantragensis,
Date:	February 3, 2015	wiison	cence ang c=US Date 2015 02 04 13 29 27 .06 50
Re:	Proficiency Test Tr	anscription Err	or on PAR-C 2014

On November 10, 2014 the Quality Division entered and submitted proficiency test results for the College of American Pathologists (CAP) Parentage and Relationship Testing Survey (PAR-C) via the CAP website. During online data entry there was a transcription error made on page 11 where a single allele was recorded at an untested marker, F13B. The online data entry information was administratively reviewed before submission; however, the transcription error was not caught at that time.

The transcription error was discovered upon the review of the expected results provided by CAP. The Quality Division is aware of the error and will be more meticulous when entering and reviewing online data entry for proficiency tests in the future. Although this error did impact the reported results, the examination documentation created during analysis shows that the correct results were obtained.

1 - 10/15 Ullie White april 15 Der Rins 2-11-15 My Recommendation on Somewhile endering 211-15 While Site MC 211-15



	Quali	ity Divisi	on use o	nlv	
Quality Tracking #	2014-004			Date Submitted	: 2/8/2016
				Date Closed	: 2/15/2016
Date of this Poport:	2/8/2016				
Date of this Report:	2/0/2010	Division:	FAD	F	CN: CTS 15-575 U2588D
Date of Incident:	2/3/2016	Section:	Biology	No	HPD incident # applicable to external proficiency test.
In this space, record o instructed by the Sec	details of the incident, in tion Manager or Divisio	nclude dates n Director(s)	. Do not inclu :	de analysts name	s unless otherwise
the result for the sper U2588D for item 4. TI DNA report has the sp error was not identifie obtained by this analy interpretations of the The DNA analyst's inter corrective actions for t CTS consensus data.	and epithelial fraction the CTS form requires the eerm fraction above the ed during TR/AR. The an st for TH01 are concord samples tested. erpretation and reporting this potential non-conse Prisile The Should	g are complia ns us, as the	al, was made 101 on the pro- e epithelial fra- ction. This co ly listed the re published dat ant with labora results reporte	when the DNA and ficiency test resul ction above the sp uld also be the rea sult obtained on t a for item 4, resul atory protocol. The d by the analysts	alyst mistakenly switched ts form for CTS 15-575 berm fraction while HFSC ason the transcriptional the DNA report. The results ting in consensus here are no planned are concordant with the
	loci and is o	n the pha	oficiary	MANV (Acturor	" prom. lum him
Additional Information	only n/ Follow Up (If applical	ble):			
Technical Personne	AR cholysi - Christ	Line Kornel	analysi)	se ployed at 1	A rest
Section Manage	r Dut (N	-100-	0	Date: 2 15/11	12-17-16
<b>Division Directo</b>	r: Jelina k	nis		Date: 2/1	5/11/2
Quality Directo	r: Suulin		- Jou Hishie	n Date: 2/18	12016
Incident Trackii Issued by: Qual	ng Report Tack ity Director Tack	FR 2.15	814 Mares	unt Issue Date	HFSC-QDiv-INCR e: March 02, 2015
	CODIS admin!	: Clux U	lot 2/14/16		Page 1 of 2



Incident Tracking Report Issued by: Quality Director



	Quality Division use	only			
Quality Tracking # 2016-083 Date Submitted: 7/5/2016					
		Date Closed: 8/25/2016			
Date of this Report:8/4/2016Date of Incident:4/5/2016	Division: FAD Section: Forensic	FCN: PARF-A 2016 (If applicable)			
In this space, record details of the incident, include dates. Do not include analysts names unless otherwise instructed by the Section Manager or Division Director(s): A class III transcriptional error, per the HFSC Quality Manual, was made when the DNA analyst mistakenly wrote allele					
"11.1" instead of "11.0" at TPOX for item 3.1 (PARF-03) on the CAP Parentage/Relationship Testing Survey Result Form for test PARF A that was submitted to CAP electronically on April 5, 2016. The "intended" allele call per CAP, 11.0, was correctly obtained through testing and reported in the HFSC DNA report					
for FCN PARF-A 2016. The non-consensus was limited to one allele at one locus for one sample on the proficiency manufacturer's results form. The interpretations for all items tested were fully concordant with CAP's published results. The DNA analyst's interpretation and reporting were fully concordant with laboratory protocol. Currently, laboratory protocol requires that technical and administrative reviewers also include the manufacturer's results					
forms in the review process for proficiency tests. However, this transcriptional error was not discovered at the technical or administrative review. A possible reason that it was not discovered during technical and administrative review could be due to the large number of data transfers onto the data testing survey as well as the electronic portal. To minimize the amount of data transfers it is recommended that data first be entered into the portal and then printed for technical and administrative review.					
The electronic submission was verified identical to the results hand-writter submitting results electronically, the verification step.	ed by a member of the Quality D on the results form. It was recor DNA allele chart might serve as	ivision. Electronically submitted results were mmended by the DNA analyst that when a second check for the data entry and			
Quality Division Use Only Additional Information/ Follow Up	(If applicable):				

Incident Tracking Report Issued by: Quality Director



Der ihre Biology sof, Arth the technical and administrative reveries unclude a reveies of data in case file & data sheets. She sof should prevent transcription errors such as these one. This does appear to be an invalid inciding to the additional action cull de takin at this time. 25/2016

**Technical Personnel:** Section Manager: **Division Director: Quality Director:** DNA Tech. Lead. Techifeviewr Admin Reviewer: CUD CODIS admin .: Clux Whit

Date:	8/12/16
Date:	081716
Date:	8.22-16
Date:	8/74/2016
Dak.	August 12,2016
Date:	8.15.16
Date	: 8/22/16

Incident Tracking Report Issued by: Quality Director



		Qualit	ty Divisi	on use only		
	Quality Tracking #	2015-006		Date	Submitted: 6/	/30/2015
				D	ate Closed: 💈	110/2015
	Date of this Report:	4/23/2015	Division:	FAD	FCN:	2014-24018, 2014- 22949
	Date of Incident:	3/23/2015	Section:	Biology		(lf applicable)
	In this space, record of instructed by the Sect	letails of the incident, in ion Manager or Divisio	nclude dates n Director(s	s. Do not include an: ):	alysts names un	less otherwise
	On February 06, 2015 39ZR15, 40ZR15, 41ZR 2015 (FCN 2014-1790)	, the following unique id 15 and 42ZR15. These i 5 and 2014-17481).	dentifiers we identifiers w	ere duplicated on QI rere originally used in	Acube Batch 10: n a Chelex Extrac	37ZR15, 38ZR15, ction dated January 21,
0	The duplication was no sets of tubes having the for the respective Fore	oticed when samples we ne same unique identifie ensic Case Numbers and	ere pulled fo ers in two di l item descri	or amplification by a fferent racks in coole ptions.	technician. The er 1. Samples we	technician found two ere pulled aside to look
	It was discovered by re Batch 10. The first set second set of samples each sample are listed	eferencing a previous ex of samples were from t were identified as bein below.	traction wo he Chelex e g associated	rksheet that these st xtraction; those unic with FCN 2014-240:	amples were in f que identifiers re 18 and 2014-229	act duplicated on Q- main the same. The 149, and the details of
	The unique identifier f This change was made	for the second set of sar on each tube and nota	nples was m ted in each (	odified by adding ar case file.	n "A" at the end a	as indicated below.
	37ZR15A (2014-24018 38ZR15A (2014-24018 39ZR15A (2014-24018 40ZR15A (2014-24018 41ZR15A (2014-24018 42ZR15A (2014-22949	Item 5.1.1 Portion of Item 5.2.1 Portion of Item 5.3.1.1 Portion o Item 5.4.1.1 Portion o Item 3.1.1 Portion of Item 3.2.1 Portion of	vaginal swa rectal swab f swab from of stain from penile swab rectal swabs	bs) 5) fingernail scrapings 1 dress) s) )	)	
	fect et	CW 08/04/15				

Incident Tracking Report Issued by: Quality Director



Quality Division Use Only Additional Information/ Follow Up (If applicable): On 7/10/15 the Quality Division sent the incident report back to the section for edits. The Quality Division also requested extraction worksheets related to this incident. Date: 07-23-2015 Technical Personnel: 7 23 2015 Section Manager: Date: Date: 8-4-15 Division Director: Date: 8/10/2015 Quality Director: There is a significant delay between dute of incident & report due to WA. Incident 2015-006 relates to a duplication unique i dentifiens. It is Not cleane how 7-24-15 this issue will be prevented in the future x whether an evaluation of the procedure was conducted by either QA or A Biblog of Shatt. This should be reviewed by the returning TL Robin Gurdoy. due Kios 7-24.15 INCR 7-24-15 COOFS Administration Muss 7 Sid off an Carton 7-24-15 an Rive 7-24-15 Gordey. Jun Rios 7 - 24.15 8/4/18: Until more complete UMS integration is realized, sample identifiers are greated by individual andusts. Once LIMS integration extends to processing of SAKS, LIMS will autopopulate worksheets with a unique identifier for each sample consisting of FCN, iten to \$ INC/ogency# Fyly growt funding tasks will be requested to expand likis indumentation beyond DNA casework- Roc \$14/15



Incident Tracking Report Issued by: Quality Director



	Qualit	y Divisi	on use only		
Quality Tracking # Z	015-007		Date Sub	mitted: 3/23	3/2015
			Date	Closed: 5/	6/2015
Date of this Report:	3/23/2015	Division:	FAD	FCN:	(If applicable)
Date of Incident:	3/18/2015	Section:	DNA	]	
In this space, record det instructed by the Section On 3-16-15 a plate that (including the positive of (Gamma), in hopes this during the analysis of the to the attention of the to run. Another request we analyzed by the DNA and and to include an additi- up the plate a 4 <sup>th</sup> time, correctly onto the plate one sample name was en- their actual sample well. The plate was set up and the advanced integration the 3130 to identify wh LIMS to preclude any po-	tails of the incident, in on Manager or Division t was processed on ge ontrol). A request was would clean up the ex- ne plate it was noticed echnician who believe as made for this plate alyst. The positive con- onal positive control to the technician discover , however during the entered twice into two ls. Therefore, the sam d processed correctly on of LIMS into DNA as ich sample is located i potential manual mislat	nclude dates n Director(s matic analyz s made by the cessive artife that the poise at this was t to be process ntrol was ag to ensure an ered the cause entering of t o consecutive ples were in on 3-20-15; ssignments i in which plat beling of sam	s. Do not include analys er Beta contained exces the DNA analyst to re-inje- facts. On 3-18-15, the pla sitive control (POS03161 the result of the machine ssed. On 3-19-15, the re- ain blank. A 3rd request acceptable positive was se of the "blank" positive the sample names into the e wells, causing the rema- jected off by one well fro- all samples and positive in the coming days, LIMS the well. Moving forward apples on the 3130 data com-	ts names unles sive artifacts in act this plate or ate was proces 5MR) was blar e running out o sults of this run was made for s present on the e. The samples he software of aining names to om their true le produced acce s will create file , we anticipate collection software	a multiple samples in the other machine sed on Gamma; ink. This was brought f polymer during the in on Gamma were the plate to be set up e plate. Before setting were loaded the genetic analyzer, o be one off from ocations on the plate. eptable data. With is that will be used by e this new feature of vare.
Quality Division Use On Additional Information DNA Work Flow 1 documentation project. Jow 516/19	nly <u>/Follow Up (If applic</u> <i>Mplementation</i> <i>for Further</i> 5	able): 1917 L detail-	IMS IS COMPLE S related to th	te. See he imple	VErification mentation

fees 330

3-30 15 Incident Tracking Report Issued by: Quality Director



**Technical Personnel:** Section Manager **Division Director:** ins Quality Director: 3/29/15

Date:	3/24/15
Date:	3/27/15
Date:	4-6-15
Date:	417/2015

Incident Tracking Report Issued by: Quality Director



		<b>Quality Divis</b>	ion use o	nly		
Quality Tracking #	2015-010			Date Submi	tted: 6,	/29/2015
				Date Clo	osed:	7/8/2015
Date of this Report:	6/30/2015	Division	FAD		FCN:	2012-23650
Date of Incident:	5/20/2015	Section	Biology			(If applicable)
In this space, record of instructed by the Sect On 5/20/15 a DNA Ext Upon filing a copy of t numbers, it was discor 66KG15.	letails of the in tion Manager o raction worksh his worksheet i vered that a DN	cident, include data or Division Director( leet was prepared w into the extraction k NA Extraction works	es. Do not inclu s): ith the followin inder where th neet dated 4/2	ng sample nur ng sample nur ne technician l 7/15 also cont	nbers: 65 heeps trac tained sar	less otherwise KG15 through 76KG ck of their sample mples 65KG15 and
duplicate sample num the issue and was inst worksheets, and all ot after the sample num The retention of a cop analyst inadvertently	bers were gene ructed to prepa her related doc pers (i.e., 65KG y of the extract did not file the 4	erated. The technici are an incident repo- cumentation pertain 15A and 66KG15A). tion worksheets has 4/27/15 copy imme	an immediatel rt, make correc ing to the 4/27 proven in the diately into the	y emailed the stions on the s /15 DNA Extra past to be effe	Acting Te sample tu action as ective up	echnical Leader abor bes/extraction follows : add an "A" until this point. The
Quality Division Use C Additional Informatio	only n/ Follow Up (I	If applicable):				
On 7/10/15 the Qua requested extraction v	lity Division ser vorksheets rela	nt the incident repo ited to this incident.	rt back to the s	ection for edit	ts. The Q	uality Division also
			() all an - 1-	wal -		
S Technical Personn	el: Karen	ETINCOD *NOTO	4 HFSC	Date:	-	
Section Manage	er: m	ingo	<u> </u>	Date:	7 23 1	2015
Incident Track		$\checkmark$				



Division Director: Quality Director: -P///

Date:	1-24-15
Date:	8/10/2015

7-24-15

CODES Administration needs to sign of f on this CAPA as per FBE Guidelines. UN 105 CAPA as per FBE Guidelines. 20015 Un his 7-2475

8/4/15: Firther UMS integration is planned. This will betend some features & LIMS integration beyond the processing of DNA casevork into other areas induding SAKS. UMS will autopopulate sample identifiers to induch FEN, iken#, & INC/agency #. This will remore the need for antipsts to manually assign case identifiers and prevent this issue from recurring - Rol s/4/15 UR Remeined 8-4-15

CU 08/04/15 CODIS Administrator Jaw 8/10/2015 Sec comment 7/24/15

Incident Tracking Report Issued by: Quality Director



	Qua	ality Divisi	on use only			
Quality Tracking # 2015-018			Date Subr	Date Submitted: 10/2/2015		
			Date (	Closed: /	0/13/2015	
Date of this Report:	10/6/2015	Division:	FAD	FCN:	2014-13585, 2014- 16474, 2014-18769, 2014-19557, 2015- 01152	
Date of Incident:	3/6/2015	Section:	Forensic Biology		(If applicable)	
February 27, 2015 (FCN The duplication was no Incident Report #2015- The unique identifier fo change was made on ea 195HN15A (2014-18769	ticed when examinat 013 (a sample switch or the first set of samp ach tube and notated ) Item 1.10.1 Portion	9557, 2015-01: ion documenta ). ples was modifi in each case fil of KSS	Identifiers were original 152). tion was reviewed during ed by adding an "A" at th e.	y used in ar the root ca e end as ind	EZ1 extraction dated use analysis for licated below. This	
OGUNITEA /2014 1000-	7 1 the set 7 7 1 (1 (1 + 1')	CUDE				
196HN15A (2014-1955) 197HN15A (2015-01152 198HN15A (RBK022715	7 Item 1.2.1 Portion 2 Item 1.5.1 Portion HN)	of KSS of KSS				
L96HN15A (2014-1955) L97HN15A (2015-01152 L98HN15A (RBK022715) Until a more complete L by individual analysts. ( his time), LIMS will aut CN and the item #, the	<ul> <li>Item 1.2.1 Portion</li> <li>Item 1.5.1 Portion</li> <li>HN)</li> <li>IMS integration is reading to the second second</li></ul>	of KSS of KSS alized for SAK c extends to the on worksheets red for analysts	asework, sample identific processing of SAKs (LIM with a unique identifier fi to maintain and track ur	ers will cont S updates a or each sam ique identi	inue to be generated re being tested at ple, consisting of the fiers.	

Incident Tracking Report Issued by: Quality Director



The significant delay between the incident and this report is not well understood; the incident was not discovered until June, 2015 during the review of the involved analyst's casework in response to a separate incident. It was realized on October 2, 2015 during discussions around the quality incidents associated with this analyst that this report was never actually created.

Quality Division Use Only Additional Information/ Follow Up (If applicable): Click here to enter text.

Technical Personnel:	affen
Section Manager:	R
<b>Division Director:</b>	Ichma Riva
Quality Director:	SWillim
casis Admin:	Clean West

Date:	10/07/15	
Date:	10/7/15	
Date:	10.7-15	
Date:	10/13/2015	
Dete.	10/1/15	

Incident Tracking Report Issued by: Quality Director



	Qu	ality Divisi	on use only	2	118/2016
Quality Tracking #	2015-022		Date Su	bmitted: 1	2/4/2015 ABW
			Date	e Closed:	2 18/2016
Date of this Report:	12/4/2015	Division:	FAD	FCN:	2015-08774, 2014- 25334, and 115623199
Date of Incident:	11/23/2015	Section:	Forensic Biology		(If applicable)
In this space, record d instructed by the Section	etails of the inciden	nt, include dates.	Do not include analys	ts names unl	ess otherwise
On November 23, 2019 2710IH15 through 273 November 17, 2015.	5 the following uniq 3IH15. These identi	ue identifiers we ifiers were origin	re duplicated on an ext ally used on an extracti	raction from on from QIAo	QlAcube Batch 88; cube Batch 87 dated
The duplication was no were two requests whi paperwork it was disco Batch 88.	oted when copies of ich both contained t overed that all of the	re-amplification the same unique e unique identifie	paperwork were being identifier. After exami ers from Batch 87 extra	made on De ning the batc ction sheet h	cember 3, 2015. There h extraction ad been duplicated in
The duplicated unique change was made on e	identifiers for the sa ach tube and notate	amples in the Ba ed in each case r	tch 88 were modified to ecord.	o contain an '	"A" at the end. This
2/2/16 - The fut from occurving.	LIMS will aut	tation of the	SAK assignmen generate uniqu	t in Uins e identifi	will prevent this iss
Quality Division Use O	nly	licable):			
The Quality Division r	equested extraction	worksheets rela	ted to this incident.		
See attached Anadint cle	email to	amy Can	tille for up	tatis 2	118/2016 JULLan
tation prog	tct. dint Form A	ectored the	4 Hallom on 2	118/16. hl	aft Anadim
Town dine on	2 12/4/15,	curvett.	/		

Incident Tracking Report Issued by: Quality Director



Technical Personnel: Section Manager: Division Director: Quality Director: FULL

Date:	01-26-16		
Date:	1/27/16		
Date:	2-10-16		
Date:	2/18/2016		

1-25-14 Technical Leurer: 3 HA HALSELL

C

on 2-12-16 I spoke to they Corstillo to see if she could assist with SAK Assignment in LIMS. She indicates she could . chue Kus 2-15%

CODIS Admin: Clua What 02/14/16

when while his for received 2/18/16

**Incident Tracking Report Issued by: Quality Director** 

### Lori Wilson, BS ASQ CQA

From: Sent:	Lori Wilson, BS ASQ CQA Thursday, February 18, 2016 7:09 AM
То:	Jennifer Clay; acastillo@houstonforensicscience.org; irios@houstonforensicscience.org;
Cc:	Aimee Grimaldi, M.S.
Subject:	SAK Assignment in LIMS as Referenced in Quality Incident 2015-022

Amy-

This incident tracking form indicates that your group will assist Biology with implementation of SAK assignments into LIMS. This is needed because there have been incidents in which the same unique identifiers were reused on casework. Please provide ongoing updates concerning this project to the Quality Division. These updates will be used as documentation of action taken to correct this issue.

1

Thanks. Please let Aimee or me know if you have any questions.

# HOUSTON POLICE DEPARTMENT CRIME LABORATORY

## CORRECTIVE AND PREVENTIVE ACTION REPORT

### CHECK IF ADDITIONAL PAGES ARE USED

## **SECTION 1**

SECTION	
Date: Apr 8, 2014	CAPA #: 2014-010
DESCRIPTION OF Contamination was detected in a reagent blank (11M ISSUE/NON- CONFORMANCE:	IS14 – RBS012714MS) for HPD Case #116874113. The observed s) positioned before the reagent blank.
CLASSIFICATION OF NONCONFORMANCE: see Quality Manual for desc	cription II PREVENTIVE ACTION ONLY
ROOT CAUSE Mary Symonds performed the differential extraction. ANALYSIS: analysis, re-amplification and genetic analysis of the r Lentz. The reagent blank was re-injected and then re were present after re-amp; however they remained co reproducibility of the contamination indicates that it during the set up for guant or amp. Either way, the a PROPOSED CORRECTIVE ACTIONS/RECOMMENDATIONS TO ADDR	Benjamin Cambridge performed the quantification, genetic re-amp. Amplification and re-injection were performed by Peter e-amplified to confirm the presence of the alleles. Fewer alleles onsistent with the DNA profile from the preceding samples. The could have occurred from sample-to-sample during extraction or issociated samples cannot be used for interpretation.
All associated samples were re-extracted and all associated reagent b poured new aliquots of reagents before re-extracting the affected sar Cambridge will continue to exercise extreme caution while handling	planks yielded acceptable data. DNA Analyst Mary Symonds mples. DNA Analyst Mary Symonds and DNA Technician Benjamin samples in the laboratory.
	Date: 4/14/14
FINAL Lee Tech Leader email dated 412 RESOLUTION: reported SINCE Jan. 2013) No to	2312014(a tatal of 3 centamination events for ther action tak on a this time.
QUALITY MANAGER: Studim	Date: 4/28/2014
LABORATORY DIRECTOR: Lun Rios	Date: 5-6-KC
Corrective and Preventive Action Form Issued By: Quality Manager	CL-QA -CAPA Issue Date: February 1, 2014 Page 1 of 1

### Wilson, Lori

From:Guidry, RobinDSent:Friday, May 09, 2014 6:06 PMTo:Wilson, LoriCc:Rios, IrmaSubject:Extraction contamination

Lori,

As you know, the Biology/DNA Unit of the Houston Forensic Science Center documents issues, such as DNA contamination, via the Corrective And Preventative Action (CAPA) form. This allows the detection of possible trends and presents any preventative measures that the lab may elect to employ.

In 2011, there were 18 CAPA-worthy events, 6 of which involved extraction contamination (33.3%). In 2012, there were 11 CAPA-worthy events, 3 of which involved extraction contamination (27.3%). In 2013, there were 18 CAPA-worthy events, 1 of which was associated with contamination at amplification in a negative PCR control (5.6%). In 2014 todate, there have been 8 CAPA-worthy events, 3 of which involved contamination (38%). Of those 3, 1 (12.5%) was associated with amplification contamination, while the other 2 (25%) were associated with extraction (1 reagent blank and 1 sample, both with low-level contamination). Please note that many of the CAPAs generated in 2013 and 2014 are associated with the massive outsourcing project of almost 10,000 cases and involve chain of custody documentation.

For perspective, the DNA lab has experienced a significant increase in production and therefore extractions. As the number of extractions increases, so does the potential for a contamiantion event.

- 472 DNA reports were issued in 2011
- 887 DNA reports were issued in 2012
- 1078 DNA reports were issued in 2013
- 330 DNA reports have been issued in 2014 (YTD)

The reduction in extraction contamination from 2011 to 2013 appears significant, and I suspect there is less due to an increased use of automation and a decreased use of manual extractions. 2014 has observed a percentage-wise increase of issues related to contamination, but year-to-date, is as high as 2012 and one half of 2011. One of the 2 extraction contaminations in 2014 was detected in a differential extraction, which is still a fully manual process; we are transitioning to an automated differential extraction at this time. The contamination events do not appear to be analyst-specific.

This lab continues to strive to completely avoid contamination through the use of good laboratory practices but also relies on mechanisms such as the extraction reagent blank to detect it when it is present. We will continue to employ good lab practices and will continue to document events and their corrective and preventative measures taken via the CAPA form. We will also continue to monitor contamination events for any trends and take action when necessary.

Thank you, Robin

Robin D. Guidry, M.S., F-ABC Police Administrator Houston Forensic Science Center Phone: 713-308-2620 Fax: 713-308-2645 Email: robind.guidry@houstonpolice.org

2014-13



# Houston Forensic Science Center

Inter-Office Correspondence

June 13, 2014

MEMORANDUM FOR:

SUBJECT: Root Cause Analysis of an Erroneous Identification made by

#### BACKGROUND SUMMARY:

- 1. The training procedure implemented by the Houston Forensic Science Center's Latent Print Unit requires all newly hired latent print examiners to be thoroughly competency tested prior to entering into any dependent supervised casework. Based on the documentation of qualifications and background experience the five (5) newly hired Certified Latent Print Examiners provided, a modified training program was implemented to test their knowledge and abilities in the area of Latent Prints. The competency testing program developed for the examiners was a two part test. A written competency test was developed consisting of 50 questions that would test the examiner's knowledge of the biology, history, processing techniques, various chemical development mediums, and the methodology if the science of friction skin identification. The second phase of the final competency testing consisted of a comparison examination developed from a three year old proficiency test from the testing agency CTS. The test was CTS Latent Print Test #11-517. The original test was scanned into Adobe Photoshop CS4 with the unknown latent images scanned at 2400 ppi resolution and the record finger and palm print cards scanned at 1000 ppi resolution. All information indicating which CTS version of the test was removed or redacted from the image. The scanned images were then printed using an Epson Stylus Pro 4900 high resolution ink jet printer. Four copies of the comparison competency test were made. The answer sheet was scanned as an Adobe PDF document with all extraneous information associated with the original CTS test cropped out.
- 2. On the cover of the final comparison competency test, the directions were as follows:

"Instructions: This is an assessment of your ability to identify or exclude latent prints when compared against known records. The test consists of twelve (12) latent images and four (4) records consisting of ten print and palm prints. You will have 8 hours to complete this assessment. No copies or scratch paper are allowed to leave the testing area. Please use a blue or black ink pen and write legibly on the answer sheet provided. You ARE allowed the use of your PC, scanner, and Photoshop software or your fingerprint loupe while in the process of completing this assessment. All work must be conducted independently."
- 3. The comparison test was administered to
  - Association for Identification. All of the above examiners successfully passed the examination.
- 4. On June 5,2014, **Example to the set of the set with the above directions**. Upon grading the test using the CTS answer key, it was discovered that he had erroneously identified Latent Image 5H. Todd was informed of this in the afternoon and advised that a resolution would be provided soon.
- 5. Per the Code of Ethics for Certified International Association for Identification Latent Print Examiners and the IAI Certification Manual Section X; subsection B under Technical Errors, the Secretary of the Certification Board, **Example 1** was notified on June 6, 2014 of the erroneous identification. Upon presentation of the facts, **Example 1** determined that since no report involving actual casework was issued and the erroneous identification was discovered in competency testing, it was unnecessary for **Example 1** to lose his status as a CLPE and in-house remedial assessments would be appropriate.

### CAUSE ANALYSIS:

- 1. **Example 1** was instructed on June 6, 2014 to scan the latent identified and also the erroneous finger into Adobe Photoshop and chart what he saw during his analysis and comparison of the latent to known to better understand the thought process and determine possible causes. He was also instructed to provide a summary of possible factors as to why he erroneously identified the latent print. **Example 1** provided me with a summary of what he found and possible causes for the misidentification. (See Attached Summary from **Example 2**).
- 2. Upon analyzing the documentation and speaking with Todd, the following possible factors were likely contributors to the erroneous identification decision:
  - A. **Executive field** was in a supervisory capacity prior to accepting the position with HFSC and did not routinely compare latent prints as a supervisor.
  - B. Although the directions stated a computer, scanner, and Photoshop software could be used, used a comparison loupe. He advised he was not aware he could have asked for access and his previous experience with comparing latent prints were conducted on the computer.
  - C. The location was taking his test was in the common area with many people walking and communicating around him.
  - D. **Example** started with the HFSC Latent Print unit on June 2, 2014 and was started with his competency testing within a few days. A summary of his explanations indicated that he also has external stressors that may have contributed to the erroneous identification.

### CORRECTIVE ACTION PLAN

- 1. All further competency testing will be conducted in an environment that is free from extraneous noise and distractions.
- 2. Notifications will be posted that testing is in progress and to not disturb the person(s) taking the tests.
- 3. **Detection of the administered a series of new competency tests to determine his skills and** abilities further. This will consist of no less than four (4) additional comparison competency tests. These tests will be conducted using Photoshop software and he will be required to chart his conclusions so there will be a documented visual representation of the process. Once competency has been established and no errors have been noted, a new final comparison test will be issued. Upon successful completion of the re-testing phase, **Detection of the dependent** will proceed into the dependent supervised casework portion of the HFSC Latent Print Training Program.
- 4. If further erroneous identifications are made during the re-evaluation phase, a re-evaluation of **Exercision** will need to be conducted to determine if he can remain in a Latent Print Examiner position with the Houston Forensic Science Center.

Timothy Schmahl, CLPE Latent Print Unit Manager

# HOUSTON FORENSIC SCIENCE CENTER

4.\*

4

Print Form

### INCIDENT REPORT

Corrective	Preventive Tracki	ng/Documentation Only	Inc. Report #: 2014 - 027
Date: Oct 31, 2014			
DESCRIPTION OF DISCREPANCY/ NON/CONFORMANCE	On 9/11/14, DNA Analyst Clay Davis obse Reagent blank sample 682MR14 was re-i reagent blank was re-amplified by a seco consistent with the known DNA profile o and loaded this reagent blank and its ass contamination was confirmed.	rved allelic activity in a ream njected the same day and t nd technician and the activ f DNA Technician Maria Rur ociated samples. The Tech	gent blank during his review of the data. he activity was replicated. On 9/12/14, the /ity was again reproduced. This activity was mble who extracted, quantified, amplified nical Leader was notified as soon as the
Date: Sep 11, 2014			
CAUSE OF DISCREPANCY/ NON-CONFORMANCE (if possible to determine)	When notified of the contamination, the contamination. All extractions by this tec the same preventative measures that she the analyst recalls following good laborat DNA was introduced to the reagent blank	analyst evaluated her action hnician since this event hav routinely incorporates into ory practices, at some poin tube.	ns and was unable to pinpoint a cause for the ve been acceptable; she believes she is using her laboratory procedures. Even though t prior to amplification, it appears her own
	handling), analysts are asked to make a ne explanation should data and/or controls e and does not recall the need to do so. Bec process, but rather only once samples hav can be very difficult to identify the exact o DNA testing process.	g an extraction (e.g., a tube ote on examination docume exhibit unusual activity late ause contamination is gene 'e been quantified, amplifie ause of the contamination	is dropped onto the bench top during entation for easier troubleshooting or r. The analyst did not make any such notes erally not detected immediately in the ed, and subjected to fragment separation, it event, especially given the sensitivity of the
LEVEL/TYPE OF DISCRE	PANCY/NON-CONFORMANCE (see Quality	Manual for description): Cl	LASS II
EFFECT OF DISCREPANCY/ NON-CONFORMANCE: (if possible to determine)	Because a reagent blank was found to be interpretation. Samples will need to be re re-extraction of the associated samples. C case due to limited sample remaining for e INC#024911686/L86-3529/2014-13476, IN 2014-14668. Consumption has been grant investigator is seeking input from the pros	unacceptable, the data of the extracted. Additional time onsumption orders have be each item. Three cases are a C# 141044213, and INC# 07 ted for all but INC#0249116 ecuting attorney.	he associated samples may not be used for e and resources will be used to complete the een requested from case officers for each associated with this reagent blank: 4776514/ 86/L86-3529/2014-13476; the case
	This is the 682nd sample extracted by Mar section-wide Forensic Biology meeting hel reminded to exercise extreme caution and things such as chairs, face, face masks, etc.	a this year and this is the fir d September 26, 2014, this awareness when handling with gloved hands and to	rst contaminated reagent blank. At the issue was discussed and analysts were samples during extraction by not touching change gloves as frequently as needed.
If no	ot discovered at this point, where else in th	e process would this incide	nt have been discovered?
technical review of data the technical review of that controls are accept	an examination documentation and contro a, this issue, if not caught when it was durin this case. The DNA review checklist require table.	ls, including reagent blanks ng the analyst's initial review the reporting analyst and	s, is a required step in data analysis and the w of the data, would have been caught in the technical reviewer to acknowledge
Daylahant	Corrective Actions/Prevention	/e Measures Taken (if appli	cable):
074776514/2014-14668	, given the unacceptable reagent blank co 3. Re-extraction is pending consumption p	ntrol, re-testing has comme ermission for INC#0249116	enced for INC# 141044213 and INC# 86/L86-3529/2014-13476.
Corrective an Issued By: Qu	d Preventive Action Form alify Director		HFSC -QDiv -CAPA Issue Date: August 19, 2014 Page 1 of 2

# HOUSTON FORENSIC SCIENCE CENTER

Print Form

### INCIDENT REPORT

Corrective	Spew Preventive	Tracking/Documentation	on Only Inc. Re	port #: 2014-027
ANALYST:	Mumbr	MARIA A. RU	MBLE Date:	10 31/14
SECTION MANAGER:	hi	ROB N D.G	UDKY Date:	10/31/14
CODIS ADMINISTRATOR (if applicable):	Cleve West	Cleva W.	eST Date:	10/31/14
ADDITIONAL INFORMATIC FOLLOW UP (if applicab	DN provide tollow le): And reported	up once all cas	ts have b	een reworked
	,			
QUALITY DIRECTOR:	Sulum		Date:	11/5/2014
LABORATORY DIRECTOR	chunk	ios	Date:	17-7-14
	Da	te Closed: IAPM 12	12 2 /2014 See	email dated 12/11/14
	Cl	ay Davis	Clay ha	WIS 10.31.14

Corrective and Preventive Action Form Issued By: Quality Director

\*

HFSC -QDiv -CAPA Issue Date: August 19, 2014 Page 2 of 2



	Qual	ity Divisi	ion use only	2	118/2015
Quality Tracking #	2015-024		Date Sub	mitted: 1	12/2016 JBW
			Date	Closed:	3/18/2016 Frid
Date of this Report:	12/11/2015	Division:	FAD	FCN:	2013-20123 /
Date of Incident:	2/27/2015	Section:	DNA		(If applicable)
In this space, record de instructed by the Section A request for YSTR and tissue/fluid from a fetu Davis. Analysis of the and was DNA from tissue/fl A comparison of the st consistent with the "ex A re-amplification was source profile with no in The extra alleles observe setup and not in the or consisted of a major co	etails of the incident, in on Manager or Divisio lysis was made on 2-16 s (Items 1.5, 1.6, 1.7 & mplified items was per uid from a fetus, a mix aff YSTR database reve tra" alleles present in I requested on 5-28-15 f ndications of a second yed in the original YSTR iginal extraction of the mponent consistent w	nclude dates n Director(s) 6-15 for case 1.8). The for formed and a ture of YSTR' ealed that the item 1.5. for Item 1.5; contributor. R amplificatio item. This the ith the biologe	Do not include analyst DO not include analyst 2073206213 (2013-2012 ar items were amplified a mixture was observed s in this item was not ar analyst that amplified t the second YSTR DNA pr n were most likely intro neory is supported by th gical mother and 2 mino	s names unle 3) for the iter with YSTRs o in Item 1.5. S aticipated. the evidence ofile produce duced at the e fact that the r alleles that	ess otherwise ms associated with n 2-20-15 by M. Bryan since this sample type with YSTRs was ed a partial single- YSTR amplification he autosomal profile are consistent with
the DNA profile develo Bryan Davis. Therefore reporting purposes.	ped on other portions , the re-amplification r	of the fetal ti results for Ite	ssue/fluid. These 2 mind m 1.5 are deemed accep	or alleles are otable and w	not consistent with M ill be used for
Quality Division Use On Additional Information	nly n/ Follow Up (If applica	able):			
The Quality Division re	equested associated el	ectropherogr	ams.	Anadem	1 11411
Mot de dored	until timi	ra 118/1. 1.ne. Ad	ated to delain	ed Alph	ting to alla
is received.		viu - oc			
See timelin	e dated by T	Allah	m 3/18/2016.		
Incident Tracki	ng Report Pleo	se Note y piles be	TL HAISEII.	H	FSC-QDiv-INCR

Date: March 02, 2015 Page 1 of 2



Technical Personnel: Boyan Davis no longes employed Date: 2.4.14 Section Manager: Jul Charges by it Psc Date: 2/8/14 **Division Director:** Quality Director: Illinn

LSA 1-261/Date: 2-16-16 Date: 3/18/2016

1-25-16

Technical Leader: SA CONFS admin. ! Clux West 2/16/16

2-16-16 Resolving Quality Incident 2015-024 was a bit lengthy. Review ras instituted for this mindent unsers' I managers were remainded of process in FAD meeting held 2-15-16. Process map was provide A. china Rios 2-16-16

Walum rec'd 2/15/16

**Incident Tracking Report Issued by: Quality Director** 

**HFSC-QDiv-INCR** Issue Date: March 02, 2015 Page 2 of 2

Time line to address delayed reporting of CAR 2015-024 regarding Incident number 073206213 to the **Quality Division** 

- 2-20-15: Item 1.5 (3225MR14) is amplified with YSTR
- 2-27-15: Item 1.5 (3225MR14) is run on CE
- 5-28-15: Item 1.5 (3225MR14) is requested for re-amplification and re-amplified
- 5-29-15: Item 1.5 (3225MR14) re-amplification is run for CE
- 12-14-15: DNA report is issued with results for Item 1.5

During the time that this case was identified and processed for YSTR analysis there was not a set schedule for the routine processing of YSTR requests. In February of 2015 two large YSTR amplifications were performed that consisted of most of the open requests. One reason for such a large run was that only two technicians were competent in processing YSTR samples. These samples were not part of an active batch and the cases were to be written by the few analysts that could issue YSTR reports. The analyst would work on these cases between their ongoing batches when they had time.

The data was initially reviewed in February 2015, but that analysis was not case specific. The first analysis was meant to check the controls and overall profiles as compared to amplified target and therefore the contamination was not detected at this time. The case was reviewed by the reporting analyst in May 2015. During the review conducted by the reporting analyst the contamination was detected.

After the re-amplification results were obtained it is possible that the complexity of the case and the case type extended the completion date. This case request was a paternity testing case in which Timeline prepares by Cloyos Itmisell Pouls (1) 03/25/16 JANU 3/18/16 UR 3.30-16 statistical analysis for paternity calculations was necessary. Due to the complexity of the case, many discussions and consultations occurred as to how it should be reported.



		QUALITY DIVIS	ION USE ONLY		
Quality CAR #	2016-005		Date Subm	itted:	3/1/2016
Non-Conformance	e Level CLASS I		Date C	losed:	6/14/2016
Date of this Repor	t: 5/23/2016	Division:	FAD	FCN :	2014- 19609/120012514 & 2014- 22128/136106214
Date of Incide	nt: 3/11/2015	Section:	Forensic Biology/DNA		(If applicable)

### Description of Discrepancy/Non-conformance:

The epithelial fraction reagent blank, RBE031115IH-1 (266IH15), was extracted on 3-11-15 on Batch 21. The extraction batch contained two cases, 2014-19609 (Incident # 120012514) and 2014-22128 (Incident # 136106214). The reagent blank was quantified on 3-12-15 and had a value of 0.0006 ng/µl. Amplification occurred on 4-3-15, with CE following on 4-6-15. The reagent blank contained a single peak above threshold with additional peaks that were distinguishable from background below analytical threshold.

The data was initially reviewed on 4-13-15, however this was not a case specific review. The reporting analyst did not review the CE run until 7-20-15 and the technical reviewer until 10-2-15.

#### Actions Taken:

Re-injection was requested on 7-27-15 and occurred on 8-5-15. The peaks persisted so the reagent blank was requested for re-amplification on 8-6-15 and occurred on 8-12-15, with CE following on 8-12-15. The peaks persisted after re-amplification.

The extraction batch and employee profile list were examined for possible sources, none were identified.

All samples from case 2014-22128 had been initially amplified. All samples with case 2014-19609 were either male negative or inconclusive, so no samples were amplified. To troubleshoot the source of the contamination, the sample immediately adjacent to the reagent blank, 265IH15, was requested for amplification on 9-3-15 and set up on 9-10-15. This profile was not consistent with the reagent blank.

All other samples from case 2014-19609 were requested for amplification on 9-15-15 and set up on 9-16-15. Several did not generate a DNA profile and those that did generate results were all consistent with the same female profile and not consistent with the contaminant.

Since no ADA was assigned to these cases to issue permission to consume, re-extraction did not occur. The acceptable sperm fractions were reported out and the associated epithelial fractions were reported as not meeting quality assurance standards.

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed



If not discovered at this point, where else in the process would this incident have been discovered?

The DNA review checklist requires the reporting analyst and the technical reviewer to acknowledge that controls are acceptable. This incident would have been discovered during review.

$\bigcirc$	
Technical Personnel:	Date: 06-10-10
Immediate Supervisor: Stynuthe Unley	Date: 6/13/16
Section Manager: Jup C	Date: 6/3/16
CODIS Administrator (if applicable):	Date: 6/3/14
Division Director: Chuna Ruiz	Date: 6/3/16
Trich Lend: Stat	5-2476

#### Summary of Root Cause Analysis:

In this particular case the contamination was reproduced after re-amplification which suggests that the contaminant was most likely introduced to the extract at either the extraction or quantification steps. A likely root cause of this particular contamination event could be attributed to poor sample handling at either of these processes. Because the source of this contaminant is not a sample processed on Batch 21 nor an employee, extraneous DNA could have been deposited into the laboratory and introduced to this reagent blank during processing.

#### Additional Information/Follow-Up:

The Forensic Biology Section will be performing lab decontamination on a routine basis. Additional PPE requirements have also been implemented to prevent contamination issues. Lab coat, gloves, hair coverings and face masks are now required during screening, extraction, quantification, and amplification. In the post-amplification laboratory, gloves and a lab coat are required. This PPE is not optional and anyone entering the areas where these procedures are performed must abide by these requirements.

Quality Director: Son Willim

Date: 6/14/2016

reliased for signatures 5/24/10 tilas.

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed

This time line addresses the delayed reporting of CAR 2016-005 regarding Incident numbers 2014-22128 (136106214) and 2014-19609 (120012514) to the Quality Division.

RBE031115IH-1 (266IH15) was extracted as part of SAK batch 2015-21.

- 3-11-15 Extraction
- 3-12-15 Quantification
- 4-3-15 Amplification
- 4-6-15 CE
- 4-13-15 Initial review for poor injections
- 7-20-15 Review by report writer
- 7-27-15 Requested for reinjection
- 8-5-15 CE of reinjection
- 8-6-15 Requested for reamplification
- 8-12-15 Reamplification
- 8-12-15 CE of reamplificaiton
- 9-1-15 Email to Tech Lead asking how to report since there was no ADA assigned. Tech lead
  responds to report acceptable fractions and others as inconclusive and an incident report will be
  necessary. TL asks about other samples being amplified. Clearly a conversation was had in
  person based on the tone of the emails.
- 9-3-15 Sample 265IH15 requested for amplification as part of troubleshooting
- 9-10-15 Amplification of 265IH15
- 9-10-15 CE of 265IH15
- 9-15-15 Additional samples requested for amplification for trouble shooting
- 9-16-15 Amplification of additional samples
- 9-16-15 CE of additional samples
- 11-30-2015- 2014-22128 reported
- 12-21-15 2014-19609 reported

The cause of the delayed reporting of this corrective action to the Quality Division it not known. However, in October 2015 a re-organization of Biology section management occurred in which an Alternate Technical Leader was designated. This restructure could have contributed to reporting delay. The TL designated at the time of this event was involved in the troubleshooting of this contamination event and investigated the event thoroughly.

The ATL notified the Quality Division that a corrective action was necessary in February 2016. Since February 2016, the Quality Division and the ATL have worked together to close this corrective action report.

Time line provided by Lloyd Halsell III, Acting Technical Leader



		Quality Div	vision use of	oniy	
Quality Tracking #	2016-032			Date Submitted: 3	/29/2016
				Date Closed: 5	110/16
Date of this Report:	3/29/2016	Divisio	FAD	FCN:	2016-02382/154.101115 2015-12890/13 121342 2015-07396/01803241
Date of Incident:	3/14/2016	Sectio	on: Biology		(If applicable)
In this space, record de instructed by the Secti Reagent blank 1343LS1 of 0.01274ng/µL. This ZR031516). The reagen concordant with the sa	etails of the inc on Manager or 6 for Extraction reagent blank v t blank produce mple's quant v	ident, include da Division Director n Batch 28-2016 v was amplified on 0 ed a clean profile alue, this reagent	tes. Do not inclu r(s): vas originally qu 03/15/16 and th with no DNA ac blank was then	ude analysts names unle aanted on 03/14/16 and nen it was loaded on 03/ tivity. Since this DNA res n re-quanted along with a	ess otherwise yielded a quant value 15/16 (project sult was not an adjacent sample,
results were N/A sugar	esting that no F	NA was present	The re-quantifi	ication result correspond	ded with the reagent
blank's DNA result of n acceptable.	o DNA activity	present. Therefo	ore, this reagent	blank and the associate	d data are deemed
Quality Division Use O Additional Information	nly	f applicable):	ore, this reagent	blank and the associate	d data are deemed
Quality Division Use O Additional Information It is unclear how extrar 0.01274 ng/µl. A thorc extraneous DNA that m basis. As of 4/8/2016 a contamination. The re- coverings.	nly <b>I/ Follow Up (li</b> neous DNA was ugh laboratory ay have been o idditional PPE r quired PPE in th	f applicable): deposited in the clean was perfor deposited. In addi requirements have he pre-amplificati	original quantifier med on 3/28/20 ition, the section e also been imp on areas include	ication of the reagent bl 016 to decontaminate th n plans to perform this la lemented as a preventiv e a lab coat, gloves, face	d data are deemed ank yielding a result of ne work areas of any ab clean on a routine e measure to prevent masks, and head
Quality Division Use O Additional Information It is unclear how extrar 0.01274 ng/µl. A thorc extraneous DNA that m basis. As of 4/8/2016 a contamination. The re- coverings. Technical Personn Section Manage Division Direct	nly n/ Follow Up (If neous DNA was nugh laboratory nay have been of ndditional PPE in the nel:	f applicable): deposited in the clean was perfor deposited. In addi requirements have he pre-amplificati	original quantifiermed on 3/28/20 ition, the section on areas include	ication of the reagent black of the decontaminate the plans to perform this land the associate the plans to perform the second	d data are deemed ank yielding a result of ne work areas of any ab clean on a routine e measure to prevent masks, and head
Quality Division Use O Additional Information It is unclear how extrar 0.01274 ng/µl. A thoro extraneous DNA that m basis. As of 4/8/2016 a contamination. The re- coverings. Technical Personn Section Manag Division Direct Quality Direct Tech. Jury	nly n/ Follow Up (If neous DNA was pugh laboratory nay have been of additional PPE in the nel: ger: for: ng Report	f applicable): deposited in the clean was perfor deposited. In addi requirements hav he pre-amplificati	original quantifiermed on 3/28/20 ition, the section e also been imp on areas include	ication of the reagent bl 016 to decontaminate th n plans to perform this la lemented as a preventive e a lab coat, gloves, face Date: $5 - 6 - 10$ Date: $5 / 6 / 10$ Date: $5 / 9 / 10$ Date: $5 / 9 / 10$ Date: $5 / 10 / 20$ F-6 - 14	d data are deemed ank yielding a result of ne work areas of any ab clean on a routine e measure to prevent masks, and head



	Qual	ity Divisi	on use on	У	
Quality Tracking #	2016-049		D	ate Submitted:	4/21/2016
				Date Closed:	4/26/2016
Date of this Report: Date of Incident:	4/4/2016 3/22/2016	Division:	FAD Forensic Biolo	gy yncid	N: 2014-15820 ent $#$ : (If applicable) 087225614
In this space, record instructed by the Sec On 3/22/16, when the basket during the ext swab in the tube. The remained with the sw The technician record record.	details of the incident, tion Manager or Divis e substrate from the p raction procedure the technician continued vab. The technician ret led this information or	, include dates ion Director(s) ortion tube co DNA technicia to transfer the ained the spin a laboratory i	Do not includ ntaining item 10 n noticed that t swab into the basket with the nformation wo	e analysts names 0.8.1 was being tra- here was a strand spin basket makin apparent hair an sksheet that was i	unless otherwise ansferred into a spin of apparent hair on the g sure the apparent hair d placed it into Freezer 1. ncluded as part of the case
On 3/24/16 a DNA an hair was observed on data. The data obtain complainant in the ca were also analyzed an Item 10.8.1. It does n 10.8.1. It is unclear w hair in the screening Item 10.8.1 will be re	alyst analyzed the data the swab from the lab ed was a major/minor ase and the minor com nd the results from the ot appear that the app here the apparent hair notes for Item 10.8.1.1 ported.	a obtained from poratory inform mixture when ponent was ins majority of the parent hair not came from as ltem 10.8.1 is a	m Item 10.8.1. T nation workshe e the major con sufficient for co lose samples we ed on the swab s the screening a a portion of "S#	The analyst had kr et and keep that in aponent was cons mparison. The oth ere consistent with had any impact o analyst did not no 8 L. wrist" swabs.	nowledge that an apparent in mind when analyzing the istent with the her samples in the case in the data obtained from in the results for Item te any observations of a The data obtained from
Quality Division Use Additional Informati	Only on/ Follow Up (If appli	icable):			

hair attached. All three screeners stated that if a hair was observed during the portioning process that it would be noted in their case notes. In addition, standard procedure is to portion one half of an evidence swab for extraction. During the portioning procedure, the technician would portion the area of the swab that did not contain the apparent hair. It is unclear if the apparent hair was present during the screening procedure and overlooked or if it was introduced during processing. Hair coverings have since been implemented as a required PPE in the screening, extraction, and pre-amplification areas of the laboratory.

Incident Tracking Report Issued by: Quality Director HFSC-QDiv-INCR Issue Date: March 02, 2015 Page 1 of 2



Technical Personnel: In Muki Section Manager: Division Director: Quality Director:

Tuh Leve: SAT HAUSEIC nakum/ u

CODIS admin: Cleve West

Date:	0-1-25-16
Date:	4/24/16
Date:	4.26-16
Date:	4/20/2016

4-25-16

4/26/16

4/24/16

The swab was in the process of analysis when the hair was first sted. Since analysis had already begun, mesample, including the ssible have, proceeded through the analytical process. Based upm I DNA results obtained, the neur did not impact the results and irefore, the results where deemed acceptable. Ron 4/20/10 SBIN

**Incident Tracking Report** Issued by: Quality Director

**HFSC-QDiv-INCR** Issue Date: March 02, 2015 Page 2 of 2

	2016-05328 2015-01631 2015-10450	HPD Incida 1 7	nt # 03980 01334 06523	8716 Jow 11215 513112010 8415	ĵ
	Qu	ality Divisi	on use on	ly	
Quality Tracking #	2016-050		D	ate Submitted:	4/22/2016
				Date Closed:	5131/2016
Date of this Report:	4/22/2016	Division:	FAD	FCN	: 2016-05328 2015-01631 2015-10459
Data of Incident:	1/12/2016	Castion	Pielogy		(If applicable
Date of meldent.	4/13/2010	Section.	Diology		
instructed by the Section Reagent blank for the end allele below analytical contamination. Re-inje good morphology. Upper reagent blank was there Upon re-amplification were deemed accepted	etails of the inciden ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele w ble.	nt, include dates, ision Director(s): f extraction batch gent blank yielden t blank was requ allele was reprod termine if this po was not present a	Do not include 39, RBE041316 d a quant value lested since the uced and now a ssible allele was nd therefore th	5LS-1 (1825LS16), p of 0.0ng/μl and sho possible allele was bove analytical thr s reproducible at th is reagent blank an	nless otherwise roduced a possible owed no other signs in a locus bin and h eshold at 58 RFUs. T ne amplification proc d the associated dat
instructed by the Section Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Upper reagent blank was ther Upon re-amplification were deemed acceptal	etails of the inciden ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele w ble.	nt, include dates, ision Director(s) f extraction batch gent blank yielden t blank was requ allele was reprod termine if this po vas not present a	Do not include 39, RBE041316 d a quant value lested since the uced and now a ssible allele wa nd therefore th	5LS-1 (1825LS16), p of 0.0ng/μl and sho possible allele was bove analytical thr s reproducible at th is reagent blank an	nless otherwise roduced a possible owed no other signs in a locus bin and h eshold at 58 RFUs. T ne amplification proc d the associated dat
instructed by the Section Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was then Upon re-amplification were deemed acceptal	etails of the inciden ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to den the possible allele w ble.	nt, include dates. ision Director(s): f extraction batch gent blank yielden t blank was requ allele was reprod termine if this po vas not present a	Do not include a 39, RBE041316 d a quant value lested since the uced and now a ossible allele was nd therefore th	analysts names un 5LS-1 (1825LS16), p of 0.0ng/µl and sho possible allele was bove analytical thr s reproducible at th is reagent blank an	nless otherwise roduced a possible owed no other signs in a locus bin and h eshold at 58 RFUs. The amplification proc d the associated dat
instructed by the Section Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was ther Upon re-amplification were deemed acceptal Quality Division Use O Additional Information In response to contamina routine basis. Addition gloves, hair coverings a amplification. In the per- anyone entering the ar	etails of the inciden ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele w ble. Only n/ Follow Up (If app ination events, the f hal PPE requirement and face masks are r ost-amplification lat reas where these pro-	nt, include dates, ision Director(s): f extraction batch gent blank yielden allele was reprod termine if this po vas not present a blicable): Forensic Biology is have also been now required dur poratory, gloves a ocedures are per	Do not include a 39, RBE041316 d a quant value lested since the uced and now a ssible allele was nd therefore th bection will be p implemented to ing screening, e and a lab coat an formed must ab	analysts names un 5LS-1 (1825LS16), p of 0.0ng/μl and sho possible allele was above analytical thr s reproducible at th is reagent blank an performing lab deco o prevent contamine extraction, quantifie re required. This P bide by these requine O 5-24-	Itess otherwise roduced a possible owed no other signs in a locus bin and h eshold at 58 RFUs. The amplification proc d the associated dat ontamination on a hation issues. Lab co cation, and PE is not optional an rements.
instructed by the Section Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was ther Upon re-amplification were deemed acceptal Quality Division Use O Additional Information In response to contamination routine basis. Addition gloves, hair coverings a amplification. In the per- anyone entering the art Technical Personn	etails of the incident ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele we ble. Only n/ Follow Up (If app ination events, the F hal PPE requirement and face masks are r ost-amplification lak reas where these pro-	nt, include dates, ision Director(s): f extraction batch gent blank yielden allele was reprod termine if this po vas not present a plicable): Forensic Biology is have also been now required dur poratory, gloves a ocedures are per	Do not include a 39, RBE041316 d a quant value lested since the uced and now a ossible allele was nd therefore th bection will be p implemented to ing screening, e and a lab coat an formed must ab	analysts names un SLS-1 (1825LS16), p of 0.0ng/μl and sho possible allele was above analytical thr s reproducible at the is reagent blank and performing lab deco o prevent contamine extraction, quantified re required. This P bide by these require O5-24- Date:	Itess otherwise roduced a possible owed no other signs in a locus bin and h eshold at 58 RFUs. The amplification proc d the associated dat ontamination on a hation issues. Lab co cation, and PE is not optional an rements.
instructed by the Secti Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was ther Upon re-amplification were deemed acceptal Quality Division Use O Additional Information In response to contami routine basis. Addition gloves, hair coverings a amplification. In the pe anyone entering the ar Section Manage	etails of the incident ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele we ble. Inly n/ Follow Up (If app ination events, the F nal PPE requirement and face masks are r ost-amplification lak reas where these pro- mel: ger: Or Content of the formation of the formation of the masks are r of the masks are r ost-amplification laker and face masks are r	nt, include dates, ision Director(s): f extraction batch gent blank yielden allele was reprod termine if this po vas not present a blicable): Forensic Biology is have also been now required dur poratory, gloves a ocedures are per	Do not include a 39, RBE041316 d a quant value lested since the uced and now a ssible allele was nd therefore th bection will be p implemented to ing screening, e and a lab coat a formed must ab	analysts names un 5LS-1 (1825LS16), p of 0.0ng/µl and sho possible allele was above analytical thr s reproducible at the is reagent blank an performing lab decor- o prevent contamine extraction, quantifier re required. This P bide by these required. Date: Date: Date: 5 25	Itess otherwise roduced a possible owed no other signs in a locus bin and his eshold at 58 RFUs. The amplification proc d the associated dat ontamination on a nation issues. Lab co cation, and PE is not optional an rements. $\partial o l \not \models$
instructed by the Secti Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was ther Upon re-amplification were deemed acceptal Quality Division Use O Additional Information In response to contami routine basis. Addition gloves, hair coverings a amplification. In the pe anyone entering the ar Section Manage Division Direct	etails of the incident ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele we ble. <b>Only</b> <b>n/ Follow Up (If app</b> ination events, the F hal PPE requirement and face masks are r ost-amplification lak reas where these pro- mel: ger: Amplification for the tor: Amplification for the form the fo	at, include dates. ision Director(s): f extraction batch gent blank vieldent t blank was requ allele was reprod termine if this po vas not present a blicable): Forensic Biology is have also been how required dur poratory, gloves a ocedures are per	Do not include a 39, RBE041316 d a quant value sested since the uced and now a ssible allele was nd therefore th bection will be p implemented to ing screening, e and a lab coat an formed must ab	analysts names un 5LS-1 (1825LS16), p of 0.0ng/µl and sho possible allele was above analytical thr s reproducible at the is reagent blank an performing lab decord o prevent contamine extraction, quantified re required. This P bide by these required 05-24- Date: Date: $5/25$ Date: $5/25$	Inters otherwise roduced a possible by wed no other signs in a locus bin and history eshold at 58 RFUs. The amplification proceed d the associated dat ontamination on a hation issues. Lab con- cation, and PE is not optional an rements. Polipication 1/10
instructed by the Secti Reagent blank for the e allele below analytical contamination. Re-inje good morphology. Up reagent blank was ther Upon re-amplification were deemed acceptal Quality Division Use O Additional Information In response to contami routine basis. Addition gloves, hair coverings a amplification. In the p anyone entering the ar Section Manage Division Direct Quality Direct	etails of the incident ion Manager or Divi epithelial fraction of threshold. This reage ection of this reager on re-injection the a n re-amplified to det the possible allele we ble. Only n/ Follow Up (If app ination events, the F hal PPE requirement and face masks are r ost-amplification lak reas where these pro- nel: ger: Autom tor: Autom	nt, include dates. ision Director(s): f extraction batch gent blank vieldent t blank was requ allele was reprod termine if this po vas not present a plicable): Forensic Biology is have also been how required dur boratory, gloves a occdures are per Micos	Do not include a 39, RBE041316 d a quant value sested since the uced and now a ssible allele was nd therefore th Section will be p implemented to ing screening, e and a lab coat au formed must ab	analysts names un 5LS-1 (1825LS16), p of 0.0ng/µl and sho possible allele was above analytical thr s reproducible at the is reagent blank an performing lab decord o prevent contamine extraction, quantified re required. This P bide by these required 05-24- Date: Date: $5/25$ Date: $5/25$ Date: $5/25$	Itess otherwise roduced a possible powed no other signs in a locus bin and he eshold at 58 RFUs. The amplification proc d the associated dat ontamination on a hation issues. Lab co cation, and PE is not optional an rements. $\partial o I p$ b f/I co f/I co f/I co f/I co



		(	QUALITY DIVISI	ON USE ON	ILY		
Quality CAR #	2016-1/	A-10			Date Submi	tted: 7/	1/2016
Non-Conformanc	ce Level	CLASS III			Date Clo	osed: 🛛	315/2016
Date of this Repo	ort: [	6/27/2016	Division:	FAD		FCN:	N/A
Date of Incid	ent:	5/9-13/2016	Section:	Forensic E	Biology/DNA		(If applicable)
Description of I	Discrepa	ancy/Non-conform	ance:			2.3 17-	
2016 Internal A	Audit Fir	ding #2:	<b>N</b>				
Source: IS	SO 5.5.6						
Requirement: T m Co Finding: R	he labo naintena ontamin	ratory shall have pr ince of measuring e ation or deteriorat	ocedures for sa equipment to en ion.	afe handling nsure prope	g, transport, stora er functioning and	age, use a d in order	nd planned to prevent
w	as bein	g completed and/o	r analysts were	not initialir	nat not all week ng and/or dating	y mainten the log as	ance listed in the SOP required.

#### **Actions Taken:**

Forensic Biology Quality Assurance Designee on 6/28/16. It does appear that there have been instances of incomplete records, primarily with regard to the weekly shut off of the Tecan 150. Given this is a daily task, the current worksheet is somewhat ambiguous regarding the documentation of the shut off. For example, if it is already off from the previous work day, an analyst might not mark the maintenance record because s/he did not actually shut off the Tecan workstation at the end of the week. Because of this ambiguity and other areas for improvement, the Tecan maintenance worksheet has been updated with input from the technicians using the instrument, while still adhering to the current SOP requirements. Further, FB management will create and complete a checklist for section management to document monthly reviews of quality-related records, including but not limited to, instrument maintenance records. Finally, the FB staff was reminded at the Forensic Biology section-wide meeting on June 30, 2016 that care should be taken to complete forms as indicated (e.g., insert initials and date if requested, not only one or the other).

If not discovered at this point, where else in the process would this incident have been discovered? If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance. Implementation of the monthly quality review by FB management should also provide opportunities for possible future non-conformances to be discovered.

Technical Personnel: DNA Technical leader	-nla-Soul	Date:	212.117
animediate supervisor.~		Date: _	113(116
Corrective Action Report	,		HFSC-QDiv-CAR
Uncontrolled When Printed		ls	sue Date: October 30, 2015 Page 1 of 2

CORRECTIVE ACTION REPOR	Т
Section Manager:	Date: 073116
DDIS Administrator (if applicable):	Date: 08/05/16
Division Director: Inn Rus	Date: 8-5-16

to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director:

Sillipm

Date: 8/5/2016

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed



	(	QUALITY DIVIS	ON USE ONLY	
Quality CAR # 2016-IA	A-11		Date Submit	ted: 7/1/2016
Non-Conformance Level	CLASS III		Date Clo	sed: 815/2016
Date of this Report:	6/27/2016	Division:	FAD	FCN: N/A
Date of Incident:	5/9-13/2016	Section:	Forensic Biology/DNA	(if applicable)
Description of Discrepa 2016 Internal Audit Fin	ncy/Non-conform ding #3:	ance:		
Source: ISO 4.3.2 Requirement: c) invalid assured a	.2 or obsolete docun against unintendec	nents are prom I use?	ptly removed from all points	of issue or use, or otherwise
Finding: The follow uncontro	wing forms were re olled or obsolete. S	emoved from th ome of these re	ne "Reagent Prep Binder" beo eagents are no longer made i	cause they were either n house.
<ul> <li>TRIS-HCI – 1N</li> <li>TRIS-HCI – 2N</li> <li>Luminol Reag</li> <li>Nuclear Fast</li> <li>Picroindigoca</li> <li>Pht Stock solu</li> <li>Pht solution N</li> <li>PBS Phosphate</li> <li>PBS 10X form</li> </ul>	1 pH 8.0 A pH 8.0 Red Solution rmine (PIC) ution form Working Form te buffered saline (not made in 2015	et (not prepare 5 nor 2016)	d in 2015 or 2016)	
DNA • Chelex salt, 2 • Carrier RNA ( • DNA reagent • QlAamp DNA • TE Buffer 10/ • Stain extracti • Sodium Dode • Sodium Dode • Sodium chlor • Sarcosyl solut • Proteinase K • EDTA Solutio • Dithiothreito • Digest Buffer	0% w/v cRNA) for EZ1 extra Prep worksheet mini kit buffer AW 0.1 Mm, pH8.0 on buffer cyl Sulfate (SDS) 20 ide, 5M tion 20% W/V solution n, 0.5 M pH 8.0 I (DTT, 0.39 M) I (DTT, 1 M) pH 7.5.	actions /1 and AW2 0%		

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed



#### Actions Taken:

The outdated forms listed above were removed from the laboratory. Additionally, FB management will create and complete a checklist for section management to document monthly reviews of quality-related records, including but not limited to, the removal of obsolete forms and SOPs from the laboratory. Finally, the FB staff was reminded at the Forensic Biology section-wide meeting on June 30, 2016 that should they encounter an obsolete form or SOP in the laboratory, they should remove it.

If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance. Implementation of the monthly quality review by FB management should also provide opportunities for possible future non-conformances to be discovered.

	, FEUI	
Technical Personnel:	-n/a- Date	2:
Immediate Supervisor:	Date	e: 7/2-0/16
Section Manager:	BCC Date	DISTIC
CODIS Administrator (if applicable):	n With Date	e: 7/20/16
Division Director:	lun his Date	8: 8-5-16

#### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director: Allelins

	2151
Date:	01012016

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed



Uncontrolled When Printed

# HOUSTON FORENSIC SCIENCE CENTER CORRECTIVE ACTION REPORT

Quality CAR #       2016-IA-12       Date Submitted:       7/1/2016         Non-Conformance Level       CLASS III       Date Closed:       8/5/2016         Date of this Report:       6/27/2016       Division:       FAD       FCN:       N/A         Date of Incident:       5/9-13/2016       Section:       Forensic Biology/DNA       (If applicable)         Description of Discrepancy/Non-conformance:       2016       Internal Audit Finding #4:       Source:       ISO 4.3.2.3         Requirement: Are management system documents generated by the lab uniquely identified? Does such identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?       Findings:         • The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")       • LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.	uality CAR #       2016-IA-12         on-Conformance Level       CLASS III         ate of this Report:       6/27/2016         Date of Incident:       5/9-13/2016         escription of Discrepancy/Non-conform.         016 Internal Audit Finding #4:         ource:       ISO 4.3.2.3	Date Submitted: 7/1/2016 Date Closed: 8/5/20 Division: FAD FCN: N/A (If Section: Forensic Biology/DNA	16
Non-Conformance Level       CLASS III       Date Closed:       8/5/2016         Date of this Report:       6/27/2016       Division:       FAD       FCN:       N/A         Date of Incident:       5/9-13/2016       Section:       Forensic Biology/DNA       (If applicable)         Description of Discrepancy/Non-conformance:       2016       Internal Audit Finding #4:       Source:       ISO 4.3.2.3         Requirement: Are management system documents generated by the lab uniquely identified? Does such identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?       Findings:         • The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")       • LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.	ate of this Report: 6/27/2016 Date of Incident: 5/9-13/2016 escription of Discrepancy/Non-conform 016 Internal Audit Finding #4: purce: ISO 4.3.2.3	Date Closed: 8/5/20 Division: FAD FCN: N/A (If Section: Forensic Biology/DNA	16
Date of this Report:       6/27/2016       Division:       FAD       FCN:       N/A         Date of Incident:       5/9-13/2016       Section:       Forensic Biology/DNA       (If applicable)         Description of Discrepancy/Non-conformance:       2016       Internal Audit Finding #4:       Source:       ISO 4.3.2.3         Requirement: Are management system documents generated by the lab uniquely identified? Does such identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?       Findings:         • The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")         • LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.	ate of this Report: 6/27/2016 Date of Incident: 5/9-13/2016 escription of Discrepancy/Non-conform 016 Internal Audit Finding #4: purce: ISO 4.3.2.3	Division: FAD FCN: N/A (If Section: Forensic Biology/DNA	
Date of Incident:       5/9-13/2016       Section:       Forensic Biology/DNA         Description of Discrepancy/Non-conformance:       2016 Internal Audit Finding #4:         Source:       ISO 4.3.2.3         Requirement: Are management system documents generated by the lab uniquely identified? Does such identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?         Findings:       • The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")         • LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.	Date of Incident: 5/9-13/2016 escription of Discrepancy/Non-conform 016 Internal Audit Finding #4: ource: ISO 4.3.2.3	Section: Forensic Biology/DNA	applicable)
Description of Discrepancy/Non-conformance:         2016 Internal Audit Finding #4:         Source:       ISO 4.3.2.3         Requirement: Are management system documents generated by the lab uniquely identified? Does such identification include the date of issue and/or revision identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?         Findings:       • The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")         • LIMS worksheets do not contain footers or headers that contain document control information (issue dissuing authority) and are not listed on the master document list.	escription of Discrepancy/Non-conform 016 Internal Audit Finding #4: ource: ISO 4.3.2.3		
<ul> <li>2016 Internal Audit Finding #4:</li> <li>Source: ISO 4.3.2.3</li> <li>Requirement: Are management system documents generated by the lab uniquely identified? Does such identification include the date of issue and/or revision identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?</li> <li>Findings: <ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul> </li> </ul>	016 Internal Audit Finding #4: ource: ISO 4.3.2.3	ance:	
<ul> <li>Source: ISO 4.3.2.3</li> <li>Requirement: Are management system documents generated by the lab uniquely identified? Does such identification include the date of issue and/or revision identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?</li> <li>Findings:         <ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul> </li> </ul>	Surce: ISO 4.3.2.3		
<ul> <li>Requirement: Are management system documents generated by the lab uniquely identified? Does such identification include the date of issue and/or revision identification, page numbering, total number of pages or a mark to signing the end of the document, and issuing authority(ies)?</li> <li>Findings: <ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue dissuing authority) and are not listed on the master document list.</li> </ul> </li> </ul>			
<ul> <li>include the date of issue and/or revision identification, page numbering, total number of pages or a mark to signit the end of the document, and issuing authority(ies)?</li> <li>Findings: <ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul> </li> </ul>	equirement: Are management system do	cuments generated by the lab uniquely identified? Does such	identification
<ul> <li>the end of the document, and issuing authority(ies)?</li> <li>Findings: <ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul> </li> </ul>	clude the date of issue and/or revision ic	entification, page numbering, total number of pages or a mar	k to signify
<ul> <li>Findings:</li> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul>	e end of the document, and issuing auth	ority(ies)?	σ,
<ul> <li>The form used to check the SERI Christmas Tree Stain reagent was not controlled with the required worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul>	ndings:		
<ul> <li>worksheet identifiers nor was it controlled in QMS. In addition, this reagent did not have a quality form a described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul>	The form used to check the SERI	Christmas Tree Stain reagent was not controlled with the requ	uired
<ul> <li>described in the SOP ("also contain the test date, signature of the analyst performing the quality control, second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul>	worksheet identifiers nor was it co	ntrolled in QMS. In addition, this reagent did not have a gual	ity form as
<ul> <li>second reader signature, if applicable, and date and any supporting documentation")</li> <li>LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.</li> </ul>	described in the SOP ("also contai	the test date, signature of the analyst performing the quality	control. a
LIMS worksheets do not contain footers or headers that contain document control information (issue d issuing authority) and are not listed on the master document list.	second reader signature, if applica	ble, and date and any supporting documentation")	concrot, a
issuing authority) and are not listed on the master document list.	<ul> <li>LIMS worksheets do not contain</li> </ul>	footers or headers that contain document control information	n (issue date
Actions Takan	issuing authority) and are not liste	d on the master document list.	(lissue dute,
Actions Takon			
	ctions Taken		
A controlled form has been created for the quality shack of the Christmas Tree Stain uniquely identified as FAD	controlled form has been created for th	a quality shack of the Christmas Tree Stein, uniqualy identified	
A controlled form has been created for the quality check of the Christmas free stain, uniquely identified as FAD-	is oc cts 1	e quality check of the christmas free stain, uniquely identified	as FAD-BIO-
WS-QC-C15.1.	S-QC-C13.1.		
The DNA Technical London has the descent for 17 to increase the data of increased in			
identification, and issuing authority/iss) on the following UNAS generated workshoots that are surrently in your	aptification and issuing authority(isc) as	request for fit to incorporate the date of issue and/or revision	1
Desting Worksheet	Partice Workshot	the following clivis-generated worksheets that are currently	in use:
Fortion Worksheet	Fortion Worksheet		
E21 Extraction worksneet	E21 Extraction Worksneet		
Duo Quantitation Worksheet	<ul> <li>Duo Quantitation Worksheet</li> </ul>		
Tecan Pre-Quant Deck Map	<ul> <li>Tecan Pre-Quant Deck Map</li> </ul>		
<ul> <li>Tecan Duo Quantitation Worksheet</li> </ul>	<ul> <li>Tecan Duo Quantitation Workshee</li> </ul>	it	
<ul> <li>ID+ Amplification Plate Worksheet</li> </ul>	<ul> <li>ID+ Amplification Plate Worksheet</li> </ul>		
<ul> <li>Tecan ID+ Amplification Setup</li> </ul>	<ul> <li>Tecan ID+ Amplification Setup</li> </ul>		
<ul> <li>Tecan ID+ Amplification Worksheet</li> </ul>	<ul> <li>Tecan ID+ Amplification Workshee</li> </ul>	t	
<ul> <li>Tecan ID+ Amplification Worksheet – Amp Calc</li> </ul>	Tecan ID+ Amplification Workshee	t – Amp Calc	
Pre-Amp Submission	Pro Amo Cubmission		
3130 Plate Submission	<ul> <li>Pre-Amp Submission</li> </ul>		
The DNA Technical Leader has also updated the master document list to include each of the worksheets listed ab	<ul> <li>3130 Plate Submission</li> </ul>	d the master document list to include each of the worksheets	listed above.
	<ul> <li>Pre-Amp Submission</li> <li>3130 Plate Submission</li> <li>DNA Technical Leader has also update</li> </ul>		
Corrective Action Report	<ul> <li>Bre-Amp Submission</li> <li>3130 Plate Submission</li> <li>DNA Technical Leader has also update</li> </ul>		
Issued by: Quality Director Issue Date: October 30, 2015	<ul> <li>Pre-Amp Submission</li> <li>3130 Plate Submission</li> <li>ne DNA Technical Leader has also update</li> <li>Corrective Action Report</li> </ul>	HESC-OF	Div-CAR

Page 1 of 2



If not discovered at this point, where else in the process would this incident have been discovered? If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

Technical Personnel: - n/a Head	Date:
-Immediate Supervisor: Fa	Date: 7/31/16
Section Manager:	Date:
CODIS Administrator (if applicable):	Date: 08 05/16
Division Director: Ihm this	Date: 8-5-16

#### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director:

Date: 8/5/2016

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed



		QUALITY DIVIS	ON USE ONLY	
Quality CAR # 2016	-IA-14		Date Subm	itted: 7/1/2016
Non-Conformance Lev	el		Date Cl	losed: 8/5/2016
Date of this Report:	6/27/2016	Division:	FAD	FCN:
Date of Incident:	5/9-13/2016	Section:	Forensic Biology/DNA	(If applicable)
Description of Discre	pancy/Non-conform	iance:		
2016 Internal Audit F Source: QM 5.4 Requirement: Section Finding: A cross of equi	inding #6: .1. aal SOPs will contain s-linker was used to l ipment was not prop	instructions for UV plastic ware erly maintained	the use of equipment. as a secondary measure of nor had an SOP on how to	decontamination when the piece use it.
Actions Taken:				

Staff was reminded at the Forensic Biology section-wide meeting on June 30, 2016 that instruments or equipment marked as "out of service" or "not for casework use" may not be used for casework applications. FB management will explore supplementing the FB SOPs with instructions for the use, maintenance, and cleaning of the cross-linkers so that they may be used in the future.

### If not discovered at this point, where else in the process would this incident have been discovered?

If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

Technical Personnel: 11/a	Date:
ONA Technical leaders 1-	Date: 1/20/16
Section Manager:	Date: 072110
CODIS Administrator (if applicable):	Date: 7/20/16
Division Director: him	Date: 8/5-/14

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed



### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director: Sulan

Date: 8/5/2016

Corrective Action Report Issued by: Quality Director **Uncontrolled When Printed** 



		QUALITY DIVISI	ON USE O	NLY	
uality CAR # 20	16-IA-15			Date Submittee	i: 7/1/2015
Ion-Conformance	Level CLASS III			Date Closed	d: 8/5/2016
Date of this Report	6/27/2016	Division:	FAD		FCN: (If applicable)
Date of Inciden	t: 5/9-13/2016	Section:	Forensic	Biology/DNA	
Description of Dis	crepancy/Non-confor	mance:			
2016 Internal Aut	4 13 2				
Requirement: Doo num Finding: The	es such identification in ober of pages or a mark page numbering and f the documentation. Th	nclude the date of k to signify the e forensic case nur is was observed	of issue and nd of the o mber on th in many ca	d/or revision identific document, and issuing ne case files is illegible ase files during case fi	ation, page numbering, total g authority(ies)? at times and is not corrected ile review.

#### Actions Taken:

Staff was reminded at the Forensic Biology section-wide meeting on June 30, 2016 that case file pagination must be reviewed to ensure that the forensic case #s and page #s are clear. If not, information must be manually corrected. FB management will look for opportunities to adjust the footer of HFSC-generated documents that may be impacted. FB management will create and complete a checklist for section management to document monthly reviews of quality-related records, including but not limited to, case file reviews.

If not discovered at this point, where else in the process would this incident have been discovered?

If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance. Implementation of the monthly quality review by FB management should also provide opportunities for possible future non-conformances to be discovered.

Technical Personnel:	-nla-
DNA Technical Leader Immediate Supervisor:	N=
Section Manager:	RAC
CODIS Administrator (if applicable):	Clein Attet
Division Director:	chur this

Date:	
Date:	7/20/16
Date:	072116
Date:	7/20/16
Date:	8-5-16

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed



### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director: FUIDm

Date: 8/5/2016

**Corrective Action Report** Issued by: Quality Director **Uncontrolled When Printed** 

		QUALITY DIVIS	ION USE ONLY	Y	
Quality CAR # 201	6-IA-16			Date Submitted	: 7/1/2016
Non-Conformance L	evel CLASS II			Date Closed	: 8/5/2016
Date of this Report:	6/27/2016	Division:	FAD	F	CN:
Date of Incident	5/9-13/2016	Section:	Forensic Bio	logy/DNA	(If applicable)
Description of Disc	repancy/Non-conform	ance:			
2016 Internal Audi	t Finding #8:				
Requirement: The list as scope to, ar	aboratory shall establis of its activities. The sy d implemented by the	h, implement, /stem's docum appropriate po	and maintain entation shall ersonnel.	a management sys be communicated	tem appropriate to the to, understood by, available
Finding: DNA scien Augu	SOP 2.5.2.1 states that tific article per month'. st 2015 and February 2	'DNA technicia There is no do 016.	ans and analys cumentation	ts shall attempt to to show that article	read at least one current as were reviewed between

### Actions Taken:

The less than consistent article reading may be attributed to the interim nature of the FB management from May, 2015 through June, 2016, as typically, article reading corresponded to meeting attendance. An acting DNA Technical Leader was in place from May, 2015 through July, 2015 due to FMLA leave; an interim Forensic Biology section manager, an interim DNA Technical Leader, and interim supervisors were in place from October, 2015 through June, 2016. The DNA SOP will be updated to require scientific article quarterly. Additionally, once implemented QUALTRAX will enable better record keeping of readings (similar to SOP and QM reviews). Finally, FB management will create and complete a checklist for section management to document monthly reviews of quality-related records, including but not limited to, required article reading.

If not discovered at this point, where else in the process would this incident have been discovered?

If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance. Implementation of the monthly quality review by FB management should also provide opportunities for possible future non-conformances to be discovered.

1101-
$\sim$
RED

Date:	
Date:	7/20/16
Date:	072110

HFSC-QDiv-CAR Issue Date: October 30, 2015 Page 1 of 2

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed

HOUS	TON FORENSIC SCIEN	CE CENTE	R
CORR	ECTIVE ACTION REPO	RT	
DDIS Administrator (if applicable):	Class what	Date:	7/20/16
Division Director:	- china hiviz	Date:	6-5-16

#### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

### Additional Information/Follow-Up:

Quality Director: Fuldin

Date: 8/5/2016

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed



		QUALITY DIVIS	ION USE ON	ILY	
Quality CAR # 2016	·IA-17			Date Subm	nitted: 7/1/2016
Non-Conformance Lev	el CLASS III			Date C	losed: \$15/2016
Date of this Report:	6/27/2016	Division:	FAD		FCN:
Date of Incident:	5/9-13/2016	Section:	Forensic B	iology/DNA	(If applicable)
Requirement: Does th	.5 le laboratory maintai	n records of re	levant autho	orizations com	atonco advectional au t
Source: ISO 5.2.	5				
professi	onal qualifications, t	raining, skills, a	ind experien	ice of all technic	betence, educational and cal personnel, including
Finding: There w	ted personnel? as no documented of	ontinuing aduc	ation as rea	wine of few Data	
Files of	nine analysts.	manung euuc	ation, as req	uired for DNA a	inalysts per FBI QAS, in the Q
One sta	ff member is authori	zed to conduct	certain task	s in biology. Ho	wever, that individual has not
provide	d an SOQ that descri	bes current dut	ies. Records	of previous tra	ining and transcripts have not
been pro	ovided to the quality	division.			
Actions Takon					
Continuing education	rocorde have here		Contraction of the second		

result of the internal audit. Continuing education requirements had been met; the records had not yet been provided to the Quality Division for each of the nine analysts in question, a provided to the Quality Division.

An SOQ, previous training records, and transcripts have since been provided for the one staff member in question, as a result of the internal audit.

Staff was reminded at the Forensic Biology section-wide meeting on June 30, 2016 that records of attendance, such as certificates of attendance, must be provided to the Quality Division as soon as is practicable after the continuing education event.

 If not discovered at this point, where else in the process would this incident have been discovered?

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 Technical Personnel:

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity to discover this non-conformance.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity.

 If not discovered at this point, it seems that a future audit would be the most probable opportunity.

 If not d

CORRECTIVE A	TION PEDODT		
DNA Technical Water Immediate Supervisor:		Date:	7/20116
Section Manager	00	Date.	110/10
Section Manager:		Date: C	72116
S Administrator (if applicable):	UNAF	Date:	7/20/16
Division Director:		Date:	\$-5-16

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director:

Date: 8/5/2016

**Corrective Action Report** Issued by: Quality Director Uncontrolled When Printed



QUALITY DIVISION USE ONLY				
Quality CAR # 2016-IA-18	Date Submitted: 7/1/2016			
Non-Conformance Level CLASS II	Date Closed: 8/5/2016			
Date of this Report: 6/27/2016 Division: FAD	FCN:			
	(If applicable)			
Date of Incident: 5/9-13/2016 Section: For	ensic Biology/DNA			
Description of Discrepancy/Non-conformance:				
2016 Internal Audit Finding #10:				
Source: DNA SOP 3.3.3.1.9				
Requirement: Signs may be posted to designate appropriate pe	rsonal protective equipment (PPE) in certain areas.			
Finding: A DNA technician was observed on three senarat.	e occasions not wearing the required hair covering in			
the extraction room.	e occasions not wearing the required half covering in			
Actions Taken:				
The DNA technician in question is no longer employed by the l	Houston Forensic Science Center as of May 31, 2016.			
However, staff was reminded at the Forensic Biology section-w	ide meeting on June 30, 2016 that PPE are required in			
the laboratory areas in which signs are posted.				
	d al fa fa st dans have been discussed 0			
At this time, the issue appears to be isolated to a particular s	a this incluent have been discovered?			
appropriate PPE appropriately cannot be predicted.	tan member. Any ratare instances of failure to don			
	7			
-+	N			
Due Technical Personnel: 17/10	Date:			
Immediate Supervisor:	Date: 7/20/16			
Section Manager:	Date: 077111-			
Sector manager State				
CODIS Administrator (if applicable):	Date: 7/20/16			
Division Director: Ince this	Date: 8/5//6			

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed



#### Summary of Root Cause Analysis:

This nonconformance was identified through the May-June 2016 internal audit. The focus of this internal audit was to verify that the quality management system and technical sections (Biology, Controlled Substances, Toxicology, Firearms, Latent Prints, Audio/Video and Digital Forensics) were compliant to the HFSC QA manual, ISO/IEC 17025 standard and ANAB requirements. There will be no root cause analysis completed on nonconformance's issued through internal audits.

Additional Information/Follow-Up:

Quality Director: SWMM

Date: 8/5/2016

Corrective Action Report Issued by: Quality Director Uncontrolled When Printed

#### NAME: Bruce Budowle

<u>TITLE:</u> Professor, Director, Center for Human Identification University of North Texas Health Science Center

BUSINESS ADDRESS, PHONE NUMBER, and EMAIL ADDRESS:

Center for Human Identification University of North Texas Health Science Center 3500 Camp Bowie Boulevard Ft. Worth, Texas 76107

bruce.budowle@unthsc.edu

BIRTH DATE: October 13, 1953

BIRTH PLACE: San Pedro, California

MARITAL STATUS: Married

EDUCATION:

King College Bristol, Tennessee

Virginia Polytechnic Institute and Ph.D. - 1979 (Genetics) State University Blacksburg, Virginia

DISSERTATION: Phase Change in Hedera helix L.

RESEARCH AND/OR PROFESSIONAL EXPERIENCE:

1974	Undergraduate Research Scientist, King College, Bristol, Tennessee
1976 - 1979	Graduate Teaching Assistantship in Biology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia
1979 - 1982	Postdoctoral Fellow in Immunogenetics, Awarded by the National Cancer Institute, University of Alabama in Birmingham, Alabama
1982	Consultant to Department of Criminal Justice University of Alabama in Birmingham
1983 - 1985	Consultant to Beckman Instruments, Inc. Palo Alto, California
1983 - 1994	Research Chemist, Forensic Science Research and Training Center, Laboratory Division, FBI Academy, Quantico, Virginia
1994 - 1997	Chief, Forensic Science Research Unit, Laboratory Division, FBI Academy, Quantico, Virginia

B.A. - 1975 (Biology)

1985 - 2008 Adjunct Professor, School of Continuing Education,

University of Virginia, FBI Academy Campus

- 1987 1988 Council Member, International Electrophoresis Society
- 1987 1988 Vice President, America's Branch of the Electrophoresis Society
- 1988 1990 Vice President, International Electrophoresis Society
- 1989 1991 Council Member, American Electrophoresis Society
- 1989 1998 Associate Editor, Applied and Theoretical Electrophoresis
- 1990 present Editorial Board, BioTechniques
- 1990 1991 Visiting Instructor, Rush Presbyterian St. Luke's Medical Center.
- 1990 present Editorial/Advisory Board, International Journal of Legal Medicine
- 1991 2005 Chairman of the DNA Commission of the International Society of Forensic Haemogenetics
- 1994 Defense Science Board, Mitochondrial DNA, AFDIL
- 1994 1998 Editor, Crime Laboratory Digest
- 1995 2000 Chairman of The Scientific Working Group on DNA Analysis Methods
- 1995 2000 DNA Advisory Board, DNA Identification Act, Federal Bureau of Investigation
- 1995 2005 Editorial Board, Genetic Analysis: Biomolecular Engineering
- 1998 2001 The Research and Development Working Group, National Commission on the Future of DNA Evidence, National Institute of Justice
- 1998 2009 Senior Scientist Biology, Laboratory Division, Federal Bureau of Investigation
- 1999 present Editorial Board, Forensic Science Communications
- 1999 present Editorial Board, Legal Medicine (Japanese Society of Legal Medicine)
- 1999 2003 Research Professor, Institute for Biosciences, Bioinformatics, and Biotechnology, George Mason University, Manassas, Virginia
- 1999 2003 Affiliate Professor, Department of Biology, George Mason University, Fairfax, Virginia
- 2000 Outside Reviewer for German Proficiency Testing System (GEDNAP)

- 2001-2002 Celera DNA Advisory Board, Mitochondrial DNA/WTC
- 2001-2003 Kinship and Data Analysis Panel for WTC Victim Identification
- 2002 Steering Committee, Colloquium on Microbial Forensics, American Society of Microbiology
- 2002 2004 Chair of Scientific Working Group Microbial Genetics and Forensics
- 2002 Co-organizer of Microbial Forensics Meeting, The Banbury Center, Cold Spring Harbor Laboratory
- 2002 2008 Adjunct Faculty, Department of Pathology, University of North Texas Health Science Center, Ft. Worth, Texas
- 2003 2008 National Biodefense Analysis and Countermeasures Center Advisory Group
- 2002 2007 National Interagency Genomics Science Coordinating Committee, National Science Foundation
- 2003 Disease Informatics Senior Coordinating Committee, National Science Foundation
- 2004 Co-organizer of Second Microbial Forensics Meeting, Identifying Gaps, sponsored by the Department of Homeland Security, The Banbury Center, Cold Spring Harbor Laboratory
- 2004 2007 Editorial Board, Forensic Science International
- 2004 Participant in Expert Meeting on Microbial Forensics, National Academy of Sciences, Washington, D.C., June 22-25, 2004
- 2004 Participant in Biosecurity Threats in the 21<sup>st</sup> Century: Reexamining how we define the "problem" and mitigate the effects, National Academy of Sciences, Minneapolis, MN, July 15, 2004
- 2004 Invited Lecturer, Post Graduate Course in Forensic Genetics, Finish Graduate School in Population Genetics and department of Forensic Medicine, University of Helsinki, Finland, September 20-21, 2004
- 2004 Member of Steering Committee on the Animal Forensics Working Group of the International Society of Animal Genetics
- 2004 present Member of Scientific Working Group for the NIAID-funded Bioinformatics Resource Center (BRC) at The Institute for Genomic Research (TIGR)
- 2005 Co-organizer of Third Microbial Forensics Meeting, sponsored by the Department of Homeland Security, Evidence Collection, Storage, and Extraction, The Banbury Center,

Cold Spring Harbor Laboratory

- 2006 Participant in Advancing the International Biosecurity Dialogue: Clarifying Definitions, National Academy of Sciences, Washington, D.C., January 27, 2006
- 2006 Participant in Genomics and Global Pathogens, The American Academy of Microbiology, Washington, D.C., September 27-28, 2006
- 2006 Lecturer in Science Exposition and Ethics Course, Watson School of Biological Science, Cold Spring Harbor, New York, November 29, 2006
- 2006 International Fellow, Institute of Environmental Science and Research, New Zealand, December 1-13, 2006
- 2006 2008 Steering Committee Member, Scientific Working Group on Chemical, Biological, Nuclear and Radiological Analyses
- 2007 Member of National Planning Committee for Workshop on Plant Pathogen Forensics: Filling the Gaps, sponsored by Oklahoma State University, Oklahoma City, Oklahoma, January 11-13, 2007
- 2007 present Editorial Board, Forensic Science International Genetics
- 2007 Co-organizer of Fourth Microbial Forensics Meeting, Enduring Research Pathways, sponsored by the Department of Homeland Security, The Banbury Center, Cold Spring Harbor Laboratory
- 2008 Invited Outside Reviewer on DNA Technology for National Research Institute of Police Science, National Police Agency, Chiba, Japan, January 15-16, 2008
- 2008 Visiting Fellow, Faculty of Health Science and Medicine, Bond University, Gold Coast, Australia, June 23-July 5, 2008
- 2008 present Visiting Professor, Faculty of Health Science and Medicine, Bond University, Gold Coast, Australia
- 2008 present Member, Expert Working Group on Human Factors in Latent Print Analysis, NIST and NIJ
- 2009 present Professor, Department of Forensics and Investigative Genetics, University of North Texas Health Science Center, Ft. Worth, Texas
- 2009 present Executive Director, Institute of Investigative Genetics, University of North Texas Health Science Center, Ft. Worth, Texas
- 2009 Invited Speaker, Overview of Microbial Forensics and the Concepts of Validation, Committee on Review of the

Scientific Approaches used during the FBI's Investigation of the 2001 *Bacillus anthracis* Mailings, First Meeting, National Academy of Sciences, July 30-31, 2009

- 2009 Invited Speaker, Low Copy Number Typing Issues, Mixture Interpretation Issues, Committee on Science, Technology and Law, National Academy of Sciences, October 19, 2009
- 2009 present Co-Editor-in-Chief, BMC Investigative Genetics
- 2010 Member of Steering Committee for Forensic Death Investigation Symposium, National Institute of Justice, Scottsdale, AZ, June 7-9, 2010
- 2010 Consultant to Cyprus Institute of Neurology and Genetics Laboratory of Forensic Genetics UN Missing Persons Identification Program, Cyprus, September 20-24, 2010
- 2010 present Adjunct Faculty, Department of Biological Sciences, University of North Texas, Denton, TX
- 2010 Co-organizer of Fifth Microbial Forensics Meeting, Microbial Forensics in the Era of Genomics, sponsored by the Department of Homeland Security, The Banbury Center, Cold Spring Harbor Laboratory, November 7-10, 2010
- 2011 Co-organizer of Lyme Disease Diagnostics in the Proteomics-Genomics Era, The Banbury Center, Cold Spring Harbor Laboratory, April 10-13, 2011
- 2011 Visiting Professor, Department of Forensic Medicine, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand, June 2011.
- 2011 Member of Organizing Committee, Microbial Evolution and Cutting Edge Tools for Outbreak Investigations, Center for Disease Control and Prevention, Atlanta, GA, September 14-16, 2011.
- 2011 present Editorial Board, American Journal of Forensic Medicine and Pathology
- 2012 present Member of Academic Committee, Key Laboratory of Forensic Genetics, Institute of Forensic Science of Ministry of Public Security, Beijing, China
- 2012 Member of planning committee for the Forum on Microbial Threats Workshop: The science and applications of microbial genomics: predicting, detecting, and tracking novelty in the microbial world, Institute of Medicine, Board on Global Health, National Academy of Sciences, June 12-13 2012.
- 2012-2017 Member of the Technical Advisory Group to the Board of the Houston Forensic Science Center, LGC, Inc.
- 2013-2016 Member of the International Expert Committee for the Biology Division of Health Sciences Authority, Singapore

- 2013- present Appointment with Center of Excellence in Genomic Medicine Research (CEGMR), King Abdulaziz University, Jeddah, Saudi Arabia.
- 2013-2014 Member of Committee for the Science Needs for Microbial Forensics: Developing an Initial International Science Roadmap, Institute of Medicine, Board on Global Health, National Academy of Sciences.
- 2013-2015 Visiting Professor, Science Without Borders, Universidade Federal Do Rio De Janeiro, Centro De Ciências Da Saúde, Instituto De Biofísica Carlos Chagas Filho
- 2014-2015 Member of Committee on PCR Standards for the BioWatch Program, Board of Life Sciences, Division on Earth and Life Sciences, Board of Health Sciences Policy, Institute of Medicine, Board on Global Health, National Research Council, National Academy of Sciences.
- 2014 present Associate Editorial Board of Biosafety and Biosecurity of Frontiers in Bioengineering and Biotechnology
- 2016 present Director of the Center for Human Identification, University of North Texas Health Science Center, Ft. Worth, Texas
- 2016 GAO Meeting on Gaps in Capabilities for Attributing the Source of a Biological Attack, Washington, DC, April 20-21, 2016.
- 2016 Tackling Low Cost Nucleic Acid Test for the Developing World: Catalyzing Innovation in Sample Preparation, Scientific Advisory Board, Bill & Melinda Gates Foundation, Seattle, WA, May 25, 2016.
- 2016 present Member of the Texas Forensic Science Commission.
- 2017 present Vice-Chair, Department of Microbiology, Immunology and Genetics, University of North Texas Health Science Center, Ft. Worth, Texas.

MEMBERSHIPS IN PROFESSIONAL AND SCHOLARLY ORGANIZATIONS:

International Society for Forensic Genetics American Society of Microbiology

HONORS AND OTHER SPECIAL COMMENTS:

```
    Pi Alpha Sigma (1972)
    Undergraduate Research Award (1974)
    Graduate State Tuition Scholarship (1976 - 1979)
    Phi Kappa Phi (1976)
    Sigma Xi (1978)
    American Academy of Forensic Sciences Recognition Award (1981)
    Attorney General's Award for Exceptional Service (1991)
    Jefferson Award, University of Virginia (1991)
    Forensic Scientist of the Year, MAAFS (1996)
    Honorary Member of the Finnish Society of Forensic Medicine (1998)
```
Director's Award for Excellence in Investigative Support (2000)
Paul L. Kirk Award, Criminalistics Section, American Academy of Forensic Sciences (2001)
University of Alabama at Birmingham's 2004 Ireland Distinguished Visiting Scholar
Honorary Member of the Mediterranean Academy of Forensic Sciences (2004)
Health Care Hero Award, Dallas Business Journal (2010)
GSA Outstanding Faculty Award 2016, GSBS, UNTHSC

RESEARCH INTERESTS:

Forensic Science Genetic Marker Systems Technique Development Molecular Biology Population Genetics Human Genetics Microbial Forensics Pharmacogenomics

## PUBLICATIONS:

1. Budowle, B., Go, R. C. P. and Acton, R. T.: Isoelectric focusing of hair proteins. In: Electrophoresis '81 (Allen, R. C. and Arnaud, P., eds.) Walter de Gruyter, Berlin, pp. 585-590, 1981.

2. Budowle, B., Go, R. C. P., Barger, B. O. and Acton, R. T.: Properdin factor B polymorphism in black Americans. J. Immunogenetics 8:519-521, 1981.

3. Budowle, B. and Acton, R. T.: A technique for the detection of variable electrophoretic patterns of hair proteins. Electrophoresis 2:333-334, 1981.

4. Budowle, B., Acton, R. T. and Barger, B. O.: A method for the dialysis of micro-samples. Anal. Biochem. 118:399-400, 1981.

5. Budowle, B., Reitnauer, P. J., Barger, B. O., Go, R. C. P., Roseman, J. M. and Acton, R. T.: Properdin factor B in type 1 (insulin-dependent) diabetic patients. Diabetologia 22(6):483-485, 1982.

6. Acton, R. T., Balch, C. M., Budowle, B., Go, R. C. P., Roseman, J. M., Soong, S-J., and Barger, B. O.: Immunogenetics of melanoma. In: <u>Melanoma</u> <u>Antigens and Antibodies</u> (Reisfeld, R. A. and Ferrone, S., eds.) Plenum Publishing Corporation, New York, pp. 1-21, 1982.

7. Reitnauer, P. J., Go, R. C. P., Acton R. T., Murphy, C. C., Budowle, B., Barger, B. O. and Roseman, J. M.: Evidence for genetic admixture as a determinant in the occurrence of IDDM in U.S. Blacks. Diabetes 31:532-537, 1982.

8. Budowle, B., Barger, B. O., Balch, C. M., Go, R. C. P., Roseman, J. M. and Acton, R. T.: Associations of Properdin factor B with melanoma. Cancer Genetics and Cytogenetics 5:247-251, 1982.

9.Budowle, B., Acton, R. T., Barger, B. O., Blackstock, R., Crist, W., Go, R. C. P., Humphrey, G., Ragab, A., Roper, M., Vietti, T. and Dearth, J.: Properdin factor B and acute lymphocytic leukemia (ALL). Cancer 50: 2369-2371, 1982.

10. Acton, R. T., Balch, C. M., Barger, B. O., Budowle, B., Go, R. C. P., Soong, S-J., and Roseman, J. M.: The occurrence of melanoma and its relationship with host, lifestyle and environmental factors. In: <u>Melanoma-1</u> (Constanzi, J. J., ed.), Martinus Nijhoff Publishers, The Hague, pp. 151-182, 1983.

11. Budowle, B., Go, R. C. P., Roseman, J. M., Barger, B. O. and Acton, R. T.: C4 phenotypes in Caucasians from the southeastern United States. In: Electrophoresis '82 (Stathakos, D., ed.), Walter de Gruyter, Berlin, pp. 715-723, 1982.

12. Budowle, B., Roseman, J. M., Go, R. C. P., Crist, W. and Dearth, J.: Complement phenotypes for prediction of risk and prognosis for acute lymphocytic leukemia (ALL). In: <u>Cancer: Etiology and Prevention</u> (Crispen, R. G., ed.) Elsevier Biomedical, New York, pp. 109-123, 1983.

13. Budowle, B., Roseman, J. M., Go, R. C. P., Louv, W. C., Barger, B. O. and Acton, R. T.: Phenotypes of the fourth complement component (C4) in black Americans from the southeastern United States. J. Immunogenetics 10 (3):199-204, 1983.

14. Budowle, B., Louv, W. C., Barger, B. O., Go, R. C. P., Roseman, J. M. and Acton, R. T.: Age at onset of insulin-dependent diabetes mellitus associated with BfF1. Immunogenetics 17:437-440, 1983.

15. Budowle, B., Dearth, J., Bowman, P., Melvin, S., Crist, W., Go, R., Kim, T., Iyer, R. J., Roseman, J., Barger, B., and Acton, R.: Genetic predisposition to acute lymphocytic leukemia in American Blacks. Cancer 55:2880-2882, 1985.

16. Budowle, B., Roseman, J. M., Go, R. C. P., Barger, B. and, Acton, R. T.: The complement component C4 in black Americans with type 1 (insulindependent) diabetes mellitus. Diabetologia 26:166-168, 1984.

17. Budowle, B.: A method to increase the volume of sample applied to isoelectric focusing (IEF) gels. Forens. Sci. Int. 24(4):273-277, 1984.

18. Budowle, B.: A reproducible method for dialysis of multiple small volume samples. BioTechniques 1(4):176-177, 1983.

19. Budowle, B.: Increasing the sensitivity of detection of group-specific component in agarose gels by double-staining with coomassie brilliant blue R250 and silver. J. Forens. Sci. 29(4):1183-1186, 1984.

20. Budowle, B. and Gambel, A.: An alternative gel system for group III gels. Crime Lab Digest 11 (1):12-13, 1984.

21. Budowle, B.: Increasing the sensitivity of protein detection of a silver stain for agarose gels. Electrophoresis 5(3):174-175, 1984.

22. Budowle, B.: Phosphoglucomutase-1 subtyping of human bloodstains on ultrathin-layer polyacrylamide gels. Electrophoresis 5(3):165-167, 1984.

23. Budowle, B.: An ultrathin-layer polyacrylamide gel isoelectric focusing method for transferrin subtyping. Electrophoresis 6(2):97-99, 1985.

24. Budowle, B.: Rapid electrofocusing of erythrocyte acid phosphatase. Electrophoresis 5(4):254-255, 1984.

25. Budowle, B.: Typing esterase D by isoelectric focusing. Electrophoresis 5(5):314-316, 1984.

26. Budowle, B. and Davidson, L.: Electrophoresis: The theory and evolution of electrophoretic methods. Crime Lab Digest 11 (3): 45-50, 1984.

27. Budowle, B. and Chow, G. H.: Discontinuous polyacrylamide gel electrophoresis for typing haptoglobin in bloodstains. J. Forens. Sci. 30(3):893-897, 1985.

28. Budowle, B. and Scott, E.: Transferrin subtyping of human bloodstains. Forens. Sci. Int. 28:269-275, 1985.

29. Budowle, B.: An agarose gel method for typing phosphoglucomutase-1, esterase D or glyoxalase I. J. Forens. Sci. 30(4):1216-1220, 1985.

30. Budowle, B., Sundaram, S. and Wenk, R.: Population data on the forensic genetic markers: phosphoglucomutase-1, esterase D, erythrocyte acid phosphatase and glyoxalase I. Forens. Sci. Int. 28:77-81, 1985.

31. Budowle, B.: A rapid method for subtyping phosphoglucomutase-1. BioTechniques 3(2):92-93, 1985.

32. Murch, R. and Budowle, B.: Applications of isoelectric focusing in forensic serology. J. Forens. Sci. 31(3):869-880, 1986.

33. Budowle, B.: Subtyping group-specific component or esterase D using the same ultrathin-layer polyacrylamide gel format. Electrophoresis 7:141-144, 1986.

34. Budowle, B. and Murch, R.: A high resolution, rapid procedure for alpha 1-antitrypsin typing. Electrophoresis 6(10):523-525, 1985.

35. Budowle, B.: Principles of isoelectric focusing. In: Proceedings of the International Symposium on the Forensic Application of Electrophoresis, Government Printing Office, Washington, D. C., pp. 121-126, 1984.

36. Budowle, B. and Davidson, L.: Selecting genetic markers for analysis of forcibly removed hairs. In: Proceedings of the International Symposium on Forensic Hair Comparisons. Government Printing Office, Washington, D.C., pp. 89-93, 1985.

37. Budowle, B. and Eberhardt, P.: Ultrathin-layer polyacrylamide gel isoelectric focusing for the identification of hemoglobin variants. Hemoglobin 10(2):161-172, 1986.

38. Budowle, B., Murch, R. S., Davidson, L. C., Gambel, A. M. and Kearney, J. J.: Subtyping phosphoglucomutase-1 in semen stains and bloodstains: A report on the method. J. Forens. Sci. 31(4):1341-1348, 1986.

39. Budowle, B.: A method for subtyping group-specific component in bloodstains. Forens. Sci. Int. 33(3):187-196, 1987.

40. Gambel, A., Budowle, B., and Terrell, L.: Glyoxalase I typing and phosphoglucomutase-1 subtyping of a single hair. J. Forens. Sci. 32(5):1175-1181, 1987.

41. Budowle, B.: Making ultrathin-layer polyacrylamide gel isoelectric focusing a reproducible methodology. In: Proceedings of the 1986 Meeting of the Americas Branch of the Electrophoresis Society. National Bureau of Standards, pp. 1-12, 1986.

42. Budowle, B. and Murch, R. S.: Applications of isoelectric focusing in forensic serology. II. In: New Directions in Electrophoretic Methods (Jorgenson, J. and Phillips, M., eds.), ACS Symposium Series 335, pp. 143-157, 1987.

43. Budowle, B. and Mudd, J. L.: An aluminum template for casting agarose gels. J. Forens. Sci. 32(3):784-787, 1987.

44. Budowle, B. and Gambel, A.: Negative gold staining for electrophoretic protein profile interpretations. Acta Histochemica et Cytochemica 19(5):647-654, 1986.

45. Allen, R. C., Budowle, B., Lack, P. M. and Graves, G.: Rehydrated polyacrylamide gels: A comparison with conventionally cast gels. In: Electrophoresis 86 (Dunn, M., ed.), VCH, Weinheim, pp. 462-473, 1986.

46. Allen, R. C., Budowle, B., Saravis, C. A. and Lack, P. M.: Enzyme and antibody detection following isoelectric focusing on ultrathin-layer rehydrated polyacrylamide gels. Acta Histochemica et Cytochemica 19(5):637-645, 1986.

47. Alexander, L. A., Reeder, D. J. and Budowle, B.: A method for routinely producing high resolution black and white journal quality photographs of electrophoretic gels. J. Forens. Sci. 32(5):1331-1341, 1987.

48. Budowle, B.: Improved separation of the common transferrin variants in gels containing pH 5-7 ampholines and HEPES. Electrophoresis 8(4):210-212, 1987.

49. Budowle, B. and Allen, R.C.: Electrophoresis Reliability. I. The contaminant issue. J. Forens. Sci. 32(6):1537-1550, 1987.

50. Budowle, B. and Gambel, A. M.: An alternative effective substrate for erythrocyte acid phosphatase phenotype determinations. J. Forens. Sci. 33(4):915-920, 1988.

51. Budowle, B. and Gambel, A. M.: A hybrid ampholyte focusing technique for esterase D subtyping of evidentiary material. J. Forens. Sci. 33(3):738-743, 1988.

52. Budowle, B., Huddleston, J. F., Go, R. C. P., Barger, B. O., and Acton, R. T.: Association of HLA-linked Factor B with gestational diabetes mellitus in Black women. Amer. J. Obstet. Gyn. 159(4):805-806, 1988.

53. Budowle, B., Deadman, H. A., Murch, R. S. and Baechtel, F. S.: An introduction to the methods of DNA analysis under investigation in the FBI Laboratory. Crime Laboratory Digest 15(1):8-21, 1988.

54. Budowle, B., Adams, D.E., Comey, C.C., and Merril, C.R.: Mitochondrial DNA: A possible genetic material suitable for forensic analysis. In: Advances in Forensic Science (Lee, H.C. and Gaensslen, R.E., eds.), Year Book Medical Publishers, Chicago, pp. 76-97, 1990.

55. Budowle, B., Adams, D.E., and Allen, R.C.: Fragment length polymorphisms for forensic science applications. In: Methods in Nucleic Acids (Karam, J., Chao, L., and Warr, G., eds.), CRC Press, Boca Raton, Florida, pp. 181-202, 1991.

56. Budowle, B.: The RFLP technique. Crime Laboratory Digest 15(4):97-98, 1988.

57. Budowle, B. and Baechtel, F.S.: Modifications to improve the effectiveness of restriction fragment length polymorphism typing. Appl. Theor. Electrophoresis 1:181-187, 1990.

58. Allen, R.C., Graves, G. and Budowle, B.: Polymerase chain reaction amplification products separated on rehydratable polyacrylamide gels and stained with silver. BioTechniques 7(7):736-744, 1989.

59. Budowle, B., Waye, J.S., Shutler, G.G., and Baechtel, F.S.: Hae III - a suitable restriction endonuclease for restriction fragment length polymorphism analysis of biological evidence samples. J. Forens. Sci. 35(3): 530-536, 1990.

60. Waye, J.S., Presley, L., Budowle, B., Shutler, G.G., and Fourney, R.M.: A simple method for quantifying human genomic DNA in forensic specimen extracts. BioTechniques 7(8):852-855, 1989.

61. Budowle, B., Baechtel, F.S., Giusti, A.M., and Monson, K.L.: Applying highly polymorphic VNTR loci genetic markers to identity testing. Clinical Biochemistry 23: 287-293, 1990.

62. Budowle, B., Baechtel, F.S., and Adams, D.E.: Validation with regard to environmental insults of the RFLP procedure for forensic purposes. In: Forensic DNA Technology, (Farley, M. and Harrington, J., eds.) Lewis Publishers, Inc., Boca Raton, Florida, pp. 83-91, 1991.

63. Monson, K.L. and Budowle, B.: A system for semi-automated analysis of DNA autoradiograms. In: Proceedings of the International Symposium on the Forensic Aspects of DNA Analysis, Government Printing Office, Washington, D.C., pp. 127-132, 1989.

64. Budowle, B. and Monson, K.L.: A statistical approach for VNTR analysis. In: Proceedings of the International Symposium on the Forensic Aspects of DNA Analysis, Government Printing Office, Washington, D.C., pp. 121-126, 1989.

65. Budowle, B.: A protocol for RFLP analysis of forensic biospecimens. In: Proceedings of an International Symposium on the Forensic Aspects of DNA Analysis, Government Printing Office, Washington, D.C., pp. 57-62, 1989.

66. Budowle, B., Giusti, A.M., and Allen, R.C.: Analysis of PCR products (pMCT118) by polyacrylamide gel electrophoresis. In: Advances in Forensic Haemogenetics 3, (Polesky, H. F. and Mayr, W. R., eds.), Springer-Verlag, Heidelberg, pp. 148 - 150, 1990.

67. Budowle, B. and Allen, R.C.: Discontinuous polyacrylamide gel electrophoresis of DNA fragments. In: Methods in Molecular Biology -Protocols in Human Molecular Genetics, Vol. 9 (Mathew, C., ed.), Humana Press Inc., Clifton, New Jersey, pp. 123-132, 1991.

68. Acton, R.T., Harmon, L., Go. R.C.P., and Budowle, B.: Comparison of VNTR allele frequencies in white and black populations. In: Proceedings for the International Symposium on Human Identification 1989, Promega Corporation, Madison, Wisconsin, pp. 5-20, 1990.

69. Budowle, B., Baechtel, F.S., Giusti, A.M., and Monson, K.L.: Data for forensic matching criteria for VNTR profiles. In: Proceedings for the International Symposium on Human Identification 1989, Promega Corporation, Madison, Wisconsin, pp. 103-115, 1990.

70. Budowle, B., Giusti, A.M., Waye, J.S., Baechtel, F.S., Fourney, R.M., Adams, D.E., Presley, L.A., Deadman, H.A., and Monson, K.L.: Fixed bin analysis for statistical evaluation of continuous distributions of allelic data from VNTR loci for use in forensic comparisons. Amer. J. Hum. Genet. 48:841-855, 1991.

71. Budowle, B., Chakraborty, R., Giusti, A.M., Eisenberg, A.J., and Allen, R.C.: Analysis of the variable number of tandem repeats locus D1S80 by the polymerase chain reaction followed by high resolution polyacrylamide gel electrophoresis. Amer. J. Hum. Genet. 48:137-144, 1991.

72. Sajantila, A., Strom, M., Budowle, B., Tienari, P.J., Ehnholm, C., and Peltonen, L.: The distribution of the HLA-DQ $\alpha$  alleles and genotypes in the Finnish population as determined by the use of DNA amplification and allele specific oligonucleotides. Int. J. Leg. Med. 104: 181-184, 1991.

73. Comey, C.T., Jung, J.M., and Budowle, B.: Use of formamide to improve PCR amplification of HLA-DQ sequences. BioTechniques 10(1):60-61, 1991.

74. Jung, J.M., Comey, C.T., Baer, D.B., and Budowle, B.: Extraction strategy for obtaining DNA from bloodstains for PCR amplification and typing of the HLA-DQ gene. Int. J. Leg. Med. 104(3):145-148, 1991.

75. Budowle, B., Comey, C.T., Jung, J.M., and Giusti, A.M.: Research regarding the polymerase chain reaction for forensic utility - HLA-DQα locus and AMP-FLPs. In: DNA-Technology and Its Forensic Application, (G. Berghaus, B. Brinkmann, C. Rittner, and M. Staak, eds.), Springer-Verlag, Berlin, pp. 71-78, 1991.

76. Budowle, B., Monson, K.L., Anoe, K., Baechtel, F.S., Bergman, D., et al.: A preliminary report on binned general population data on six VNTR loci in Caucasians, Blacks, and Hispanics from the United States. Crime Laboratory Digest 18(1): 9-26, 1991.

77. Hochmeister, M., Budowle, B., and Baechtel, F.S.: Effects of presumptive test reagents on the ability to obtain RFLP patterns from human blood and semen stains. J. Forens. Sci. 36(3): 656-661, 1991.

78. Adams, D.E., Presley, L.A., Baumstark, A.L., Hensley, K.W., Hill, A.L., Anoe, K.S., Campbell, P.A., Mclaughlin, C.M., Budowle, B., Giusti, A.M., Smerick, J.B., and Baechtel, F.S.: DNA analysis by restriction fragment length polymorphisms of blood and other body fluid stains subjected to contamination and environmental insults. J. Forens. Sci. 36(5): 1284-1298, 1991.

79. Hochmeister, M.N., Budowle, B., Borer, U.V., Eggmann, U.T., Comey, C.T., and Dirnhofer, R.: Typing of DNA extracted from compact bone tissue from human remains. J. Forens. Sci. 36 (6): 1649-1661, 1991.

80. Comey, C.T. and Budowle, B.: Validation studies on the analysis of the HLA-DQalpha locus using the polymerase chain reaction. J. Forens. Sci. 36 (6): 1633-1648, 1991.

81. Sajantila, A., Strom, M., Budowle, B., Karhunen, P.J., and Peltonen, L.: The polymerase chain reaction and post-mortem forensic identity testing: application of amplified D1S80 and HLA-DQalpha loci to the identification of fire victims. Forens. Sci. Int. 51 (1): 23-34, 1991.

82. Hochmeister, M.N., Budowle, B., Jung, J., Borer, U.V., Comey, C.T., and Dirnhofer, R.: PCR-based typing of DNA extracted from cigarette butts. Int. J. Legal Med. 104: 229-233, 1991.

83. Chakraborty, R., de Andrade, M., Daiger, S.P., and Budowle, B.: Apparent heterozygote deficiencies observed in DNA typing data and their implications in forensic applications. Annals of Human Genetics 56: 45-57, 1992.

84. Budowle, B. and Stafford, J.: Response to expert report by D.L. Hartl submitted in the case of United States versus Yee. Crime Laboratory Digest 18(3): 101-108, 1991.

85. Budowle, B. and Stafford, J.: Response to "population genetic problems in the forensic use of DNA profiles" by R.C. Lewontin submitted in the case of United States versus Yee. Crime Laboratory Digest 18(3): 109-112, 1991.

86. Giusti, A.M. and Budowle, B.: The effect of storage conditions on RFLP analysis of DNA bound to positively charged nylon membranes. J. Forens. Sci. 37(2): 597-603, 1992.

87. Sajantila, A., Budowle, B., Strom, M., Johnsson, V., Lukka, M., Peltonen, L, and Ehnholm, C.: PCR amplification of alleles at the D1S80 locus: Comparison of a Finnish and a North American Caucasian population sample, and forensic case-work evaluation. Am. J. Hum. Genet. 50(4): 816-825, 1992.

88. Budowle, B., Baechtel, F.S., and Comey, C.T.: Some considerations for use of AMP-FLPs for identity testing. In: Advances in Forensic Haemogenetics 4 (C. Rittner and P.M. Schneider, eds.), Springer-Verlag, Berlin, pp. 11-17, 1992.

89. Comey, C.T., Baechtel, F.S., Alevy, M.C., Parson, G.L., Wilson, M., and Budowle, B.: Analysis by PCR of VNTR loci. In: New Technologies, Standardization of Methods and Data Sharing for DNA Typing Laboratories. Proceedings from The Second International Symposium on Human Identification 1991, Promega Corporation, Madison, Wisconsin, pp. 53-61, 1991.

90. Robertson, J., Ziegle, J., Kronick, M., Madden, D., and Budowle, B.: Genetic typing using automated electrophoresis and fluorescent detection. In: DNA Fingerprinting Approaches and Application, (T. Burke, G. Doff, A.J. Jeffreys, and R. Wolff, eds.), Birkhauser Verlag, Basel, pp. 391-398, 1991.

91. Baechtel, F.S., Monson, K.L., Forsen, G.E., Budowle, B., and Kearney, J.J.: Tracking the violent criminal offender through DNA typing profiles - a national database system concept. In: DNA Fingerprinting Approaches and Applications, (T. Burke, G. Doff, A.J. Jeffreys, and R. Wolff, eds.), Birkhauser Verlag, Basel, pp. 356-360, 1991.

92. Sajantila, A. and Budowle, B.: Identification of individuals with DNA testing. Annals of Medicine 23(6): 637-642, 1991.

93. Budowle, B., Sajantila, A., Hochmeister, M.N., and Comey, C.T.: The application of PCR to forensic science. In: The Polymerase Chain Reaction, (F. Ferre, K. Mullis, and R. Gibbs, eds.), Birkhauser Verlag, Boston, pp. 244-256, 1994.

94. Budowle, B., Monson, K.L., and Wooley, J.R.: The reliability of statistical estimates in forensic DNA typing. In: DNA Identification (Billings, P.R., ed.), Cold Spring Harbor Press, New York, pp. 79-90, 1992.

95. Robertson, J., Schaefer, T., Kronick, K., and Budowle, B.: Automated analysis of fluorescent amplified fragment length polymorphisms for DNA typing. In: Advances in Forensic Haemogenetics 4 (C. Rittner and P.M. Schneider, eds.), Springer-Verlag, Berlin, pp. 35-37, 1992.

96. Comey, C.T., Budowle, B., Adams, D.E., Baumstark, A.L., Lindsey, J.A., and Presley, L.A.: PCR amplification and typing of the HLA-DQα gene in forensic samples. J. Forens. Sci. 38(2): 239-249, 1993.

97. Budowle, B. and Monson, K.L.: Perspectives on the fixed bin method and the floor approach/ceiling principle. In: Proceedings from the Third International Symposium on Human Identification 1992, Promega Corporation, Madison, Wisconsin, pp. 391-406, 1992.

98. Hochmeister, M.N., Budowle, B., Borer, U., and Dirnhofer, R.: Effects of nonoxinol-9 on the ability to obtain DNA profiles from postcoital vaginal swabs. J. Forens. Sci. 38(2): 442-447, 1993.

99. Rand, S., Puers, C., Skowasch, K., Wiegand, P., Budowle, B., and Brinkmann, B.: Population genetics and forensic efficiency data of four AMPFLPs. Int. J. Leg. Med. 104: 329-333, 1992.

100. Allen, R.C., Budowle, B., and Reeder, D.J.: Resolution of DNA in the presence of mobility modifying polar and non-polar compounds by discontinuous electrophoresis on rehydratable polyacrylamide gels. Appl. Theor. Electrophoresis 3(3/4): 173-181, 1993.

101. Budowle, B., Comey, C.T., and Baechtel, F.S.: Forensic Analysis. In: DNA Probes (G.H. Keller and M.M. Manak, eds.), Macmillan Publishers, Basingstoke, England, pp. 617-640, 1993.

102. Budowle, B. and Monson, K.L.: The approach used by the FBI for calculating ceiling frequencies. Crime Laboratory Digest 19(3): 84-94, 1992.

103. Wiegand, P., Budowle, B., Rand, S., and Brinkmann, B.: Forensic validation of the STR systems SE 33 and TC 11. Int. J. Leg. Med. 105 (6): 315-320, 1993.

104. Presley, L.A., Lindsey, J.A., Baumstark, A., Dixon, A., Comey, C.T., and Budowle, B.: The implementation of polymerase chain reaction (PCR) HLA DQ alpha typing by the FBI Laboratory. In: Proceedings from the Third International Symposium on Human Identification 1992, Promega Corporation, Madison, Wisconsin, pp. 245-269, 1992.

105. Kloosterman, A.D., Daselaar, P., Budowle, B., and Riley, E.L.: Population genetic study on the HLA DQ $\alpha$  and the D1S80 locus in Dutch Caucasians. In: Proceedings from the Third International Symposium on Human Identification 1992, Promega Corporation, Madison, Wisconsin, pp. 329-344, 1992.

106. Kloosterman, A.D., Budowle, B., and Daselaar, P.: PCR-amplification and detection of the human D1S80 VNTR locus: Amplification conditions, population genetics, and application in forensic analysis. Int. J. Leg. Med. 105: 257-264, 1993.

107. Kloosterman, A.D., Budowle, B., and Riley, E.L.: Population data of the HLA  $DQ\alpha$  locus in Dutch Caucasians: Comparison with seven other population studies. Int. J. Leg. Med. 105(4): 233-238, 1993.

108. Monson, K.L. and Budowle, B.: A comparison of the fixed bin method to the floating bin and direct count methods: Effect of VNTR profile frequency estimation and reference population. J. Forens. Sci. 38: 1037-1050, 1993.

109. Budowle, B., Monson, K.L., Giusti, A.M., and Brown, B.: The assessment of frequency estimates of Hae III-generated VNTR profiles in various reference databases. J. Forens. Sci. 39:319-352, 1994.

110. Budowle, B., Monson, K.L., Giusti, A.M., and Brown, B.: Evaluation of Hinf I-generated VNTR profile frequencies determined using various ethnic databases. J. Forens. Sci. 39:988-1008, 1994.

111. Elliot, J.C., Budowle, B., Aubin, R.A., and Fourney, R.M.: Quantitative reproduction of DNA typing minisatellites resolved on ultra-thin silverstained polyacrylamide gels with X-ray duplicating film. BioTechniques 14 (5): 702-704, 1993.

112. Chakraborty, R., Jin, L., Zhong, Y., Srinivasan, M.R., and Budowle, B.: On allele frequency computation from DNA typing data. Int. J. Leg. Med. 106: 103-106, 1993.

113. Baechtel, F.S., Smerick, J.B., Presley, K.W., and Budowle, B.: Multigenerational amplification of a reference ladder for alleles at locus D1S80. J. Forens. Sci. 38 (5): 1176-1182, 1993.

114. Sajantila, A., Pacek, P., Lukka, M., Syvanen, A-C., Noikelainen, Sistonen, P., Peltonen, L., and Budowle B.: A microsatellite polymorphism in von Willebrand Factor gene: comparison of allele frequencies in different population samples and evaluation for forensic medicine. Forens. Sci. Int. 68: 91-102, 1994.

115. Budowle, B. and Monson, K.L.: The forensic significance of various reference population databases for estimating the rarity of variable number of tandem repeat (VNTR) loci profiles. In: DNA Fingerprinting: State of the Science, (D.J. Pena, R. Chakraborty, J.T. Epplen, and A.J. Jeffreys, eds.), Berkhauser Verlag, Basel, Switzerland, pp. 177-191, 1993.

116. Budowle, B., Monson, K.L., and Giusti, A.M.: A reassessment of frequency estimates of Pvu II-generated VNTR profiles in a Finnish, an Italian, and a general United States Caucasian database: No evidence for ethnic subgroups affecting forensic estimates. Amer. J. Hum. Genet. 55:533-539, 1994.

117. Replogle, J., Lord, W.D., Budowle, B., Meinking, T.L., and Taplin, D.: Identification of host DNA by amplified fragment length polymorphism analysis: Preliminary analysis of human crab louse (*Anoplura Pediculidae*) excreta. J. Med. Entomol. 31: 686-690, 1994.

118. Budowle, B. and Monson, K.L.: A perspective on the polemic on DNA statistical inferences in forensics. In: Fourth International Symposium on Human Identification 1993, Promega Corporation, Madison, Wisconsin, pp. 1-10, 1993.

119. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva, E.: Sequence multiplex amplification of genetic markers from an individual sample. In: Fourth International Symposium on Human Identification 1993, Promega Corporation, Madison, Wisconsin, pp. 173-175, 1993.

120. Allen, R.C. and Budowle, B.: The use of the polymerase chain reaction and the detection of amplified products. In: PCR Protocols: Current Methods and Applications, Methods in Molecular Biology, Vol. 15, (B.A. White, ed.), Humana Press, Inc., Totawa, New Jersey, pp. 113-128, 1993.

121. Presley, L.A. and Budowle, B.: The application of polymerase chain reaction (PCR) based technologies to forensic analyses. In: PCR Technology: Current Innovations, Griffin, H.G. and Griffin, A.M. (eds.), CRC Press, Inc., Boca Raton, Florida, pp. 259-276, 1994.

122. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva, E.: Composite PAGE: an alternate method for increased separation of amplified short tandem repeat alleles. Int. J. Leg. Med. 106: 69-73, 1993.

123. Budowle, B., Klevan, L., and Eisenberg, A.J.: RFLP typing: a new highly polymorphic VNTR locus and chemiluminescent detection. In: Advances in Forensic Haemogenetics 5, Bar, W., Fiori, A., and Rossi, U. (eds.), Springer-Verlag, Berlin, pp. 245-252, 1994.

124. Lorente, J.A., Lorente, M., Budowle, B., Wilson, M.R., and Villanueva, E.: Analysis of HUMTH01 allele frequencies in the Spanish population. J. Forens. Sci. 39 (5): 1270-1274, 1994.

125. Chakraborty, R., Zhong, Y., Jin, L., and Budowle, B.: Nondetectability of restriction fragments and independence of DNA fragment sizes within and between loci in RFLP typing of DNA. Amer. J. Hum. Genet. 55: 391-401, 1994.

126. Haas, H., Budowle, B., and Weiller, G.: Horizontal polyacrylamide gel electrophoresis (PAGE) for the separation of DNA fragments. Electrophoresis 15: 153-158, 1994.

127. Hochmeister, M.N., Budowle, B., Borer, U.V., and Dirnhofer, R.: Swiss population data on the loci HLA-DQ $\alpha$ , LDLR, GYPA, HBGG, D7S8, Gc, and D1S80. Forens. Sci. Int. 67(3): 175-184, 1994.

128. Wilson, M.R., Holland, M.M., Stoneking, M., DiZinno, J.A., and Budowle, B.: Guidelines for the use of mitochondrial DNA sequencing in forensic science. Crime Lab. Dig. 20(4): 68-77, 1994.

129. Budowle, B. and Monson, K.L.: Greater differences in forensic DNA profile frequencies estimated from racial groups than from ethnic subgroups. Clinica Chimica Acta 228: 3-18, 1994.

130. Hochmeister, M.N., Jung, M.M., Budowle, B., Borer, U.V., and Dirnhofer, R.: Swiss population data on three tetrameric short tandem repeat loci - vWA, HUMTH01, and F13A1 - derived using multiplex PCR and laser fluorescence detection. Int. J. Leg. Med. 107: 34-36, 1994.

131. Budowle, B., Baechtel, F.S., Smerick, J.B., Presley, K.W., Giusti, A.M., Parsons, G., Alevy, M., and Chakraborty, R.: D1S80 population data in African Americans, Caucasians, Southeastern Hispanics, Southwestern Hispanics, and Orientals. J. Forens. Sci. 40(1): 38-44, 1995.

132. Lorente, J.A., Lorente, M., Budowle, B., Wilson, M.R., and Villanueva, E.: Analysis of the short tandem repeat (STR) HUMVWA in the Spanish population. Forens. Sci. Int. 65(3): 169-175, 1994.

133. Huang, N.E. and Budowle, B.: Chinese population data on the PCR-based loci HLA-DQa, LDLR, GYPA, HBGG, D7S8, and Gc. Human Heredity 45:34-40, 1995.

134. Butler, J.M., McCord, B.R., Jung, J.M., Wilson, M. R., Budowle, B., and Allen, R.O.: Quantification of polymerase chain reaction products by capillary electrophoresis using laser fluorescence. J. Chromatography B 658:271-280, 1994.

135. Budowle, B., Lindsey, J.A., DeCou, J.A., Koons, B.W., Giusti, A.M., and Comey, C.T.: Validation and population studies of the loci LDLR, GYPA, HBGG, D7S8, and Gc (PM loci), and HLA-DQ $\alpha$  using a multiplex amplification and typing procedure. J. Forens. Sci. 40(1):45-54, 1995.

136. Budowle, B. and Giusti, A.M.: Fixed Bin Frequency Distributions for the VNTR Locus D5S110 in General United States Reference Databases. J. Forens. Sci. 40: 236-238, 1995.

137. Monson, K.L., Moisan, J.P., Pascal, O., McSween, M., Aubert, D., Giusti, A., Budowle, B., and Lavergne, L.: Description and analysis of allele distribution for four VNTR markers in French and French Canadian populations. Human Heredity 45: 135-143, 1995.

138. Huang, N.E., Chakraborty, R., and Budowle, B.: D1S80 allele frequencies in a Chinese population. Int. J. Leg. Med. 107: 118-120, 1994.

139. Huang, N.E. and Budowle, B.: Fixed bin population data for the VNTR loci D1S7, D2S44, D4S139, D5S110, and D17S79 in Chinese from Taiwan. J. Forens Sci. 40: 287-290, 1995.

140. Huang, N.E., Schumm, J., and Budowle, B.: Chinese Population Data on Three Tetrameric Short Tandem Repeat Loci - HUMTH01, TPOX, AND CSF1PO -Derived Using Multiplex PCR and Manual Typing. Forens. Sci. Int. 71: 131-136, 1995.

141. Budowle, B.: The effects of inbreeding on DNA profile frequency estimates using PCR-based loci. Genetica 96: 21-25, 1995.

142. Budowle, B.: Finns and Italians as categorical support for population substructure, the effects of inbreeding, and the probability of innocence - are these real concerns regarding DNA forensic statistics? In: Fifth International Symposium on Human Identification 1994, Promega Corporation, Madison, Wisconsin, PP. 43-48, 1995.

143. Hochmeister, M.N., Budowle, B., Borer, U.V., and Dirnhofer, R.: A method for the purification and recovery of genomic DNA from an HLA DQA1 amplification product and its subsequent amplification and typing with the Amplitype PM PCR Amplification and Typing Kit. J. Forens. Sci. 40(4): 649-653, 1995.

144. Hochmeister, M.N., Budowle, B., Borer, U.V., Rudin, O., Bohnert, M., and Dirnhofer, R.: Confirmation of the identity of human skeletal remains using multiplex PCR amplification and typing kits. J. Forens. Sci. 40(4): 701-705, 1995.

145. Hochmeister, M.N., Budowle, B., Borer, U.V., and Dirnhofer, R.: Swiss population data on three tetrameric short tandem repeat loci - HUMTH01, TPOX, CSF1PO - derived using the GenePrint Triplex PCR Amplification Kit. Int. J. Leg. Med. 107(5): 246-249, 1995.

146. Lander, E.S. and Budowle, B.: DNA fingerprinting controversy laid to rest. Nature 371: 735-738, 1994.

147. Woo, K.M. and Budowle, B.: Korean population data on the PCR-based loci LDLR, GYPA, HBGG, D7S8, Gc, HLA-DQA1, and D1S80. J. Forens. Sci. 40(4): 645-648, 1995.

148. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva, E.: Sequential multiplex amplification (SMA) of genetic loci: a method for recovery template DNA for subsequent analyses of additional loci. Int. J. Leg. Med. 107:156-158, 1994.

149. Budowle, B., Baechtel, F.S., Comey, C.T., Giusti, A.M., and Klevan, L.: Simple protocols for typing forensic biological evidence: chemiluminescent detection for human DNA quantitation and RFLP analyses and manual typing of PCR amplified polymorphisms. Electrophoresis 16(9):1559-1567, 1995.

150. Hayes, J.M., Budowle, B., and Freund, M.: Arab population data on the PCR-based loci: HLA-DQA1, LDLR, GYPA, HBGG, D7S8, Gc, and D1S80. J. Forens. Sci. 40:888-892, 1995.

151. Wilson, M.R., Polanskey, D., Butler, J., DiZinno, J.A., Replogle, J., and Budowle, B.: Extraction, PCR amplification, and sequencing of mitochondrial DNA from human hair shafts. BioTechniques 18:662-669, 1995.

152. Scholl, S., Budowle, B., Radecki, K., and Salvo, M.: Navajo, Pueblo, and Sioux population data on the loci HLA-DQA1, LDLR, GYPA, HBGG, D7S8, Gc, and D1S80. J. Forens. Sci. 41:47-51, 1996.

153. Gutowski, S., Budowle, B., Auer, J., and van Oorschot, R.: Statistical analysis of an Australian population for the loci Gc, HLA-DQA1, D1S80, and HUMTHO1. Forens. Sci. Int. 76:1-6, 1995.

154. Giusti, A.M. and Budowle, B.: Chemiluminescence-based detection system for human DNA quantitation and restriction fragment length polymorphism (RFLP) analysis. Applied and Theoretical Electrophoresis 5: 89-98, 1995.

155. Hochmeister, M.N., Budowle, B., Eisenberg, A., Borer, U.V., and Dirnhofer, R.: Using multiplex PCR amplification and typing kits for the analysis of DNA evidence in a serial killer case. J. Forens. Sci. 41:155-162, 1996.

156. Sovinski, S.M., Baird, L.S., Budowle, B., Caruso, J.F., Davender, P.S., Cheema, M.S., Duncan, G.T., Hamby, P.P., Masibay, A.S., Sharma, V.J., and Tahir, M.A.: The development of a deoxyribonucleic acid (DNA) restriction fragment length polymorphism (RFLP) database for Punjabis in East Punjab, India. Forens. Sci. Int. 79:187-198, 1996.

157. Butler, J.M., McCord, B.R., Jung, J.M., Lee, J.A., Budowle, B., and Allen, R.O.: Application of dual internal standards for precise sizing of polymerase chain reaction products using capillary electrophoresis. Electrophoresis 16:974-980, 1995.

158. Martin, P., Alonso, A., Budowle, B., Albarran, C., Garcia, O., and Sancho, M.: Spanish population data on seven tetrameric short tandem repeat loci. Int. J. Leg. Med. 108 (3):145-149, 1995.

159. Budowle, B., Monson, K.L., and Chakraborty, R.: Estimating minimum allele frequencies for DNA profile frequency estimates for PCR-based loci. Int. J. Leg. Med. 108:173-176, 1996.

160. Wilson, M.R., DiZinno, J.A., Polanskey, D., Replogle, J., and Budowle, B.: Validation of mitochondrial DNA sequencing for forensic casework analysis. Int. Journal Leg. Med. 108:68-74, 1995.

161. Budowle, B., Koons, B.W., and Errera, J.D.: Multiplex Amplification and Typing Procedure for the Loci D1S80 and Amelogenin. J. Forens. Sci. 41:660-663, 1996.

162. Budowle, B., Woller, J., Koons, B.W., Furedi, S., Errera, J.D., and Padar, Z.: Hungarian population data on seven PCR-based loci. J. Forens. Sci. 41:667-670, 1996.

163. Kirby, L.T., Fourney, R.M., and Budowle, B.: DNA fingerprinting analysis. In: Molecular Biology and Biotechnology, A Comprehensive Desk Reference, Meyers, R.A. (eds.), VCH, New York, New York, pp. 219-224, 1995.

164. Comey, C.T. and Budowle, B.: Approaches to genetic analyses: Forensics. In: Nucleic Acid Analysis: Principles and Bioapplications, Dangler, C. A. (ed,), Wiley-Liss, Inc., New York, pp. 79-104, 1996.

165. Budowle, B., Koons, B.W., Keys, K.M., and Smerick, J.B.: Methods for typing the STR triplex CSF1PO, TPOX, and HUMTH01 that enable compatibility among DNA typing laboratories. In: Advances in Forensic Haemogenetics 6, (eds. A. Carracedo, B. Brinkmann, and W. Bar), Springer-Verlag, Berlin, pp 107-114, 1996.

166. Martin, P., Alonso, A., Budowle, B., Albarran, C., Garcia, O., and Sancho, M.: Spanish population data on 13 PCR-based systems. In: Advances in Forensic Haemogenetics 6, (eds.), Springer-Verlag, Berlin, pp. 578-580, 1996.

167. Garcia, O., Martin, P., Budowle, B., Albarran, C., and Alonso, A.: Allele frequencies of HLA-DQ $\alpha$ , LDLR, GYPA, HBGG, D7S8, and Gc in the resident and autochthonous populations of the Basque country. In: Advances in Forensic Haemogenetics 6, (eds.), Springer-Verlag, Berlin, pp. 532-534, 1996.

168. Penacino, G., Smerick, J., Perez Calvo, J., Baechtel, F.S., Budowle, B., and Corach, D.: D1S80 AMP-FLP attributes in two different ethnic groups of Argentinean populations. In: Advances in Forensic Haemogenetics 6, (eds.), Springer-Verlag, Berlin, pp. 665-667, 1996.

169. Ambach, E., Parson, W., Niederstatter, H., and Budowle, B.: Multiplex PCR and automated detection of four tetrameric STRs in a western Austrian population. In: Advances in Forensic Haemogenetics 6, Springer-Verlag, Berlin, pp. 483-485, 1996.

170. Lorente, M., Lorente, J.A., Alvarez, J.C., Budowle, B., and Villanueva: Sequential multiplex amplification (SMA) in cases with minimal amounts of DNA. In: Advances in Forensic Haemogenetics 6, Springer-Verlag, Berlin, pp. 356-358, 1996.

171. Lorente, M., Lorente, J.A., Alvarez, J.C., Budowle, B., and Villanueva: Spanish population data on seven loci (D1S80, D17S5, HUMTH01, HUMVWA, ACTBP2, D21S11, and DQA1): equilibrium and independence. In: Advances in Forensic Haemogenetics 6, Springer-Verlag, Berlin, pp. 569-571, 1996.

172. Lorente, M., Lorente, Budowle, B., and Villanueva: Science and conscience: regulation or guidelines for forensic haemogenetics? In: Advances in Forensic Haemogenetics 6, Springer-Verlag, Berlin, pp. 689-691, 1996.

173. Budowle, B. and Monson, K.L.: Clarification of additional issues regarding statistics and population substructure effects on forensic DNA profile frequency estimates. In: Sixth International Symposium on Human Identification 1995, Promega Corporation, Madison, Wisconsin pp.1-6, 1996.

174. Keys, K.M., Budowle, B., Andelinovic, S., Definis-Gojanovic, M., Drmic, I., Mladen, M., and Primorac, D.: Northern and southern Croatian population data on seven PCR-based loci. Forens. Sci. Int. 81:191-199, 1996.

175. Budowle, B. and Allen, R.C.: Protocols for analyzing amplified fragment length polymorphisms (VNTR/STR loci) for human identity testing. In: Methods in Molecular Biology - Forensic DNA Profiling Protocols, Vol. 98, (Lincoln, P. and Thomsom, J., eds.), Humana Press Inc., Totowa, New Jersey, pp.155-171, 1998.

176. Murch, R.S. and Budowle, B.: Are developments in forensic applications of DNA technology consistent with privacy protections? In: Genetic Secrets: Protecting Privacy and Confidentiality in the Genetic Era, (Rothstein, M.A., ed.), Yale Press, New Haven, pp. 212-230, 1997.

177. Woller, J., Budowle, B., Furedi, S., and Padar, Z.: Hungarian population data on the loci HLA-DQ $\alpha$ , LDLR, GYPA, HBGG, D7S8, and Gc. Int. J. Leg. Med. 108(5):280-282, 1996.

178. Isenberg, A.R., McCord, B.R., Koons, B.W., Budowle, B., and Allen, R.O.: DNA typing of a PCR-amplified D1S80/amelogenin multiplex using capillary electrophoresis and a mixed entangled polymer matrix. Electrophoresis 17(9):1505-1511, 1996.

179. Furedi, S., Budowle, B., Woller, J., and Padar, Z.: Hungarian population data on 6 STR loci - HUMVWA31/1, HUMTHO1, HUMCSF1PO, HUMFES/FPS, HUMTPOX, AND HUMHPRTB - derived using multiplex PCR amplification and manual typing. Int. J. Leg. Med. 109(2):100-101, 1996.

180. Gehrig, C., Hochmeister, H., Budowle, B., and Reynolds, R.: Subtyping the HLA-DQA1 locus in the Swiss Population. Forens. Sci. Int. 83:27-30, 1996.

181. Park, S.J., Lee, W.G., Lee, S.W., Kim, S.H., Koo, B.S., Budowle, B., and Rho, H.M.: Genetic variation at four tetrameric tandem repeat loci in Korean population. J. Forens. Sci. 42(1):125-129, 1997.

182. Budowle, B., Jankowski, L.B., Corey, H.W., Swec, N.T., Freck-Tootell, S., Pino, J.A., Schwartz, R., Kelley, C.A., and Tarver, M.L.: Evaluation of independence assumptions for PCR-based and protein-based genetic markers in New Jersey Caucasians. J. Forens. Sci. 42(2):223-225, 1997.

183. Budowle, B., Smerick, J.B., Keys, K.M., and Moretti, T.R.: United states population data on the multiplex short tandem repeat loci - HUMTH01, TPOX, and CSF1PO and the variable number tandem repeat locus D1S80. J. Forens. Sci. 42(5):846-849, 1997.

184. Bell, B., Budowle, B., Martinez-Jarreta, B., Casalod, Y., Abecia, E., and Castellano, M.: Distribution types for six PCR-based loci LDLR, GYPA, HBGG, D7S8, Gc, and HLA-DQA1 in central Pyrenees and Teruel (Spain). J. Forens. Sci. 42(3):510-513, 1997.

185. Santos, S.M.M., Budowle, B., Smerick, J.B., Keys, K.M., Koons, B.W., and Moretti, T.R.: Portuguese population data on the six short tandem repeat loci - CSF1PO, TPOX, THO1, D3S1358, VWA, and FGA. Forens. Sci. Int. 83: 229-235, 1996.

186. Budowle, B., Moretti, T.R., Keys, K.M., Koons, B.W., and Smerick, J.B.: Validation Studies of the CTT STR Multiplex System. J. Forens. Sci. 42(2):701-707, 1997.

187. Bar, W., Brinkmann, B., Budowle, B., Carracedo, A., Gill, P., Lincoln, P., Mayr, W., Olaisen, B.: DNA recommendations. Further report of the DNA Commission of the ISFH regarding the use of short tandem repeat systems, International Society for Forensic Haemogenetics. Int. J. Leg. Med. 110(4):175-176, 1997.

188. Duncan, G.T., Balamurugan, K., Budowle, B., and Tracy, M.L.: Hinf I/Tsp509 I polymorphisms in the flanking regions of the human VNTR locus D1S80. Genetic Analysis: Biomolecular Engineering 13:119-121, 1996.

189. Tahir, M., Caruso, J., Budowle, B., and Novick, G.E.: Distribution of HLA-DQA1, and Polymarker (LDLR, GYPA, HBGG, D7S8, and GC) alleles in Arab and Pakistani populations living in Abu Dhabi, United Arab Emirates. J. Forens. Sci. 42(5):914-918, 1997.

190. McCord, B. R., Budowle, B., Isenberg, A.R., and Allen, R.O.: Capillary electrophoresis for the automated analysis of multiplexed STRs using multiwavelength fluorescence detection. In: Seventh International Symposium on Human Identification 1996, Promega Corporation, Madison, Wisconsin, pp. 116-122, 1997.

191. Budowle, B. and Monson, K.L.: Accepted practices by the forensic DNA community supported by the NRC II Report. In: Seventh International Symposium on Human Identification 1996, Promega Corporation, Madison, Wisconsin pp. 27-38, 1997.

192. Alkhayat, A., Alshamali, F., and Budowle, B.: Population data on the PCR-based loci, LDLR, GYPA, HBGG, D7S8, Gc, HLA-DQA1, and D1S80 from Arabs from Dubai. Forens. Sci. Int. 81:29-34, 1996.

193. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva: Spanish population data on seven loci: D1S80, D17S5, HUMTH01, HUMVWA, ACTBP2, D21S11, and DQA1. Forens. Sci. Int. 86:163-171, 1997.

194. Moura-Neto, R.S. and Budowle, B.: Fixed bin population data for the VNTR loci D1S7, D2S44, D4S139, D5S110, D10S28, and D14S13 in a population sample from Rio de Janeiro, Brazil, J. Forens. Sci. 42(5):926-928, 1997.

195. Ambach, E., Parson, W., Niederstatter, H., and Budowle, B.: Austrian Caucasian population data for the quadruplex plus amelogenin: refined mutation rate for HumvWFA31/A. J. Forens. Sci. 42(6):1136-1139, 1997.

196. Wilson, M., Polanskey, D., Replogle, J., DiZinno, J.A., and Budowle, B.: A family exhibiting heteroplasmy in the human mitochondrial DNA control region reveals both somatic mosaicism and pronounced segregation of mitotypes. Human Genetics 100:167-171, 1997.

197. Duncan, G.T., Balamurugan, K., Budowle, B., Smerick, J., and Tracy, M.L.: Microvariation at the human D1S80 locus. Int. J. Leg Med. 110:150-154, 1997.

198. Tahir, M.A., Alkhayat, A.Q., Shamali, F.A., Budowle, B., and Novick, G.E.: Distribution of HLA-DQA1 alleles in Arab and Pakistani individuals from Dubai, United Arab Emirates. Forens. Sci. Int. 85:219-223, 1997.

199. Lorente, M., Lorente, J.A., Alvarez, J.C., Budowle, B., Wilson, M.R., and Villanueva, E.: Sequential multiplex amplification: utility in forensic casework with minimal amounts of DNA and partially degraded samples. J. Forens. Sci. 42(5):923-925, 1997.

200. Bayoumi, R.A., Al-Gazali, L.I., Jaffer, U., Nur-E-Kamal, M.S.A., Dawodu, A., Bener, A., Eapen, V., and Budowle, B.: United Arab Emirate population data on three short tandem repeat loci: HUMTH01, TPOX, and CSF1PO - derived using multiplex PCR and manual typing. Electrophoresis 18:1637-1640, 1997.

201. Miller, M. L., McCord, B. R., Martz, R., and Budowle, B.: The analysis of EDTA in dried blood stains by ionspray LC/MS/MS and ion chromatography. J. Analyt. Toxicol. 21(7):521-528, 1997.

202. Jorquera, H. and Budowle, B.: Chilean population data on ten PCR-based loci. J. Forens. Sci. 43:171-173, 1998.

203. Budowle, B., Koons, B.W., and Moretti, T.R.: Subtyping of the HLA-DQA1 locus and independence testing with PM and STR/VNTR loci. J. Forens. Sci. 43:657-660, 1998.

204. Mansfield, E.S., Robertson, J.M., Vainer, M., Isenberg, A.R., Frazier, R.R., Ferguson, K., Chow, S.T., Harris, D.W., Barker, D.L., Gill, P.D., Budowle, B., and McCord, B.R.: Analysis of multiplexed STR systems using capillary array electrophoresis. Electrophoresis 19(1):101-107, 1998.

205. Isenberg, A.R., Allen, R.O., Keys, K.M., Smerick, J.B., Budowle, B., and McCord, B.R.: Analysis of two multiplexed STR systems using capillary electrophoresis and multiwavelength fluorescence detection. Electrophoresis 19(1):94-100, 1998.

206. Lord, W.D., DiZinno, J.A., Wilson, M.R., Budowle, B., Taplin, D., and Meinking, T.L.: Isolation, amplification, and sequencing of human mitochondrial DNA obtained from human crab louse, <u>Pthirus pubis</u> (L.), blood meals. J. Forens. Sci. 43(5):1097-1100, 1998.

207. Garofano, L., Lago, G., Vecchio, C., Pizzamiglio, M., Zanon, C., Virgili, A., Albonici, L., Manzari, V., and Budowle, B.: Italian population data on the polymarker system and on the five short tandem repeat loci CSF1PO, TPOX, TH01, F13B, VWA. J. Forens. Sci.43:837-840, 1998.

208. Budowle, B., Nhari, L.T., Moretti, T.R., Kanoyangwa, S.B., Masuka, E., Defenbaugh, D.A., and Smerick, J.B.: Zimbabwe black population data on the six short tandem repeat loci - CSF1PO, TPOX, TH01, D3S1358, VWA, and FGA. Forens. Sci. Int. 90:215-221, 1997.

209. Cariolou, M.A., Manoli, P., Christophorou, M., Bashiardes, E., Karagrigoriou, A., and Budowle, B.: Greek Cypriot allele and genotype frequencies of Amplitype PM-DQA1 and D1S80 loci. J. Forens. Sci. 43:661-664, 1998.

210. Martinez-Jarreta, B., Budowle, B., Abecia, E., Bell, B., Casalod, Y., and Castellano, M.: PM and D1S80 in the Zaragoza population of North Spain. J. Forens. Sci. 43(5):1094-1096, 1998.

211. Monson, K.L. and Budowle, B.: Effect of reference database on frequency estimates of polymerase chain reaction (PCR)-based DNA profiles. J. Forens. Sci. 43(3): 483-488, 1998.

212. Bar, W., Brinkmann, B., Budowle, B., Carracedo, A., Gill, P., Holland, M., Lincoln, P.J., Mayr, W., Morling, N., Olaisen, B., Schneider, P.M., Tully, G., and Wilson, M.: DNA Commission of the International Society for Forensic Genetics: guidelines for mitochondrial DNA typing. Int. J Leg. Med. 113(4):193-196, 2000; and Forens. Sci. Int. 110(2):79-85, 2000.

213. Budowle, B. and Isenberg, A.R.: Capillary electrophoresis for forensic DNA typing analyses. In: Advances in Forensic Haemogenetics 7, (Olaisen, B., Brinkmann, B., and Lincoln, P.J., eds.), Elsevier, Amsterdam, pp. 61-67, 1998.

214. Budowle, B. and Monson, K.L.: Database size for frequency estimation of PCR profiles. In: Eighth International Symposium on Human Identification 1997, Promega Corporation, Madison, Wisconsin pp 26-37, 1998.

215. Wilson, M.R., DiZinno, J.A., Stewart, J.E.B., Pokorak, E., Polanskey, D., and Budowle, B.: Mitochondrial DNA testing on evidentiary specimens in the FBI Laboratory: Casework examples and future directions. In: Eighth International Symposium on Human Identification 1997, Promega Corporation, Madison, Wisconsin pp 129-131, 1998.

216. Lorente, M., Entrala, C., Lorente, J.A., Alvarez, J.C., Villaneuva, E., and Budowle, B.: Dandruff as a potential source of DNA in forensic casework. J. Forens. Sci. 43:901-902, 1998.

217. Woller, J., Budowle, B., Angyal, M., Furedi, S., and Padar, Z.: Population data on the loci HLA-DQA1, LDLR, GYPA, HBGG, D7S8, GC, and D1S80 in a Hungarian Romany population. In: Advances in Forensic Haemogenetics 7, (Olaisen, B., Brinkmann, B., and Lincoln, P.J., eds.), Elsevier, Amsterdam, pp. 381-383, 1998.

218. Jankowski, L.B., Budowle, B., Swec, N.T., Pino, J.A., Freck-Tootell, S., Corey, H.W., Schwartz, R., LaRue, E.J., Rochin, W.L., Kearner, C.J., and Tarver, M.L.: New Jersey Caucasian, African American, and Hispanic population data on the PCR-based loci HLA-DQA1, LDLR, GYPA, HBGG, D7S8, and Gc. J. Forens. Sci.43 (5): 1037-1040, 1998.

219. Garcia, O., Martin, P., Budowle, B., Uriarte, J., Albarran, C., and Alonso, A.: Basque Country autochthonous population data on 7 short tandem repeat loci. Int. J. Leg. Med. 111 (3):162-164, 1998.

220. Budowle, B., Baechtel, F.S., and Fejeran, R.: Polymarker, HLA-DQA1, and D1S80 Allele Frequency Data in Chamorro and Filipino Populations from Guam. J. Forens. Sci. 43(6): 1195-1198, 1998.

221. Garofano, L., Pizzamiglio, M., Vecchio, C., Lago, G., Floris, T., D'Errico, G., Brembilla, G., Romano, A., and Budowle, B.: Italian population data on thirteen short tandem repeat loci: TH01, D21S11, D18S51, VWA, FGA, D8S1179, TPOX, CSF1PO, D16S539, D7S820, D13S317, D5S818, D3S1358. Forens. Sci. Int. 97:53-60, 1998.

222. Moretti, T.R., Koons, B.W., and Budowle, B.: Enhancement of PCR amplification yield and specificity using AmpliTaq Gold<sup>TM</sup> DNA polymerase. BioTechniques 25:716-722, 1998.

223. Tomsey, C.S., Basten, C.J., Budowle, B., Giles, B. A., Ermlick, S., and Gotwald, S.: Use of combined frequencies for RFLP and PCR based loci in determining match probability. J. Forens. Sci. 44:385-388, 1999.

224. Wolfarth, R., Nhari, T., Budowle, B., Kanoyangwa, S.B., Masuka, E., Defenbaugh, D.A., Koons, B.W., and Smerick, J.B.: Polymarker, HLA-DQA1, and D1S80 allele data in a sub-Saharan sample population. Int. J. Leg. Med. 113:300-301, 2000.

225. Kupferschmid, T.D., Calicchio, T., and Budowle, B.: Maine Caucasian population DNA database using twelve short tandem repeat loci. J. Forens. Sci. 44:392-395, 1999.

226. Budowle, B. and Moretti, T.R.: Forensics: Analysis of short tandem repeat loci by multiplex PCR and real-time fluorescence detection during capillary electrophoresis. In: DNA Profiling and DNA Fingerprinting, (J.T. Epplen and T. Lubjuhn, eds.), Birkhauser, Basel, Switzerland, pp. 101-116, 1999.

227. Budowle, B., Moretti, T.R., Niezgoda, S.J., and Brown, B.L.: CODIS and PCR-based short tandem repeat loci: Law enforcement tools. In: Second European Symposium on Human Identification 1998, Promega Corporation, Madison, Wisconsin pp 73-88, 1998.

228. DiZinno, J.A., Wilson, M.R., and Budowle, B.: Typing of DNA derived from hairs. In: Forensic Examination of Human Hair (J. Robertson, ed.), Taylor & Francis Forensic Science Series, London, pp. 155-173, 1999.

229. Balamurugan, K., Abdel-Rehman, H., Duncan, G.T., Budowle, B., Anderson, S., Macechko, J. and Tahir, M. Distribution of D1S80 alleles in the Jordanian population. Int. J. Leg. Med. 111(5):276-277, 1998.

230. Gehrig, C., Hochmeister, M., Borer, U.V., and Budowle, B.: Swiss Caucasian population DNA data for 13 STR loci using AmpFlSTR Profiler Plus and Cofiler PCR amplification kits. J. Forens. Sci. 44(5):1035-1038, 1999.

231. Entrala, C., Lorente, M., Lorente, J.A., Alvarez, J.C., Moretti, T., Budowle, B., and Villanueva, E.: Fluorescent multiplex analysis of nine STR loci and the amelogenin locus: Spanish population data. Forens. Sci. Int. 98:179-183, 1998.

232. Budowle, B., Wilson, M.R., DiZinno, J.A., Stauffer, C., Fasano, M.A., Holland, M.M., and Monson, K.L.: Mitochondrial DNA regions HVI and HVII population data. For. Sci. Int. 103:23-35, 1999.

233. Hochmeister, M.N., Budowle, B., Sparkes, R., Rudin, O., Gehrig, C., Thali, M., Schmidt, L., Cordier, A., and Dirnhofer, R.: Validation studies of an immunochromatographic 1-step test for the forensic identification of human blood. J. Forens. Sci. 44(3):597-602, 1999.

234. Lorente, M., Lorente, J.A., Entrala, C., Alvarez, J.C., Wilson, M.R., and Budowle, B.: Minimal amounts of DNA: Improving the result of the analysis in forensic casework. In: Advances in Forensic Haemogenetics 7, (Olaisen, B., Brinkmann, B., and Lincoln, P.J., eds.), Elsevier, Amsterdam, pp. 120-122, 1998.

235. Lorente, J.A., Lorente, M., Entrala, C., Alvarez, J.C., Villaneuva, E., and Budowle, B.: Dandruff as a source of DNA: Validation studies. In: Advances in Forensic Haemogenetics 7, (Olaisen, B., Brinkmann, B., and Lincoln, P.J., eds.), Elsevier, Amsterdam, pp.123-125, 1998. 236. Martinez-Jarreta, B., Diaz Roche, P., Budowle, B., Abecia, E., Castellano, M., and Casalod, Y.: Pyrenean population data on 3 tetrameric short tandem repeat loci - HUMTH01, TPOX, and CSF1PO - derived using a STR multiplex system. In: Advances in Forensic Haemogenetics 7, (Olaisen, B., Brinkmann, B., and Lincoln, P.J., eds.), Elsevier, Amsterdam, pp.312-314, 1998.

237. Entrala, C., Lorente, J.A., Lorente, M., Alvarez, J.C., Budowle, B., and Villanueva, E.: Spanish population data on the loci D13S317, D7S820, D16S539 generated using silver staining (SilverSTR III<sup>™</sup> Multiplex). J. Forens. Sci. 44(5):1032-1034, 1999.

238. Hochmeister, M.N., Budowle, B., Rudin, O., Gehrig, C., Borer, U., Thali, M., Thalmann, G.N., Dirnhofer, R.: Evaluation of prostate-specific antigen (PSA) membrane test assays for the forensic identification of seminal fluid. J. Forens. Sci. 44:1057-1060, 1999.

239. Tahir, M.A., Balamurugan, K., Tahir, U.A., Amjad, M., Owan, M.B., Chaudhary, O.R., Hamby, J.E., Budowle, B., and Herrera, R.: Allelic distribution of nine short tandem repeat (STR), HLA-DQA1, and Polymarker loci in an Omani sample population. Forens. Sci. Int. 109:81-85, 2000.

240. Garofano, L., Pizzamiglio, M., Bizzaro, G.P., Donato, F., Rossetti, M., and Budowle, B.: Italian population data on two new short tandem repeat loci: D6S477 and D19S433. Forens. Sci. Int. 101:203-208, 1999.

241. Sinha, S., Amjad, M., Rogers, C., Hamby, J.E., Tahir, U., Balamurugan, K., Al-Kubaidan, N. A., Choudry, A.R., Budowle, B., and Tahir, M.: Typing of eight short tandem repeat (STR) loci in a Saudi Arabian population. Forens. Sci. Int. 104:143-146, 1999.

242. Tahir, M., Rogers, C., Alkhayat, M., Gohary, M., Budowle, B., and Balamurugan, K.: Distribution of D1S80 alleles in the Bahrainian population. J. Forens. Sci. 44:1314-1315, 1999.

243. Budowle, B., Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M.: Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. J. Forens. Sci. 44:1277-1286, 1999.

244. Entrala, C., Lorente, J.A., Lorente, M., Alvarez, J.C., Budowle, B., and Villanueva, E.: Population studies and casework application with the new GenePrint<sup>™</sup> SilverSTR III<sup>™</sup> multiplex (D16S539, D7S820, D13S317). In: Proceedings from the Second European Symposium on Human Identification 1998, Promega Corporation, Madison, Wisconsin pp 45-7, 1998.

245. Smith, J.A.L. and Budowle, B.: Source identification of body fluid stains using DNA profiling. In: Proceedings from the Second European Symposium on Human Identification 1998, Promega Corporation, Madison, Wisconsin pp 89-90, 1998.

246. Drobnic, K., Regent, A., and Budowle, B.: The Slovenian population data on the PCR based HLA-DQA1, LDLR, GYPA, HBGG, D7S8, GC, and D1S80. J. Forens. Sci. 45(3):689-691, 2000.

247. Padula, R.A., Gangitano, D., Juvenal, G.J., and Budowle, B.: Allele frequencies in the population of Buenos Aires (Argentina) using AmpliType PM + DQA1. J. Forens. Sci. 44:1320, 1999. 248. Martinez-Jarreta, B., Nievas Marco, P., Abecia Martinez, E., Lareu Huidoboro, M.V., and Budowle, B.: Population genetics of the D18S535, D1S1656, and D12S391 loci in Asturias (North Spain). J. Forens. Sci. 45:442-444, 2000.

249. Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., and Budowle, B.: Validation of short tandem repeats (STRs) for forensic usage: Performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. J. Forens. Sci. 46(3):647-660, 2001.

250. Chakraborty, R., Stivers, D.N., Su, B., Zhong, Y., and Budowle, B.: The utility of STR loci beyond human identification: Implications for the development of new DNA typing systems. Electrophoresis 20:1682-1696, 1999.

251. Drobnic, K. and Budowle, B.: The analysis of three short tandem repeat (STR) loci in the Slovene population by multiplex PCR. J. Forens. Sci. 45(4):893-895, 2000.

252. Biondo, R., Spinella, A., Montagna, P., Walsh, S., Holt, C., and Budowle, B.: Regional Italian allele frequencies at nine short tandem repeat loci. Forens. Sci. Int. 115:95-98, 2001.

253. Budowle, B. And Moretti, T.R.: Genotype profiles for six population groups at the 13 CODIS short tandem repeat core loci and other PCR-based loci. Forensic Science Communications 1(2) July 1999. Available: http://www.fbi.gov/programs/lab/fsc/current/budowle.htm.

254. Garofano, L., Pizzamiglio, M., Donato, F., Biondo, F., Rossetti, M., and Budowle, B.: Italian population data on two new short tandem repeat loci: D2S1338 and Penta E. Forens. Sci. Int. 105:131-136, 1999.

255. Peterson, B.L., Su, B., Chakraborty, R., Budowle, B., and Gaensslen, R.E.: World population data for the HLA-DQA1, PM and D1S80 loci with least and most common profile frequencies for combinations of loci estimated following NRC II guidelines. J. Forens. Sci. 45(1):118-146, 2000.

256. Budowle, B., Defenbaugh, D.A., and Keys, K.M.: Genetic variation at nine short tandem repeat loci in Chamorros and Filipinos from Guam. Legal Medicine 2(1):26-30, 2000.

257. Binda, S., Borer, U.V., Gehrig, C., Hochmeister, M., and Budowle, B.: Swiss Caucasian population data for the STR loci D2S1338 and D19S433 using the AmpFlSTR SGM Plus PCR amplification kit. Forens. Sci. Int. 108(2):117-120, 2000.

258. Budowle, B., Leggitt, J.L., Defenbaugh, D.A., Keys, K.M., and Malkiewicz, S.F.: The Presumptive Reagent Fluorescein for Detection of Dilute Bloodstains and Subsequent STR Typing of Recovered DNA. J. Forens. Sci. 45:1090-1092, 2000.

259. Tahir, M.A., Sinha, S.K., Al-Kubaidan, N.A., Tahir, U.A., Budowle, B., and Amjad, M.: Distribution of amplified fragment length polymorphism D1S80 alleles in Saudi Arabian population. J. Forens. Sci. 45:1159, 2000.

260. Tahir, M.A., Herrera, R.J., Khan, A.A., Kashyap, V.K., Duncan, G., Barna, C., Budowle, B., Rowold, D.J., Sinha, S. and Amjad, M.: Distribution of HLA-DQA1, polymarker, CSF1PO, vWA, TH01, TPOX, D16S539, D7S820, D13S317, and D5S818 alleles in East Bengali and West Punjabi populations from Indo-Pak subcontinent. J. Forens. Sci. 45:1320-1323, 2000.

261. Stewart, J.E.B, Fisher, C.L., Aagaard, P.J., Wilson, M.R., Isenberg, A.R., Polanskey, D., Pokorak, E., DiZinno, J.A., and Budowle, B.: Length variation in HV2 of the human mitochondrial DNA control region. J. Forens. Sci. 46(4):862-870, 2001.

262. Budowle, B., DiZinno, J.A., and Wilson, M.R.: Interpretation guidelines for mitochondrial DNA sequencing. In: Tenth International Symposium on Human Identification 1999, Promega Corporation, Madison, Wisconsin, At: http://www.promega.com/ussymp10proc/default.htm.

263. Tahir, M.A., Sinha, S., Rogers, C., Tahir, U., Balamurugan, K., Al-Kubaidan, N.A., Choudry, A.R., Budowle, B., and Amjad, M.: Distribution of HLA-DQA1, Amplitype PM loci in a Saudi Arabian sample population. J. Forens. Sci. 45(1):236, 2000.

264. Budowle, B.: STR allele concordance between different primer sets - a brief summary. Profiles in DNA 3(3):10-11, 2000.

265. Gehrig, C., Hochmeister, M., and Budowle, B.: Swiss allele frequencies and haplotypes of 7 Y-specific STRs. J. Forens. Sci. 45:436-439, 2000.

266. Martinez-Jarreta, B., Nievas, P., Albecia, E., and Budowle, B.: Genetic analysis of the short tandem repeat loci D16S539, D7S820, D13S317, D18S535, D1S1656, and D12S391 in two Spanish populations. In: Progress in Forensic Genetics (Sensabaugh, G.F., Lincoln, P.J., and Olaisen, B., eds.), Elsevier, Amsterdam, pp. 190-192, 2000.

267. Prades, A., Calafell, F., Budowle, B., Bertranpetit, J., and Martinez-Jarreta, B.: Sequence analysis of mitochondrial DNA (mtDNA) control region in Aragon (North Spain). An anthropological view, In: Progress in Forensic Genetics (Sensabaugh, G.F., Lincoln, P.J., and Olaisen, B., eds.), Elsevier, Amsterdam, pp. 332-334, 2000.

268. Morales, J., Monterrosa, J.C., Alvarez, J.C., Entrala, C., Lorente, J.A., Lorente, M., Villaneuva, E., and Budowle, B.: El Salvador (Central America) population data for the D1S80 and D17S5 (YNZ22) loci. In: Progress in Forensic Genetics (Sensabaugh, G.F., Lincoln, P.J., and Olaisen, B., eds.), Elsevier, Amsterdam, pp. 359-361, 2000.

269. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., Alvarez, J.C., and Villaneuva, E.: Improvement in the yield of mitochondrial DNA amplification products: implications for the analysis of old and degraded biological samples. In: Progress in Forensic Genetics (Sensabaugh, G.F., Lincoln, P.J., and Olaisen, B., eds.), Elsevier, Amsterdam, pp. 485-486, 2000.

270. Lorente, M., Lorente, J.A., D'Aloja, E., Fiori, A., Budowle, B., and Villaneuva, E.: Genetic databases: past, present, and future. Criminal databases in forensic sciences. In: Progress in Forensic Genetics (Sensabaugh, G.F., Lincoln, P.J., and Olaisen, B., eds.), Elsevier, Amsterdam, pp. 616-618, 2000.

271. Martinez-Jarreta, B., Prades, A., Calafell, F., and Budowle, B.: Mitochondrial DNA HVI and HVII variation in a North-east Spanish population. J. Forens. Sci. 45:1162-1163, 2000.

272. Budowle, B., Shea, B., Niezgoda, S., and Chakraborty, R.: CODIS STR loci data from 41 sample populations. J. Forens. Sci. 46(3):453-489, 2001.

273. Budowle, B. and Sprecher, C.J.: Concordance study on population database samples using the PowerPlex<sup>TM</sup> 16 Kit and AmpFlSTR<sup>®</sup> Profiler Plus<sup>TM</sup> Kit and AmpFlSTR<sup>®</sup> COfiler<sup>TM</sup> Kit. J. Forens. Sci. 46(3):637-641, 2001.

274. Balamurugan, K., Budowle, B., and Tahir, M.: Allele frequencies for nine STR loci in African American and Caucasian populations from Marion County, Indiana, USA. J. Forens. Sci.45:744-746, 2000.

275. Scherczinger, C.A., Hintz, J.L., Peck, B.J., Adamowicz, M.S., Bourke, M.T., Coyle, H.M., Ladd, C., Yang, N.C.S., Budowle, B., and Lee, H.C.: Allele frequencies for the CODIS core STR loci in Connecticut populations. J. Forens. Sci. 45(4):938-940, 2000.

276. Budowle, B., Hudlow, W.H., and Lee, S.B.: Using a CCD camera imaging system (the CCDBIO<sup>TM</sup> 16C) instead of film as a recording device to quantify human DNA by slot blot hybridization. BioTechniques 30(3):680-685, 2001.

277. Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., and Budowle, B.: Validation of STR Typing by Capillary Electrophoresis. J. Forens. Sci. 46(3):661-676, 2001.

278. Budowle, B., Chakraborty, R. Carmody, G. and Monson, K.L.: Source Attribution of a Forensic DNA Profile. Forensic Science Communications 2(2) July 2000. At: http://www.fbi.gov/programs/lab/fsc/current/budowle.htm.

279. Holt, C.L., Stauffer, C., Wallin, J.M., Lazaruk, K.D., Nguyen, T., Budowle, B., and Walsh, P.S.: Practical applications of genotypic surveys for forensic STR testing. Forens. Sci. Int. 112:91-109, 2000.

280. Fisher, F.L., Isenberg, A.R., Stewart, J.E.B., Miller, K.O., Theisen, C.E., Wilson, M.R., DiZinno, J.A., and Budowle, B.: Mitochondrial DNA: today and tomorrow. In: Eleventh International Symposium on Human Identification 2000, Promega Corporation, Madison, Wisconsin. At: http://www.promega.com/ussympl1proc/default.htm.

281. Budowle, B.: STR primer concordance data - validation studies. In: Eleventh International Symposium on Human Identification 2000, Promega Corporation, Madison, Wisconsin. At: http://www.promega.com/ussympl1proc/default.htm.

282. Vanek, D., Roman, H., and Budowle, B.: Czech population data on ten short tandem repeat loci of SGM Plus STR system kit using DNA purified in FTA cards. Forens. Sci. Int. 119:107-108, 2001.

283. Bashiardes, E., Manoli, P., Budowle, B., and Cariolou, M.A.: Data on nine STR loci used for forensic and paternity testing in the Greek Cypriot population of Cyprus. Forens. Sci. Int. 123:225-226, 2001.

284. Drobnic, K., Regent, A., and Budowle, STR data for the AmpFlSTR SGM Plus from Slovenia. Forens. Sci. Int. 115:107-109, 2001.

285. Lorente, J.A., Entrala, C., Alvarez, J.C., Lorente, M., Villaneuva, E., Carrasco, F., and Budowle, B.: Missing persons identification: genetics at work for society. Science 290:2257, 2000.

286. Pagano, S., Alvarez, J.C., Entrala, C., Lorente, J.A., Lorente, M., Budowle, B., and Villaneuva, E.: Uruguayan population data for eight STR loci (using Powerplex 1.2<sup>™</sup> kit). J. Forens. Sci. 46:178, 2001.

287. Gangitano, D., Juvenal, G.J., Lorente, J.A., Budowle, B. and Padula, R.A.: Population data on eight STR loci in Buenos Aires (Argentina). J. Forens. Sci. 46:183, 2001.

288. Balamurugan, K., Granoff, M., Budowle, B., and Tahir, M.: Allele frequencies for four STR loci (D16S539, TH01, TPOX, and CSF1PO) in African American and Caucasian populations from Marion County, Indiana, USA. J. Forens. Sci. 46:189, 2001.

289. Budowle, B. and Chakraborty, R.: Population variation at the CODIS core short tandem repeat loci in Europeans. Legal Med 3(1):29-33, 2001.

290. Gangitano, D.A., Garofalo, M.G., Juvenal, G.J., Budowle, B., and Padula, R.A.: Distribution of HumHPRTB and HumF13A01 in Buenos Aires population (Argentina). J. Forens. Sci. 46(2):418, 2001.

291. Miller, K.W.P. and Budowle, B.: A Compendium of Human Mitochondrial DNA Control Region: Development of an International Standard Forensic Database. Croatian Medical Journal 42(3):315-327, 2001.

292. Lorente, J.A., Entrala, C., Alvarez, J.C., Arce, B., Heinrichs, B., Lorente, M., Carrasco, F., Budowle, B., and Villanueva, E.: Identification of missing persons: the Spanish Phoenix Program. Croatian Medical Journal 42:267-270, 2001.

293. Budowle, B.: Genotype profiles for five population groups at the short tandem repeat loci D2S1338 and D19S433. Forensic Science Communications 3(3) July 2001. Available: http://www.fbi.gov/hq/lab/fsc/current/budowle.htm.

294. Budowle, B., Collins, P.J., Dimsoski, P., Ganong, C.K., Hennessy, L.K., Leibelt, C.S., Rao-Coticone, S., Shadravan, F., Reeder, D.J.: Population data on the STR loci D2S1338 and D19S433. Forensic Science Communications 3(3)July 2001. Available: http://www.fbi.gov/hq/lab/fsc/current/budowle.htm.

295. Budowle, B. and Brown, B.L.: The use of DNA typing for forensic identification. Forensica 1(1):9-37, 2001.

296. Akbasak, B.S., Budowle, B., Reeder, D.J., Redman, J., and Kline, M.C.: Turkish population data with the CODIS short tandem repeat loci. Forens. Sci. Int. 123:227-229, 2001.

297. Arce, B., Heinrichs, B., Armenteros, M.F., Carrasco, F., Lorente, J.A., and Budowle, B.: Spanish population data on nine STR loci. J. Forens. Sci. 46(4):1003-1004, 2001.

298. Gill, P., Brenner, C., Brinkmann, B., Budowle, B., Carracedo, A., Jobling, M.A., de Knijff, P., Kayser, M., Krawczak, M., Mayr, W.R., Morling, N., Olaisen, B., Pascali, V., Prinz, M., Roewer, L., Schneider, P.M., Sajantila, A., and Tyler-Smith, C.: DNA commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Ychromosome STRs. Int. J. Leg. Med. 114(6):305-309, 2001. 299. Budowle, B., Masibay, A., Anderson, S.J., Barna, C., Biega, L., Brenneke, S., Brown, B.L., Cramer, J., DeGroot, G.A., Douglas, D., Duceman, B., Eastman, A., Giles, R., Hamill, J., Haase, D.J., Janssen, D.W., Kupferschmid, T.D., Lawton, T., Lemire, C., Llewellyn, B., Moretti, T., Neves, J., Palaski, C., Schueler, S., Sgueglia, J., Sprecher, C., Tomsey, C., Yet, D.: STR primer concordance study. Forens. Sci. Int. 124:47-54, 2001.

300. Lorente, J.A., Entrala, C., Alvarez, J.C., Lorente M., Carrasco, F., Arce, B., Heinrich, B., Budowle, B., and Villanueva, E.: Social benefits of non-criminal genetic databases: missing persons and human remains identification. Int. J. Leg. Med. 116: 187-190, 2002.

301. Budowle, B., Biancavilla, R.P., and Adams, D.E.: Another powerful forensic genetic tool: mitochondrial DNA typing. United States Attorneys' Bulletin 49(5):5-28, 2001.

302. Budowle, B., Chakraborty, R., Carmody, G., and Monson, K.L.: Reply to Weir (2001). Forens. Sci. Comm. 3(1), 2001. Available: http://www.fbi.gov/hq/lab/fsc/backissu/jan2001/budowle.htm

303. Budowle, B., Allard, M., Fisher, C.L., Isenberg, A.R., Monson, K.L., Stewart, J.E.B., Wilson, M.R., and Miller, K.W.P.: HVI and HVII Mitochondrial DNA population data in Apaches and Navajos. Int. J. Leg. Med. 116(4):212-215, 2002.

304. Budowle, B.: Population studies on 17 STR loci routinely used in forensic analyses. In: Progress in Forensic Genetics 9, (Brinkmann, B., and Carracedo, A., eds.), Elsevier, Amsterdam, pp. 71-74, 2003.

305. Miller, K.W.P., Brown, B.L., and Budowle, B.: The Combined DNA Index System (CODIS). In: Progress in Forensic Genetics 9, (Brinkmann, B., and Carracedo, A., eds.), Elsevier, Amsterdam, pp. 617-620, 2003.

306. Budowle, B., Hobson, D.L., Smerick, J.B., and Smith, J.A.L.: Low Copy Number - Consideration and Caution. In: Twelfth International Symposium on Human Identification 2001, Promega Corporation, Madison, Wisconsin, 2001. Available: http://www.promega.com/ussymp12proc/default.htm.

307. Balamurugan, B., Prabakaran, N., Duncan, G., Budowle, B., Tahir, M., and Tracy, M.: Allele frequencies of 13 STR loci and D1S80 in a Tamil population. J. Forens. Sci.: 46:1515-1517, 2001.

308. Gangitano, D.A., Garofalo, M.G., Juvenal, G.J., Budowle, B., and Padula, R.A.: Typing of the locus DYS19 from DNA derived from fingernail clippings using PCR Concert<sup>™</sup> Rapid Purification system. J. Forens. Sci. 47(1):175-177, 2002.

309. Gangitano, D.A., Garofalo, M.G., Juvenal, G.J., Budowle, B., Lorente, J.A., and Padula, R.A.: STR data for the PowerPlex® 16 loci in Buenos Aires population (Argentina). J. Forens. Sci. 47(2):418-420, 2002.

310. Monson, K.L., Miller, K.W.P., Wilson, M.R., DiZinno, J.A., and Budowle, B.: The mtDNA population database: an integrated software and database resource for forensic comparison. Forensic Science Communications 4(2) April 2002. Available: http://www.fbi.gov/hq/lab/fsc/current/index.htm. 311. Morales, J.A., Monterrosa, J.C., Alvarez, J.C., Entrala, C., Lorente, J.A., Lorente, M., Budowle, B., and Villaneuva, E.: Population data on nine STR loci in an El Salvadoran (Central American) sample population. J. Forens. Sci. 47(4):900-901, 2002.

312. Cerda-Flores, R.M., Budowle, B., Jin, L., Barton, S.A., Deka, R., and Chakraborty, R.: Maximum likelihood estimates of admixture in Northeastern Mexico using 13 short tandem repeat loci. Am. J. Hum. Biol. 14:429-439, 2002.

313. Budowle, B., Allard, M.W., and Wilson, M.R.: Critique of interpretation of high levels of heteroplasmy in the human mitochondrial DNA hypervariable region I from hair. Forens. Sci. Int. 126:30-33, 2002.

314. Dugan, K.A., Lawrence, H.S., Hares, D.R., Fisher, C.L., and Budowle, B.: An improved method for post-PCR purification for mtDNA sequence analysis. J. Forens. Sci. 47(4):811-818, 2002.

315. Houck, M.M. and Budowle, B.: Correlation of microscopic and mitochondrial DNA hair comparisons. J. Forens. Sci. 47:964-967, 2002.

316. Allard, M.W., Miller, K., Wilson, M.R., Monson, K.L., and Budowle, B.: Characterization of the Caucasian haplogroups present in the SWGDAM forensic mtDNA data set for 1771 human control region sequences. J. Forens. Sci. 47(6):1215-1223, 2002.

317. Sinha, S.K., Budowle, B., Arcot, S.S., Richey, S.L., Chakraborty, R., Jones, M.D., Wojtkiewicz, P.W., Schoenbauer, D.A., Gross, A.M., Sinha, S.K., and Shewale, J.G.: Development and validation of a multiplexed Y-chromosome STR genotyping system, Y-PLEX<sup>TM</sup>6, for forensic casework. J. Forens. Sci. 48(1):93-103, 2003.

318. Wilson, M.R., Allard, M.W., Monson, K., and Budowle, B.: Recommendations for coding variants in the human mitochondrial DNA control region. Forens. Sci. Int. 129(1):35-42, 2002.

319. Wilson, M.R., Allard, M.W., Monson, K., Miller, K.W.P., and Budowle, B.: Further Discussion of the Consistent Treatment of Length Variants in the Human Mitochondrial DNA Control Region. Forens. Sci. Comm. 4(4) October 2002. Available: http:// www.fbi.gov/hq/lab/fsc/current/index.htm.

320. Budowle, B., Chidambaram, A., Strickland, L., Beheim, C.W., Taft, G.M., and Chakraborty, R.: Population data at 13 STR loci for three Native Alaska population groups. Forens. Sci. Int. 129(1):51-57, 2002.

321. Alshamali, F.H., Alkhayat, A.I., Budowle, B., and Watson, N.D.: Allele frequency distributions and other population genetic parameters for 13 STR loci in a UAE local population from Dubai. In: Progress in Forensic Genetics 9, (Brinkmann, B., and Carracedo, A., eds.), Elsevier, Amsterdam, pp. 249-258, 2003.

322. Henke, L., Aaspollu, A., Biondo, R., Budowle, B., Drobnic, K., van Eede, P.H., Felske-Zech, H., Fernandez de Simon, L., Garafano, L., Gehrig, C., Luckenbach, C., Malik, N., Muche, M., Parson, W., Primorac, D., Schneider, P.M., Thomson, J., and Vanek, D.: Evaluation of the STR typing kit PowerPlex<sup>™</sup> 16 with respect to technical performance and population genetics: a multicenter study. In: Progress in Forensic Genetics 9, (Brinkmann, B., and Carracedo, A., eds.), Elsevier, Amsterdam, pp. 789-7 94, 2003. 323. Martinez-Jarreta, B., Nievas, P., Abecia, E., Hinojal, R., and Budowle, B.: Haplotype distribution of nine Y-chromosome STR-loci in two northern Spanish populations (Asturias and Aragon). J. Forens. Sci. 48:204-205, 2003.

324. Budowle, B., Allard, M.W., and Wilson, M.R.: Characterization of heteroplasmy and hypervariable sites in HV1: critique of D'Eustachio's interpretations. Forens. Sci. Int. 130:68-70, 2002.

325. Stewart, J.E.B., Aagaard, P.J., Pokorak, E.G., Polanskey, D., and Budowle, B.: Evaluation of a multicapillary electrophoresis instrument for mitochondrial DNA typing. J. Forens. Sci. 48(3):571-580, 2003.

326. Budowle, B.: Defining a new forensic discipline: Microbial Forensics. In: Thirteenth International Symposium on Human Identification 2002, Promega Corporation, Madison, Wisconsin, Profiles in DNA 6(1):7-10, 2003. At: http://www.promega.com/ussymp13proc/default.htm

327. Bertoni, B., Budowle, B., Sans, M., and Chakraborty, R.: Admixture in Hispanics: distribution of ancestral population contributions in the continental United States. Human Biology 75(1):1-11, 2003.

328. Coyle, H.M., Budowle, B., Bourke, M.T., Carita, E., Hintz, J.L., Ladd, C., Roy, C., Yang, N.C.S., Palmbach, T., and Lee, H.C.: Population data for seven Y-chromosome STR loci from three different population groups residing in Connecticut. J. Forens. Sci. 48:435-437, 2003.

329. Garofalo, M.G., Gangitano, D.A., Juvenal, G.J., Budowle, B., Lorente, J.A., and Padula, R.A.: Six Y-chromosome STR frequencies in a population from Argentina. J. Forens. Sci. 48:455-456, 2003.

330. Fenandez-Rosado, F., Martinez-Espin, E., Rodriguez, T., Entrala, C., Alavarez, J.C., Lorente, J.A., Lorente, M., Budowle, B., and Villaneuva, E.: Population data of Ecuador for fifteen STR loci (PowerPlex<sup>™</sup> 16). J. Forens. Sci. 48:224-226, 2003.

331. Martinez-Espin, E., Fenandez-Rosado, F., Alvarez, J.C., Entrala, C., Lorente, J.A., Oviedo de Duarte, M., and Budowle, B.: Paraguayan population data on the fifteen STR loci included in the PowerPlex  $16^{\text{TM}}$  kit. J. Forens. Sci. 48:253-255, 2003.

332. Budowle, B., Allard, M.W., Wilson, M.R., and Chakraborty, R.: Forensics and mitochondrial DNA: applications, debates, and foundations. Ann. Rev. Genomics Hum. Genetics 4:119-141, 2003.

333. Frégeau, C.J., Aubin, R.A., Budowle, B., and Fourney, R.M.: DNA typing analysis. In: Encyclopedia of Molecular Cell Biology and Molecular Medicine, (Meyers, R.A., ed.), Wiley-VCH Verlag, Weinheim, Germany pp.477-506, 2004.

334. Anghel, A., Marian, C., Pitulescu, M., Daba, A., Sirbu, I.O., Rusu, V., and Budowle, B.: Population genetic study of eight short tandem repeat loci CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, F13B and LPL in western Romanian Population. Forens. Sci. Int. 131:218-219, 2003.

335. Sinha, S.K., Nasir, H., Gross, A.M., Budowle, B., and Shewale, J.G.: Development and validation of the Y-PLEX<sup>™</sup>5, a Y-chromosome STR genotyping system for forensic casework. J. Forens. Sci. 48:985-1000, 2003. 336. Leibelt, C., Budowle, B., Collins, P., Dimsoski, P., Ganong, C., Moretti, T., Nunn, G., Rao-Coticone, S., Reeder, D., Roby, R., and Shadravan, F.: Identification of a D8S1179 primer binding site mutation and the validation of a primer designed to recover null alleles. Forens. Sci. Int. 133:220-227, 2003.

337. Budowle, B., Planz, J., Campbell, R., and Eisenberg, A.: SNPs and microarray technology in forensic genetics: development and application to mitochondrial DNA. Forens. Sci. Rev. 16:22-36, 2004.

338. Budowle, B., Burans, J., Breeze, R.G., Wilson, M.R., and Chakraborty, R.: Microbial Forensics. In: Microbial Forensics, Schutzer, S., Breeze, R., and Budowle, B. (eds.), Academic Press, Amsterdam, pp. 1-25, 2005.

339. Budowle, B., Sinha, S.K., Lee H.S., and Chakraborty, R.: Utility of Ychromosome STR haplotypes in forensic applications. Forens. Sci. Rev. 15(2):153-164, 2003.

340. Budowle, B. and SWGMGF Members: Quality assurance guidelines for laboratories performing microbial forensic work. Forens. Science Communications October 5(4): 2003, At: www.fbi.gov/hq/lab/fsc/current/2003 10 guide01.htm.

341. Figueiredo, M.S., Fernando-Rosao, F., Kunii, I., Pacheco, A.C., Lorente, J.A., and Budowle, B.: Brazilian Caucasian population data for 15 STR loci (PowerPlex 16<sup>™</sup> kit). J. Forens. Sci. 49:167-169, 2004.

342. Melendez, E., Martinez-Espin, E., Karlson, I.S., Lorente, J.A., and Budowle, B.: Population data on 15 STR loci (PowerPlex  $16^{\text{TM}}$  kit) in a Costa Rica (Central America) sample population. J. Forens. Sci. 49:170-172, 2004.

343. Marjanovic, D., Kapur, L., Drobnic, K., Budowle, B., Pojskic, N., and Hadzjselimovis, R.: Comparative study of genetic variation at fifteen STR loci in three isolated populations of Bosnia mountain area. Human Biology 76(1):15-31, 2004.

344. Allard, M.W., Wilson, M.R., Monson, K.L., and Budowle, B.: Control region sequences for East Asian individuals in the SWGDAM forensic mtDNA data set. Legal Med. 6(1): 11-24, 2004.

345. Budowle, B., Schutzer, S.E., Einseln, A., Kelley, L.C., Walsh, A.C., Smith, J.A.L., Marrone, B.L., Robertson, J., and Campos, J.: Building microbial forensics as a response to Bioterrorism. Science 301: 1852-1853, 2003.

346. Alshamali, F, Alkhayat, AQ, Budowle, B, and Watson, N.: Y chromosome in forensic casework and paternity testing. In: Progress in Forensic Genetics 10, (Doutremepuich, C., and Morling, N., eds.), Elsevier, Amsterdam, pp. 353-356, 2004.

347. Budowle, B. And Chakraborty, R.: Genetic considerations for interpreting molecular microbial forensic evidence. In: Progress in Forensic Genetics 10, (Doutremepuich, C., and Morling, N., eds.), Elsevier, Amsterdam, pp. 56-58, 2004.

348. Vecchio, C., Garofano, L., Saravo, L., Spitalen S., Iacovacci, G., Santacroce, M., Manzari, V., and Budowle, B.: Allele frequencies for CODIS loci in a Sicilian population sample. In: Progress in Forensic Genetics 10, (Doutremepuich, C., and Morling, N., eds.), Elsevier, Amsterdam, pp. 136-138, 2004.

349. Budowle, B., Campbell, R., Eisenberg, A., Wilson, M., and Chakraborty, R.: Microbial forensic biocrimes and HIV. In: Fourteenth International Symposium on Human Identification 2003, Promega Corporation, Madison, Wisconsin. At: http://www.promega.com/ussymp14proc/default.htm.

350. Flores-Obando, R.E., Budowle, B., and Huete-Pérez, J.A.: Allele frequencies for markers CSF1PO, TPOX, TH01, F13A01, FESFPS, vWA, D16S539, D7S820, D13S317 in the general population of Nicaragua. J. Forens. Sci. 49(2):416-417, 2004.

351. Vasquez. P., Martinez-Jarreta, B., Budowle, B., Abecia, E., and De Blas, I.: Population genetic study of Y-chromosome haplotypes in the population of El Salvador (San Salvador, Central America). In: Progress in Forensic Genetics 10, (Doutremepuich, C., and Morling, N., eds.), Elsevier, Amsterdam, pp. 305-306, 2004.

352. Budowle, B., Planz, J.V., Campbell, R., and Eisenberg, A.J.: Molecular diagnostic applications in forensic science. In: Molecular Diagnostics, Patrinos, G. and Ansorge, W., eds., Elsevier, Amsterdam, pp. 267-280, 2005.

353. Ryan, J.H., Barrus, J.K., Budowle, B., Shannon, C.M., Thompson, V.W., and Ward, B.E.: The application of an automated allele concordance analysis system (CompareCalls<sup>SM</sup>) to ensure accuracy of single source STR DNA profiles. J. Forens. Sci. 49(3): 492-499, 2004.

354. Gill, P., Werrett, D.J., Budowle, B., and Guerrieri, R.: An assessment of whether SNPs will replace STRs in national DNA databases - joint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). Science & Justice 44(1):51-53, 2004.

355. Martinez-Jarreta, B., Vasquez, P., Abecia, E., Garde, M., De Blas, I., and Budowle, B.: Autosomic STR loci (HUMTPOX, HUMTH01, HUMVWA, D18S535, D1S1656, and D12S391) in San Salvador (El Salvador, Central America). J. Forens. Sci. 49(3):633-634, 2004.

356. Sinha, S., Budowle, B., Chakraborty, R., Paunovic, A., Guidry, R.D., Larsen, C., Lal, A., Shaffer, M., Pineda, G., Sinha, S.K., Schneida, E., Nasir, H., and Shewale, J.G.: Utility of the Y-STR Y-PLEX<sup>™</sup> 6 and Y-PLEX<sup>™</sup> 5 in forensic casework and 11 Y-STR haplotype database for three major population groups in the United States. J. Forens. Sci. 49:691-700, 2004.

357. Shewale, J.G., Nasir, H., Schneida E., Gross, A.M., Budowle, B., and Sinha, S.K.: Y-chromosome STR system, Y-Plex<sup>™</sup> 12, for forensic casework: development and validation. J. Forens. Sci. 49(6):1278-1290, 2004.

358. Krenke, B.E., Viculis, L., Richard, M.L., Prinz, M., Milne, S.C., Ladd, C., Gross, A.M., Gornall, T., Frappier, J.R.H., Eisenberg, A.J., Barna, C., Aranda, X.G., Adamowicz, M.S., and Budowle, B.: Validation of a malespecific, 12-locus fluorescent Short Tandem Repeat (STR) multiplex. Forens. Sci. Int. 148(1):1-14, 2005. 359. Budowle, B., Polanskey, D., Allard, M.W., and Chakraborty, R.: Addressing the use of phylogenetics for identification of sequences in error in the SWGDAM mitochondrial DNA database. J. Forens. Sci. 49(6):1256-1261, 2004.

360. Allard, M.W., Wilson, M.R., Miller, K., Monson, K.L., and Budowle, B.: Characterization of 1257 human control region sequences for the African American haplogroups in the SWGDAM forensic mtDNA data set. Forens. Sci. Int. 148(2-3):169-179, 2005.

361. Budowle, B.: Genetics and attribution issues that confront the microbial forensics field. Forensic Sci. Int. 146 Suppl:S185-S188, 2004. 362. Budowle, B.: SNP typing strategies. Forensic Sci. Int. 146 Suppl: S139-S142, 2004.

363. Ang, H.C., Sornarajah, R., Lim, S.E.S., Syn, C.K.C., Tan-Siew, W.F., Chow, S.T., and Budowle, B.: STR data for the 13 CODIS loci in Singapore Malays. Forensic Sci. Int. 148(2-3):243-245, 2005.

364. Lim, S.E.S., Tan-Siew, W.F., Syn, C.K.C., Ang, H.C., Chow, S.T., and Budowle, B.: Genetic data for the 13 CODIS STR loci in Singapore Indians. Forensic Sci. Int. 148(1):65-67, 2005.

365. Syn, C.K.C., Chuah, S.Y., Ang, H.C., Lim, S.E.S., Tan-Siew, W.F., Chow, S.T., and Budowle, B.: Genetic data for the 13 CODIS STR loci in Singapore Chinese. Forensic Sci. Int. 152:285-288, 2005.

366. Polanskey, D., and Budowle, B.: Summary of the Findings of a Quality Review of the Scientific Working Group on DNA Analysis Methods Mitochondrial DNA Database. Forensic Sci. Comm. 7(1), 2005; At: http//www.fbi.gov/hq/lab/fsc/current/research/2005research.htm.

367. Chakraborty, R., Lee, H.S., and Budowle, B.: Response to Krane et al. J. Forens. Sci. 49(6):1390-1393, 2004.

368. Alshamali, F., Alkhayat, A., Budowle, B., and Watson, N.D.: STR population diversity in nine ethnic populations living in Dubai. Forens. Sci. Int. 152:267-279, 2005.

369. Martinez-Gonzalez, L.J., Martinez-Espin, E., Fernandez-Rosado, F., Moguel, M.A., Entrala, C., Alvarez, J.C., Lorente, J.A., and Budowle, B.: Mexican population data on fifteen STR loci (Identifiler® Kit) in a Chihuahua (northern central Mexico) sample. J. Forens. Sci. 50(1):236-238, 2005.

370. Allard, M.W., Budowle, B., and Wilson, M.R.: Systematics in forensic science. In: McGraw-Hill Yearbook of Science and Technology 2005, McGraw-Hill, New York, pp. 355-358, 2005.

371. Budowle, B., Schutzer, S.E., Ascher, M.S., Atlas, R.M., Burans, J.P., Chakraborty, R., Dunn, J.J., Fraser, C.M., Franz, D.R., Leighton, T.J., Morse, S.A., Murch, R.S., Ravel, J., Rock, D.L., Slezak, T.R., Velsko, S.P., Walsh, A.C., and Walters, R.A.: Towards a system of microbial forensics: from sample collection to interpretation of evidence. Applied and Environmental Microbiology 71(5):2209-2213, 2005. 372. Budowle, B., Adamowicz, M., Aranda, X., Barna, C., Chakraborty, R., Eisenberg, A.J., Frappier, R., Gross, A.M., Lee, H.S., Milne, S., Prinz, M., Saldanha, G., and Krenke, B.E.: Twelve short tandem repeat loci Y chromosome haplotypes: genetic analysis on populations residing in North America. Forens. Sci. Int. 150(1):1-15, 2005.

373. Budowle, B. and Polanskey, D.: FBI mtDNA database: a cogent perspective. Science 307:845-846, 2005.

374. Budowle, B. and Eisenberg, A.J.: Forensic Genetics. In: Emery and Rimoin's Principles and Practice of Medical Genetics, fifth edition, Vol. 1, Rimoin, D.L., Connor, J.M., Pyeritz, R.E., and Korf, B.R., eds., Elevier, Philadelphia, pp.501-517, 2007.

375. Budowle, B., Bieber, F.R., and Eisenberg, A.J.: Forensic aspects of mass disasters: strategic considerations for DNA-based human identification. Legal Med. 7(4):230-243, 2005.

376. Shriver, M., Frudakis, T., and Budowle, B.: Getting the science and the ethics right in forensic genetics. Nat. Genet. 37(5):449-450, 2005.

377. Budowle, B., Murch, R.S., and Chakraborty, R.: Microbial forensics: the next forensic challenge. Int. J. Leg. Med. 119:317-330, 2005.

378. Tang J.S.W., Wong, H.Y., Syn, C.K.C., Tan-Siew, W.F., Chow, S.T., and Budowle, B.: Population study of 11 Y-chromosomal STR loci in Singapore Chinese. Forens. Sci. Int. 158:65-71, 2006.

379. Budowle, B., Gyllensten, U., Chakraborty R., Allen, M.: Forensic analysis of the mitochondrial coding region and association to disease. Int. J. Leg. Med. 119:314-315, 2005.

380. Ecker, D.J., Sampath, R., Willet, P., Samant, V., Massire, C., Hall, T.A., Kumar, H., McNeil, J.A., Buchen-Osmond, C., and Budowle, B.: The microbial rosetta stone III: global and emerging infectious microorganisms. BioMed Central Microbiology 5(1):19, 2005.

381. Ecker, D.J., Sampath, R., Willet, P., Samant, V., Massire, C., Hall, T.A., Kumar, H., McNeil, J.A., Buchen-Osmond, C., and Budowle, B.: The microbial rosetta stone I: A Common structure for microbial biosecurity threat agents. J. Forens. Sci. 50:1380-1385, 2005.

382. Budowle, B., Garofano, P., Hellman, A., Ketchum, M., Kanthaswamy, S, Parson, W., van Haeringen, W., Fain, S., and Broad, T.: Recommendations for animal DNA forensic and identity testing. Int. J. Legal Med. 119:295-302, 2005.

383. Hall, T., Budowle, B., Jiang, Y., Blyn, L., Eshoo, M., Sannes-Lowery, K., Samant, V., White, N., Ecker, D.J., and Hofstadler, S.: Base composition analysis of human mitochondrial DNA using electrospray ionization mass spectrometry: a novel tool for the identification and differentiation of humans. Anal. Biochem. 344:53-69, 2005.

384. Budowle, B., and Harmon, R.: HIV legal precedent useful for microbial forensics. Croatian Med. J. 46(4):514-521, 2005.

385. Budowle, B., Johnson, M.D., Fraser, C.M., Leighton, T.J., Murch, R.S., and Chakraborty, R.: Genetic analysis and attribution of microbial forensics evidence. Critical Rev. Microbiol. 31(4):233-254, 2005.

386. Schutzer, S., Budowle, B., and Atlas, R.: Microbial forensics and the physician. PLoS Med 2(12):e337, 2005.

387. Martínez-Jarreta, B., Vásquez, P., Abecia, E., Budowle, B., Luna, A., and Peiró, F.: Characterization of 17 Y-STR loci in a population from El Salvador (San Salvador, Central America) and their potential for DNA profiling. J. Forens. Sci. 50:1243-1246, 2005.

388. Allard, M.W., Polanskey, D., Wilson, M.R., Monson, K.L., and Budowle, B.: Evaluation of variation in control region sequences for Hispanic individuals in the SWGDAM mtDNA data set. J. Forens. Sci. 51:566-573, 2006.

389. Andreasson, H., Nilsson, M., Budowle, B., Lundberg, H., and Allen, M.: Nuclear and mitochondrial DNA quantification of various forensic materials. Forens. Sci. Int. 164:56-64, 2006.

390. Budowle, B., Buscaglia, J., and Schwartz Perlman, R.: Review of the scientific basis for friction ridge comparisons as a means of identification: committee findings and recommendations. Forens. Sci. Comm. 8(1), 2006, At: http://www.fbi.gov/hq/lab/fsc.

391. Budowle, B. and Dickenson, D.: Mitochondrial DNA SNP detection: design issues and the use of mass spectrometry as an analysis platform. Sixteenth International Symposium on Human Identification 2005, Promega Corporation, Madison, Wisconsin, 2005, http://www.promega.com/ussympl6proc/default.htm.

392. Biesecker, L.G., Bailey-Wilson, J., Ballantyne, J., Baum, H., Bieber, F., Brenner, C., Budowle, B., Butler, J., Carmody, G., Conneally, P.M., Duceman, B., Eisenberg, A., Forman, L., Kidd, K., LeClair, B., Niezgoda, S., Parsons, T., Pugh, E., Shaler, R., Sherry, S., and Sozer, A.: Identification of the remains of victims from the World Trade Center attack: scientific challenges and policy implications. Science 310:1122-1123, 2005.

393. Marian, C., Anghel, A., Dressler, M.L., and Budowle, B.: Population data for the D5S8181, D13S317, D7S820, and D16S539 STR loci in a Romanian population sample. J. Forens. Sci. 50:1512, 2005.

394. Chang, C.W., Mulero, J.J., Budowle, B., Calandro, L.M., and Hennessy, L.K.: Identification of a novel polymorphism in the X-chromosome region homologous to the DYS456 locus. J. Forens. Sci. 51(2):344-348, 2006.

395. Cariolou, M.A., Manoli, P., Demetriou, N., Bashiardes, E., Karagrigoriou, A., and Budowle, B.: Allele distribution of 15 STR loci used for human identity purposes in the Greek Cypriot population of the island of Cyprus. Forens. Sci. Int. 164:75-78, 2006.

396. Shewale, J.G., , Bhushan, A., Nasir, H., Schneida, E., Washington, B., Fleming, Sinha, S.K., Gross, A.M., Budowle, B., and Sinha, S.K.: Population data for four population groups from the United States for the eleven Y-chromosome STR loci recommended by SWGDAM. J. Forens. Sci. 51:700-702. 2006.

397. Henry, R.C., Alleyne, L.E., and Budowle, B.: Population data on eight STR loci in the Barbadian population. J. Forens. Sci. 51:440-441, 2006.

398. Andreasson, H., Nilsson, M., Budowle, B., Frisk, S., and Allen, M.: Quantification of mtDNA mixtures in forensic evidence materials using pyrosequencing. Int. J. Leg. Med. 120:383-390, 2006. 399. Morse, S.A. and Budowle, B.: Microbial forensics- application to bioterrorism preparedness and response. Infectious Disease Clinics of North America 20: 455-473, 2006.

400. Harmon R. and Budowle, B.: Questions about forensic science. Science 311:607, 2006.

401. Smrz, M.A., Burmeister, S.G., Einseln, A., Fisher, C.L., Fram, R., Stacey, R.B., Theisen, C.E., and Budowle, B.: Review of FBI latent print unit processes and recommendations to improve practices and quality. J. Forens. Ident. 56(3):402-434, 2006.

402. Mulero, J.J., Budowle, B., Butler, J.M., and Gusmao, L.: Nomenclature and allele repeat structure update for the Y-STR locus GATA H4. J. Forensic Sci.51:694, 2006.

403. González-Andrade, F., Sánchez, D., Martínez-Jarreta, B., and Budowle, B.: Y-chromosome STR haplotypes in three different population groups from Ecuador (South America). J. Forens. Sci. 53(2):512-514, 2008.

404. Fletcher, J., Bender, C., Budowle, B., Cobb, W.T., Gold, S.E., Ishimaru, C.A., Luster, D., Melcher, U., Murch, R., Scherm, H., Seem, R.C., Sherwood, J.L., Sobral, B.W., and Tolin, S.: Plant pathogen forensics: capabilities, needs and recommendations. Microbiology and Molecular Biology Reviews 70(2):450-471, 2006.

405. Martinez-Gonzalez, L.J., Lorente, J.A., Martinez-Espin, E., Alvarez, J.C., Fernandez-Rosado, F., Entrala, C., Lorente, M., Villanueva, E., and Budowle, B.: Intentional mixed buccal cell reference sample in a paternity case. J. Forens. Sci. 52:397-399, 2007.

406. Budowle, B., Schutzer, S.E., Burans, J.P., Beecher, D.J., Cebula, T.A., Chakraborty, R., Cobb, W.T., Fletcher, J., Hale, M.L., Harris, R.B., Heitkamp, M.A., Keller, F.P., Kuske, C., LeClerc, J.E., Marrone, B.L., McKenna, T.S., Morse, S.A., Rodriguez, L.L., Valentine, N.B., Yadev, J.: Quality sample collection, handling, and preservation for an effective microbial forensics program. Applied and Environmental Microbiology 72(10):6431-6438, 2006.

407. Martinez-Espin, E., Martínez-Gonzalez, L.J., Fernandez-Rosado, F., Entrala, C., Alvarez, J.C., Lorente, J.A., Budowle, B., and Gutierrez-de-Monroy, M.O.: Guatemala Mestizo population data on fifteen STR loci (Identifiler kit). J. Forens. Sci. 51:1216-1218, 2006.

408. Budowle, B., Planz, J.V., Chakraborty, R., Callaghan, T.F., and Eisenberg, A.J.: Clarification of statistical issues related to the operation of CODIS. Seventeenth International Symposium on Human Identification 2006, Promega Corporation, Madison, Wisconsin, 2006, At: http://www.promega.com/ussymp17proc/default.htm.

409. Gross, A.M. and Budowle, B.: Minnesota population data on 15 STR loci using the Identifiler kit. J. Forens. Sci. 51:1410-1413, 2006.

410. Wong, H.Y., Tang, J.S., Budowle, B., Allard, M.W., Syn, C.K., Tan-Siew, W.F., Chow, S.T.: Sequence polymorphism of the mitochondrial DNA hypervariable regions I and II in 205 Singapore Malays. Legal Med. 9:33-37, 2007.

411. Marian, C., Anghel, A., Bel, S.M., Ferencz, B.K., Ursoniu, S., Dressler, M., Popescu, O., and Budowle, B.: STR data for the 15 AmpFlSTR identifiler loci in the Western Romanian population. Forens. Sci. Int. 170(1):73-75, 2007.

412. Alvarez, J.C., Johnson, D.L.E., Lorente, J.A., Martinez-espin, E., Martinez-Gonzalez, L.J., Allard, M., Wilson, M.R., and Budowle, B.: Characterization of human control region sequences for Spanish individuals in a forensic mtDNA data set. Legal Medicine 6:293-304, 2007.

413. Henke, L., Muche, M., Blaauw, A., van Eede, P.H., Martin, W., Helmken, C., Budowle, B., and Henke, J.: Validation of a new short tandem repeat (STR) fluorescent multiplex system and report of population genetic data. Clin. Lab. 53:477-482, 2007.

414. Budowle, B., Beaudry, J.A., Barnaby, N.G., Giusti, A.M., Bannon, J.D., and Keim, P.: Law enforcement response and microbial forensics role in investigation of bioterrorism. Croatian Med. J. 48:437-449, 2007.

415. Bügl, H., Danner, J.P., Molinari, R.J., Mulligan, J., Roth, D.A., Wagner, R., Budowle, B., Scripp, R.M., Smith, J.A.L., Steele, S.J., Church, G., and Endy, D.: A practical perspective on DNA synthesis and biological security. Nature Biotechnology 25(6):627-629, 2007.

416. Eisenberg, A.J., Klevan, L., and Budowle, B.: An overview of forensic DNA typing: tools, databases and future technological prospects. Journal of Japanese Society of DNA Polymorphism Research 15:11-26, 2007.

417. Budowle, B., Ge J., and Chakraborty, R.: Basic principles for estimating the rarity of Y-STR haplotypes derived from forensic evidence. Eighteenth International Symposium on Human Identification 2007, Promega Corporation, Madison, Wisconsin, 2007, At: http://www.promega.com/ussymp18proc/default.htm.

418. Budowle, B., Fisher, C.L., Polanskey, D., Den Hartog, B.K., Kepler, R.B., and Elling, J.W.: Stabilizing mtDNA sequence nomenclature with an operationally efficient approach. Forens. Sci. Int. Genetics Supplement Series 1:671-673, 2008.

419. Butler, J.M., Budowle, B., Gill, P., Kidd, K.K., Phillips, C., Schneider, P.M., Vallone, P.M., and Morling, N.: Report on ISFG SNP panel discussion. Forens. Sci. Int. Genetics Supplement Series 1:471-472, 2008.

420. McCurdy, L.D., Gioeni, L.J., Penella, T., Fisher, C.L., Isenberg, A.R., Hall. T.A., Sannes-Lowery, K.A., Hofstadler, S.A., and Budowle, B.: Multiplex PCR electrospray-ionization mass spectrometry (ESI-MS): application to forensic mitochondrial DNA examinations. Forens. Sci. Int. Genetics Supplement Series 1:52-54, 2008.

421. Hunt, S.Y., Morse, S.A., Barnaby, N.G., and Budowle, B.: Forensic Microbiology. In: Encyclopedia of Microbiology, Schaechter, M., (ed.), Elsevier, Oxford, pp. 539-551, 2009.

422. Morse, S.A and Budowle, B.: Microbial Forensics. In: Encyclopedia of Life Sciences, John Wiley & Sons, Ltd., West Sussex, UK (DOI:10.1002/9780470015902.a0004035), 2008.

423. Budowle, B. and van Daal, A.: Forensically relevant SNP classes. BioTechniques 44(5):603-610, 2008.

424. Hari, K.L., Goates, A.T., Jain, R., Towers, A. Harpin, V.S., Robertson, J.M., Wilson, M.R., Samant, V.S., Ecker, D.J., McNeil, J.A., and Budowle, B.: The Microbial Rosetta Stone: A database system for tracking infectious microorganisms. Int. J. Leg. Med. 123(1):65-69, 2009.

425. Budowle, S.A., Gonzales, S., Budowle, B., Eisenberg, A.J., and Grange, R.W.: A novel SNaPshot® assay to detect the mdx mutation. Muscle and Nerve 37(6):731-735, 2008.

426. Budowle, B., Baechtel, F.S., and Chakraborty, R.: Partial matches in heterogeneous offender databases do not call into question the validity of random match probability calculations. Int. J. Leg. Med. 123(1):59-63, 2009.

427. Budowle, B., Aranda, X., Lagace, R.E., Hennessy, L.K., Planz, J.V., Rodriguez, M., and Eisenberg, A.J.: Null allele sequence structure at the DYS448 locus and implications for profile interpretation. Int. J. Leg. Med. 122:421-427, 2008.

428. McLaren, R.S., Ensenburger, M., Budowle, B., Rabbach, D., Fulmer, P., Sprecher, C., Bessetti, J., Sundquist, T., and Storts, D.: Post-injection hybridization of complementary DNA strands on capillary electrophoresis platforms: a novel solution for dsDNA artifacts. Forens. Sci. Int. Genetics 2:257-273, 2008.

429. Budowle, B., Onorato, A.J., Callaghan, T.F., Della Manna, A., Gross, A.M., Guerrieri, R.A., Luttman, J.C., and McClure, D.L.: Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. J. Forens. Sci. 54:810-821, 2009.

430. Budowle, B., Schutzer, S.E., Morse, S.A., Martinez, K.F., Chakraborty, R., Marrone, B.L., Murch, R.S., Jackson, P.J., Williamson, P., Harmon, R., and Velsko, S.P.: Guidance for validation in microbial forensics. Applied and Environmental Microbiology 74:5599-5607, 2008.

431. Kastelic, V., Budowle, B., and Drobnic, K.: Validation of SRY marker for forensic casework analysis. J. Forens. Sci. 54(3):551-555, 2009.

432. Budowle, B., Ge, J., Low, J., Lai, C., Yee, W.H., Law, G., Tan, W.T., Chang, Y.M., Mizuno, N., Kasai, K., Sekiguchi, K., and Chakraborty, R.: The effects of Asian population substructure on Y STR forensic analyses. Leg. Med. 11:64-69, 2009.

433. Kanthaswamy, S., Tom, B.K., Mattila, A., Johnston, E., Dayton, M., Halverson, J., Fantin, D., DeNise, S., Kou, A., Malladi, V., Satkoski, J., Budowle, B., Smith, D.G., and Koskinen, M.T.: Canine population data generated from a multi-plex STR kit for use in forensic casework. J. Forens. Sci. 54:829-840, 2009.

434. Budowle, B., Ge, J., Aranda, X.G., Planz, J.V., Eisenberg, A.J., and Chakraborty, R.: Texas population substructure and estimating the rarity of Y STR haplotypes in forensic analyses. J. Forens. Sci. 54(5):1016-1021, 2009.

435. Nunez, A.N., Kavlick, M.F., Robertson, J.M., and Budowle, B: Application of circular ligase to provide template for rolling circle amplification of low amounts of fragmented DNA. Nineteenth International Symposium on Human Identification 2008, Promega Corporation, Madison, Wisconsin, 2008, http://www.promega.com/ussymp19proc/default.htm.

436. Alshamali, F., Pereira, L., Budowle, B., Poloni, E.S., and Currat, M.: Local population structure in Arabian Peninsula revealed by Y-STR diversity. Human Heredity 68:45-54, 2009.

437. Budowle, B., Bottrell, M.C., Bunch, S.G., Fram, R., Harrison, D., Meagher, S., Oien, C.T., Peterson, P.E., Seiger, D.P., Smith, M.B., Smrz,, M.A., Soltis, G.L., and Stacey, R.B.: A perspective on errors, bias, and interpretation in the forensic sciences and direction for continuing advancement. J. Forens. Sci. 54:798-809, 2009.

438. Ge, J., Budowle, B., Aranda, X.G., Planz, J.V., Eisenberg, A.J., and Chakraborty, R.: Mutation rates at Y chromosome short tandem repeats in Texas populations. Forens. Sci. Int. Genetics 3(3):179-184, 2009.

439. Maybruck, J.L., Hanson, E., Ballantyne, J., Budowle, B., and Feurst, P.A.: A comparative analysis of two different sets of Y-chromosome short tandem repeats (Y-STRs) on a common population panel. Forens. Sci. Int. Genetics 4(1):11-20, 2009.

440. Budowle, B. and van Daal, A.: Extracting evidence from forensic DNA analyses: future molecular biology directions. BioTechniques 46(5):339-350, 2009.

441. Smith, B.G., Lee, B., and Budowle, B.: Population data for 15 STR loci (Identifiler® kit) in a Filipino population. Leg. Med. 11(3):159-161, 2009.

442. Budowle, B., Eisenberg, A.J., and van Daal. A.: Validity of low copy number typing and applications to forensic science. Croatian Med. J. 50(3):207-217, 2009.

443. Tom, B.K., Koskinen, M.T., Dayton, M., Mattila, A.M., Johnston, E., Fantin, D., DeNise, S., Spear, T., Smith, D.G., Satkoski, J., Budowle, B., and Kanthaswamy, S.: Development of a nomenclature system for a canine STR multiplex reagent kit. J. Forens. Sci. 55(3):597-604, 2010

444. Dayton, M., Koskinen, M.T., Tom, B.K., Mattila, A.M., Johnston, E., Halverson, J., Fantin, D., DeNise, S., Budowle, B., Smith, D.G., and Kanthaswamy, S.: Developmental validation of an short tandem repeat reagent kit for forensic DNA profiling of canine biological material. Croatian Med. J. 50(3):268-285, 2009.

445. Smalling, B.B. Satkoski, J.A., Tom, B.K., Szeto, W.Y., Erickson B.J., Spear, T.F., Smith, D.G., Budowle, B., Webb, K., Allard, M., and Kanthaswamy, S.: Geographic differences in mitochondrial DNA (mtDNA) distribution among United States (US) domestic dog populations. The Open Forensic Science Journal 3:22-32, 2010.

446. Hall, T.A., Sannes-Lowery, K.A., McCurdy, L.D., Fisher, C., Anderson, T., Henthorne, A., Budowle, B., and Hofstadler, S.A.: Base composition profiling of human mitochondrial DNA using PCR and direct automated electrospray ionization mass spectrometry. Analytical Chem. 81(18):7515-7526, 2009.

447. Budowle, B., Eisenberg, A.J., Gonzalez, S., Planz, J.V. Sannes-Lowery, K.A., Hall, T.A., Paulsen, J.E., and Hofstadler, S.A.: Validation of mass spectrometry analysis of mitochondrial DNA. Forens. Sci. Int. Gen. Suppl. Series 2:527-528, 2009.
448. Cummings, C.A., Bormann Chung, C.A., Fang, R., Barker, M., Brzoska, P.M., Williamson, P., Beaudry, J.A., Matthews, M., Schupp, J.M., Wagner, D.M., Furtado, M.R., Keim, P., and Budowle, B.: Whole-genome typing of *Bacillus anthracis* isolates by next-generation sequencing accurately and rapidly identifies strain-specific diagnostic polymorphisms. Forens. Sci. Int. Gen. Suppl. Series 2:300-301, 2009.

449. Budowle, B., Eisenberg, A.J., and van Daal, A.: Low copy number typing has yet to achieve "General Acceptance". Forens. Sci. Int. Gen. Suppl. Series 2:551-552, 2009.

450. Planz, J.V., Budowle, B., Hall, T., Eisenberg, A.J., Sannes-Lowery, K., and Hofstadler, S.A.: Enhanced resolution and statistical power by using mass spectrometry for detection of SNPs within the short tandem repeats. Forens. Sci. Int. Gen. Suppl. Series 2:529-531, 2009.

451. Hofstadler, S.A., Hall, T.A., Sannes-Lowery, K.A., Manalili, S., Paulsen, J.E., McCurdy, L.D., Gioeni, L., Penella, T., Eisenberg, A.J., Planz, J.V., and Budowle, B.: Analysis of DNA forensic markers using high throughput mass spectrometry. Forens. Sci. Int. Gen. Suppl. Series 2:524-526, 2009.

452. Den Hartog, B.K., Elling, J.W., and Budowle, B.: The Impact of Jumping Alignments on mtDNA Population Analysis and Database Searching. Forens. Sci. Int. Gen. Suppl. Series 2:315-316, 2009.

453. Roby, R.K., Gonzalez, S.D., Phillips, N.R., Planz, J.V., Thomas, J.L., Pantoja Astudillo, J.A., Ge, J., Aguirre Morales, E., Eisenberg, A.J., Chakraborty, R., Bustos, P., and Budowle, B.: Autosomal STR allele frequencies and Y-STR and mtDNA haplotypes in Chilean sample populations Forens. Sci. Int. Gen. Suppl. Series 2:532-533, 2009.

454. Polanskey, D., Den Hartog, B.K., Elling, J.W., Fisher, C.L., Kepler, R.B., and Budowle, B.: Comparison of Mitotyper rules and phylogenetic-based mtDNA nomenclature systems. J. Forens. Sci. 55(5):1184-1189, 2010.

455. Budowle, B., Polanskey, D., Fisher, C.L., Den Hartog, B.K., Kepler, R.B., and Elling, J.W.: Automated alignment and nomenclature for consistent treatment of polymorphisms in the human mitochondrial DNA control region. J. Forens. Sci. 55(5):1190-1195, 2010.

456. Cheong, P.Y., Liew, P.V.O., Ibrahim, H., and Budowle, B.: A genetic database for DNA-based forensic analysis in Brunei Darussalam. Brunei Darussalam Journal of Health 3:1-6, 2008.

457. Budowle, B., Chakraborty, R., and van Daal, A.: Response to commentary by Gill and Buckleton. J. Forens. Sci. 55(1)269-273, 2010.

458. Budowle, B.: Response to Krane et al. J. Forens. Sci. 55(1)275-276, 2010.

459. Schutzer, S., Keim, P., Czerwinski, J., and Budowle, B.: Use of forensic methods under exigent circumstances prior to full validation. Science Translational Medicine 1(8cm7): 1-3, 2009.

460. Nilsson, M., Possnert, G., Edlund, H., Budowle, B., Kjellström, A., and Allen, M.: Analysis of the putative remains of a European patron saint-St. Birgitta. PloS One 5(2):e8986, 2010.

461. Ge, J., Budowle, B., Planz, J.V., and Chakraborty, R.: Haplotype block: a new type of forensic DNA marker. Int. J. Leg. Med. 124(5):353-361, 2010.

462. Ge, J., Budowle, B., and Chakraborty, R.: Choosing relatives for DNA identification of missing person identification. J. Forens. Sci. 56 Suppl 1:S23-8, 2011.

463. Ge, J., Budowle, B., and Chakraborty, R.: DNA identification by pedigree likelihood ratio with population substructure and mutations. BMC Investigative Genetics 1:8, 2010.

464. Ge, J., Budowle, B., and Chakraborty, R.: Interpreting Y chromosome STR mixture. Leg. Med. 12(3):137-143, 2010.

465. Cummings, C.A., Bormann-Chung, C.A., Fang, R., Barker, M., Brzoska, P., Williamson, P.C., Beaudry, J., Matthews, M., Schupp, J., Wagner, D.M., Birdsell, D., Vogler, A.J., Furtado, M.R., Keim P., and Budowle, B.: Accurate, rapid, and high-throughput detection of strain-specific polymorphisms in Bacillus anthracis and Yersinia pestis by next-generation sequencing. BMC Investigative Genetics 1:5, 2010.

466. Budowle, B., Eisenberg, A., and van Daal, A.: Response to Comment on "Low copy number typing has yet to achieve "general acceptance"" (Budowle et al., 2009. Forensic Sci. Int. Genetics: Supplement Series 2, 551-552) by Theresa Caragine, Mechthild Prinz., Forens. Sci. Int. Genetics 5(1):5-7, 2011.

467. Budowle, B. and van Daal, A.: Comment on "A universal strategy to interpret DNA profiles that does not require a definition of low copy number" by Peter Gill and John Buckleton, 2010, Forensic Sci. Int. Genetics 4, 221-227. Forens. Sci. Int. Genetics 5(1):15, 2011.

468. Nuñez, C., Baeta, M., Sosa, C., Casalod, Y., Ge, J., Budowle, B., González-Andrade, F., and Martínez-Jarreta, B.: Reconstructing the population history of Nicaragua by means of mtDNA, Y-chromosome STR and autosomal STR markers. Amer. J. Phys. Anthropol. 143(4):591-600, 2010.

469. Budowle, B.: Low copy number typing still lacks robustness and reliability. Profiles in DNA 13(2), 2010; At: www.promega.com/profiles/1302/1302 02.html.

470. Budowle, B.: Familial searching: extending the investigative lead potential of DNA typing. Profiles in DNA 13(2), 2010, At: www.promega.com/profiles/1302/1302 07.html.

471. Ge, J., Budowle, B., Planz, J., Eisenberg, a., Ballantyne, J., and Chakraborty, R.: U.S. forensic Y chromosome short tandem repeats database. Leg. Med. 12(6):289-295, 2010.

472. Budowle, B. and van Daal, A.: Reply to Comments by Buckleton and Gill on "Low copy number typing has yet to achieve 'general acceptance'" by Budowle, B., et al, 2009. Forensic Sci. Int. Genetics: Supplement Series 2, 551-552. Forens. Sci. Int. Genetics 5(1):12-14, 2011.

473. Ge, J., Eisenberg, A., Yan, J., Chakraborty, R., and Budowle, B.: Pedigree likelihood ratio for lineage markers. Int. J. Leg. Med. 125(4):519-525, 2011. 474. Ge, J., Budowle, B., and Chakraborty, R.: Comments on "Interpreting Y chromosome STR haplotype mixture". Leg. Med. 13(1):52, 2011.

475. Balamurugan, K., Kanthimathi, S., Vijaya, M., Suhasini, G., Duncan, G., Tracey, M., and Budowle, B. Genetic variation of 15 autosomal microsatellite loci in a Tamil population from Tamil Nadu, Southern India. Leg. Med. 12(6):320-323, 2010.

476. Sajantila, A., Palo, J.U., Ojanperä, I., Davis, C., and Budowle, B.: Pharmacogenetics in medico-legal context. Forens. Sci. Int. 203(1-3):44-52, 2010.

477. Budowle, B., Ge, J., Chakraborty, R., Eisenberg, A.J., Green, R., Mulero, J., Lagace, R., and Hennessy, L.: Population Genetic Analyses of the NGM STR Loci. Int. J. Leg. Med. 125:101-109, 2011.

478. Ge, J., Chakraborty, R., Eisenberg, A. and Budowle, B.: Comparisons of the familial DNA database searching policies. J. Forens. Sci. 56(6):1448-1456, 2011.

479. Kavlick, M.F., Lawrence, H.S., Merritt, R.T., Fisher, C., Isenberg, A., Robertson, J.M., and Budowle, B.: Quantification of human mitochondrial DNA using synthesized DNA standards. J. Forens. Sci. 56(6):1457-1463, 2011.

480. Ge, J., Yan, J., Budowle, B., Chakraborty, R., and Eisenberg, A.: Issues on China forensic DNA database. Chinese Journal of Forensic Medicine 26(3): 252-255, 2011.

481. Budowle, B. and Williamson, P.C.: Microbial forensics - a scientific discipline for response to bioterrorism and biocrime. Jamieson A. and Moenssens A., eds., Wiley Encyclopedia of Forensic Science, John Wiley & Sons, Ltd., Chichester, UK, 2011, DOI: 10.1002/9780470061589.fsa1031.

482. Frumkin, D., Wasserstrom, A., Budowle, B., and Davidson, A.: DNA methylation-based forensic tissue identification. Forens. Sci. Int. Genet. 5(5):517-524.

483. Lee, S.B., Clabaugh, K.C., Silva, B., Odigie, K.O., Coble, M.D., Loreille, O., Scheible, M., Fourney, R.M., Stevens, J., Carmody, G.R., Parsons, T.J., Selmanovic, A., Eisenberg, A.J., Budowle, B., Ahmad, T., Miller, R.W., and Crouse, C.A.: Assessing a novel room temperature DNA storage medium for forensic biological samples. Forens. Sci. Int. Genet. 6(1):31-40, 2012.

484. Budowle, B., Kayser, M.K., and Sajantila, A.: The demise of UK's Forensic Science Service (FSS): loss of world-leading engine of innovation and development in the forensic sciences. BMC Investigative Genetics 2:4, 2011.

485. Davis, C., Ge, J., Chidambaram, A., King, J., Turnbough, M., Collins, M., Dym, O., Chakraborty, R., Eisenberg, A.J., and Budowle, B.: Y-STR loci diversity in native Alaskan populations. Int. J. Leg. Med. 125:559-563, 2011.

486. Chakraborty, R., Ge, J., and Budowle, B.: Response to: DNA identification by pedigree likelihood ratio accommodating population substructure and mutations - authors' reply. BMC Investigative Genetics 2:8, 2011.

487. Nuñez, A.N., Tate, C.M., Goldstein, C.A., Gomes, I., Kavlick, M.F., Robertson, J.M., and Budowle, B.: Evaluation of circular DNA substrates for whole genome amplification prior to forensic analysis. Forens. Sci. Int. Genet. 6:185-190, 2012.

488. Núñez C., Sosa, C., Baeta, M., Geppert, M., Turnbough M., Phillips N., Casalod, Y., Bolea, M., Roby R., Budowle B., Roewer, L., and Martínez-Jarreta, B.: Ancient DNA analysis of skeletons from a medieval burial in the Aragonese Pyrenees. Croatian Med. J. 52(3):336-343, 2011.

489. Budowle, B., Ge, J., Chakraborty, R., and Gill-King, H.: Use of prior odds for missing persons identifications. BMC Investigative Genetics 2:15, 2011.

490. Budowle, B., Ge, J., Chakraborty, R., and Gill-King, H.: Reply to Biedermann, Taroni, and Margot. BMC Investigative Genetics 3:3, 2012.

491. Davis, C., King, J., Budowle, B., Eisenberg, A.J., and Turnbough, M.: Extraction system-platform evaluations: a comparison of Automate Express™, EZ1<sup>®</sup> Advanced XL, and Maxwell<sup>®</sup> 16. Leg. Med. 14(1):36-9, 2012.

492. LaRue, B.L., Ge, J., King, J.L., and Budowle, B.: A validation study of the Qiagen Investigator DIPplex<sup>®</sup> Kit; an INDEL based assay for human identification. Int. J. Leg. Med. 126(4):533-540, 2012.

493. Davis, C., Ge, J., King, J., Malik, N., Weirich, V., Eisenberg, A.J., and Budowle, B.: Variants observed for STR locus SE33: a concordance study. Forens. Sci. Int. Genetics 6(4):494-497, 2012.

494. Ge, J., Eisenberg, A., and Budowle, B.: Developing criteria and data to determine best options for expanding the core CODIS loci. BMC Investigative Genetics 3:1, 2012.

495. Myers, B., King, J., and Budowle, B.: Validation of direct amplification of STRs using PowerPlex® 18D and Identifiler® Direct systems. Forens. Sci. Int. Genetics 6(5):640-645.

496. Planz, J.V., Sannes-Lowery, K.A., Duncan, D.D., Manalili, S., Budowle, B., Chakraborty, R., Hofstadler, S.A., and Hall, T,A.: Automated analysis of sequence polymorphism in STR alleles by PCR and direct electrospray ionization mass spectrometry. Forens. Sci. Int. Genet. 6(5):594-606, 2012.

497. Li, L., Ge, J., Zhang, S., Guo, J., Zhao, S., Li, C., Tang, H., Davis, C., Budowle, B., Hou, Y., and Liu, Y.: Maternity exclusion with a very high autosomal STRs kinship index. Int. J. Leg. Med. 126(4):645-648, 2012.

498. Davis, C., Illescas, M., Tirado, C., Lopez, R., Budowle, B., and Dawson Cruz, T.: A Case of Amelogenin Y null: A simple primer binding site mutation or unusual genetic anomaly? Leg. Med. 14(6):320-323, 2012.

499. Ge, Y. and Budowle, B.: Kinship index variations among populations and thresholds for familial searching. PLoS One 7(5): e37474, 2012.

500. Davis, C., Ge, J., Sprecher, C., Chidambaram, A., Thompson, J., Ewing, M., Fulmer, P., Rabbach, D., Storts, D., and Budowle, B.: Prototype PowerPlex<sup>®</sup> Y23 System: A Concordance Study. Forens. Sci. Int. Genet. 7(1):204-208, 2013.

501. Alvarez-Cubero, M.J., Saiz, M., Martinez-Gonzalez, L.J., Alvarez, J.C., Eisenberg, A.J., Budowle, B., and Lorente, J.A.: Genetic identification of missing persons: DNA analysis of human remains and compromised samples. Pathobiology 79(5):228-238, 2012.

502. Warshauer, D.H., Marshall, P., Kelley, S., King, J., and Budowle, B.: An evaluation of the transfer of saliva-derived DNA. Int. J. Leg. Med. 126(6):851-861, 2012.

503. Warshauer, D.H., King, J., Eisenberg, A.J., and Budowle, B.: Validation of the PLEX-ID<sup>™</sup> mass spectrometry mitochondrial DNA assay. Int. J. Leg. Med. 127(2):277-286, 2013.

504. Li, B., Ge, J., Wu, F., Ye, L., Budowle, B., and Chen, Y.: Population genetic analyses of the STR loci of the AmpFlSTR NGM SElect<sup>™</sup> kit for Han population in Fujian Province, China. Int. J. Leg. Med. 127(2):345-346, 2013.

505. LaRue, B.L., King, J.L., and Budowle, B.: A validation Study of the Nucleix DSI-Semen Kit - a Methylation-Based Assay for Semen Identification. Int. J. Leg. Med. 127(2):299-308, 2013.

506. Budowle, B., Schmedes, S., and Murch, R.S.: The microbial forensics pathway for use of massively-parallel sequencing technologies. The science and applications of microbial genomics. Institute of Medicine, Washington, DC, The National Academies Press, pp. 117-133, 2013.

507. LaRue, B.L., Sinha, S.K., Montgomery, A.H., Thompson, R., Klaskala, L., Ge, J., King, J., Turnbough, M., and Budowle, B.: INNULs, a new strategy for human identification based on retrotransposable elements. Hum. Hered. 74(1):27-35, 2012.

508. Marshall, P.L., King, J.L., Lawrence, N.P., Lazarev, A., Gross, V.S., and Budowle, B.: Pressure cycling technology (PCT) reduces effects of inhibitors of the PCR. Int. J. Leg. Med. 127(2):321-333, 2013.

509. Keating, B., Bansal, A.T., Walsh, S., Millman, J., Newman, J., Kidd, K., Budowle, B., Eisenberg, A., Donfack, J., Gasparini, P., Budimlija, Z., Henders, A.K., Chandrupatla, H., Duffy, D.L., Gordon, S.D., Hysi, P., Liu, F., Medland, S.E., Rubin, L., Martin, N.G., Spector, T.D., and Kayser M.: First all-in-one inference tool for DNA forensics: parallel genome-wide inference of bio-geographic ancestry, appearance, relatedness and gender with Identitas forensic chip. Int. J. Leg. Med. 127(3):559-572, 2013.

510. Schmedes, S., Marshall, P., King, J.L., and Budowle, B.: Effective removal of co-purified inhibitors from extracted DNA samples using synchronous coefficient of drag alteration (SCODA) technology. Int. J. Leg. Med. 127(4):749-755, 2013.

511. Budowle, B.: Editors' Pick: Normal aging versus Alzheimer's disease - expression patterns may discern the differences. BMC Investigative Genetics 3(1):11, 2012.

512. Budowle, B.: Editors' Pick: ENCODE and its first impractical application. BMC Investigative Genetics 4(4), 2013.

513. Jin, H.X., Seo, S.B., Lee, H.Y., Cho, S., King, J., Budowle, B., and Lee, S.D.: Differences of PCR efficiency between two-step PCR and standard three-step PCR protocols in short tandem repeat amplification. Australian Journal of Forensic Sciences 46(1):80-90, 2014.

514. Alenizi, M., Ge, J., Ismael, S., Alenezi, H., AlAwadhi, A., AlDuaij, W., AlSaleh, B., Ghulloom, Z., and Budowle, B.: Population genetic analyses of the 15 STR loci of seven forensically-relevant populations residing in Kuwait. Forens. Sci. Int. Genet. 7(4):e106-107, 2013.

515. Warshauer, D.H.; Lin, D., Hari, K., Jain, R., Davis, C., LaRue, B., King, J., and Budowle, B.: STRait Razor: A length-based forensic STR allelecalling tool for use with second generation sequencing data. Forens. Sci. Int. Genet. 7:409-417, 2013.

516. Seo, S.B., King, J., Warshauer, D., Davis, C., Ge, J., and Budowle, B.: Single nucleotide polymorphism typing with massively parallel sequencing for human identification. Int. J. Leg. Med. 127(6):1079-1086, 2013.

517. Budowle, B., Warshauer, D.H., Seo, S.B., King, J.L., Davis, C., and LaRue, B.: Massively parallel sequencing provides comprehensive multiplex capabilities. Forensic Sci. Int.: Genetics Supplement Series 4:e334-e335, 2013.

518. Ge, J. and Budowle, B.: Modeling one complete versus triplicate analyses in Low Template DNA typing. Int. J. Leg. Med. 128(2):259-267, 2014.

519. Seo, S.B., Ge, J., King, J.L., and Budowle, B.: Reduction of stutter ratios in short tandem repeat loci typing of low copy number DNA samples. Forens. Sci. Int. Genet. 8(1):213-218, 2014.

520. LaRue, B.L., Lagacé, R., Chang, C., Holt, A., Hennessy, L., Ge, J., King, J.L., Chakraborty, R., and Budowle, B.: Characterization of 114 insertion/deletion (INDEL) polymorphisms, and selection of a global INDEL panel for human identification. Leg. Med. 16(1):26-32, 2014.

521. Ambers, A., Gill-King, H., Dirkmaat, D., Benjamin, R., King, J., and Budowle, B: Autosomal and Y-STR analysis of degraded DNA from the 120-year-old skeletal remains of Ezekiel Harper. Forens. Sci. Int. Genet. 9:33-41, 2014.

522. Budowle, B.: Editors' pick: re-'colon'-ization of healthy microbiota after recurrent C. difficile infection. Invest. Genet. 4(1):28, 2013.

523. Kayser, M., Sajantila, A., and Budowle, B.: A tribute to DNA fingerprinting. 4(1):19, 2013.

524. Flores, S.K., Sun, J., King, J., and Budowle, B.: Validation of the GlobalFiler™ Express PCR Amplification Kit for the direct amplification of single-source DNA samples on a high-throughput automated workflow. Forens. Sci. Int. Genet. 10:33-39, 2014.

525. Ambers, A., Turnbough, M., Benjamin, R., King, J., and Budowle, B.: Assessment of the role of DNA repair in damaged forensic samples. Int. J. Leg. Med. 128(6):913-921, 2014.

526. Li, S., Liu, C., Liu, H., Ge, J., Budowle, B., Liu, C., Zheng, W., Li, F., and Ge, B.: Developmental validation of the EX20+4 system. Forens. Sci. Int. Genet. 11:207-213, 2014.

527. Schmedes, S.E., Budowle, B.: Forensic Microbiology, Reference Module in Biomedical Sciences, Elsevier, pp. 1-13, doi:10.1016/B978-0-12-801238-3.02483-1, 2015.

528. Vuorio, A., Laukkala, T., Navathe, P., Budowle, B., Eyre, A., and Sajantila, A.: Aircraft-assisted pilot suicides - data from United States, Germany, United Kingdom and Finland from 1990 to 2012. Aviation, Space, and Environmental Medicine 85(8):841-846, 2014.

529. Marshall, P.L., King, J.L., and Budowle, B.: Utility of amplification enhancers in low copy number DNA analysis. Int. J. Leg. Med. 129(1):43-52, 2015.

530. Ge, J., Sun, H., Li, H., Liu, C., Yan, J., Budowle, B.: Future directions of forensic DNA databases. Croatian Med. J. 55:163-166, 2014.

531. LaRue, B.L., Moore, A., King, J.L., Marshall, P.A., and Budowle, B.: Evaluation and validation of the RapidHIT<sup>™</sup> system for reliably genotyping reference samples. Forens. Sci. Genet. Int. 13:104-111, 2014.

532. Mulero, J.J., Ballantyne, J., Ballantyne, K., Budowle, B., Coble, M., Gusmao, L., Ralf, A., Kayser, M., and Roewer, L.: Nomenclature update and Allele repeat structure for the markers DYS518 and DYS449. Forens. Sci. Genet. Int. 13:e3, 2014.

533. Purps, J., Siegert, S., Willuweit, S., Nagy, M., Budowle, B., Roewer, L.: A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forens. Sci. Int. Genet. 12:12-13, 2014.

534. Sajantila, A., Budowle, B.: Post mortem medico-legal genetic diagnostics also require reporting guidance. Eur. J. Hum. Genet. 24(3):329-30, 2016.

535. Alenizi, M., Ge, J., Salih, A., Alenizi, H., Al jabber, J., Ziab, J., Al harbi, E., Isameal, S., Budowle, B.: Population data on 25 autosomal STRs for 500 unrelated Kuwaitis. Forens. Sci. Genet. Int. 12:126-127, 2014.

536. King, J.L., Sajantila, A., and Budowle, B.: mitoSAVE: mitochondrial sequencing analysis of variants in excel. Forens. Sci. Genet. Int. 12:122-125, 2014.

537. King, J.L., LaRue, B.L., Novroski, N., Stoljarova, M., Seo, S.B., Zeng, X., Warshauer, D., Davis, C., Parson, W., Sajantila, A., and Budowle, B.: High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. Forens. Sci. Int. Genet. 12:128-135, 2014.

538. Marshall, P.L., Stoljarova, M., Larue, B.L., King, J.L., and Budowle, B.: Evaluation of a novel material, Diomics X-Swab<sup>™</sup>, for collection of DNA. Forens. Sci. Genet. Int. 12:192-18, 2014.

539. Marshall, P.L., Stoljarova, M., Schmedes, S.E., King, J.L., and Budowle, B.: A high volume extraction and purification method for recovering DNA from human bone. Forens. Sci. Genet. Int. 12:155-160, 2014.

540. Budowle, B., Connell, N.D., Bielecka-Oder, A., Colwell, R.R., Corbett, C.R., Fletcher, J., Forsman, M., Kadavy, D.R., Markotic, A., Morse, S.A., Murch, R.S., Sajantila, A., Schmedes, S.E., Ternus, K.L., Turner, S.D., Minot, S.: Validation of high throughput sequencing and microbial forensics applications. BMC Invest. Genet. 5:9, 2014.

541. Flores, S., Sun, J., King, J., Eisenberg, A., and Budowle, B.: Allele frequencies for 15 autosomal STR loci and haplotype data for 17 Y-STR loci in a population from Belize. Int. J. Leg. Med. 129(6):1217-1218, 2015.

542. Budowle, B.: Molecular genetic investigative leads to differentiate monozygotic twins. BMC Invest. Genet. 5:11, 2014.

543. Seo, S.B., Zeng, X., King, J.L., Larue, B.L., Assidi, M., Al-Qahtani, M.H., Sajantila, A., and Budowle, B.: Underlying data for sequencing the mitochondrial genome with the massively parallel sequencing platform Ion Torrent<sup>™</sup> PGM<sup>™</sup>. BMC Genomics 16 Suppl. 1:S4, 2015.

544. Davis, C., Peters, D., Warshauer, D., King, J., and Budowle, B.: Sequencing the hypervariable regions of human mitochondrial DNA using massively parallel sequencing: Improved methods for DNA samples encountered in forensic testing. Leg. Med. 17(2):123-127, 2015.

545. Warshauer, D.H., Davis, C.P., Holt, C., King, J.L., and Budowle, B.: Massively parallel sequencing of forensically-relevant single nucleotide polymorphisms using TruSeq<sup>™</sup> Forensic Amplicon. Int. J. Leg. Med. 129(1):31-36, 2015.

546. Warshauer, D.H., King, J.L., and Budowle, B.: STRait Razor v2.0: the improved STR allele identification tool - razor. Forens. Sci. Int. Genet. 14:182-186, 2015.

547. Moura-Neto, R.S, Silva, R., Mello, I.C., Nogueira, T., Al-Deib, A.A., LaRue, B., King, J., and Budowle, B.: Evaluation of a 49 InDel Marker HID Panel in Two Specific Populations of South America and One Population of Northern Africa. Forens. Sci. Int. Genet. 129(2):245-249, 2015.

548. Zeng, X., King, J.L., Stoljarova, M., Warshauer, D.H., LaRue, B.L., Sajantila, A., Patel, J., Storts, D.R., and Budowle, B.: High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing. Forens. Sci. Int. Genet. 16C:38-47, 2014.

549. Taqi, Z., Al-enizi, M., Alenizi, H., Isameal, S., Aziz Bin Dukhyil, A., Nazir, M., Sanqoor, S., Al harbi, E., Al-jaber, J., Theyab, J., Budowle, B.: Population genetics of 23 Y-STR markers in Kuwaiti population. Forens. Sci. Int. Genet. 16C:203-204, 2015.

550. Churchill, J.D., Chang, J., Ge, J., Rajagopalan, N., Lagacé, R., Liao, W., King, J.L., Budowle, B.: Blind study evaluation illustrates utility of the Ion PGM™ System for use in human identity DNA typing. Croat. Med. J. 56(3):218-229, 2015.

551. Santos, C.G.M. Moura-Neto, R.S. Pimentel-Coelho, P.M., Dornelas-Ribeiro, M., Pompeu, F.A.M.S., Budowle, B., and Silva, R.: The heritable path of human physical performance: from single polymorphisms to the "next generation". Scandinavian Journal of Medicine and Science in Sports 26(6):600-612, 2016.

552. Zeng, X., King, J., Hermanson, S., Patel, J., Storts, D.R., and Budowle, B.: An evaluation of the PowerSeq<sup>™</sup> Auto system: a multiplex short tandem repeat marker kit compatible with massively parallel sequencing. Forens. Int. Genet. Int. 19:172-179, 2015.

553. Stoljarova, M., King, J.L., Takahashi, M., Aaspõllu, A., and Budowle, B.: Whole mitochondrial genome genetic diversity in the Estonian Population sample. Forens. Int. Genet. Int. 130(1):67-71, 2016.

554. Warshauer, D.H., Churchill, J.D., Novroski, N., King, J.L., and Budowle, B.: Novel Y-chromosome short tandem repeat variants detected through the use of massively parallel sequencing. Genomics, Proteomics, and Bioninformatics 13(4):250-257, 2015.

555. Moretti, T.R., Budowle, B., and Buckleton, J.S. Erratum. J. Forens. Sci. 60(4):1114-1116, 2015.

556. Moretti, T.R., Budowle, B., and Buckleton, J.S. Authors' Response. J. Forens. Sci. 60(6):1669-1670, 2015.

557. Schmedes, S.E., King, L., and Budowle, B.: Correcting inconsistences and errors in bacterial genome metadata using an automated curation tool in Excel (AutoCurE). Frontiers in Bioengineering and Biotechnology 3:138, 2015.

558. Vuorio, A., Laukkala, T., Pooshan, N., Budowle, B., Eyre, A., and Sajantila, A.: On doctors' accountability and flight deck safety. Croatian Med. J. 56(4):385-386, 2015.

559. Churchill, J.D., Schmedes, S.E., King, J.L., and Budowle, B.: Evaluation of the Illumina® beta version ForenSeq<sup>™</sup> DNA Signature Prep Kit for use in genetic profiling. Forens. Int. Genet. Int. 20:20-29, 2015.

560. Ambers, A., Turnbough, M., Benjamin, R., Gill-King, H., King, J., Sajantila, A., and Budowle, B.: Modified DOP-PCR for improved STR typing of degraded DNA from human skeletal remains and bloodstains. Leg. Med. 22:54-63, 2016.

561. Zeng, X., Chakraborty, R., King, J.L., LaRue, B., Moura-Neto, R.S., and Budowle, B.: Selection of highly informative SNP markers for population affiliation of major U.S. populations. Int. J. Leg. Med. 130(2):341-52, 2016.

562. Parson, W., Ballard, D., Budowle, B., Butler, J., Hares, D., Gettings, K., Gill, P., Gusmão, L., Irwin, J., King, J., de Knijff, P., Morling, N., Prinz, M., Schneider, P.M., Van Neste, C., Willuweit, S., and Phillips, C.: Massively Parallel Sequencing of forensic STRs: Considerations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forens. Sci. Int. Genet. 22:54-63, 2016.

563. Wendt, F., Zeng, X., Churchill, J., King, J., and Budowle, B.: Analysis of short tandem repeat (STR) and single nucleotide polymorphism (SNP) loci from single source samples using a custom HaloPlex Target Enrichment System panel. Amer. J. Forens. Med. Pathol. 37(2):99-107, 2016.

564. Zeng, X., Warshauer, D.H., King, J.L., Churchill, J.D., Chakraborty, R., and Budowle, B.: Empirical testing of four major US populations with a 23-AIMs panel. Int. J. Leg. Med. 130(4):891-896, 2016.

565. Rahikainen, A., Palo, J.U., de Leeuw, W., Budowle, B., and Sajantila, A.: DNA quality and quantity from up to 16 years old post-mortem blood stored on FTA cards. Forens. Sci. Int. 261:148-153, 2016.

566. Schmedes, S., Sajantila, A., and Budowle, B.: Expansion of microbial forensics. J. Clin. Microbiol. 54(8):1964-1974, 2016.

567. Phillips, C., Parson, W., Amigo, J., King, J.L., Coble, M.D., Steffen, C.R., Vallone, P.M., Gettings, K.B., Butler, J.M., and Budowle, B.: D5S2500 is an ambiguously characterized STR: Identification and description of forensic DNA markers in the genomics age. Forens. Sci. Int. Genet. 23:19-24, 2016.

568. Churchill, J.D., King, J.L., Chakraborty, R., and Budowle, B.: Effects of the Ion  $PGM^{m}$  Hi-Q<sup>m</sup> sequencing chemistry on sequence data quality. Int. J. Leg. Med. 130(5):1169-80, 2016.

569. Ambers, A., Churchill, J.D., King, J.L., Stoljarova, M., Gill-King, H., Assidi, M., Abu-Elmagd, M., Buhmeida, A., Al-Qahtani, M., and Budowle, B.: Characterization of unidentified 140-year-old human skeletal remains using massively parallel DNA sequencing. BMC Genomics 17(Suppl. 9):750, 2016.

570. Nazir, M., Alhaddad, H., Alenizi, M., Alenizi, H., Taqi, Z., Sanqoor, S., Alrazouqi, A., Hassan, A., Alfalasi, R., Gaur, S., Al Jaber, J., Ziab, J., Al-Harbi, E., Moura-Neto, R.S., and Budowle, B.: A genetic overview of 23Y-STR markers in UAE population. Forens. Sci. Int. Genet. 23:150-152, 2016.

571. Wendt, F., Churchill, J.D., Novroski, N.M., King, J.L., Ng, J., Oldt, R.F., McCulloh, K.L., Weise, J.A., Smith, D.G., Kanthaswamy, S., and Budowle, B.: Genetic analysis of the Yavapai Native Americans from west-central Arizona. Forens. Sci. Int. Genet. 24:18-23, 2016.

572. Bieber, F.R., Buckleton, J., Budowle, B., Butler, J., and Coble, M.D.: Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. BMC Genetics 17(1):125, 2016.

573. Al-Attis, A., Assidi, M., Al-Maghrabi, J., Dallol, A., Schulten, H-J., Abu-Elmagd, M., Chaudhary, A., Abuzenadah, A., Budowle, B., Buhmeida, A., and Al-Qahtani, M.: Enhancement of pathologist's routine practice: reuse of DNA extracted from immunostained formalin-fixed paraffin-embedded (FFPE) slides in downstream molecular analysis of cancer. Cancer Genomics & Proteomics 13(5):399-406, 2016.

574. Ng, J., Oldt, R.F., McCulloh, K.L., Weise, J.A., Viray, J., Budowle, B., Smith, D.G., Kanthaswamy, S.: Native American population data based on the Globalfiler® autosomal STR loci. Forens. Sci. Int. Genet. 24:e12-13, 2016.

575. Novroski, N.M, King, J.L., Churchill, J.D., Seah, L.H., and Budowle, B.: Characterization of genetic sequence variation of 58 STR loci in four major population groups. Forens. Sci. Int. Genet. 25:214-226, 2016.

576. Vuorio, A., Laukkala, T., Pooshan, N., Budowle, B., Bor, R., and Sajantila, A.: Bipolar disorder in aviation medicine. Aerospace Medicine & Human Performance 88(1):42-47, 2017.

577. Wendt, F.R., Warshauer, D.H., Zeng, X., Churchill, J.D., Novroski, N.M., Song, B., King, J.L., LaRue, B.L., and Budowle, B.: Massively parallel sequencing of 68 insertion/deletion markers identifies novel microhaplotypes for utility in human identity testing. Forens. Sci. Int. Genet. 25:198-209, 2016.

578. Budowle, B., Capt, C., Chakraborty, R., and Ge, J.: Paternity calculations in a di-spermy case. Int. J. Leg. Med. 131(2):339-343, 2017.

579. McCulloh, K.L., Ng, J., Oldt, R.F., Weise, J.A., Viray, J., Budowle, B., Smitha, D.G., and Kanthaswamy, S.: The genetic structure of Native Americans in North America based on the Globalfiler® STRs. Leg. Med. 23:49-54, 2016.

580. Monnerat-Cahli, G., Paulúcio, D., Moura Neto, R., Silva, R., Pompeu, F., Budowle, B., and Santos, C.G.: Are the doors opened to "A genetic-based algorithm for personalized resistance training"? Biology of Sport 34:27-29, 2016.

581. Vuorio, A., Asmayawati, S., Budowle, B., Griffiths, R., Strandberg, T., and Sajantila, A.: General aviation pilots over 70 years old: a new challenge for physicians. Aerospace Medicine & Human Performance 88(2):142-145, 2017.

582. Abu-Elmagd, M., Assidi, M., Dallol, A., Buhmeida, A., Natesan Pushparaj, P., Kalamegam, G., Ahmed, W., Al-Hamzi, E., Shay, J., Scherer, S., Agarwal, A., Budowle, B., Gari, M., Chaudhary, A., Abuzenadah, A., and Al-Qahtani, M.: The third international genomic medicine conference (3<sup>rd</sup> IGMC, 2015): Overall activities and outcome highlights. BMC Genomics 17(Suppl. 9):747, 2016.

583. Lindberg, M.R., Schmedes, S.E., Hewitt, C., Ternus, K., Kadavy, D., and Budowle, B.: A Comparison and integration of MiSeq and MinION platforms for sequencing single source and mixed mitochondrial genomes. PLoS ONE 11(12):e0167600, 2016.

584. Pakstis, A.J., Kang, L., Liu, L., Zhang, Z., Jin, T., Grigorenko, E.L., Wendt, F.R., Budowle, B., Hadi, S., Al Qahtani, M.S., Morling, N., Mogensen, H.S., Themudo, G.E., Soundararajan, S., Rajeevan, H., Kidd, J.R., and Kenneth, K.K: Increasing the reference populations for the 55 AISNP panel: the need and benefits. Int. J. Leg. Med. 131(4):913-917, 2017.

585. Martínez-Jarreta, B., Sosa, C., Laliena, C., Budowle, B., and Hedges, R.: Stable isotopes and radiocarbon dating of the remains of the medieval royal house of Aragon (Spain) shed light on their diets, life histories and identities. Archaeometry (in press).

586. Gittelson, S., Moretti, T.R., Onorato, A.J., Budowle, B., Weir, B., and Buckleton, J.: The factor of 10 in forensic DNA match probabilities. Forens. Sci. Int. Genet. 28:178-187, 2017.

587. Wendt, F.R., Sajantila, A.., Chakraborty, R., and Budowle, B.: Global genetic variation of select opiate metabolism genes in self-reported healthy individuals. Pharmacogenomics Journal (in press).

588. Wendt, F., King, J.L., Novroski, N.M., Churchill, J.D., Ng, J., Oldt, R.F., McCulloh, K.L., Weise, J.A., Smith, D.G., Kanthaswamy, S., and Budowle, B.: Flanking region variation of ForenSeq<sup>™</sup> DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans. Forens. Sci. Int. Genet. 28:146-154, 2017.

589. King, J.L., Wendt, F.R., Sun, J., and Budowle, B.: STRait Razor v2s: Advancing sequence-based STR allele reporting and beyond to other marker systems. Forens. Sci. Int. Genet. 29:21-28, 2017.

590. Churchill, J.D., Novroski, N.M.M., King, J.L., Seah, L.H., and Budowle, B.: Population and performance analyses of four major populations with Illumina's FGx Forensic Genomics System. Forens. Sci. Int. Genet. 30:81-92, 2017.

591. Översti, S., Onkamo, P., Stoljarova, M., Budowle, B., Sajantila, A., and Palo, J.: Local demographic patterns buried in the present mtDNA genome pool: Finland as an example. Sci. Rep. 7(1):6193, 2017.

592. Brown, H., Thompson, R., Murphy, G.P., Peters, D., LaRue, B., King, J., Montgomery, A.H., Carroll, M., Baus, J., Sinha, S., Wendt, F., Song, B., Chakraborty, R., Budowle, B., and Sinha, S.K.: Development and validation of a novel multiplexed DNA analysis system, InnoTyper<sup>®</sup> 21. Forens. Sci. Int. Genet.29:80-99, 2017.

593. Moretti, T.R. and Budowle, B.: Reiteration of the statistical basis of DNA source attribution determinations in view of the Attorney General's directive on "reasonable scientific certainty" statements. J. Forens. Sci. 62(4):1114-1115, 2017.

594. Alonso, A., Müller, P., Roewer, L., Willuweit, S., Budowle, B., Parson, W.: European survey on forensic applications of massively parallel sequencing. Forens. Sci. Int. Genet. 29:e23-e25, 2017.

595. Budowle, B., Schmedes, S.E., and Wendt, F.R.: Increasing the reach of forensic genetics with massively parallel sequencing. Forensic Science, Medicine and Pathology 13:342-349, 2017.

596. Young, B., King, J.L., Budowle, B., and Armogida, L.: A technique for setting analytical thresholds in massively parallel sequencing-based forensic DNA analysis. PLoS ONE 12(5):e0178005, 2017.

597. Zeng, X., King, J., and Budowle, B.: Investigation of the STR loci noise distribution of PowerSeq<sup>™</sup> Auto System. Croat. Med. J. 58(3):214-221, 2017.

598. Woerner, A.E., King, J.L., and Budowle, B.: Fast STR allele identification with STRait Razor 3.0. Forens. Sci. Int. Genet. 29:21-28, 2017.

599. Vanek, D., Budowle, B., Dubska-Votrubova, J., Ambers, A., Frolik, J., Pospisek, M., Anwar Al Afeefi, A., Ismaeil Al Hosani, K., Allen, M., Saeed Al Naimi, K., Al Salafi, D., Ali Rashid Al Tayyari, W., Arguetaa, W., Bottinelli, M., Bus, M.M., Cemper-Kiesslich, J., Cepil, O., De Cock, G., Desmyter, S., El Amri, H., El Ossmani, H., Galdies, R., Grün, S., Guidet, F., Hoefges, A., Bogdan Iancu, C., Lotz, P., Maresca, A., Nagy, M., Novotny, J., Rachid, H., Rothe, J., Stenersen, M., Stephenson, M., Stevanovitch, A., Strien, J., Sumita, D.R., Vella, J., and Zander, J.: Results of a collaborative study on DNA identification of aged bone samples. Croat. Med. J. 58(3):203-213, 2017.

600. Heraclides, A., Bashiardes, E., Fernández-Domínguez, E., Chimonas, M., Christofi, V., King, J., Budowle, B., Manoli, P., Cariolou, M.A.: Ychromosomal analysis investigating similarities and differences in the paternal ancestry of Greek Cypriots and Turkish Cypriots. PLoS ONE 12(6):e0179474, 2017.

601. Laukkala, T., Bor, R., Budowle, B., Sajantila, A., Navathe, P., Sainio, M., and Vuorio, A.: Attention-deficit/hyperactivity disorder and fatal accidents in aviation medicine. Aerospace Medicine and Human Performance 88(9):871-875.

602. Cabral, B., Hoffmann, L., Budowle, B., Ürményi, T., Moura-Neto, R., Azevedo, S., and Silva, R.: Planktonic microbial profiling in water samples from a Brazilian Amazonian reservoir. MicrobiologyOpen 7(2):e00523, 2018.

603. Moura-Neto, R.S., Mello, I.C.T., Silva, R., Maette, A.P.C., Bottino, C.G., Woerner, A., King, J., Wendt, F., and Budowle, B.: Evaluation of InnoTyper® 21 in a sample of Rio de Janeiro population as an alternative forensic panel. Int. J. Leg. Med. 132(1):149-151, 2018.

604. Jeanguenat, A.M., Budowle, B., and Dror, I.E.: Strengthening forensic DNA decision making through a better understanding of the influence of cognitive bias. Science&Justice 57(6):415-420, 2017.

605. Schmedes, S.E., Woerner, A.E., and Budowle, B.: Forensic human identification using skin microbiomes. Applied Environ. Microbiol. (in press).

606. Gettings, K., Borsuk, L.A., Ballard, D., Bodner, M., Budowle, B., Devesse, L., King, J.L., Parson, W., Phillips, C., and Vallone, P.M.: STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. Forens. Sci. Int. Genet.31:111-117, 2017.

607. Elwick, K., Zeng, X., King, J., Budowle, B., and Hughes-Stamm, S.: Comparative tolerance of two massively parallel sequencing systems to common PCR inhibitors. Int. J. Leg. Med. 132(4):983-995, 2018.

608. Churchill, J.D., Peters, D., Capt, C., Strobl, C., Parson, W., and Budowle, B.: Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework. Forensic Science International: Genetics Supplement Series 6: e388-e389, 2017.

609. Churchill, J.D., Stoljarova, M., King, J.L., and Budowle, B.: Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data. Forensic Science International: Genetics Supplement Series 6: e439-e441, 2017.

610. Votrubova, I., Ambers, A., Budowle, B., and Vanek, D.: Comparison of standard capillary electrophoresis based genotyping method and ForenSeq DNA Signature Prep kit (Illumina) on a set of challenging samples. Forensic Science International: Genetics Supplement Series 6: e140-e142, 2017.

611. Wiley, R., Sage, K., Larue, B., and Budowle, B.: Internal validation of the RapidHIT<sup>®</sup> ID System. Forens. Sci. Int. Genet. 31:180-188, 2017.

612. Wendt, F.R., Sajantila, A., Moura-Neto, R.S., Woerner, A.E., and Budowle, B. Full-gene haplotypes refine CYP2D6 metabolizer phenotype inferences. Int. J. Leg. Med. 132(4):1007-1024, 2018.

613. Schmedes, S.E., Woerner, A.E., Novroski, N.M.M., Wendt, F., King, J.L., and Budowle, B.: Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. Forens. Sci. Int. Genet. 32:50-61, 2017.

614. Ambers, A., Wiley, R., Novroski, N., and Budowle, B.: Direct PCR amplification of DNA from human bloodstains, saliva, and touch samples collected with microFLOQ<sup>®</sup> Swabs. Forens. Sci. Int. Genet. 32:80-87, 2017.

615. Woerner, A.E., King, J.L., and Budowle, B.: Flanking variation influences rates of stutter in simple repeats. Genes 8(11):329, 2017.

616. Wendt, F.R., Sajantila, A., and Budowle, B.: Predicted activity of UGT2B7, ABCB1, OPRM1, and COMT using full-gene haplotypes and their association with the *CYP2D6*-inferred metabolizer phenotype. Forens. Sci. Int. Genet. 33:48-58, 2018.

617. Churchill, J.D., Stoljarova, M., King, J., and Budowle, B.: Massively Parallel Sequencing-Enabled Mixture Analysis of Mitochondrial DNA Samples. Int. J. Leg. Med. (in press).

618. Ambers, A., Votrubova, J., Vanek, D., Sajantila, A., and Budowle, B.: Improved Y-STR typing for disaster victim identification, missing persons investigations, and historical human skeletal remains. Int. J. Leg. Med. (in press).

619. Laukkala, T., Vuorio, A., Bor, R., Budowle, B., Navathe, P., Pukkala, E., and Sajantila, A.: Copycats in pilot aircraft-assisted suicides after the Germanwings incident. International Journal of Environmental Research and Public Health 15(3):E491, 2018.

620. Laukkala, T., Bor, R., Budowle, B., Navathe, P., Sajantila, A., Sainio, M., and Vuorio, A.: Pilot`s post-traumatic stress disorder and fatal aviation accidents: a descriptive study. Aviation Psychology and Applied Human Factors (in press).

621. Novroski N.M.M., Woerner A.E., and Budowle, B.: Insertion within the flanking region of the D10S1237 Locus. Forens. Sci. Int. Genet. 35:e4-e6, 2018.

622. Alonso, A., Barrio, P.A., Müller, P., Köcher, S., Berger, B., Martin, P., Bodner, M., Willuweit, S., Parson, W., Roewer, L., and Budowle, B.: Current state-of-art of STR sequencing in forensic genetics. Electrophoresis (in press).

623. Wendt, F.R., Woerner, A.E., Sajantila, A., Moura-Neto, R.S., and Budowle, B.: Exploring the 1000 Genomes Project haplotype reporting for the *CYP2D6* pharmacogene. Int. J. Leg. Med. (in press).

624. Vuorio, A., Budowle, B., Sajantila, A., Laukkala, T., Junttila, I., Kravik, S.E., and Griffiths, R.: Duty of notification and aviation safety - a study of fatal aviation accidents in the United States in 2015. International Journal of Environmental Research and Public Health 15(6): E1258, 2018.

625. King, J.L., Churchill, J.D., Novroski, N.M.M., Zeng, X., Warshauer, D., Seah, L.H., and Budowle, B.: Increasing the discrimination power of ancestryand identity-informative SNP amplicons within the ForenSeq<sup>™</sup> DNA Signature Prep Kit. Forens. Sci. Int. Genet. 36:60-76, 2018.

626. Junttila, I.S., Vuorio, A., Budowle, B., Laukkala, T., and Sajantila, A.: Challenges in investigation of diabetes related aviation fatalities - an analysis of 1491 subsequent aviation fatalities in USA during 2011-2016. Aerospace Medicine and Human Performance (in press).

627. Buckleton, J.S., Bright, J.A., Gittelson, S., Moretti, T.R., Onorato, A.J., Bieber, F.R., Budowle, B., and Taylor, D.A.: The probabilistic genotyping software STRmix: Utility and evidence for its validity. J. Forens. Sci. (in press).

628. Woerner, A.E., Ambers, A., Wendt, F.R., King, J.L., Moura-Neto, R.S., Silva, S., and Budowle, B.: Mitochondrial genome sequencing with the Precision ID Whole Genome Panel on two massively parallel sequencing systems. Forens. Sci. Int. Genet. (in press).

## BOOKS, REPORTS, and VIDEOS

Federal Bureau of Investigation: <u>VNTR Population Data: A Worldwide Study</u>, Volumes I-IV, Forensic Science Research and Training Center, FBI Academy, Quantico, Virginia, 1993.

Allen, R.C. and Budowle, B.: <u>Gel Electrophoresis of Proteins and Nucleic</u> Acids: Selected Techniques, Walter de Gruyter, Berlin, pp. 1-352, 1994.

Allen, R.C. and Budowle, B.: <u>Protein Staining and Identification Techniques</u>, BioTechniques® Books -Eaton Publishing, Natick, MA, 99. 1-139, 1999.

Budowle, B., Smith, J.A., Moretti, T. and DiZinno, J.: <u>DNA Typing Protocols:</u> <u>Molecular Biology and Forensic Analysis</u>, BioTechniques Books, BioForensic Sciences Series, Eaton Publishing, Natick, MA, 2000.

Hochmeister, M., Lee, H.C., and Budowle, B.: <u>DNA Evidence: Guidelines for</u> Collection, Packaging, and Preservation.

Breeze, R.G., Budowle, B., and Schutzer, S. (eds.): <u>Microbial Forensics</u>, Academic Press, Amsterdam, 2005.

Budowle, B., Schutzer, S.E., Breeze, R., Keim, P.S., and Morse, S.A. (eds.): Microbial Forensics, Second Edition, Academic Press, Amsterdam, 2011.

Science Needs for Microbial Forensics: Developing Initial International Research Priorities, Committee for the Science Needs for Microbial Forensics: Developing an Initial International Science Roadmap, Board on Life Sciences, National Research Council of the National Academies, National Academies Press, Washington, D.C., 2014.

Familial DNA Searching: Current Approaches, Final Report. National Institute of Justice, Office of Investigative and Forensic Sciences, 2015; At: https://rti.connectsolutions.com/p49iz1rzbpi/.

Biowatch, PCR Assays, Building Confidence, Ensuring Reliability, Board of Life Sciences, Division on Earth and Life Sciences, Board of Health Sciences Policy, Institute of Medicine, Board on Global Health, National Research Council of the National Academies. National Academy of Sciences, 2015.

Amorim, A. and Budowle B.: <u>Handbook of Forensic Genetics: Biodiversity and</u> <u>Heredity in Civil and Criminal Investigations</u>, World Scientific, New Jersey, pp. 1-632, 2017.

## PATENTS

Quantification of Human Mitochondrial DNA Using Synthesized DNA Standards; Mark F. Kavlick and Bruce Budowle, FBI; U.S. Patent No. 9,080,205; issued July 14, 2015.

Quantification of Human Mitochondrial DNA Using Synthesized DNA Standards; Mark F. Kavlick and Bruce Budowle, FBI; U.S. Patent No. 9,765,400; issued September 19, 2017.

## ABSTRACTS AND PRESENTATIONS

1. Budowle, B. and Esen, A.: Enzymatic change associated with juvenile and adult forms of English Ivy. 57th Annual Meeting of the Virginia Academy of Sciences, Richmond, Virginia, 1979.

2. Reitnauer, P. J., Acton, R. T., Barger, B. O., Budowle, B., Murphy, C. C., Roseman, J. M. and Go, R. C. P.: A population genetics study of insulindependent diabetes mellitus in young black Americans. Amer. Soc. Hum. Genet., New York City, New York, Amer. J. Hum. Genet. 32(6):149A, 1980.

3. Budowle, B., Barger, B. O., Go, R. C. P., Murphy, C. C., Reitnauer, P. J., Roseman, J. M. and Acton, R. T.: Properdin factor B (Bf) phenotypes in Blacks with insulin-dependent diabetes mellitus (IDDM). FASEB, Atlanta, Georgia, Fed. Proc. 40:1113, 1981.

4. Barger, B. O., Budowle, B., Go, R. C. P. and Acton, R. T.: HLA-A-Bf and HLA-B-Bf Black haplotype frequencies, American Association for Clinical Histocompatibility Testing, Orlando, Florida, 1981.

5. Budowle, B., Go, R. C. P. and Acton, R. T.: Isoelectric focusing of hair proteins, International Electrophoresis Society, Charleston, South Carolina, 1981.

6. Budowle, B., Balch, C. M., Barger, B. O., Go, R. C. P., Roseman, J. M. and Acton, R. T.: Properdin factor B in malignant melanoma, Amer. Assoc. Cancer Res., Washington, D. C., Proc. Amer. Assoc., Cancer Res. 22:71, 1981.

7. Budowle, B., Acton, R. T. and Allen, R. C.: Structural proteins of hair as a forensic marker, Southern Association of Forensic Scientists, Birmingham, Alabama, 1981.

8. Budowle, B. and Allen, R. C.: Electrophoretic methods in forensic medicine, Southern Association of Forensic Scientists, Birmingham, Alabama, 1981.

9. Budowle, B., Acton, R. T., Barger, B. O., Blackstock, R., Crist, W., Go, R. C. P., Humphrey, G. B., Ragab, A., Roper, M., Vietti, T. and Dearth, J.: Properdin factor B (Bf) phenotypes predict risk of contracting acute lymphocytic leukemia (ALL), Amer. Soc. Hemat., San Antonio, Texas, Blood 58(5):136A, 1981.

10. Budowle, B., Barger, B. O., Go, R. C. P. and Acton, R. T.: C4 phenotypes in Caucasians from the southeastern United States, International Electrophoresis Society, Athens, Greece, 1982.

11. Budowle, B.: A simple, rapid and inexpensive method for drying polyacrylamide slab gels, International Electrophoresis Society, Athens, Greece, 1982.

12. Conary, J. T., Budowle, B. and Thompson, J. M.: Cold focus for isoelectric focusing: Separation of B-hexosaminidase A and B isozymes, Alabama Academy of Science, Birmingham, Alabama, J. Alabama Academy of Science 53(3):84, 1982.

13. Budowle, B., Huddleston, J. F., Barger, B. O., Go. R. C. P. and Acton, R. T.: Properdin factor B as a predictor of non-obese gestational diabetes in black American women, American Diabetes Association, San Francisco, California, Diabetes 31(Suppl. 2):65A, 1982.

14. Budowle, B.: Advances in electrophoresis for forensic medicine, American Academy of Forensic Sciences, Orlando, Florida, 1982.

15. Budowle, B., Crist, W., Dearth, J., Go, R. C. P. and Roseman, J. M.: Complement phenotypes for prediction of risk and prognosis for acute lymphocytic leukemia (ALL), The Seventh Chicago Cancer Symposium, Chicago, Illinois, 1982.

16. Budowle, B., Dearth, J., Bowman, P., G, R., Crist, W. and Acton, R. T.: Black children with certain factor B and C4 phenotypes are genetically predisposed to ALL, Amer. Soc. Hemat. Washington, D. C., Blood 60(5) (suppl. 1):121a, 1982.

17. Budowle, B. and Mertens, J.: The removal of salts from small semen samples, A Forensic Science Symposium on the Analysis of Sexual Assault Evidence, FBI Academy, Quantico, Virginia, 1983.

18. Budowle, B., Gambel, A., and Baechtel, F. S.: Silver staining agarose gels for the forensic laboratory, Electrophoresis Society of America, Boston, Massachusetts, 1983.

19. Budowle, B. and Gambel, A.: Group-specific component in Bloodstains, Electrophoresis Society of America, Boston, Massachusetts, 1983.

20. Budowle, B.: Ultrathin-layer polyacrylamide gel isoelectric focusing for PGM subtyping, Mid-Atlantic Association of Forensic Scientists, Harper's Ferry, West Virginia, 1983.

21. Budowle, B.: Phenotyping esterase D by isoelectric focusing. International Society of Blood Transfusion, Munich, Germany, 1984. Murch, R. S. and Budowle, B.: Evaluation of erythrocyte acid phosphatase typing by isoelectric focusing using forensic casework samples, An International Symposium on the Forensic Applications of Electrophoresis, FBI Academy, Quantico, Virginia, 1984.

22. Budowle, B.: Methods for increasing resolution and sensitivity of detection of electrophoretic markers, An International Symposium on the Forensic Applications of Electrophoresis, FBI Academy, Quantico, Virginia, 1984.

23. Budowle, B.: Problems associated with lack of water control for phosphoglucomutase subtyping. NBS Workshop-Electrophoresis Standardization: Approaches and Needs, National Bureau of Standards, Gaithersburg, Maryland, 1984.

24. Budowle, B.: Obtaining reproducible, non-distorted results using ultrathin-layer polyacrylamide isoelectric focusing gels, Electrophoresis Society of America, Tucson, Arizona, 1984.

25. Budowle, B. and Murch, R.S.: Ultrathin polyacrylamide isoelectric focusing of phosphoglucomutase (PGM1) allotypes: further modifications, American Chemical Society, Miami, Florida, 1985.

26. Davidson, L. and Budowle, B.: Glyoxalase I typing and phosphoglucomutase-1 subtyping of a single hair, An International Symposium on Forensic Hair Comparisons, FBI Academy, Quantico, Virginia, 1985. 27. Davidson, L. and Budowle, B.: An agarose gel electrophoretic method for typing glyoxalase I, Mid-Atlantic Association of Forensic Scientists, Washington, D.C., 1985.

28. Budowle, B.: Genetic markers in hair, An International Symposium on Forensic Hair Comparisons, FBI Academy, Quantico, Virginia, 1985.

29. Budowle, B.: Ultrathin-layer isoelectric focusing for genetic marker typing, American Chemical Society, Chicago, Illinois, 1985.

30. Budowle, B.: Ultramicro gel electrophoresis: Forensic and genetic applications, Electrophoresis Society of America, Gaithersburg, Maryland, 1986.

31. Gambel, A., Budowle, B. and Murch, R.S.: Alpha 1-antitrypsin (Pi) phenotyping by ultrathin layer isoelectric focusing, Electrophoresis Society of America, Gaithersburg, Maryland, 1986.

32. Budowle, B.: Immunologic probes and silver staining for rapid detection of serum proteins after electrophoresis, Second Joint Meeting of the American and Japanese Histochemical Societies, San Francisco, California, 1986.

33. Allen, R. C. and Budowle, B.: A comparison of immunoprint-techniques following isoelectric focusing of the Gc protein: printing on cellulose acetate and on large pore ultrathin-layer polyacrylamide gels, An International Symposium on Forensic Immunology, FBI Academy, Quantico, Virginia, 1986.

34. Budowle, B. and Murch, R. S.: Current theory and applications of electrophoretic analyses in forensic serology, Combined meeting of Forensic Science Societies, Lexington, Kentucky, 1986.

35. Budowle, B.: Isoelectric focusing followed by silver staining of transferrin derived from human bloodstains, International Electrophoresis Society, London, England, 1986.

36. Gambel, A. and Budowle, B.: Glyoxalase I and phospho-glucomutase-1 analyses of hair sheath, International Electrophoresis Society, London, England, 1986.

37. Allen, R. C., Budowle, B., Lack, P. M. and Graves, G.: Rehydrated polyacrylamide gels: A comparison with conventionally cast gels, International Electrophoresis Society, London, England, 1986.

38. Budowle, B.: Validity and reliability of electrophoresis and current electrophoretic methods in use at the FBI, Mid-Atlantic Association of Forensic Scientists, Ocean City, Maryland, 1986.

39. Budowle, B.: Electrophoretic and histochemical developments in forensic serology, Electrophoresis Society of America, San Francisco, California, 1987.

40. Budowle, B.: An improved method for subtyping transferring derived from bloodstains, 11th Meeting of International Association of Forensic Sciences, Vancouver, Canada, 1987.

41. Coleman, H. C., Gambel, A., Howard, J. D., Fligner, C. L., Nakamura, Y., O'Connell, P., Budowle, B., and Reay, D. T.: Evaluation of DNA in decomposed tissues, 11th Meeting of International Association of Forensic Sciences, Vancouver, Canada, 1987.

42. Budowle, B.: Application of molecular biology to forensic Serology, Mid-Atlantic Association of Forensic Scientists, Alexandria, Virginia, 1987.

43. Budowle, B.: Forensic applications of DNA probes, DNA probes in the practice of medicine II, American Medical Association Conference, Los Angeles, California, 1987.

44. Murch, R. S., Baechtel, F. S. and Budowle, B.: Methods for the recovery of DNA from liquid blood and bloodstains, American Academy of Forensic Sciences, Philadelphia, Pennsylvania, 1988.

45. Budowle, B., Baechtel, F. S. and Murch, R. S.: Forensic applications of variable number tandem repeat DNA probes, American Academy of Forensic Sciences, Philadelphia, Pennsylvania, 1988.

46. Budowle, B.: DNA probes - practical approaches for practice, American Pathology Foundation Meeting, Charleston, South Carolina, 1988.

47. Budowle, B., Defenbaugh, D., Brinkman, J. and Baechtel, F. S.: Enhancing sensitivity of detection of the restriction fragment length polymorphism methodology, Electrophoresis Society of America, Charleston, South Carolina, 1988.

48. Budowle, B., Baechtel, F. S., Deadman, H. A., Brinkman, J. E., and Defenbaugh, D.: DNA typing approaches for characterization of forensic biological materials, California Association of Criminalists, Berkeley, California, 1988.

49. Budowle, B., Baechtel, F. S., Deadman, H. A., and Murch, R. S.: DNA typing in the FBI laboratory, Mid-Atlantic Association of Forensic Scientists, Virginia Beach, Virginia, 1988.

50. Budowle, B.: Restriction fragment length polymorphisms and multi-locus polymorphisms, DNA Technology in Forensic Science, FBI Academy, Quantico, Virginia, 1988.

51. Budowle, B.: A simple RFLP technique for detection of small quantities of DNA, International Academy of Legal Medicine and Social Medicine. The Society for Forensic Haemogenetics, Liege, Belgium, 1988.

52. Budowle, B.: An introduction to the methods of DNA analysis, American Chemical Society, Los Angeles, California, 1988.

53. Budowle, B.: Validation of DNA typing methods for application to forensic biological evidentiary materials, American Chemical Society, Los Angeles, California, 1988.

54. Budowle, B., Baechtel, F.S., and Adams, D.E.: Parameters for consideration in the design of RFLP methodology for forensic serology, Canadian Society of Forensic Science Meeting, Toronto, Canada, 1988.

55. Deadman, H.A., Budowle, B., and Comey, C.: PCR for the analysis of evidentiary biological material, Canadian Society of Forensic Science Meeting, Toronto, Canada, 1988.

56. Budowle, B.: Forensic Pathology, DNA probes in the practice of medicine: An update. American Medical Association Conference, San Diego, California, 1988.

57. Baechtel, F.S., Brinkmann, J.E., Hill, A.L., and Budowle, B.: DNA recovery from body fluid stains, American Academy of Forensic Sciences, Las Vegas, Nevada, 1989.

58. Budowle, B., Shutler, G., Waye, J., Adams, D.E., and Baechtel, F.S.: Selection of restriction endonuclease and interprobe comparison for RFLP technology, American Academy of Forensic Sciences, Las Vegas, Nevada, 1989.

59. Adams, D.E., Baechtel, F.S., and Budowle, B.: DNA analysis of body fluid stains subjected to environmental, chemical, and biological insults, American Academy of Forensic Sciences, Las Vegas, Nevada, 1989.

60. Budowle, B.: High resolution electrophoresis of PCR amplified DNA for identity, First International Symposium on PCR, London, England, 1989.

61. Budowle, B.: Casework and statistical analyses with regard to VNTR-RFLPs, California Association of Criminalists, Sacramento, California, 1989.

62. Budowle, B.: DNA probes for forensic and identity tests, Diagnostic Applications of Nucleic Acid Probes in the Clinical Laboratory. National Academy of Clinical Biochemistry, Toronto, Canada, 1989.

63. Giusti, A.M., Monson, K.L., Baechtel, F.S. and Budowle, B.: The distribution frequencies of restriction fragment lengths for ten variable number tandem repeat (VNTR) regions in a Black population, American Electrophoresis Society Meeting, Washington, D.C., 1989.

64. Baechtel, F.S., Adams, D.E., Monson, K.L., and Budowle, B.: Genetic typing of biological evidence by restriction fragment length polymorphism analysis - an approach to method validation and data interpretation, Eastern Analytical Symposium, New York, New York, 1989.

65. Budowle, B.: Forensic applications of molecular probe technologies, Association of Medical Laboratory Immunologists - Second Annual Meeting, Albany, New York, 1989.

66. Budowle, B.: RFLP, blotting and hybridization for DNA analysis, An International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1989.

67. Budowle, B.: Statistics of DNA analysis and database Development, An International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1989.

68. Allen, R.C., Lack, P.M., Graves, G.M., and Budowle, B.: Silver-stain visualization of amplified fragment length polymorphisms following polyacrylamide gel electrophoresis in discontinuous buffers, An International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1989.

69. Budowle, B.: Validation criteria and data for DNA typing for forensic application, Genetics Society of America, Atlanta, Georgia, 1989.

70. Budowle, B.: Molecular biology technology and applications for identity testing, American Electrophoresis Society Meeting, Washington, D.C., 1989.

71. Budowle, B.: New Aspects of VNTR analysis using PCR, Canadian Society of Forensic Science Meeting, Edmonton, Canada, 1989. Journal of the Canadian Society of Forensic Sciences 22(3): 289, 1989.

72. Budowle, B.: Analysis of polymerase chain reaction (PCR) products by polyacrylamide gel electrophoresis, International Society for Forensic Haemogenetics, New Orleans, Louisiana, 1989.

73. Budowle, B.: DNA probes in forensic pathology, The Third Annual Medical Association Conference on DNA Probes in the Practice of Medicine, San Diego, California, 1989.

74. Budowle, B.: DNA data analysis at the FBI Laboratories, The International Symposium on Human Identification - Data Acquisition and Statistical Analysis for DNA Typing Laboratories, Madison, Wisconsin, 1989.

75. Budowle, B.: Consideration for statistical analysis of VNTR Profiles, American Academy of Forensic Sciences, Cincinnati, Ohio, 1990.

76. Budowle, B.: Fixed bin analysis for DNA profile comparisons, American Academy of Forensic Sciences, Cincinnati, Ohio, 1990.

77. Budowle, B. and Allen, R.C.: AMP-FLP analysis by discontinuous polyacrylamide gel electrophoresis and silver staining, American Academy of Forensic Sciences, Cincinnati, Ohio, 1990.

78. Budowle, B.: Population genetics, frequencies and databases, Legal Aspects of Forensic DNA Analysis, FBI Academy, Quantico, Virginia, 1990.

79. Budowle, B.: Databases for interpretation: Statistical Considerations, The European Forensic Science DNA Symposium-Trevi Conference, London, England, 1990.

80. Budowle, B.: Use of DNA probes in forensic medicine, American College of Obstetricians and Gynecologists - Thirty-Eighth Annual Clinical Meeting, San Francisco, California, 1990.

81. Budowle, B.: Matching criteria and population statistics, Mid-Atlantic Association of Forensic Scientists, Fredericksburg, Virginia, 1990.

82. Budowle, B.: DNA technology in bloodstain analysis, International Symposium on DNA Technology for Forensic Analysis, Cologne Germany, 1990.

83. Budowle, B.: New advances in DNA analysis at the FBI Laboratories, Canadian Society of Forensic Science Meeting, Ottawa, Canada, 1990.

84. Budowle, B.: Case experience at the FBI Laboratories, Canadian Society of Forensic Science Meeting, Ottawa, Canada, 1990.

85. Giusti, A. M., Monson, K. L. and Budowle, B.: Determination of allele frequencies for six variable number tandem repeat (VNTR) loci for two racial groups, Canadian Society of Forensic Science Meeting, Ottawa, Canada, 1990.

86. Budowle, B., Giusti, A. M., and Chakraborty, R.: Discretized allelic data for a VNTR locus by amplified fragment length polymorphism (AMP-FLP) analysis, American Society of Human Genetics, Cincinnati, Ohio, 1990 Amer. J. Hum. Genet. 47 (3): A129, 1990.

87. Budowle, B.: Consideration regarding molecular biology analysis in forensic pathology, Pediatric Symposium, San Diego, California, 1990.

88. Giusti, A. M. and Budowle, B.: Determination of allele frequencies for the VNTR locus D10S28 in random population sample groups: Evaluation for identity testing, Amer. J. Hum. Genet. 47 (3): A135, 1990.

89. Weir, B. and Budowle, B.: Testing for disequilibrium at VNTR loci with forensic application, Amer. J. Hum. Genet. 47 (3): A148, 1990.

90. Baechtel, F. S., Monson, K. L., Forsen, G. E., Budowle, B., and Kearney, J. J.: Tracking the violent criminal offender through DNA typing profiles - A national database system concept, First International Conference on DNA Fingerprint, Berne, Switzerland, 1990.

91. Budowle, B., Giusti, A. M., Monson, K. L., Baechtel, F. S.: Restriction fragment length allele frequencies for six VNTR loci in several racial/ethnic groups, First International Conference on DNA Fingerprinting, Berne, Switzerland, 1990.

92. Robertson, J., Ziegle, J., Kronick, M., Madden, D., and Budowle, B.: Human identity testing using automated electrophoresis and fluorescence detection, First International Conference on DNA Fingerprinting, Berne, Switzerland, 1990.

93. Budowle, B.: Issues concerning the applicability of DNA typing of forensic biological evidence, International Association of Forensic Sciences, Adelaide, Australia, 1990.

94. Budowle, B., and Comey, C. T.: Amplification by PCR of VNTR loci. International Association of Forensic Sciences, Adelaide, Australia, 1990.

95. Monson, K. L. and Budowle, B.: A computerized system for measurement of RFLP fragments, International Association of Forensic Sciences, Adelaide, Australia, 1990.

96. Budowle, B., Monson, K. L., and Weir, B.: Statistical approaches for inculpatory data by using VNTR profiles, International Association of Forensic Sciences, Adelaide, Australia, 1990.

97. Robertson, J., Ziegle, J., Kronick, M., McBride, L., and Budowle, B.: Identity testing using automated electrophoresis and multi-wavelength fluorescence detection, International Association of Forensic Sciences, Adelaide, Australia, 1990.

98. Monson, K. L., Baechtel, F. S., Budowle, B., Kearney, J. J., and Forsen, G. E.: Development of nationwide statistical and investigative DNA databases, International Association of Forensic Sciences, Adelaide, Australia, 1990.

99. Budowle, B., Monson, K. L., Giusti, A. M., and Weir, B.: Population and statistical considerations for the use of highly polymorphic VNTR loci, American Academy of Forensic Sciences, Anaheim, California, 1991.

100. Hochmeister, M., Eggmann, U., Borer, U., and Budowle, B.: Extraction and typing of DNA from compact bone - a tool for the identification of decomposed bodies and human remains, American Academy of Forensic Sciences, Anaheim, California, 1991.

101. Comey, C. T. and Budowle, B.: Amplification by PCR of VNTR loci, American Academy of Forensic Sciences, Anaheim, California, 1991.

102. Monson, K. L., Baechtel, F. S., Budowle, B., Kearney, J. J. and Forsen, G. E.: Development and testing of a prototype system for nationwide access statistical and investigative DNA databases, American Academy of Forensic Sciences, Anaheim, California, 1991.

103. Robertson, J. M., Kronick, M., and Budowle, B.: Automated analysis of fluorescent PCR products for DNA typing, American Academy of Forensic Sciences, Anaheim, California, 1991.

104. Budowle, B.: The FBI program in DNA-based identification, American Association for Advancement of Science, Washington, D.C., 1991.

105. Allen, R.C., Graves, G.M., Budowle, B., and Reeder, D. J.: Matrix modification of rehydratable polyacrylamide gels for the separation of nucleic acids and proteins on homogeneous gel, International Meeting of the Electrophoresis Society, Washington, D.C., 1991.

106. Budowle, B.: Case studies. The application of DNA technology to Forensics, Riverside, California, 1991.

107. Budowle, B.: The potential and limits of RFLP analysis in Forensics, The Application of DNA Technology to Forensics, Riverside, California, 1991.

108. Budowle, B.: AMP-FLP analysis and potential use of forensics, European Forensic Science PCR Symposium, Trevi Conference, London, England, 1991.

109. Budowle, B.: AMP-FLPs-genetic markers for forensic Identification, An International Seminar on the Forensic Applications of PCR Technology, FBI Academy, Quantico, Virginia, 1991.

110. Allen, R.C., Reeder, D.J., and Budowle, B.: Strategies for resolution of PCR-amplified DNA in polyacrylamide gels, An International Seminar on the Forensic Applications of PCR Technology, FBI Academy, Quantico, Virginia, 1991.

111. Smith, T.A., Frasca, D.L., Alevy, M.C., and Budowle, B.: PCR amplification of the VNTR polymorphism located 3' to the human type II collagen gene, An International Seminar on the Forensic Applications of PCR Technology, FBI Academy, Quantico, Virginia, 1991.

112. Budowle, B.: PCR-status of validation studies, American Chemical Society, New York, New York, 1991.

113. Budowle, B.: Practical implications regarding DNA typing for forensics, 70th meeting of the German Society of Legal Medicine, Lausanne, Switzerland, 1991.

114. Budowle, B.: Application considerations regarding AMP-FLP genetic markers for identity testing purposes, 14th Congress of the International Society of Forensic Haemogenetics, Mainz, Germany, 1991.

115. Budowle, B.: Population genetic issues of VNTRs for forensic applications, Forensic DNA Symposium, New York, New York, 1991.

116. Budowle, B.: Population genetics of VNTRs for forensic applications, 7th Annual Symposium on Biotechnology - DNA Fingerprinting/Profiling, London, England, 1991.

117. Budowle, B.: DNA - RFLP/PCR testing and the future, The Expert Witness and DNA Testing, San Diego, California, 1992.

118. Klevan, L., Budowle, B., Fourney, R.M., and Carlson, D.P.: Chemiluminescent quantitation of human DNA from biological samples, American Academy of Forensic Sciences, New Orleans, Louisiana, 1992.

119. Fourney, R.M., Budowle, B., Carmody, G.R., Stewart, P., and Elliott, J.C.: Evaluation and statistical comparisons of amplified VNTR probes Col2A1, ApoB, and pMCT118 in North American Aboriginal populations, American Academy of Forensic Sciences, New Orleans, Louisiana, 1992.

120. Comey, C.T., Budowle, B., Adams, D.E., Presley, L.A., and Lindsey, J.A.: PCR amplification and typing of the DQalpha gene in old case samples, American Academy of Forensic Sciences, New Orleans, Louisiana, 1992.

121. Budowle, B., Alevy, M.C., Baechtel, F.S., Comey, C.T., Parsons, G.L., and Wilson, M.R.: Nomenclature and population distributions for AMP-FLP markers for application to forensic identity analyses, American Academy of Forensic Sciences, New Orleans, Louisiana, 1992.

122. Monson, K.L. and Budowle, B.: Estimation of RFLP allele frequencies: fixed bins, floating bins, and choice of reference data base, American Academy of Forensic Sciences, New Orleans, Louisiana, 1992.

123. Klevan, L., Budowle, B., Fourney, R.M., and Carlson, D.P.: Chemiluminescent quantitation of human DNA in biological fluids, 1992 International Symposium on Human Identification, Scottsdale, Arizona, 1992.

124. Lorente, J.A., Lorente, M., Budowle, B., Comey, C.T., and Villanueva, E.: HLA-DQalpha types in the Spanish population, 1992 International Symposium on Human Identification, Scottsdale, Arizona, 1992.

125. Budowle, B.: Forensic DNA analysis: A global perspective, 1992 International Symposium on Human Identification, Scottsdale, Arizona, 1992.

126. Lorente, J.A., Lorente, M., Budowle, B., and Villanueva, E.: Spanish population distribution of several PCR-based genetic marker systems, German Society for Legal Medicine Meeting, Berlin, Germany, 1992.

127. Budowle, B.: Forensic significance of VNTR profile frequency estimates determined in various reference databases, The Use of DNA Statistics in Crime Cases, Metropolitan Police Forensic Science Laboratory, London, England, 1993.

128. Wilson, M.R. and Budowle, B.: Inhibition of Taq polymerase by melanin - possible solutions for forensic applications, American Academy of Forensic Sciences, Boston, Massachusetts, 1993.

129. Monson, K.L. and Budowle, B.: Frequency assessment of VNTR profiles in databases from around the world, American Academy of Forensic Sciences, Boston, Massachusetts, 1993.

130. Budowle, B., Baechtel, F.S., Smerick, J.B., Hensley, K.W., Replogle, J., Alevy, M.C., and Parsons, G.: Population studies on D1S80, D17S5, and MBP, American Academy of Forensic Sciences, Boston, Massachusetts, 1993.

131. Budowle, B.: World population data, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

132. Merel, P., Pigeonnier, V., Comeau, F., Destrebecq, R., Richir, C., and Budowle, B.: DNA typing at the locus D2S44 in a sub-population from Togo, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

133. Tahir, M.A., Hamby, P., Asghar, A., Caruso, J., and Budowle, B.: Distribution of HLA-DQA alleles in deoxyribonucleic acid (DNA) from Caucasian and Black populations of Marion County, Indiana, USA, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

134. Riley, E. and Budowle, B.: The HLA DQA frequencies in Caribbean Blacks, data from three island populations, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

135. Gross, A.M. and Budowle, B.: Evaluation of the polymerase chain reaction (PCR) based technologies for Native American population studies, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

136. Lorente, M., Lorente, J., Wilson, M., Budowle, B., and Villanueva, E.: Spanish population data for the short tandem repeat TC11, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

137. Hawley, W.A. and Budowle, B.: Amplified fragment length polymorphisms (AMP-FLPS) in mosquito bloodmeals used to identify individual hosts and detect multiple feedings, The Second International Symposium on the Forensic Aspects of DNA Analysis, FBI Academy, Quantico, Virginia, 1993.

138. Budowle, B.: Lack of population substructure effects on forensic DNA profile frequencies, The Mid-Atlantic Association of Forensic Scientists, Baltimore, Maryland, 1993.

139. Budowle, B.: History and future of genetic markers in forensic science, National Institute of Forensic Science - Forensic PCR Workshop, Adelaide, Australia, 1993.

140. Budowle, B.: How do we satisfy the courts with our PCR data?, National Institute of Forensic Science - Forensic PCR Workshop, Adelaide, Australia, 1993.

141. Budowle, B.: Population genetics and statistical issues in forensics, National Institute of Forensic Science - Forensic Statistics Workshop, Adelaide, Australia, 1993.

142. Budowle, B.: Population data and its implications in DNA typing, Fourth International Symposium on Human Identification, Scottsdale, Arizona, 1993. 143. Budowle, B.: DNA markers, validation studies, and population genetic inferences for forensic analysis, International Society of Forensic Haemogenetics, Venice, Italy, 1993. 144. Tahir, M.A., Hamby, P.P., Asghar, A., Caruso, J.F., and Budowle, B.: Distribution of HLA-DQA alleles in DNA from Caucasian and Black populations of Marion County, Indiana, USA, International Society of Forensic Haemogenetics, Venice, Italy, 1993.

145. Lorente, M., Lorente, J., Wilson, M., Budowle, B., and Villanueva, E.: SE33 allele frequencies in the Spanish population, International Society of Forensic Haemogenetics, Venice, Italy, 1993.

146. Budowle, B.: Current approaches to the forensic uses of DNA, National Institute of Statistical Sciences Forum - DNA Fingerprinting, Chapel Hill, North Carolina, 1993.

147. Adams, D.E. and Budowle, B.: Validation and population studies for DNA RFLP probe D5S110, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

148. Monson, K.L., Budowle, B., Giusti, A., Lavergne, L., Aubert, D., Pascal, O., and Moisan, J.-P.: Allele distribution of four VNTR markers in French, French Canadian, and United States populations, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

149. Lorente, J.A., Lorente, M., Budowle, B., Wilson, M.R., Alvarez, J.C., and Villanueva, E.: Analysis of D21S11 allele frequencies in the Spanish population, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

150. Comey, C.T. and Budowle, B.: A denaturing gel system for analyzing short tandem repeat loci, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

151. Wilson, M.R., Budowle, B., DiZinno, J.A., and Polansky, D.: Human mitochondrial DNA polymorphisms, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

152. Budowle, B.: Validation studies on the analysis of a multiplex PCR system for Amplitype PM and HLA-DQ alpha analysis, American Academy of Forensic Sciences, San Antonio, Texas, 1994.

153. Budowle, B.: The application of hypervariable loci to identity issues in forensics, American Association of Physical Anthropologists, Denver, Colorado, 1994.

154. Budowle, B.: Past, present and future trends in forensic DNA technologies in North America, XVI<sup>TH</sup> Congress of the International Academy of Legal Medicine and Social Medicine, Strasbourg, France, 1994.

155. Presley, L.A., Lindsey, J., and Budowle, B.: Implementation of Amplitype PM (Polymarker) typing into forensic casework, XVI<sup>TH</sup> Congress of the International Academy of Legal Medicine and Social Medicine, Strasbourg, France, 1994.

156. Hochmeister, M., Budowle, B., Borer, U.V., and Dirnhofer, R.: The Amplitype PM Forensic DNA Amplification and Typing Kit population data, research observations and casework experience, XVI<sup>TH</sup> Congress of the International Academy of Legal Medicine and Social Medicine, Strasbourg, France, 1994.

157. Lorente, M., Lorente, J. A., Budowle, B., Alvarez, J.C., Wilson, M.R., and Villanueva, E.: PCR generated MBP allele frequencies in the Spanish population, XVI<sup>TH</sup> Congress of the International Academy of Legal Medicine and Social Medicine, Strasbourg, France, 1994.

158. Budowle, B.: Forensic Analysis, A Decade of PCR, Cold Spring Harbor, New York, 1994.

159. Budowle, B.: Population substructure, inbreeding effects, probability of innocence - are these concerns for statistical applications in forensic DNA typing?, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

160. Alkhayat, A., Alshamali, F., and Budowle, B.: HLA-DQ , LDLR, GYPA, HBGG, D7S8, and Gc allele and genotype frequency data on an Arab population sample from Dubai, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

161. Al-Awadhi, A., Tahir, M., Caruso, J.F., and Budowle, B.: Deoxyribonucleic acid (DNA typing of the HLA-DQ and Polymarker (LDLR, Gc, GYPA, HBGG, and D7S8) alleles from Arab and Pakistani populations living in Abu Dhabi, United Arab Emirates, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

162. Comey, C.T., Koons, B.W., and Budowle, B.: Analysis of four populations at the tetrameric short tandem repeat (STR) loci CSF1PO, TPOX, and HUMTHO1, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

163. Lindsey, J.A., Presley, L.A., and Budowle, B.: Results of validation, population and casework studies of the AmpliType PM (Polymarker) typing procedure, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

164. Lorente, M., Lorente, J.A., Alvarez, J.C., Wilson, M., Budowle, B., and Villanueva, E.: Spanish population data on four short tandem repeat loci (HUMTHO1, HUMVWA, ACTBP2, and D21S11): Equilibrium and independence, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

165. Tahir, M.A., Duncan, G.T., Baird, L.S., Caruso, J.F., Hamby, P.P., Masibay, A.S., Sovinski, S.M., and Budowle, B.: The development of a deoxyribonucleic acid (DNA) restriction fragment length polymorphism (RFLP) database for Punjabis in East Punjab, India, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

166. Wilson, M.R., DiZinno, J.A., Polansky, D., Replogle, J., and Budowle, B.: A mock case for mitochondrial DNA analysis, Fifth International Symposium on Human Identification, Scottsdale, Arizona, 1994.

167. Budowle, B.: The reliability of statistical inferences for forensic DNA profiling - the American experience, Robertson Symposium, Australian National University, Canberra, Australia, 1994.

168. Budowle, B.: Considerations for the application of PCR-based analyses in forensics, 12<sup>th</sup> Australian and New Zealand International Symposium on the Forensic Sciences, Auckland, New Zealand, 1994.

169. Gutowski, S., Budowle, B., van Oorschot, R., Robinson, S., and Auer, J.: Statistical analysis of genetic loci used at the State Forensic Science Laboratory, 12<sup>th</sup> Australian and New Zealand International Symposium on the Forensic Sciences, Auckland, New Zealand, 1994.

170. Budowle, B.: DNA typing strategies for forensic analyses, Third International Conference on DNA Fingerprinting, Hyderabad, India, 1994.

171. Wilson, M. R., Polansky, D., DiZinno, J. A., Budowle, B., and Butler, J.: Mitochondrial DNA sequencing of DNA extracted from human hair shafts, American Academy of Forensic Sciences, Seattle, Washington, 1995.

172. DiZinno, J. A., Wilson, M. R., Polansky, D., and Budowle, B.: The application of mitochondrial DNA technology to human identification in forensic casework, American Academy of Forensic Sciences, Seattle, Washington, 1995.

173. Budowle, B.: Evaluation of the effects of population substructure on DNA profile estimates using PCR-based loci, American Academy of Forensic Sciences, Seattle, Washington, 1995.

174. Lorente, M., Lorente, J., Wilson, M. R., Budowle, B., and Villaneuva, E.: Sequence multiplex amplification (SMA) in forensic casework, American Academy of Forensic Sciences, Seattle, Washington, 1995.

175. Comey, C. T., Koons, B. W., and Budowle, B.: Validation of multiplexed short tandem repeat systems for forensic use, American Academy of Forensic Sciences, Seattle, Washington, 1995.

176. Lindsey, J., Giusti, A., and Budowle, B.: Validation studies concerning the use of chemiluminescent detection in RFLP analysis, American Academy of Forensic Sciences, Seattle, Washington, 1995.

177. DiZinno, J. A., Wilson, M. R., Lord, W. D., and Budowle, B.: Mitochondrial DNA sequencing of Beetle larvae (Nitidulidae: Omosita) attached to human bone, American Academy of Forensic Sciences, Seattle, Washington, 1995.

178. Budowle, B.: Chemiluminescent detection, PCR analysis and statistics, American Academy of Forensic Sciences, Seattle, Washington, 1995.

179. Budowle, B.: Meeting challenges to DNA statistics, Pennsylvania District Attorneys Association, Pittsburgh, Pennsylvania, 1995.

180. Budowle, B.: Electrophoretic analysis of DNA markers used in human identity testing, Electrophoresis '95, USA, Gaithersburg, Maryland, 1995.

181. Budowle, B.: DNA Testimony, Northwest Association of Forensic Scientists, Anchorage, Alaska, 1995.

182. Budowle, B.: Status of STRs in the international community and the FBI's direction, Florida DNA Training Session III: Advanced PCR Applications, Orlando, FL, 1995.

183. Budowle, B.: DNA polymorphisms and their application to human identity testing, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

184. Lorente, M., Lorente, J.A., Alvarez, J.C., and Villaneuva, E.: Sequential multiplex amplification (SMA) utility in cases with minimal amounts of DNA, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

185. Garcia, O., Martin, P., Budowle, B., Albarran, C., and Alonso, A.: Allele frequencies of HLA-DQ, LDLR, GYPA, HBGG, D7S8, and Gc in the resident and autochthonous populations of the Basque country, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

186. Lorente, M., Lorente, J.A., Alvarez, J.C., and Villaneuva, E.: Spanish population data on seven loci (D1S80, D17S5, HUMTHO1, HUMVWA, ACTBP2, D21S11, and DQA1): equilibrium and independence, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

187. Martin, P., Alonso, A., Budowle, B., Albarran, C., Garcia, O., and Sancho, M.: Spanish population data on 13 PCR-based systems, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

188. Penacino, G., Sala, A., Smerick, J., Perez Calvo, J., Baechtel, F.S., Budowle, B., and Corach, D.: D1S80 AMP-FLP attributes in two different ethnic groups of Argentinean populations, International Society of Forensic Haemogenetics, Santiago de Compostela, Spain, 1995.

189. Budowle, B.: Methods for typing STR loci and statistical considerations for forensic applications, Sixth International Symposium on Human Identification, Scottsdale, Arizona, 1995.

190. Fisher, D.L., Koons, B.W., Lindsey, J.L., and Budowle, B.: The evaluation of Taq-induced signal intensity loss at the Gc locus of the AmpliType<sup>™</sup> PM system and proposed techniques as safeguards, Sixth International Symposium on Human Identification, Scottsdale, Arizona, 1995. 191. Al-Shamali, F., Alkhayat, A., and Budowle, B.: D1S80 allele frequencies in a Dubaian Arab Population, Sixth International Symposium on Human Identification, Scottsdale, Arizona, 1995.

192. Budowle, B.: Forensic issues and legal questions, American Society of Human Genetics, Minneapolis, Minnesota, 1995.

193. Budowle, B.: DNA/PCR typing of trace biological evidence, The Second Forensic Experts Conference - Trace Evidence at Crime Scene, Dubai, U.A.E., 1996.

194. Lorente, J.A., Lorente, M., Stone, A., Alvarez, J.C., Stoneking, M., Budowle, B., and Wilson, M.R.: Extraction and amplification strategies of ancient DNA from the royal bones of Queen Blanca de Navarra and the Prince of Viana, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

195. Budowle, B., Keys, K.M., Koons, B.W., and Smerick, J.B.: Validation of multiplex analysis of the STR loci CSF1PO, TPOX, and HUMTHO1, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

196. Monson, K.L. and Budowle, B.: Frequency estimates of PCR-based DNA profiles in reference databases of various size and origin, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

197. Fisher D.L., Lindsey, J., and Budowle, B.: Evaluation of amplification of two polymerase chain reaction based multiplexes - CSF1PO, TPOX, HUMTHO1 and D1S80/amelogenin on forensic samples, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

198. Lindsey, J., Giusti, A., Fisher, D.L., and Budowle, B.: Current methods of DNA analyses applied to casework in the FBI laboratory, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

199. DiZinno, J.A., Wilson, M.R., Polansky, D., and Budowle, B.: The implementation of mitochondrial DNA sequencing technology into forensic casework, American Academy of Forensic Sciences, Nashville, Tennessee, 1996.

200. Lorente, J.A., Lorente, M., Alvarez, J.C., Stoneking, M., Budowle, B., and Villanueva, E.: Spanish Caucasian population data for the loci HUMTHO1, TPOX, and CSF1PO using multiplex PCR amplification, American Academy of Forensic Sciences, Nashville, Tennessee, 1996. 201. Budowle, B.: RFLP - present and future. DNA Forensics: Science, Practice, and Future, Cambridge Symposium, Santa Fe, New Mexico, 1996.

202. Budowle, B.: Methods in DNA Analyses, The Mid-Atlantic Association of Forensic Scientists, Harrisburg, Pennsylvania, 1996.

203. Budowle, B.: DNA evidence, First Annual Law Enforcement/ Prosecutor Training Seminar, Tulsa, Oklahoma, 1996.

204. Budowle, B.: Primer in forensic DNA typing, California District Attorneys Association DNA Workshop, San Diego, California, 1996.

205. Budowle, B.: Various approaches for typing STR loci and validation studies to support forensic STR use, First European Symposium on Human Identification, Toulouse, France, 1996.

206. Budowle, B., Moretti, T.R., and Robertson, J.R.: STR loci for forensic identification - methods, population data, and validation studies, International Congress on Human Genetics, Rio De Janeiro, Brazil, 1996.

207. Budowle, B.: Population studies on forensically important PCR-based genetic markers, 14TH Meeting of the International Association of Forensic Sciences, Tokyo, Japan, 1996.

208. Woller, J., Budowle, B., Egyed, B., and Furedi, S.: Linkage analysis of 11 PCR-based and 3 protein genetic marker systems in Hungary, 14TH Meeting of the International Association of Forensic Sciences, Tokyo, Japan, 1996.

209. Budowle, B.: Validity of STR typing of forensic biological specimens, 13TH Australian and New Zealand International Symposium on the Forensic Sciences, Sydney, Australia, 1996.

210. Budowle, B.: Establishment of QA standards for forensic DNA typing, 13TH Australian and New Zealand International Symposium on the Forensic Sciences, Sydney, Australia, 1996.

211. Budowle, B.: Application of DNA statistics before and after the NRC II Report, The Seventh International Symposium on Human Identification, Scottsdale, Arizona, 1996.

212. Robertson, J., Moretti, T.R., and Budowle, B.: STR collaborative exercise, The Seventh International Symposium on Human Identification, Scottsdale, Arizona, 1996.

213. Robertson, J.M., Walsh, P.S., and Budowle, B.: Refinement of the CTT multiplex STR system, The Seventh International Symposium on Human Identification, Scottsdale, Arizona, 1996.

214. Budowle, B., Jankowski, L.B., Corey, H.W., Swec, N.T., Freck-Tootell, S., Pino, J., Schwartz, R., Kelley, C.A., and Tarver, M.: Evaluation of independence assumptions for PCR-based and protein-based genetic markers in New Jersey Caucasians, The Seventh International Symposium on Human Identification, Scottsdale, Arizona, 1996.

215. Budowle, B.: DNA past, present and future, 24<sup>TH</sup> Annual Florida Medical Examiners Fall Education Conference. St. Petersburg, Florida, 1996.

216. Budowle, B.: Population studies on forensically important STR loci, American Academy of Forensic Sciences, New York, New York, 1997.

217. Budowle, B., Jankowski, L.B., Corey, H.W., Swec, N.T., Freck-Tootell, S., Pino, J.A., Schwartz, R., Kelley, C.A., and Tarver, M.L.: Evaluation of independence assumptions for PCR-based and protein-based genetic markers in New Jersey Caucasians, American Academy of Forensic Sciences, New York, New York, 1997.

218. Moretti, T., Koons, B.W., Wilson, M.R., DiZinno, J.A., Reynolds, R., and Budowle, B.: Capacity of sequence specific oligonucleotide probe strips to detect variation of human mitochondrial DNA, American Academy of Forensic Sciences, New York, New York, 1997.

219. Lorente, M., Alvarez, J.C., Entrala, C., Lorente, J.A., Villanueva, E., Revelles, F., Wilson, M.R., and Budowle, B.: Organic and inorganic extraction procedures: good but not enough - increasing the DNA recovery from filtration devices, American Academy of Forensic Sciences, New York, New York, 1997.

220. Lorente, J.A., Entrala, C., Alvarez, J.C., Lorente, M., Villanueva, and Budowle, B.: Dandruff as a potential source of DNA in forensic science, American Academy of Forensic Sciences, New York, New York, 1997.

221. Robertson, J.M., Moretti, T., and Budowle, B.: Cooperative validation of DNA typing with short tandem repeat loci using fluorescence detection, American Academy of Forensic Sciences, New York, New York, 1997.

222. Cariolou, M.A., Manoli, P., Christophorou, M., Bashiardes, E., Karagrigoriou, A., and B. Budowle: Greek Cypriot allele and genotype frequencies of AmpliType PM and D1S80 loci, American Academy of Forensic Sciences, New York, New York, 1997.

223. Budowle, B.: Statistical calculations as specified in the NRC II report, The Mid-Atlantic Association of Forensic Scientists, Roanoke, Virginia, 1997.

224. Budowle, B.: DNA identification: CODIS system, Albany Symposium of Evidence V, Albany State University, Albany, Georgia, 1997.

225. Budowle, B.: DNA typing, Classification Society of North America, Washington, D.C., 1997.

226. Budowle, B.: Capillary electrophoresis in forensic science, 17th International Society of Forensic Haemogenetics Congress, Oslo, Norway, 1997.

227. Lorente, M., Lorente, J.A., Entrala, C., Alvarez, J.C., Wilson, M.R., Budowle, B., and Villaneuva, E.: Minimal amounts of DNA: improving the results of the analysis in forensic casework, 17th International Society of Forensic Haemogenetics Congress, Oslo, Norway, 1997.

228. Lorente, M., Lorente, J.A., Entrala, C., Alvarez, J.C., Villaneuva, E., and Budowle, B.: Dandruff as a source of DNA: validation studies, 17th International Society of Forensic Haemogenetics Congress, Oslo, Norway, 1997.

229. Woller, J., Budowle, B., Angyal, M., Furedi, S., Padar, Z.: Population data on the loci HLA-DQA1, LDLR, GYPA, HBGG, D7S8, GC, and D1S80 in a Hungarian Romany population, 17th International Society of Forensic Haemogenetics Congress, Oslo, Norway, 1997.

230. Budowle, B.: Forensic DNA databases: FBI CODIS. HUGO - EC Euroconference on Variation in the Human Genome: Acquiring, Handling, and Storing the Data, Helsinki, Finland, 1997.

231. Budowle, B.: Worldwide study of PCR-based markers, The Eighth International Symposium on Human Identification, Scottsdale, Arizona, 1997.

232. Smith, J.A.L. and Budowle, B.: Unique identification of body fluid stains using DNA profiling, The Eighth International Symposium on Human Identification, Scottsdale, Arizona, 1997.

233. McCord, B.R., Budowle, B., Isenberg, A.R., and Allen, R.O.: Precision and resolution studies utilizing capillary electrophoresis: Investigations of the effect of polymer type and concentration, The Eighth International Symposium on Human Identification, Scottsdale, Arizona, 1997.

234. Budowle, B.: Mitochondrial DNA typing of hairs, bone, and teeth, Forensic Medicine - A Modern Science - An International Symposium, Gdansk, Poland, 1997.

235. Budowle, B.: Studies for selecting core STR loci for CODIS, DNA Forensics: Science, Evidence, and Future Prospects, Cambridge Healthtech Institute, McLean, Virginia, 1997.

236. Budowle, B.: Standards and quality in forensic DNA typing methods, Forensic DNA Analysis Workshop, Ministry of Science, Jerusalem, Israel, 1997.

237. Moretti, T.R. and Budowle, B.: The CODIS STR project: Evaluation of fluorescent multiplex STR systems, American Academy of Forensic Sciences, San Francisco, California, 1998.

238. Budowle, B. And Moretti, T.R.: United States population data sets on forensically important STR loci, American Academy of Forensic Sciences, San Francisco, California, 1998.

239. Lorente, M., Lorente, J.A., Alvarez, J.C., Entrala, C., Villanueva, E., and Budowle, B.: The establishment of a genetic identification program for missing people in Spain, American Academy of Forensic Sciences, San Francisco, California, 1998.

240. Wilson, M.R., DiZinno, J.A., Polansky, D., and Budowle, B.: Assessing heteroplasmy in the control region of human mitochondrial DNA, American Academy of Forensic Sciences, San Francisco, California, 1998.

241. Budowle, B.: Results of the collaborative STR research project, Northwest Association of Forensic Scientists, Portland, Oregon, 1998.

242. Budowle, B.: STR loci - basics and use, Mid-Atlantic Association of Forensic Scientists. Rockville, Maryland, 1998.

243. Budowle, B.: Standards and training, Third Annual Conference on the future of DNA, Chicago, Illinois, 1998.

244. Budowle, B.: Selection criteria for STR loci, Jornadas de GenéticaForense, Bilbao, Spain, 1998.245. Budowle, B.: Forensic application of mitochondrial DNA sequencing,Jornadas de Genética Forense, Bilbao, Spain, 1998.

246. Budowle, B. And Moretti, T.R.: The U.S. national database - beyond the core STR locus selection, The Second European Symposium on Human Identification, Innsbruck, Austria 1998.

247. Lorente, J.A., Entrala, C., Lorente, M., Alvarez, J.C., Villanueva, E., and Budowle, B.: Population studies and casework application with the new GenePrint SilverSTR III Multiplex (D16S539, D7S820, D13S317), The Second European Symposium on Human Identification, Innsbruck, Austria 1998.

248. Smith, J.A.L. and Budowle, B.: Unique identification of body fluid stains using DNA profiling, The Second European Symposium on Human Identification, Innsbruck, Austria 1998.

249. Sinha, S. Tahir, U., Rogers, C., Montgomery, A., Kubidan, N., Budowle, B., and Tahir, M.: Distribution of DQA1, polymarkers, D1S80, and D5S818, D13S317, D7S820, D16S539, VWA, THO1, TPOX and CSF1PO loci in a Saudi Arabian population, The Second European Symposium on Human Identification, Innsbruck, Austria 1998.

250. Sinha, S., Amjad, M., Budowle, B., and Tahir, M.: Distribution of polymarker, DQA1, and D5S818, D13S317, D7S820, D16S539, VWA, THO1, TPOX and CSF1PO loci in Bengali and Punjabi populations, The Second European Symposium on Human Identification, Innsbruck, Austria 1998.

251. Budowle, B.: Testifying about the statistics, Expert Witness Testimony, The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

252. Budowle, B. and Moretti, T.R.: CODIS genetic marker databases, The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

253. Jorquera, H., Budowle, B., Moreno, F., Aguirre, E., Acuna, M., and Cifuentes, L.: Chilean population data on thirteen PCR-based loci, The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

254. Alkhayat, A., Alshamali, F., and Budowle, B.: Allele frequencies of three STR loci: CSF1PO, TPOX, and HUMTHO1 in a Dubaian Arab population, The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

255. Alkhayat, A., Alshamali, F., and Budowle, B.: Determination of the allele and genotype frequencies of the loci: HLA-DQA1, LDLR, GYPA, HBGG, D7S8, and Gc in a population of Pakistanis living in Dubai, The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

256. Morales, J.A., Monterrosa, J.C., Lorente, J.A., Entrala, C., Alvarez, J.C., Lorente, M., Villaneuva, E., and Budowle, B.: El Salvador (Central America) population data with the GenePrint<sup>™</sup> SilverSTR<sup>™</sup> III multiplex (D16S539, D7S820, and D13S317), The Ninth International Symposium on Human Identification, Orlando, Florida, 1998.

257. Budowle, B.: DNA analyses in forensic sciences, 50<sup>TH</sup> Anniversary of the Finnish Society of Forensic Medicine. Helsinki, Finland, 1998.

258. Budowle, B.: Forensic DNA analysis and case reports in the USA,  $7^{\text{TH}}$  Japanese Society for DNA Polymorphism Research. Matsumoto, Japan, 1998.

259. Moretti, T.R. and Budowle, B.: Capillary electrophoresis of STRs in the FBI Laboratory: Performance testing, optimization, validation, and implementation, American Academy of Forensic Sciences, Orlando, Florida, 1999.

260. Budowle, B., Wilson, M.R., Stauffer, C., Moretti, T.R., Monson, K.L., and DiZinno, J.A.: Mitochondrial DNA control region population data, American Academy of Forensic Sciences, Orlando, Florida, 1999.

261. Lorente, M., Entrala, C., Lorente, J.A., Alvarez, J.C., Villaneuva, E., Budowle, B., and Moretti, T.R.: Spanish population data for the nine loci included in the Profiler Plus<sup>™</sup> Kit, American Academy of Forensic Sciences, Orlando, Florida, 1999.

262. Budowle, B.: Forensic databases, Human Genome Meeting, Brisbane, Australia, 1999.

263. Lorente, M., Lorente, J.A., Budowle, B., D'Aloja, E., Fiori, A., and Villaneuva, E.: Looking ahead: to seek or not to seek genetic information, the declaration on the human genome and human rights. Human Genome Meeting, Brisbane, Australia, 1999.

264. Lorente, M., Lorente, J.A., Lorente, M.J., Budowle, B., D'Aloja, E., Fiori, A., and Villaneuva, E.: Ethical, legal and social implications of a program for genetic identification of newborns, Human Genome Meeting, Brisbane, Australia, 1999.

265. Budowle, B.: Fighting crime with DNA, Human Genome Meeting, Brisbane, Australia, 1999.

266. Budowle, B.: Scientific Working Group on DNA Analysis Methods, International Symposium on Setting Quality Standards for the Forensic Science Community, San Antonio, Texas, 1999.

267. Budowle, B.: CODIS and 13 STR core loci, IV Jornadas de Genetica Forense, La Gomera, Spain, 1999.

268. Drades, A., Nievas, D., Martinez-Jarreta, B. and Budowle, B.: Polimorfismos del AND mitocondrial, variabilidad en poblacion aragonesa y apliacaciones medico-forenses, IV Jornadas de Genetica Forense, Gomera, Spain, 1999. 269. Budowle, B.: STR's and new DNA techniques in criminal investigations, Biotechnology 2001 Conference, Blacksburg, Virginia, 1999.

270. Lorente, M., Lorente, J.A., Budowle, B., Wilson, M.R., and Villaneuva, E.: Improvement in the yield of mitochondrial DNA amplification products: implications for the analysis of old and degraded biological samples, Eighteenth Congress of the International Society for Forensic Haemogenetics, San Francisco, California, 1999.

271. Morales, J.A., Monterrosa, J.C., Alvarez, J.C., Entrala, C., Lorente, J.A., Lorente, M., Villaneuva, E., and Budowle, B.: El Salvador (Central America) population data for the D1S80 and D17S5 (YNZ22) loci, Eighteenth Congress of the International Society for Forensic Haemogenetics, San Francisco, California, 1999.

272. Prades, A., Calafell, F., Budowle, B., Bertranpetit, J., and Martinez-Jarreta, B.: Sequence analysis of mitochondrial DNA (mtDNA) control region in Aragon (north Spain), an anthropological view. Eighteenth Congress of the International Society for Forensic Haemogenetics, San Francisco, California, 1999.

273. Nievas, P., Martinez-Jarreta, B., Abecia, E., and Budowle, B.: Genetic analysis of the short tandem repeat loci D16S539, D7S820, D13S317, D18S535, D1S1656, and D12S391 in two Spanish populations, Eighteenth Congress of the International Society for Forensic Haemogenetics, San Francisco, California, 1999.

274. Lorente, M., Lorente, J.A., D'Aloja, E., Fiori, A., Budowle, B., and Villaneuva, E.: Genetic databases: past, present and future, Criminal databases in forensic sciences. Eighteenth Congress of the International Society for Forensic Haemogenetics, San Francisco, California, 1999.

275. Budowle, B.: Interpretation guidelines for mtDNA typing, The Tenth International Symposium on Human Identification, Orlando, Florida, 1999.

276. Budowle, B.: Perspectives of genetic research applied to criminal investigation, Konferencja Naukowo-Szkoleniowa, Lublin, Poland, 1999.

277. Budowle, B.: Statistics and interpretation wash-up session, First International Conference on Forensic Human Identification in the Millenium, London, England, 1999.

278. Budowle, B.: Mitochondrial DNA analysis in the FBI Laboratory, First International Conference on Forensic Human Identification in the Millenium, London, England, 1999.

279. Budowle, B.: Future considerations for DNA technology, Interpol, Lyon, France 1999.

280. Lorente, M., Lorente, J.A., D'Aloja, E., Fiori, A., Budowle, B., and Villanueva, E.: Criminal genetic databases: Where are the limits? The conflict between social and technical perspectives, American Academy of Forensic Sciences, Reno, Nevada, 2000.

281. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva, E.: Increasing the recovery of mitochondrial DNA amplicon purification: microcon-100 vs. Microcon-30, American Academy of Forensic Sciences, Reno, Nevada, 2000.
282. Stewart, J.E.B., Fisher, C.L., Aagaard, P., Wilson, M.R., Polansky, D., Pokorak, E., DiZinno, J.A., Isenberg, A.R., and Budowle, B.: Length variation patterns in the human mitochondrial DNA control region, American Academy of Forensic Sciences, Reno, Nevada, 2000.

283. Budowle, B.: CODIS STR population data, American Academy of Forensic Sciences, Reno, Nevada, 2000.

284. Lorente, M., Lorente, J.A., Wilson, M.R., Budowle, B., and Villanueva, E.: Improvement in the yield of mitochondrial DNA amplification products: Implications for the analysis of old and degraded biological samples, American Academy of Forensic Sciences, Reno, Nevada, 2000.

285. Budowle, B., Leggitt, J.L., Defenbaugh, D.A., Keys, K.M, and Malkiewicz, S.F.: The presumptive reagent fluorescein for detection of dilute bloodstains and subsequent STR typing of recovered material, American Academy of Forensic Sciences, Reno, Nevada, 2000.

286. Budowle, B.: Analysis of DNA: Utility in criminal and civil proceedings, First Ibero-American Symposium on Criminalistics and Criminology of the AICEF-GITAD. Montevideo, Uruguay, 2000.

287. Budowle, B.: Quality management issues, 15TH Australian and New Zealand International Symposium on the Forensic Sciences, Gold Coast, Australia, 2000.

288. Budowle, B.: DNA databases, 15TH Australian and New Zealand International Symposium on the Forensic Sciences, Gold Coast, Australia, 2000.

289. Budowle, B.: The core CODIS STR loci, 15TH Australian and New Zealand International Symposium on the Forensic Sciences, Gold Coast, Australia, 2000.

290. Budowle, B.: Mitochondrial DNA: Its uses in forensic science, 15TH Australian and New Zealand International Symposium on the Forensic Sciences, Gold Coast, Australia, 2000. 291. Budowle, B.: FTA paper as a storage medium, 15TH Australian and New Zealand International Symposium on the Forensic Sciences, Gold Coast, Australia, 2000.

292. Budowle, B.: FTA paper for automation and as a storage medium of forensic reference samples, DNA Forensics, Cambridge Healthtech Institute, Springfield, VA, 2000.

293. Budowle, B.: Concordance and validation issues, National Symposium on STR Systems, Lake Geneva, WI, 2000.

294. Budowle, B.: History and future of DNA typing, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

295. Budowle, B.: Validation efforts of STR loci in multiplex systems, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

296. Monson, K.L., Miller, K.W.P., and Budowle, B.: Mitosearch: software for managing and searching mitochondrial DNA profiles, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

297. Lorente, J.A., Gangitano, D.A., Juvenal, G.J., Budowle, B., and Padula, R.A.: Argentinean population data for 8 STR loci using silver-staining based technologies, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

298. Lorente, J.A., Lorente, M., Alvarez, J.C., Entrala, C., Budowle, B., and Villaneuva, E.: Sequential multiplex amplification (SMA) with the Powerplex<sup>™</sup> 16, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

299. Hudlow, W.R., Budowle, B., and Lee, S.B.: Rapid, accurate digital DNA quantitation using the CCDBIO 16HC, The Eleventh International Symposium on Human Identification, Biloxi, Mississippi, 2000.

300. Budowle, B.: Development of DNA technology: what it makes possible, what it will make possible, DNA and the Criminal Justice System. Harvard University, Cambridge, Massachusetts, 2000.

301. Budowle, B.: Validation of new markers and kits, FBI Laboratory's 6<sup>th</sup> CODIS User's Conference, Arlington, Virginia, 2001.

302. Chakraborty, R., Bieber, F.R., and Budowle, B.: STR mixtures and statistical interpretation issues, FBI Laboratory's 6<sup>th</sup> CODIS User's Conference, Arlington, Virginia, 2001.

303. Sinha, S., Paunovic, A., Lal, A., Chakraborty, R., Budowle, B., Warren, J., Planz, J., Richey, S., Arcot, S., Bulot, D., Larsen, C., Cook, P., Eisenberg, A.J., Jones, M.D., Wojtkicz, P., Schoenbauer, D., and Gross, A.M.: Forensic validation and population genetics on the Y-Plex<sup>™</sup> kit for Ychromosome analysis, American Academy of Forensic Sciences, Seattle, Washington, 2001.

304. Budowle, B.: Statistics for forensic DNA analysis, American Academy of Forensic Sciences, Seattle, Washington, 2001.

305. Morales, J.A., Lorente, J.A., Monterrosa-Pashaca, J., Alvarez, J.C., Entrala, C., Lorente, M., Budowle, B., and Villaneuva, E.: Population data for the Profiler Plus Nine<sup>™</sup> Loci in El Salvador (Central America), American Academy of Forensic Sciences, Seattle, Washington, 2001.

306. Pagano, S., Lorente, J.A., Alvarez, J.C., Entrala, C., Mechoso, B., Budowle, B., Villaneuva, E., and De Armas, L.: Uruguay population data for 8 STR loci (PowerPlex 1.2), American Academy of Forensic Sciences, Seattle, Washington, 2001.

307. Budowle, B.: Population genetic studies on forensically-employed short tandem repeat loci, American Academy of Forensic Sciences, Seattle, Washington, 2001.

308. Stewart, J.E.B., Aagaard, P.J., Polansky, D., Pokorak, E.G., DiZinno, J.A., Smrz, M., and Budowle, B.: The FBI national missing person DNA database, American Academy of Forensic Sciences, Seattle, Washington, 2001.

309. Monson, K.L., Budowle, B., Miller, K.W.P.: MitoSearch: integrated software and database for managing and searching mitochondrial DNA profiles, American Academy of Forensic Sciences, Seattle, Washington, 2001.

310. Budowle, B.: Molecular biology tools for human identity testing and the significance of results, The Second Francine and Michael Saferstein Memorial Lecture in Forensic Science, The Barnett Institute of Biological and Chemical Analysis, Northeastern University, Boston, Massachusetts, 2001.

311. Budowle, B.: Genomic tools for identity testing and human population genetics, Human Genetics and Genomics, Keystone Symposium, Breckenridge, Colorado, 2001.

312. Budowle, B.: Genetic aspects of forensic science, The 29th Center for Information Biology Seminar, Mishima, Japan, 2001.

313. Budowle, B.: Forensic molecular biology tools for identity testing and population genetic inferences, EMBO Course: Advanced techniques in Molecular Biology, Uppsala, Sweden, 2001.

314. Budowle, B.: Forensic DNA analysis: Challenges and Solutions, Canadian Federation of Biological Societies 44th Annual Meeting, Ottawa, Canada, 2001. 315. Chakraborty, R., Jin, L., Deka, R., Kimmel, M., and Budowle, B.: Signatures of recurrent mutations at single nucleotide polymorphism sites in the hypervariable domains of the mitochondrial control region and their implications for evolutionary studies, American Association of Physical Anthropologists, St. Louis, Missouri, 2001.

316. Kimmel, M., Bobrowski, A., Wang, N., Budowle, B., and Chakraborty, R.: Non-homogeneous infinite sites model under demographic changes of population size: application to mitochondrial DNA data, American Association of Physical Anthropologists, St. Louis, Missouri, 2001.

317. Budowle, B.: Multiple platforms for SNP analysis, International Society for Forensic Genetics, Munster, Germany, 2001.

318. Budowle, B.: Population studies on 17 STR loci routinely used in forensic analyses, International Society for Forensic Genetics, Munster, Germany, 2001.

319. Miller, K.W.P., Brown, B.L., and Budowle, B.: The Combined DNA Index System, International Society for Forensic Genetics, Munster, Germany, 2001.

320. Henke, L., Biondi, R., Branicki, W., Budowle, B., Drobnic, K., van Eede, P.H., Felske-Zech, H., Fernandez de Simon, L., Gagnor, C., Garafano, L., Gehrig, C., Kaeser, M., Luckenbach, C., Malik, N., Muche, M., Parson, W., Primorac, D., Schneider, P.M., Thomson, J., and Vanek, D.: Evaluation of the STR typing kit PowerPlex 16 with respect to technical performance and population genetics: a multicenter study, International Society for Forensic Genetics, Munster, Germany, 2001.

321. Alshamali, F., Alkhayat, A.Q., Budowle, B., and Watson, N.: Allele frequency distributions and other population genetic parameters for 13 STR loci in a UAE local population from Dubai, International Society for Forensic Genetics, Munster, Germany, 2001.

322. Budowle, B.: Past and future on DNA typing, The Second European-American Intensive Course in Clinical and Forensic Genetics, Dubrovnik, Croatia, 2001.

323. Budowle, B.: Validation of STRs and mitochondrial DNA, The Second European-American Intensive Course in Clinical and Forensic Genetics, Dubrovnik, Croatia, 2001.

324. Budowle, B., Hobson, D., Smerick, J.B., and Smith, J.A.L.: Low copy number STR typing: cautions and considerations The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

325. Budowle, B.: Allele call criteria for felon databank samples, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

326. Sinha, S., Shewale, J.G., Lal, A., Gross, A.M., Wojtkiewicz, P., Tahir, M., and Budowle, B.: Validation, database, and case work applications of Y-Plex<sup>TM</sup>6 multiplex Y-chromosome STR genotyping system, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

327. Dugan, K.A., Lawrence, H.S., Hares, D.R., Fisher, C.L., and Budowle, B.: An improved method for post-PCR purification for mtDNA sequence analysis, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

328. Pokorak, E.G., Stewart, J.E.B., Aagaard, P.J., Polansky, D., and Budowle, B.: Comparison of mitochondrial DNA sequencing instruments for use by the FBI National Missing Persons DNA Database Program, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

329. Carlson, D., Ubil, E., Lo, J-Y., Lee, S.B., Hendson, M., Chapman, W., Shah, M., Crouse, C., Konotop, F., Duncan, G., Marchese, D., Tracey, M., Ballester, M., Young, J.W., Ortuzar, I., Schumm, J., Amin, A., Fox, J., Butler, J.M., Vallone, P.M., Levin, B.C., Hancock, D.K., Coble, M., Harvie, C., Eisenberg, A., and Budowle, B.: Interlaboratory studies on multiplexed mtDNA HV and Y chromosome SNP typing using an automated liquid bead array system, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

330. Leibelt, C., Budowle, B., Collins, P., Daoudi, Y., Dimsoski, P., Ganong, C., Hennessy, L., Moretti, T., Rao-Coticone, S., Reeder, D., Roby, R., and Shadravan, F.: Identification of a D8S1179 primer binding site mutation and addition of a primer designed to recover null alleles, The Twelfth International Symposium on Human Identification, Biloxi, Mississippi, 2001.

331. Budowle, B.: Validation of new markers and kits, FBI Laboratory's 7<sup>th</sup> CODIS User's Conference, Arlington, Virginia, 2002.

332. Budowle, B., Chakraborty, R., Bieber, F.R.: Future, FBI Laboratory's 7<sup>th</sup> CODIS User's Conference, Arlington, Virginia, 2002.

333. Budowle, B.: Statistical analysis of mtDNA sequence data, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

334. Budowle, B.: ISFG recommendations about Y-STR allele designations and genetic variations of Y-STR in U.S. populations, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

335. Lorente, J.A., Budowle, B., Gangitano, D., Figueiredo, M., Jorquera, H., Melendez, E., Pagano, S., Entrala, C., Alvarez, J.C., Lorente, M., and Villaneuva, E.: Comparison of DNA data (Fst) from five Latin American populations using 15 STR loci, American Academy of Forensic Sciences, Atlanta, Georgia, 2002. 336. Polansky, D., Stewart, J.E.B., Budowle, B., Aagaard, P.J., and Pokorak, E.G.: A case study of DNA contamination from an osteological sample, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

337. Dugan, K.A., Lawrence, H.S., Craig, R., Smerick, J.B., Hobson, D., and Budowle, B.: Evaluation of AluQuant<sup>™</sup> for forensic DNA quantitation, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

338. Stewart, J.E.B., Aagaard, P.J., Polansky, D., Pokorak, E.G., and Budowle, B.: Evaluation of multicapillary electrophoresis for use in mitochondrial DNA typing, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

339. Allard, M.W., Wilson, M., Monson, K.L., Budowle, B., and Miller, K.: Characterization of the Caucasian haplogroups present in the SWGDAM forensic mtDNA database for 1771 human control region sequences, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

340. Lee, S.B., Hendson, M., Pak, S., Carlson, D., Ubil, E., Yo J.L., Alley, D., Crouse, C., Konotop, F., Duncan, G., Marchese, D., Tracey, M., Ballester, M., Young, J.W., Ortuzar, I., Schumm, J., Amin, A., Fox, J., Butler, J.M., Vallone, P.M., Levin, B.C., Hancock, D.K., Parsons, T., Coble, M., Harvie, C., Eisenberg, A., Gross, A.M., Sinha, S.K., Shewale, J., Buoncristiani, M., Riggs, L., Kienker, L., and Budowle, B.: Interlaboratory studies on multiplexed mtDNA HV and Y chromosome SNP kits using an automated liquid bead array system, American Academy of Forensic Sciences, Atlanta, Georgia, 2002.

341. Budowle, B.: Needs, validation and admissibility issues for microbial forensics, New Frontiers in Chemical and Biological Terrorism Defense. Gordon Research Conference, Ventura, CA, 2002.

342. Budowle, B.: Investigative strategies to prevent bio-terrorism attacks and current trends in DNA forensic research, Innovazioni Scientifiche per L'Analisi di Tracce Nell'Investigazione Forense, Fondazione per le Biotecnologie, Torino, Italy, 2002.

343. Budowle, B.: Evidence, expert witness, and quality, 16TH Australian and New Zealand International Symposium on the Forensic Sciences, Canberra, Australia, 2002.

344. Budowle, B.: Heteroplasmy: is there a concern about its frequency in hair?, 16TH Australian and New Zealand International Symposium on the Forensic Sciences, Canberra, Australia, 2002.

345. Budowle, B.: Defining the application of low copy number typing, 16TH Australian and New Zealand International Symposium on the Forensic Sciences, Canberra, Australia, 2002.

346. Budowle, B.: SNPs and platforms for forensic analyses, 16TH Australian and New Zealand International Symposium on the Forensic Sciences, Canberra, Australia, 2002.

347. Budowle, B.: Constructing a microbial forensic program, Cambridge Healthtech Institute Meeting on DNA Forensics, Washington, DC, 2002.

348. Budowle, B.: DNA data banks: types, compatibility, data exchange, privacy, 16th Meeting of the International Association of Forensic Sciences, Montpelier, France 2002.

349. Budowle, B.: A review of STR population databases and associated reporting issues, 16th Meeting of the International Association of Forensic Sciences, Montpelier, France 2002.

350. Budowle, B.: Defining a new forensic discipline: microbial forensics, The Thirteenth International Symposium on Human Identification, Phoenix, Arizona, 2002.

351. Dugan, K., Olivastro, E., Underhill, P., and Budowle, B.: SNP analysis of the Y chromosome, The Thirteenth International Symposium on Human Identification, Phoenix, Arizona, 2002.

352. Wilson, M.R., Allard, M.W., Miller, K.W.P., Monson, K., and Budowle, B.: Phylogenetic characterization of the SWGDAM forensic mtDNA data set, The Thirteenth International Symposium on Human Identification, Phoenix, Arizona, 2002.

353. Budowle, B.: Expert systems for the technical review of data, FBI Laboratory's 8<sup>th</sup> CODIS User's Conference, Arlington, Virginia, 2002.

354. Budowle, B.: The microbial forensic needs for law enforcement, Microbial forensics, The Banbury Center, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 2002.

355. Stewart, J.E.B., Miller, K.W. P. and Budowle, B.: Implementation of CODIS<sup>mt</sup>: The national mitochondrial DNA database, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

356. Fernandez-Rosado, F., Martinex-Espin, E., Rodriguez, T., Entrala, C., Alvarez, J.C., Lorente J.A., Lorente, M., Budowle, B., and Villanueva, E.: Population data of Ecuador for fifteen STR loci (Powerplex<sup>™</sup> 16), American Academy of Forensic Sciences, Chicago, Illinois, 2003.

357. Martinex-Espin, E., Fernandez-Rosado, F., Alvarez, J.C., Entrala, C., Lorente J.A., Lorente, M., Oviedo de Duarte, M., and Budowle, B.: Paraguayan population data on the fifteen STR loci included in the Powerplex<sup>™</sup> 16 kit, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

358. Dugan, K.A., Olivastro, E., and Budowle, B.: SNP analysis of the Y chromosome using SNaPshot, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

359. Eckenrode, B.A., Levert, K., Wilson, M.R., and Budowle, B.: Developments in SNP analysis via quadrupole MS for forensic applications, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

360. Budowle, B.: Y chromosome markers for identity testing, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

361. Budowle, B.: Low copy number DNA typing: an alternate view, American Academy of Forensic Sciences, Chicago, Illinois, 2003.

362. Budowle, B. and Herkenham, D.: DNA: technology, legislation, and policy, Privacy in the Information Age, National Academy of Sciences Meeting, Miami, Florida, 2003.

363. Budowle, B.: Practical implications of microbial forensics, Microbial forensics: a scientific assessment, American Association for the Advancement of Science, Denver, Colorado, 2003.

364. Budowle, B. and Schutzer, S.: Discussion on microbial forensic research and quality assurance guidelines, Future Directions for Biodefense Research, ASM Biodefense Research Meeting, Baltimore, Maryland, 2003.

365. Budowle, B.: Proactive response to use of bioweapons, 5<sup>th</sup> International Congress on Anthrax, Nice, France, 2003.

366. Budowle, B.: A framework for microbial forensics, American Society of Microbiology, Washington, D.C., 2003.

367. Budowle, B.: Issues in the use of genetic technologies in forensics, Inaugural Meeting of the Secretary's Advisory Committee on Genetics, Health, and Society, NIH, Washington, D.C., 2003.

368. Budowle, B.: Microbial forensics assets, Chemical and Biological National Security Program, National Nuclear Security Administration, DOE, Washington, D.C., 2003.

369. Budowle, B.: Attribution of acts of bioterrorism and biocrimes using microbial genetics and forensics, XIX International Congress of Genetics, Melbourne, Australia, 2003.

370. Budowle, B.: Privacy issues in the use of forensic genetics, XIX International Congress of Genetics, Melbourne, Australia, 2003.

371. Levert, K.L., Eckenrode, B.A., Wilson, M., and Budowle, B.: SNP genotyping via quadrupole mass spectrometry, 51<sup>st</sup> ASMS Conference, Montreal, Canada, 2003.

372. Budowle, B.: Attribution statistics, Association of Forensic DNA Analysts and Administrators, Austin, Texas, 2003.

373. Budowle, B.: Forensic biodefense, Association of Forensic DNA Analysts and Administrators, Austin, Texas, 2003.

374. Budowle, B.: Microbial forensics issues and needs for Burkholderia, Biothreat and the Biology of Burkholderia, Center for Homeland Security, Los Alamos National Laboratory, Santa Fe, New Mexico, 2003.

375. Budowle, B.: The current situation with the national DNA database in North America, International Society of Forensic Genetics, Arcachon, France, 2003.

376. Budowle, B.: Genetics and other forensic tools for attribution of microbiological agents, International Society of Forensic Genetics, Arcachon, France, 2003.

377. Vecchio, C., Garofano, L., Saravo, L., Spitalen, S., Santacroce, M., Manzan, V., and Budowle, B.: Allele frequencies for CODIS loci in a Sicilian population sample, International Society of Forensic Genetics, Arcachon, France, 2003.

378. Vasquez, P., Martinez-Jarreta, B., Budowle, B., and De Blas, I.: Population genetic study of Y-chromosome haplotypes in the population of El Salvador (San Salvador, Central America), International Society of Forensic Genetics, Arcachon, France, 2003. 379. Alshamali, F., Alkhayat, A.Q., and Budowle, B.: Y chromosome testing in forensic casework and paternity testing, International Society of Forensic Genetics, Arcachon, France, 2003.

380. Budowle, B.: Biothreats and biocrimes - applying microbial genetics and forensic analyses, International Symposium on Forensic DNA Technologies. Munster, Germany, 2003.

381. Fernandez-Rosado, F., Martinez-Espina, E., Rodriguez, T., Entrala, C., Alvarez, J.C., Lorente, J.A., Lorente, M., Budowle, B., and Villaneuva, E.: Population data of Ecuador for fifteen STR loci (Powerplex<sup>™</sup> 16), International Symposium on Forensic DNA Technologies. Munster, Germany, 2003. 382. Budowle, B.: ISFG Y marker recommendations and SWGDAM validation studies, 3<sup>rd</sup> European Academy of Forensic Science Meeting, Istanbul, Turkey, 2003.

383. Budowle, B.: Assessing bioterrorism and biocrimes through microbial forensics, 3<sup>rd</sup> European Academy of Forensic Science Meeting, Istanbul, Turkey, 2003; Forens. Sci. Int. 136 (Suppl. 1): 3929, 2003.

384. Budowle, B.: Population genetics and interpretation with Y-STRs, 14<sup>th</sup> International Symposium on Human Identification, Phoenix, Arizona, 2003.

385. Budowle, B.: Microbial forensic biocrime cases and interpretation issues, 14<sup>th</sup> International Symposium on Human Identification, Phoenix, Arizona, 2003.

386. Budowle, B.: SNPS and their use in forensic identification, FBI Laboratory's 8<sup>th</sup> CODIS User's Conference, Leesburg, Virginia, 2003.

387. Budowle, B.: Genomics for supporting microbial forensic analyses, Genomics and Pathogenesis. American Academy of Microbiology Colloquium, Key Largo, Florida, 2003.

388. Budowle, B.: Human DNA identification history and the CODIS program in the USA, Second International Symposium on Human Identification through DNA, Rio de Janeiro, Brazil, 2003.

389. Budowle, B.: Mixtures and mitochondrial DNA: addressing the issues, American Academy of Forensic Sciences, Dallas, Texas, 2004.

390. Budowle, B.: Understanding and interpreting Y STR evidence, American Academy of Forensic Sciences, Dallas, Texas, 2004.

391. Lorente, J.A., Alvarez, C., Entrala, C., Martinez-Espin, E., Fernandez-Rosado, F., Martinez-Gonzalez, L.J., Lorente, M., Villaneuva, E., Arce, B., Heinrich, B., Cano, J.A., and Budowle, B.: Missing persons: genetic tools that can help identify remains, American Academy of Forensic Sciences, Dallas, Texas, 2004.

392. Budowle, B.: Tracking microbial biocrime: the evolving role of clinical and public health laboratories, International Conference on Emerging Infectious Diseases, Atlanta, Georgia, 2004.

393. Budowle, B.: Countering bioterrorism with the newly evolving field of microbial forensics, 17TH Australian and New Zealand International Symposium on the Forensic Sciences, Wellington, New Zealand, 2004.

394. Budowle, B.: Issues to consider for the application of Y-STR loci, 17TH Australian and New Zealand International Symposium on the Forensic Sciences, Wellington, New Zealand, 2004.

395. Budowle, B.: Mitochondrial DNA: methods and interpretation, 17TH Australian and New Zealand International Symposium on the Forensic Sciences, Wellington, New Zealand, 2004.

396. Budowle, B., Sinha, S., Gross, M.A., Nasir, H., and Shewale, J.: Ychromosome STR system Y-Plex<sup>™</sup> 12 for forensic casework: development and validation, 17TH Australian and New Zealand International Symposium on the Forensic Sciences, Wellington, New Zealand, 2004.

397. Budowle, B: Points to consider for microbial forensics, Advances in Microbial forensics, The Banbury Center, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 2004.

398. Budowle, B.: Approaches for Typing SNPs, Mediterranean Academy of Forensic Sciences Meeting, Reggio Calabria, Italy, 2004.

400. Budowle, B.: Preparing Forensics for Bioterrorism and Biocrimes, Mediterranean Academy of Forensic Sciences Meeting, Reggio Calabria, Italy, 2004.

401. Murch, R.S. and Budowle, B.: Forensic issues in plant agroterrorism, Annual Meeting of the American Phytopathological Society, Anaheim, California, 2004.

402. Budowle, B.: Quality assurance measures for animal forensics, 29<sup>th</sup> International Congress on Animal Genetics, Tokyo, Japan, 2004.

403. Budowle, B.: Animal genetics and forensics: exploring focal points, 29<sup>th</sup> International Congress on Animal Genetics, Tokyo, Japan, 2004.

404. Budowle, B.: Interpreting Y STR evidence, 15<sup>th</sup> International Symposium on Human Identification, Phoenix, Arizona, 2004.

405. Alshamali, F.H., Alkhayat, A.I., Budowle, B., and Watson, N.D.: A case report of a family with a rare mutation in the Amelogenin gene: comparison of two different approaches to resolve the issue of correct sex typing, 15<sup>th</sup> International Symposium on Human Identification, Phoenix, Arizona, 2004.

406. Martinez-Gonzalez, L.J., Fernandez-Rosado, F., Martinez-Espin, E., Alvarez, J.C., Entrala, C., Lorente, J.A., and Budowle, B.: Biological stains collected from crime scenes using FTA® paper, American Academy of Forensic Sciences, New Orleans, Louisiana, 2005.

407. Martinez-Gonzalez, L.J., Moguel, M., Martinez-Espin, E., Entrala, C., Alvarez, J.C., Fernandez-Rosado, F., Lorente, J.A., Lorente, M., Villaneuva, E., and Budowle, B.: Mexican (Chihuahua) population data for the 15 STR loci included in the Identifiler kit, American Academy of Forensic Sciences, New Orleans, Louisiana, 2005.

408. Budowle, B.: Laboratory aspects of forensic molecular biology analyses, LabAutomation 2005, Association for Laboratory Automation, San Jose, California, 2005.

409. Budowle, B.: Mass Spectrometry for forensic mitochondrial DNA analysis, American Society for Mass Spectroscopy, Clearwater, Florida, 2005.

410. Budowle, B.: The use of DNA testing as an investigation tool and as a presumptive identification test, Human Identification E-Symposium, http://www.humid.e-symposium.com/, 2005.

411. Martinez-Jarreta, B., Vasquez, P., Abecia, E., Budowle, B., and Luna, A.: Characterization of 17 Y-STR loci in a population from El Salvador (San Salvador, Central America) and their potential for DNA profiling, 17<sup>th</sup> Meeting of the International Association of Forensic Sciences, Hong Kong, 2005.

412. Budowle, B., Chakraborty, R., and Fung, W.: Workshop on DNA statistics - mixture, parentage, and kinship determination, 17<sup>th</sup> Meeting of the International Association of Forensic Sciences, Hong Kong, 2005.

413. Budowle, B.: A robust SNP typing methodology: overcoming limitations of mitochondrial DNA analysis, 16<sup>th</sup> International Symposium on Human Identification, Grapevine, Texas, 2005.

414. Alshamali, F., Budowle, B., and Watson, N.D.: The bones can tell: skeletal remains identified after 11 years, 16<sup>th</sup> International Symposium on Human Identification, Grapevine, Texas, 2005.

415. Budowle, B.: Microbial forensics: sample collection, preservation, and extraction/purification/concentration, Third Microbial Forensics Meeting, The Banbury Center, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 2005.

416. Budowle, B.: Attribution of microbial forensic evidence, 2005 International Forensic Science Symposium, Taipei, Taiwan, 2005.

417. Budowle, B.: SNP typing methodologies for forensic analyses and addressing assay limitations, 2005 International Forensic Science Symposium, Taipei, Taiwan, 2005.

418. Budowle, B.: Laboratory testing of DNA for forensic use: protocols, quality assurance, training and accreditation issues, Forensic Science: The Nexus of Science and the Law, Arthur M. Sackler Colloquium of the National Academy of Sciences, Washington, D.C., 2005.

419. Budowle, B.: Bioforensics, law enforcement challenges, and case studies, Preventing Bio-Terrorism South Africa Workshop, Interpol, Cape Town, South Africa, 2005.

420. Budowle, B. and Baechtel, F.S.: Random match probabilities and database search estimates provide different answers for different questions, American Academy of Forensic Sciences, Seattle, Washington, 2006.

421. Martinez-Gonzalez, L.J., Martinez-Espin, E., Fernandez-Rosada, J., Entrala, C., Alvarez, J.C., Lorente, J.A., Lorente, M., Villaneuva, E., and Budowle, B.: Mixed buccal cells in a paternity case, American Academy of Forensic Sciences, Seattle, Washington, 2006.

422. Hennessy, L., Chien-Wei, C., Budowle, B., Calandro, L., and Mulero, J.: Characterization of a novel stutter product in the Y-STR marker DYS392 and a rare polymorphic variant in the DYS456 homologue identified using the AmpFlSTR Yfiler PCR Amplification Kit, American Academy of Forensic Sciences, Seattle, Washington, 2006.

423. Budowle, B.: The current status and future of microbial forensics, ASM Biodefense Research Meeting, Washington, D.C., 2006.

424. Budowle, B.: Forensic responses to bioterrorism, 2<sup>nd</sup> Annual Present and Future Technological Advances in Human Identification Conference, The Virginia Institute of Forensic Science and Medicine, Roanoke, Virginia, 2006.

425. Budowle, B.: What might be standards for microbial forensics, Expert Panel on the Development of Standards for Biodefense, Necessary Assurances to Protect National Security, Washington, D.C., 2006.

426. Budowle, B.: DNA databanks: uses, misapplications, and privacy issues, The Third Annual Forensic DNA Technology Workshop, Centre of Forensic Sciences, Toronto, Canada, 2006.

427. Budowle, B.: Assessing the significance of Y-STR evidence, The Third Annual Forensic DNA Technology Workshop, Centre of Forensic Sciences, Toronto, Canada, 2006.

428. Budowle, B.: SNP typing methodologies: practical applications, The Third Annual Forensic DNA Technology Workshop, Centre of Forensic Sciences, Toronto, Canada, 2006.

429. Budowle, B.: Identification in disasters and bioterrorism, Human Genome Organization Meeting, Helsinki, Finland, 2006.

430. Budowle, B.: Proper use of CODIS data, Association of Forensic DNA Analysts and Administrators, Austin, Texas, 2006.

431. Budowle, B.: CODIS hits and match probabilities - a proper interpretation, 17<sup>th</sup> International Symposium on Human Identification, Nashville, Tennessee, 2006.

432. Budowle, B.: Defining the differences between partial matches and familial searching, CODIS Users' Meeting, Crystal City, Virginia, 2006.

433. Budowle, B.: CODIS and current operational statistical applications, CODIS State Administrators Meeting, Crystal City, Virginia, 2006.

434. Budowle, B.: Forensic DNA data banking, Japanese DNA Polymorphism Research Meeting, Fukuyama, Japan, 2006.

435. Budowle, B.: Focal points of microbial forensics for enhancing biosecurity, 5<sup>th</sup> Biannual ESR Conference, Christchurch, New Zealand, 2006.

436.Budowle, B.: Tools and approaches for assessing missing person data, American Academy of Forensic Sciences, San Antonio, Texas, 2007.

437. Planz, J.V. and Budowle, B.: Validation theory, interpretation and statistical analysis of DNA mixtures, American Academy of Forensic Sciences, San Antonio, Texas, 2007.

438. Lorente, J., Martinez-Gonzalez, L.J., Martinez-Espin, E., Alvarez, J.C., Lorente, M., Villanueva, E., Budowle, B., and Monroy, M.O.: Autosomal STRs data on two aboriginal populations of Guatemala, American Academy of Forensic Sciences, San Antonio, Texas, 2007.

439. Roby, R., Budowle, B., Eisenberg, A.J., and Lorente, J.A.: Analysis of dye terminator sequence data: pattern recognition and signal background, American Academy of Forensic Sciences, San Antonio, Texas, 2007.

440. Budowle, B. And Buscaglia, J.: Evaluating and enhancing the forensic sciences: scientific foundations and best practices, American Academy of Forensic Sciences, San Antonio, Texas, 2007.

441. Budowle, B.: Biosecurity risks and responding with microbial forensics, Workshop on Plant Pathogen Forensics: Filling the Gaps, sponsored by Oklahoma State University, Oklahoma City, Oklahoma, 2007.

442. Budowle, B.: Moderate stringency matches or familial searching, California District Attorneys Association Winter Workshop, San Luis Obispo, California, 2007.

443. Budowle, B.: The power of forensic DNA typing, 72<sup>nd</sup> Meeting of the Israel Chemical Society, Tel Aviv, Israel, 2007.

444. Budowle, B.: Current status of microbial forensics, 2007 ASM Biodefense and Emerging Diseases Research Meeting, Washington, D.C., 2007.

445. Thomas, R.M., Budowle, B., and Polanskey, D.: Integrating the SWGDAM forensic mitochondrial DNA database into the anthropology community, 76th annual meeting of the American Association of Physical Anthropologists, Philadelphia, Pennsylvania, in: Amer. J. Phys. Anthropol. Supplement 44:231, 2007.

446. Budowle, B.: Advances in molecular biology for identification of mass disaster victims, missing persons, and evidentiary materials, International Medical and Health Congress 2007, Kota Bharu, Malaysia, 2007.

447. Budowle, B.: Human DNA forensics in the courts, Scientists and Science Behind CSI and Law and Order, A Science Inquiry Workshop Designed by Students for Students, The New York Academy of Sciences, New York, New York, 2007.

448. Budowle, B.: Forensic sciences: issues and directions, Committee on Identifying the Needs of the Forensic Sciences Community, Third Conference, National Academy of Sciences, Washington, D.C., 2007.

449. Budowle, B., Fisher, C.L., Polanskey, D., Den Hartog, B.K., Kepler, B.K., Elling, J.W.: Standardizing the nomenclature for mtDNA haplotypes with an intuitive hierarchal execution software program, International Society of Forensic Genetics Meeting, Copenhagen, Denmark, 2007.

450. Budowle, B.: Considerations for SNPs for forensic identity testing, International Society of Forensic Genetics Meeting, Copenhagen, Denmark, 2007.

451. Budowle, B.: Microbial forensic investigation of biocrime and bioterrorism, 5th ISABS Conference in Forensic Genetics and Molecular Anthropology. Split, Croatia, 2007.

452. Budowle, B.: Statistical issues surrounding national DNA databases, 5th ISABS Conference in Forensic Genetics and Molecular Anthropology. Split, Croatia, 2007.

453. Budowle, B., Ge J., and Chakraborty, R.: Guidelines for interpreting the significance of Y STR haplotypes derived from forensic evidence, 18th International Symposium on Human Identification, Hollywood, CA, 2007.

454. Budowle, B.: Looking into the DNA crystal ball, 18th International Symposium on Human Identification, Hollywood, CA, 2007.

455. Ge J., Budowle, B., and Chakraborty, R.: DNA identification by pedigree likelihood ratio, 18th International Symposium on Human Identification, Hollywood, CA, 2007.

456. Clabaugh, K., Silva, B., Odigie, K., Guroff, S., Fourney, R., Stevens, J., Carmody, G., Coble, M., Loreille, O., Scheible M., Kline, M., Parsons, T., Pozder A., Eisenberg, A., Budowle, B., and Lee, S.: Storage of DNA samples at ambient temperature using DNA SampleMatrix<sup>®</sup>, 18th International Symposium on Human Identification, Hollywood, CA, 2007.

457. Planz, J., Eisenberg, A., and Budowle, B.: Significance of kinship statistics and their interpretational implications in familial searches, 18th International Symposium on Human Identification, Hollywood, CA, 2007.

458. Budowle, B.: Enduring technologies, Microbial Forensics: Enduring Research Pathways, Banbury Center, Cold Spring Harbor, New York, 2007.

459. Budowle, B.: Interpretation issues, Microbial Forensics: Enduring Research Pathways, Banbury Center, Cold Spring Harbor, New York, 2007.

460. Budowle, B.: Guidelines for the interpretation of mixtures, 13<sup>th</sup> National CODIS Conference, San Francisco, California, 2007.

461. Budowle, B.: Interpretation issues regarding mixed stains, International DNA Symposium 2007 - Forensic DNA: Now and Beyond, Kuala Lumpur, Malaysia, 2007.

462. Budowle, B.: DNA database statistics issues, International DNA Symposium 2007 - Forensic DNA: Now and Beyond, Kuala Lumpur, Malaysia, 2007.

463. Budowle, B.: Microbial forensics and law enforcement, Microbial Forensics: Nexus Between Science, Public Health, and Law Enforcement, American Association for the Advancement of Science Center for Science, Technology, and Security Policy and The National Academies Committee on Science Technology, and Law, Washington, D.C., 2008.

464. Rolff, M., Muller-Cohn, J., Fourney, R.M., Coble, M. D., Kline, M.C., Parsons, T., Eisenberg, A.J., Budowle, B., Roberts, K.A., and Lee, S.P.: Optimizing collection, shipping, and storage of forensic biological samples, American Academy of Forensic Sciences, Washington, D.C., 2008.

465. McCurdy, L.D., Hall, T.A., Penella, T., Gioeni, L.J., Fisher, C.L., Sannes-Lowery, K.A., Isenberg, A.R., Hofstadler, S.A., and Budowle, B.: Base composition analysis of human mitochondrial DNA by electrospray ionization mass spectrometry: applications for forensic examinations, American Academy of Forensic Sciences, Washington, D.C., 2008.

466. Budowle, B., Aranda, X., Calandro, L.C., Hennessey, L.K., Lagace, R.E., Ge, J., Chakraborty, R., Planz, J.V., and Eisenberg, A.J.: Genetic and population characterization of the 17 Y STR loci in three Texas populations, American Academy of Forensic Sciences, Washington, D.C., 2008.

467. Clabaugh, K.C., Silva, B., Odigie, K.O., Fourney, R.M., Stevens, J., Carmody, G.R., Coble, M.D., Loreille, O., Scheible M., Kline, M.C., Parsons, T.J., Pozder, A., Eisenberg, A.J., Budowle, B., and Lee, S.B.: Storage of DNA samples at ambient temperature using DNA-SampleMatrix®, American Academy of Forensic Sciences, Washington, D.C., 2008.

468. Budowle, B.: Forensic challenges to the bioterrorism threat, Research Appreciation Day, University of North Texas Health Science Center, Ft. Worth, Texas, 2008.

469. Budowle, B.: Mixture analysis, Seventh Annual Advanced DNA Technical Workshop, Captiva Island, Florida, 2008.

470. Budowle, B., Fisher, C., Polanskey, D., Hartog, B.D., Elling, J., and Kepler, R.: Software program for standardizing an operational mtDNA nomenclature, DNA in Forensics 2008, Ancona, Italy, 2008.

471. Budowle, B., Jianye, G., Eisenberg, A.J., Aranda, X.G., and Chakraborty, R.: Interpreting Y STR profiles: substructure and mutation rates, DNA in Forensics 2008, Ancona, Italy, 2008.

472. Hennessy, L.K., Budowle, B., Aranda, X., Lagace, R., Planz, J.V., Rodriguez, M., and Eisenberg, A.J.: Null allele sequence structure at the DYS448 locus and implications for profile Interpretation, DNA in Forensics 2008, Ancona, Italy, 2008.

473. van Daal, A. and Budowle, B.: Forensic use of SNP markers for forensic analyses, DNA in Forensics 2008, Ancona, Italy, 2008.

474. Budowle, B.: Forensic science - issues and direction, 2008 Forensic DNA Technology Workshop, Toronto, Canada, 2008.

475. Budowle, B.: Developing mixture interpretation protocols, 2008 Forensic DNA Technology Workshop, Toronto, Canada, 2008.

476. Budowle, B.: The weight of Y STR evidence, 2008 Forensic DNA Technology Workshop, Toronto, Canada, 2008.

477. Budowle, B.: Low copy number DNA typing and considerations for routine laboratory work, International Society of Animal Genetics, Amsterdam, The Netherlands, 2008.

478. Ge, J., Xi, H., Budowle, B., and Chakraborty, R.: Haplotype block: a new type of forensic DNA markers, 18TH Meeting of the International Association of Forensic Sciences, New Orleans, LA, 2008.

479. Williamson, P.C. and Budowle, B.: Development of biological resources for pathogen identification in microbial forensic investigations, 18TH Meeting of the International Association of Forensic Sciences, New Orleans, LA, 2008.

480. Nunez, A., Kavlick, M., Robertson, J., and Budowle, B.: Application of circular ligase to provide template for rolling circle amplification of low amounts of fragmented DNA, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

481. Budowle, B., Planz, J.V., and Eisenberg, A.J.: Guidelines for the interpretation of mixtures, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

482. Hofstadler, S.A., Hall, T., Manalli, S., McCurdy, L.D., Penella, T., and Budowle, B.: Analysis of DNA forensic markers using high throughput mass spectrometry, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

483. Planz, J.V., Budowle, B., Lowery, K., Eisenberg, A.J., Hofstadler, S.A., and Budowle, B.: Drilling deeper into the STR allele: enhanced resolution and statistical power through SNP distributions within the short tandem repeats, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

484. McLaren, R.S., Ensenburger, M.G., Budowle, B., Rabbach, D., Fulmer, P.M., Sprecher, C.J., Bessetti, J., Sundquist, T.M., and Storts, D.R.: A solution for the split peak and -10 artifacts seen at the vWA locus PowerPlex® 16 and PowerPlex® ES, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

485. Nunez, A.N., Kavlick, M.F., Robertson, J.M., and Budowle, B.: Application of circular ligase to provide template for rolling circle amplification of low amounts of fragmented DNA, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

486. Kavlick, M.F., Lawrence, H.S., Merritt, T., Fisher, C., Isenberg, A., Robertson, J.M., and Budowle, B.: Real-time quantitative PCR assay for quantification of mitochondrial DNA, 19th International Symposium on Human Identification, Hollywood, CA, 2008.

487. Budowle, B.: Basic inheritance, Pharmacogenomics for Dummies, Society of Forensic Toxicologists, Inc., Phoenix, AZ, 2008.

488. Budowle, B.: Interpretations and statistics for Y-STR analysis, International DNA Symposium 2008: Towards the International Quality, Bangkok, Thailand, 2008.

489. Budowle, B.: Statistic issues that arise when using DNA Databases, International DNA Symposium 2008: Towards the International Quality, Bangkok, Thailand, 2008.

490. Budowle, B.: Criteria for validating microbial forensic methodologies, Ibis Biosciences Microbial Bioforensic T5000 Applications Workshop, Carlsbad, CA, 2008.

491. Baeta, M., Nunez, C., Casalod, Y., Gascon, S., Ge, J., Chakraborty, R., Martinez-Jarreta, B., and Budowle, B.: Characterization of Y-STR loci in a population from Nicaragua (Central America) and study of population substructure, American Academy of Forensic Sciences, Denver, CO, 2009.

492. Koskinen, M.T., Eisenberg, A.J., Planz, J.V., and Budowle, B.: Highperformance PCR for multiplexing STR loci directly from whole blood, American Academy of Forensic Sciences, Denver, CO, 2009.

493. Kavlick, M.F., Lawrence H.S., Merritt, R.T., Fisher, C.L., Isenberg, A.R., Robertson, J.M., and Budowle, B.: Real-time quantitative PCR assay for mitochondrial DNA quantitation, American Academy of Forensic Sciences, Denver, CO, 2009.

494. Lorente, J.A., Alvarez-Cubero, M.J., Gomez-Martin, A., Martinez-Gonzalez, L.J., Entrala, C., Fernandez-Rosado, F.J., Martinez-Espin, E., Alvarez, J.C., Budowle, B., and Villaneuva, E.: Fighting human trafficking with DNA - the Prokids program, American Academy of Forensic Sciences, Denver, CO, 2009.

495. Budowle, B., Cummings, C., Barker, M., Beaudry, J.A., Fang, R., Furtado, M.R., and Keim, P.: Detection by SOLiD<sup>™</sup> short-read sequencing of *Bacillus anthracis* and *Yersinia pestis* SNPs for strain identification and attribution in microbial forensics applications, Advances in Genome Biology and Technology, Marco Island, FL, 2009.

496. Budowle, B.: Future directions, Mitochondrial and STR DNA analysis by mass spectrometry using the Ibis Biosciences, Inc. platform, Technology Transition Workshop, Carlsbad, CA 2009.

497. Budowle, B.: Statistical inferences on genetic data from challenged samples: from low copy number human identification to attribution in microbial forensics, Cincinnati Symposium on Probability Theory and Applications, University of Cincinnati, Cincinnati. OH, 2009.

498. Budowle, B. and Eisenberg, A.: Mixture interpretation workshop. Sixth Annual Advanced DNA Technical Workshop - West, San Diego, CA, 2009.

499. Budowle, B. and Eisenberg, A.: Ethics in forensic science. Sixth Annual Advanced DNA Technical Workshop - West, San Diego, CA, 2009.

500. Budowle, B.: New Technologies. Sixth Annual Advanced DNA Technical Workshop - West, San Diego, CA, 2009.

501. Budowle, B.: Forensic science at the crossroads: issues and change. Meeting the Forensic Challenges of the  $21^{st}$  Century Conference, Dubai, UAE, 2009.

502. Budowle, B.: Forensic science meeting the challenges of Biodefense. Meeting the Forensic Challenges of the  $21^{st}$  Century Conference, Dubai, UAE, 2009.

503. Budowle, B.: The future of molecular biology in forensic evidence analysis. Meeting the Forensic Challenges of the 21<sup>st</sup> Century Conference, Dubai, UAE, 2009.

504. Budowle, B. and Eisenberg, A.: DNA evidence: single source and mixture evidence and kinship - interpretation and statistics. Meeting the Forensic Challenges of the 21<sup>st</sup> Century Conference, Dubai, UAE, 2009.

505. Budowle, B. and Eisenberg, A.: Mixture interpretation workshop. Sixth Annual Advanced DNA Technical Workshop - East, Amelia Island, FL, 2009.

506. Budowle, B. and Eisenberg, A.: Ethics in forensic science. Sixth Annual Advanced DNA Technical Workshop - East, Amelia Island, FL, 2009.

507. Budowle, B.: New Technologies. Sixth Annual Advanced DNA Technical Workshop, Amelia Island - East, FL, 2009.

508. Budowle, B.: Mass spectrometry methods for human mtDNA typing and microbial forensic applications. 10<sup>th</sup> International Symposium on Mutations in the Genome, Paphos, Cyprus, 2009.

509. Budowle, B.: Low copy number typing - we have the technology, but should we use it? The Politics and Technology of DNA Databases; Creating the Future - Computers, Freedom, & Privacy Conference 2009, Washington, D.C., 2009.

510. Budowle, B.: Engaging plant pathologists to meet law enforcement needs, Annual Meeting of the American Phytopathological Society, Portland, Oregon, 2009.

511. Budowle, B., Eisenberg, A.J., Gonzalez, S., Planz, J.V., Roby, R.K., and van Daal, A.: The challenges to the use of low copy number analysis, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

512. Budowle, B., Eisenberg, A.J., Gonzalez, S., Planz, J.V., Sannes-Lowery, K.A., Hall, T.A., Paulsen, J.E., and Hofstadler, S.A.: Validation of Mass Spectrometry Analysis of mtDNA, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

513. Budowle, B., Williamson, P., Cummings, C., Barker, M., Beaudry, J.A., Fang, R., Furtado, M.R., and Keim, P.: Detection of Bacterial Variation by Next Generation SOLiD<sup>™</sup> Sequencing for Microbial Forensics Investigations, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

514. Gonzalez, S., Roby, R.K., Phillips, N.R., Planz, J.V., Thomas, J.L., Pantoja Astudillo, J.A., Ge, J., Aguirre Morales, E., Eisenberg, A.J., Chakraborty, R., and Budowle, B.: STR allele frequencies and Y haplotypes in five Chilean sample populations, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

515. Hofstadler, S., Hall, T., Sannes-Lowery, K., Manalili, S., Paulsen, J., McCurdy, L., Gioeni, L., Penella, T., Eisenberg, A., Planz, J., and Budowle, B.: Analysis of DNA forensic markers using high throughput mass spectrometry, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

516. Planz, J.V., Budowle, B., Hall, T., Eisenberg, A.J., Sannes-Lowery, K.A., and Hofstadler, S.A.: Enhanced resolution and statistical power through evaluation of SNPs distributed within the short tandem repeats utilizing mass spectrometry, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

517. Den Hartog, B.K., Elling, J.W., and Budowle, B.: The impact of jumping alignments on clustering and database searches, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

518. Budowle, B.: Base composition analysis by electrospray ionization time of flight mass spectrometry for human mitochondrial DNA typing, Abbott Symposium, 23rd World Congress of the International Society for Forensic Genetics, Buenos Aires, Argentina, 2009.

519. Cummings, C., Bormann Chung, C., Fang, R., Brzoska, P., Williamson, P., Wagner, D., Birdsell, D., Vogler, A., Schupp, J., Beaudry, J., Matthews, M., Budowle, B., Keim, P., Barker, M., and Furtado. M.: High-throughput, wholegenome strain typing of microbial pathogens for forensics and epidemiology, Wellcome Trust Applied Bioinformatics and Public Health Microbiology 2009, Hinxton, UK, 2009. 520. Harmon, R. and Budowle, B.: The 2009 NAS report on DNA: What did you expect? Texas District & County Attorneys Association, Corpus Christi, TX, 2009.

521. Larsen, C., Budowle, B., Josserand, M., and Eisenberg, A.: Autosomal STRs alone often may not be sufficient for the identification of human remains, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

522. Budowle, B. and van Daal, A.: Ethics and forensic science, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

523. Gonzalez, S., Feller, E., Budowle, B., and Eisenberg, A.: Pressure cycling technology (PCT) applications for DNA extractions from challenging forensic samples, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

524. Feller, E.; Gonzalez, S.; Smuts, A.; Budowle, B.; and Eisenberg, A.J.: DNA extraction from hair using pressure cycling technology, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

525. Ge, J., Budowle, B., and Chakraborty, R.: Interpreting Y chromosome STR haplotype mixture, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

526. Budowle, B.: Presentation in Low Copy Number Session, 20th International Symposium on Human Identification, Las Vegas, NV, 2009.

527. Budowle, B.: Genomics and Bioterrorism, Forensic Genomics Consortium Netherlands, The Hague, Netherlands, 2009.

528. Nunez-Illas, A., Kavlick, M.F., Tate, C., Guerrieri, R., Robertson, J.M., and Budowle, B.: Application of circular ligase to provide template for rolling circle amplification of fragmented DNA, American Academy of Forensic Sciences, Seattle, WA, 2010.

529. Budowle, B.: Trace DNA: Low copy and low quality templates, novel approaches, DNA repair enzymes, and their utility in forensics, American Academy of Forensic Sciences, Seattle, WA, 2010.

530. Budowle, B.: Utility of SNPs in forensic casework and investigative leads, American Academy of Forensic Sciences, Seattle, WA, 2010.

531. Schulttheis, S.C., Peters, D., Eisenberg, A.J., and Budowle, B.: Evaluation of quantitation methods for implementation in forensic casework, American Academy of Forensic Sciences, Seattle, WA, 2010.

532. Budowle, B. and Williamson, P.C.: Need for standards and standard materials for microbial forensics, Development of Biothreat Agent Standards and Reference Materials, 8th Annual ASM Biodefense and Emerging Diseases Research Meeting, Washington, D.C., 2010.

533. Budowle, B.: Microbial forensics and next generation sequencing as a foundational tool to assist investigating biocrime, Forensic User Meeting, Bahrain, 2010.

534. Abbott, A.L., Hsiao, M.S., Fox, E.A., Murch, R., Budowle, B., Short, N.J., Misra, S., Kozievitch, N.P., and Park, S.H.: Toward a quantitative basis for sufficiency in friction ridge pattern detail, International Association of Identification, Spokane, WA, 2010.

535. Budowle, B.: What do the numbers mean?, Missing Persons and Unidentified Remains Workshop, NIJ, Ft. Lauderdale, FL, 2010.

545. Budowle, B. and Eisenberg, A.: Ethics in forensic science. 9<sup>th</sup> Annual Advanced DNA Technical Workshop, San Diego, CA, and Amelia Island, FL, 2010.

546. Budowle, B.: Low copy number -how low should you go?. 9<sup>th</sup> Annual Advanced DNA Technical Workshop, San Diego, CA, and Amelia Island, Florida, 2010.

547. Budowle, B.: Pressure cycling technology (PCT) augments sensitivity of detection and robustness in forensic DNA analyses, Applications of Ultra-high Pressure in Biotechnology, Harvard Medical School, Boston, MA, 2010.

547. Budowle, B.: DNA mixture interpretation, Asian Forensic Sciences Network 2<sup>nd</sup> Annual Meeting and Symposium, Brunei Darussalam, 2010.

548. Cheong, P.Y., Liew, P.V.O., Lee, E.Y., Jaludin, D.A.M.P., and Budowle, B.: Population frequency study for 15 STR loci for Brunei Darussalam Malay and Chinese, Asian Forensic Sciences Network 2<sup>nd</sup> Annual Meeting and Symposium, Brunei Darussalam, 2010.

549. Budowle, B.: Progress on the research for "Improved Tools and Interpretation Guidelines for Examining Limited Low Copy Number DNA Obtained from Degraded Single Source Samples: Bones, Teeth, and Hairs", The NIJ Conference 2010, National Institute of Justice, Arlington, VA, 2010.

550. Abbott, A.L., Hsiao, M.S., Fox, E.A., Murch, R., Budowle, B., Short, N.J., Misra, S., Kozievitch, N.P., and Park, S.H.: Development of a quantitative basis for sufficiency in friction ridge pattern detail, NIJ Panel on Impression Evidence, The NIJ Conference 2010, National Institute of Justice, Arlington, VA, 2010

551. Abbott, A.L., Hsiao, M.S., Fox, E.A., Murch, R., Budowle, B., Short, N.J., Misra, S., Kozievitch, N.P., and Park, S.H.: Toward a quantitative basis for sufficiency in friction ridge pattern detail, Impression and Pattern Evidence Symposium, Clearwater Beach, FL, 2010.

552. Budowle, B.: The future of DNA typing (molecular biology) in forensic biological evidence analysis, What is the Future for DNA Analysis in Judicial Practice, Laboratoire d'Hematologie Medico-Legale, Universite Victor Segalen Bordeaux, Bordeaux, France, 2010.

553. Budowle, B.: The interpretation of DNA case reports - when associations are made using Genetic data. What do the numbers mean? Missing Persons and Unidentified Remains Workshop, NIJ, Seattle, WA, 2010.

554. Budowle, B.: Forensic identification of missing persons: strategies and experiences in the USA, International Seminar on Ancient DNA of the University of Zaragoza: Applications in the Study of Human Remains of Historical Interest, Jaca, Spain, 2010.

555. Budowle, B.: Optimization of forensic analysis of difficult samples, International Seminar on Ancient DNA of the University of Zaragoza: Applications in the Study of Human Remains of Historical Interest, Jaca, Spain, 2010.

556. Budowle, B.: Perspectives on error rate reporting in forensic casework and testimony. NIJ Impression and Pattern Evidence Symposium, Clearwater, FL, 2010.

557. Budowle, B.: Low copy number typing is unwieldy and has been problematic to implement. 20<sup>th</sup> Australian and New Zealand International Symposium on the Forensic Sciences, Sydney, Australia, 2010.

558. Budowle, B.: Base composition analysis by electrospray ionization time of flight mass spectrometry: an invaluable tool for microbial forensics and for human identification (mitochondrial DNA). 20<sup>th</sup> Australian and New Zealand International Symposium on the Forensic Sciences, Sydney, Australia, 2010.

559. Budowle, B.: Base composition analysis by electrospray ionization time of flight mass spectrometry: a tool for forensics analysis of biological material. 20<sup>th</sup> Australian and New Zealand International Symposium on the Forensic Sciences, Sydney, Australia, 2010.

560. Ge J., Budowle, B., Eisenberg, A., and Chakraborty, R.: Comparing DNA based familial searching policies. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

561. Turnbough, M.A., Davis, C.P., King, J.L., Dixon, B., Liu, J.Y., Budowle, B., and Eisenberg, A.E.: Competitive extraction robot audit: a comparison of the Applied Biosystems<sup>™</sup> Automate Express<sup>™</sup>, Qiagen<sup>®</sup> EZ1<sup>®</sup> Advanced XL, and the Promega Maxwell<sup>®</sup> 16. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

562. Tate C., Nunez, A., Kavlick, M., Robertson, J., and Budowle, B.: Evaluation of circular DNA substrates for whole genome amplification prior to forensic analysis. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

563. Nunez, C., Baeta M., Sosa, C., Casalod Y., Ge, J., Budowle, B., and Martinez-Jarreta, B.: Characterization of Y-STR, autosomal STR loci, and mtDNA control region in a population from Nicaragua and study of the population substructure. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

564. Turnbough, M.A., Brownleader, M., Eisenberg, A.E., Gill-King, H., Benjamin, R.C., and Budowle, B.: Hi-Flow<sup>®</sup> - novel large volume columns for DNA extraction. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

565. Marshall, P., King, J., Dimitrijevich, D., Turnbough, M., Eisenberg, A.E., and Budowle, B.; Pressure cycling technology (PCT) applications for forensic DNA analysis. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

566. Davis, C., Chidambaram, A., King, J., Ge, J., Turnbough, M., Collins, M., Chakraborty, R., Eisenberg, A.J., and Budowle, B.: Examination of Y STR loci to enhance paternal lineage forensic analyses. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

567. Budowle, B.: Introduction to familial searching, Familial Search Panel Discussion. 21<sup>st</sup> International Symposium on Human Identification, San Antonio, TX, 2010.

568. Budowle, B.: Setting the stage, Microbial Forensics in the Era of Genomics, Department of Homeland Security, The Banbury Center, Cold Spring Harbor Laboratory, New York, 2010.

569. Budowle, B.: Archives and database needs, Microbial Forensics in the Era of Genomics, Department of Homeland Security, The Banbury Center, Cold Spring Harbor Laboratory, New York, 2010.

570. Wasserstrom, A., Frumkin, D., Davidson, A., and Budowle, B.: Forensic tissue identification based on DNA methylation, American Academy of Forensic Sciences, Chicago, IL, 2011.

571. Ge, J., Budowle, B., and Chakraborty, R.: Choosing relatives for DNA identification of missing person identification, American Academy of Forensic Sciences, Chicago, IL, 2011.

572. Swienton, A.R., Murch, R., and Budowle, B.: A strategic approach to improving forensic science performance: sufficiency as an example, American Academy of Forensic Sciences, Chicago, IL, 2011.

573. Budowle, B.: Human genetic and microbial repositories: concepts and needs. Lyme Disease in the Proteomics-Genetics Era, The Banbury Center, Cold Spring Harbor, New York, 2011.

574. Budowle, B.: Validation: Good Test - Bad Test. Lyme Disease in the Proteomics-Genetics Era, The Banbury Center, Cold Spring Harbor, New York, 2011.

575. Budowle, B.: Next generation technologies for forensic DNA testing, Third Asian Forensic Sciences Network Annual Meeting and Symposium, Seoul, Korea, 2011.

576. Barash, M., Budowle, B., Kumar, K., and van Daal, A.: Identification of single nucleotide polymorphisms (SNPs) involved in the determination of facial morphology, 7th ISABS Conference in Forensic, Anthropologic and Medical Genetics and Mayo Clinic Lectures in Translational Medicine, Bol, Croatia, 2011.

577. Ge, J., Budowle, B., and Eisenberg, A.: Expanding the CODIS loci in the United States, how many and which loci make the most sense. 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

578. Budowle, B.: New approaches for DNA testing, Latin America Working Group, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

579. LaRue, B., Frumkin, D. Wasserton, A., Davidson, A., and Budowle, B: Development and validation of a semen-specific DNA-based methylation assay. 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011. 580. Schmedes, S., Mai, L., Marshall, P., King, J., Marziali, A., and Budowle, B.: The use of synchronous coefficient of drag alteration (SCODA) technology to extract, purify and concentrate DNA from challenging or degraded forensic samples, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

581. Ge, J., Eisenberg, A., and Budowle, B.: Familial searching software: MPKin FS Edition<sup>™</sup>, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

582. LaRue, B., King, J., and Budowle, B.: Indel markers for human identification: validation of the Investigator Dipplex Human Identification Kit, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

583. Marshall, P., King, J., Schmedes, S., Turnbough, M., Eisenberg, A., and Budowle, B.: Improved tools for examining low copy number (LCN) DNA obtained from challenged or degraded samples,  $22^{nd}$  International Symposium on Human Identification, National Harbor, MD, 2011.

584. Myers, B., King, J.L., and Budowle, B.: Validation of direct amplification of STRs using Powerplex® 18D and Identifiler® Direct systems, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

585. Davis, C., King, J., Malik, N., Weirich, V., Eisenberg, A.J., and Budowle, B.: Variants observed for the STR locus SE33: a concordance study, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

585. Turnbough, M., Flores, S.K., Sun, J., Budowle, B., and Eisenberg, A.: Establishment of an accelerated training certificate program in automated, high-throughput, single source DNA sample processing at the University of North Texas Health Science Center, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

586. Budowle, B.: Issues in interpretation and advances in missing persons operations, Missing Persons Workshop, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

587. Davis, C., Ge, J., Chidambaram, A., King, J., Collins, M., Dym, O., Chakraborty, R., Eisenberg, A., and Budowle, B.: Examination of novel Y STR loci to enhance paternal lineage forensic analyses, 22<sup>nd</sup> International Symposium on Human Identification, National Harbor, MD, 2011.

588. Budowle, B.: The gaps and strategies for a robust microbial forensics program, Medical Biodefense Conference, Bundeswehr Institute of Microbiology, Munich, Germany, 2011.

589. Budowle, B.: PLEX-ID system - a versatile biodefense forensic tool, Medical Biodefense Conference, Bundeswehr Institute of Microbiology, Munich, Germany, 2011.

590. Budowle, B.: Addressing the forensic science processes with new forensic technologies. Shanghai Forum on Crime Scene Physical Evidence Technology, Shanghai, China, 2011.

591. Budowle, B.: Tackling the problems of forensic science, DNA and Civil Liberties Conference II, Mass Bay Community College, Wellesley Hills, MA, 2011.

592. Budowle, B.: DNA typing - current and future, DNA and Civil Liberties Conference II, Mass Bay Community College, Wellesley Hills, MA, 2011.

593. Budowle, B.: Low copy number typing in DNA based identifications, DNA and Civil Liberties Conference II, Mass Bay Community College, Wellesley Hills, MA, 2011.

594. Budowle, B.: Kits, validation, and mixtures, 2011 International Symposium on Forensic Genetics Progress (China), Beijing, China, 2011.

595. Budowle, B.: Low copy number typing of DNA evidence, 2011 International Symposium on Forensic Genetics Progress (China), Beijing, China, 2011.

596. Budowle, B.: Microbial forensics, 2011 International Symposium on Forensic Genetics Progress (China), Beijing, China, 2011.

597. Lorente, J.A., Alvarez-Cubero, M.J., Alvarez, J.C., Saiz-Guinaldo, M., Lorente, M., Budowle, B., and Eisenberg, A.J.: Update on DNA-PROKIDS: fighting human trafficking with DNA analysis, American Academy of Forensic Sciences, Atlanta, GA, 2012.

598. Bailon, J., Kirkpatrick, S., Planz, J., Budowle, B., and Eisenberg, A.: Direct amplification of human mitochondrial DNA using electrospray ionization mass spectrometry, Research Appreciation Day, University of North Texas Health Science Center, Ft. Worth, Texas, 2012.

599. Budowle, B.: The forensic challenges of bioterrorism, 1<sup>st</sup> Saudi International Conference of Forensic Medical Sciences, Riyadh, Saudi Arabia, 2012.

600. Budowle, B. and Simon T.: The Amanda Knox case: what role did DNA transfer and contaminations issues play? NACDL & CACJ's 5<sup>th</sup> Annual Forensic Science Seminar, Las Vegas, NV, 2012.

601. Budowle, B.: Forensic genetics and molecular methods for assessing biodiversity: a look at the past, present, and future, Molecules in the Mountains: Highlighting Molecular Strategies in Modern Biodiversity and Forensic Sciences Western Carolina University, Cullowhee, NC, 2012.

602. Budowle, B.: Is DNA forensic analysis an error-prone process? The Hidden Side of DNA Profiles. Artifact, errors and uncertain evidence, Rome, Italy, 2012.

603. Budowle, B.: The uses and limitations of forensic DNA typing, Center for International Security and Cooperation Seminar series, Stanford University, Stanford, CA, 2012.

604. Budowle, B.: Considerations regarding forensic DNA typing and future directions, 2012 Texas Forensic Science Seminar, Austin, TX 2012.

605. Budowle, B.: Microbial forensics - gaps, gaps, uncertainty, and data fusion, Forum on Microbial Threats Workshop: The science and applications of microbial genomics: predicting, detecting, and tracking novelty in the

microbial world, Institute of Medicine, Board on Global Health, National Academy of Sciences, Washington, DC, 2012.

606. Budowle, B.: Technology advances to enhance analyses of human remains, Workshop on DNA Typing of Bone Samples, Prague, Czech Republic, 2012.

607. Budowle, B.: Forensic identification of missing persons: issues, strategies and experiences, Workshop on DNA Typing of Bone Samples, Prague, Czech Republic, 2012.

608. Budowle, B.: Logistics of rapid DNA typing: desires, practicalities and constraints, Workshop: Microfluidic Systems for Rapid Forensic DNA Analysis: Update and Potential Impact, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

609. Budowle, B.: The power of Y STR typing: development, applications and practices, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

610. Davis, C., Warshauer, D., and Budowle, B.: DNA profiling of database reference samples using second generation sequencing, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

611. Seo, S.B., King, J., and Budowle, B.: Forensic mitochondrial DNA typing using the Ion Torrent PGM<sup>™</sup>, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

612. Seo, S.B., King, J., and Budowle, B.: A systematic approach for reduction of STR stutter peak heights from LCN samples, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

613. Marshall, P., King, J.L., and Budowle, B.: Application of pressure cycling technology (PCT) reduces impact of PCR inhibitors, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

614. Larue, B., Sinha, S.K., Montgomery, A.H., Thompson, R., Klaskala, L., Pineda, G., Ge. J., King, J., Turnbough, M., and Budowle, B.: Innuls, a new strategy for human identification based on retrotransposable elements, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

615. Warshauer, D., King, J., Eisenberg, A., and Budowle, B.: Validation of the PLEX-ID<sup>TM</sup> mtDNA assay for use in forensics,  $23^{rd}$  International Symposium on Human Identification, Nashville, TN, 2012.

616. Warshauer, D., Marshall, P., Kelley, S., King, J., and Budowle, B.: An investigation of the transfer of saliva-derived DNA, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

617. Ge, J. and Budowle, B: Kinship index variations among populations and thresholds for familial searching, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

618. Li, B., Ge, J., Wu, F., Ye, L., Seo, S.S., Eisenberg, A., Budowle, B., and Chen, Y.: Concordance study on major STR multiplex kits and the effect of using multiple kits on the China national database, 23<sup>rd</sup> International Symposium on Human Identification, Nashville, TN, 2012.

619. Ge, J. and Budowle, B.: Kinship index variations among populations and thresholds for familial searching. American Society of Human Genetics, San Francisco, CA, 2012.

620. Budowle, B.: Forensic mitochondrial DNA and SNP typing strategies using the Ion Torrent Personal Genome Machine<sup>™</sup>. Asian Forensic Science Network 4<sup>th</sup> Annual Meeting and Symposium, Bangkok, Thailand, 2012.

621. Davis, C., Warshauer, D., and Budowle, B.: Development of DNA profiling for reference sample databases using next generation sequencing. Asian Forensic Science Network 4<sup>th</sup> Annual Meeting and Symposium, Bangkok, Thailand, 2012.

622. Davis, C., Warshauer, D.H., and Budowle, B.: DNA profiling of database reference samples using second generation sequencing. 120<sup>th</sup> Semi-Annual Seminar (Fall 2012) California Association of Criminalists, San Jose, CA, 2012.

623. Budowle, B.: The impact of the next generation technologies on the use of DNA databases. 1<sup>st</sup> Israeli Human Identification Meeting, Tel Aviv, 2013.

624. Budowle, B.: Genomics and technologies for the next generation forensic laboratory. Joint Conference of HGM 2013 and  $21^{st}$  International Congress of Genetics, Singapore, 2013.

625. Budowle, B.: The challenges of forensic molecular biology. 2013 Illumina Asia Pacific Scientific Summit, Phuket, Thailand, 2013.

626. Budowle, B. and Kroupa, K.: Update on the next generation of DNA typing technologies. American Society of Crime Laboratory Directors 40<sup>th</sup> Anniversary Meeting, Durham, North Carolina, 2013.

627. Budowle, B. and Eisenberg, A.: A view of the new DNA technologies and their potential impact on the next generation forensic laboratory. American Society of Crime Laboratory Directors 40<sup>th</sup> Anniversary Meeting, Durham, North Carolina, 2013.

628. Budowle, B.: The genetic technology revolution. 3<sup>rd</sup> Annual Life Sciences Symposium - Improving the Quality of Life Through DNA Technology, Ft. Worth, TX, 2013.

629. Martinez-Jarreta, B., Sosa, C., Casalod, Y., Baeta, M., Nunez, C., Lorenzo, J., Gimeno, B., Bolea, M., Laliena, C., Budowle, B., Hedges, R., and The "Reyes De Aragon" Team: Skeletal analyses allow to retrieve valuable data of early medieval ancestors Of the Spanish royal family: an interdisciplinary approach. Environmental and Archaeological Science Conference, AEA & UKAS 2013, Cardiff University, England, 2013.

630. Budowle, B.: Enhancing quality of extracted DNA. Technology Transition Workshop: a DNA Revolution - next generation technologies, Forensic Technology Center of excellence, National Institute of Justice, Ft. Worth, TX, 2013.

631. Budowle, B.: Single nucleotide polymorphisms - our future forensic markers. Technology Transition Workshop: a DNA Revolution - next generation technologies, Forensic Technology Center of excellence, National Institute of Justice, Ft. Worth, TX, 2013.

632. Budowle, B.: Comprehensive sequencing to address forensic needs. Technology Transition Workshop: a DNA Revolution - next generation

technologies, Forensic Technology Center of excellence, National Institute of Justice, Ft. Worth, TX, 2013.

633. Budowle, B., Warshauer, D.H., Seo, S.B., King, J.L., Davis, C., and LaRue, B.: Next generation sequencing provides comprehensive multiplex capabilities, 25th Congress of the International society of Forensic Genetics, Melbourne, Australia, 2013.

634. Flores, S.K., Sun, J., King, J., Eisenberg, A.J., and Budowle, B.: Validation of the GlobalFiler™ Express PCR Amplification Kit for the direct amplification of reference DNA samples, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

635. Sinha, S.K, Montgomery, A.H., Pineda, G., Thompson, R., LaRue, B.L., Ge, J., and Budowle, B.: Development of a novel multiplexed DNA analysis system for highly degraded DNA samples, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

636. Seo, S.B., King, J., Warshauer, D., Ge, J., and Budowle, B.: Large panels of SNPs for human identity typing are feasible with current generation sequencing (CGS) technology, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

637. Warshauer, D.H., Lin, D., Hari, K., Jain, R., Davis, C., LaRue, B., King, J.L., and Budowle, B: STRait Razor: a bioinformatic tool for lengthbased STR allele-calling in massively parallel sequencing data, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

638. LaRue, B.L., King, J.L., and Budowle, B.: Highly reliable reference sample genotyping utilizing an automated rapid DNA typing platform, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

639. Zeng, X., Seo, S.B., LaRue, B., King, J., and Budowle, B.: Whole mitochondrial genome typing on Ion Torrent<sup>™</sup> PGM<sup>™</sup> platform, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

640. Ge, J. and Budowle, B.: One complete versus triplicate analyses in Low Template DNA typing, 24<sup>th</sup> International Symposium on Human Identification, Atlanta, GA, 2013.

641. Budowle, B.: Validation and reference materials for microbial forensics, Science Needs for Microbial Forensics: Developing an International Science Roadmap, National Academy of Sciences, Zagreb, Croatia, 2013.

642. Minot, S., Ternus, K., Allen, J., Budowle, B., and Kadavy, D.: Evaluating novel metagenomic classification algorithms for forensic microbial detection, Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 2013.

643. Budowle, B.: Global trends in life sciences and genetics, Division on Engineering and Physical Sciences, National Academy of Sciences, Washington, DC, 2013.

644. Budowle, B., King, J., Moore, A., and Larue, B.: Rapid DNA and advancements in DNA extraction technology, 5<sup>th</sup> Asian Forensic Sciences Network Annual Meeting & Symposium, Singapore, 2013.

645. Budowle, B.: Familial searching of DNA databases, 5<sup>th</sup> Asian Forensic Sciences Network Annual Meeting & Symposium, Singapore, 2013.

646. Budowle, B., Ambers, a., and King, J.: DNA repair and whole genome amplification, Post-Symposium HSA DNA Workshop, Singapore, 2013. 647. Budowle, B., Marshall, P., Seo, S.B., and King, J.: Considerations and limitations of low template analysis, Post-Symposium HSA DNA Workshop, Singapore, 2013.

648. Budowle, B.: Validation and reference materials for microbial forensics, Science Needs for Microbial Forensics: Developing an Initial International Science Roadmap, Institute of Medicine, Board on Global Health, National Academy of Sciences, Zagreb, Croatia, 2013.

649. Seo, S.B., Zeng, X., Assidi, M., LaRue, B., King, J., Sajantila, A., and Budowle, B.: High throughput whole mitochondrial genome sequencing by two platforms of massively parallel sequencing, Second International Genomic Medicine Conference in November 2013 (24th-27th) by CEGMR at King Abdulaziz University, Jeddah, Saudi Arabia, 2013.

650. Budowle, B.: Principles and chemistries of next generation sequencing technologies, American Academy of Forensic Sciences, Seattle, WA, 2014.

651. Sinha, S.K., Montgomery, A.H., Pineda, G., Thompson, R., King, J., LaRue, B.L., Ge, J., Chakraborty, R., Budowle, B.: Development of a novel and sensitive DNA analysis multiplex based on INNUL markers for highly degraded forensic DNA samples, American Academy of Forensic Sciences, Seattle, WA, 2014.

652. Budowle, B.: Technologies of the future have arrived and communicating with the legal community, 2014 International Symposium on Forensic DNA in Law, Seoul, Korea, 2014.

653. Budowle, B.: Communicating scientific evidence in the legal system, Forensic Medical Science and Jurisprudence under Islamic Law, Riyadh, Saudi Arabia, 2014.

654. Budowle, B., Ambers, a., and King, J.: DNA repair and whole genome amplification - what they offer for forensic DNA typing, Bode Technology, 11th Annual DNA Technical Workshop - West, San Diego, CA, 2014.

655. Vuorio, A., Laukkala, T., Navathe, P., Budowle, B., Eyre, A., and Sajantila, A.: Aircraft-assisted pilot suicides, 15th European Symposium on Suicide and Suicidal Behaviour, Tallinn, Estonia, 2014.

656. Budowle, B., Ambers, a., and King, J.: DNA repair and whole genome amplification - what they offer for forensic DNA typing, Bode Technology, 13th Annual DNA Technical Workshop - East, Buena Vista, FL, 2014.

657. Budowle, B.: Massively parallel sequencing and forensic identity testing, Fifth Annual Prescription for Criminal Justice Forensics, The ABA Criminal Justice Section and the Louis Stein Center for Law & Ethics, Fordham University, New York, New York, 2014.

658. Churchill, J.D., Chang, J., Ge, J., Rajagopalan, N., Lagacé, R., Liao, W., King, J.L., and Budowle, B.: Blinded genetic analysis of twelve genomic samples using the Ion Torrent PGM System, Green Mountain Conference, Burlington, VT, 2014.

659. Zeng, X., King, J.L., Stoljarova, M., Warshauer, D.H., LaRue, B.L., Sajantila, A., Patel, J., Storts, D.R., and Budowle, B.: High sensitivity multiplex short tandem repeat loci analyses with massively parallel sequencing, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

660. Stoljarova, M., King, J.L., Churchill, J.D., Budowle, B.: Massively parallel sequencing of multiplex short amplicons of mtDNA from challenged forensic samples, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

661. Novroski, N., Kindt, T., Schmedes, S., King, J., Marshall, P., and Budowle, B.: Diomics X-Swab™: a novel bio-specimen collection tool for increased trace material recovery and PCR enhancement, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

662. Churchill, J.D., Chang, J., Ge, J., Rajagopalan, N., Lagacé, R., Liao, W., King, J.L., and Budowle, B.: Evaluation of the Ion PGM™ System for use in human identity DNA typing, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

663. Schmedes, S.E., Churchill, J., King, J., and Budowle, B.: Genetic profiling using the Illumina® ForenSeq<sup>™</sup> DNA Signature Prep Kit on the MiSeq Desktop Sequencer, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

664. Warshauer, D.H., King, J.L., and Budowle, B.: STRait Razor v2.0: the improved STR Allele Identification Tool - Razor, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

665. Zeng, X., King, J., Hermanson, S., Patel, J., Storts, D.R., and Budowle, B.: Evaluation of the PowerSeq<sup>™</sup> Auto System by massively parallel sequencing, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

666. King, J.L., LaRue, B.L., Novroski, N.M., Stoljarova, M., Seo, S.B., Zeng, X., Warshauer, D.H., Davis, C.P., Parson, W., Sajantila, A., and Budowle, B.: The use of Massively Parallel Sequencing (MPS) to accurately and rapidly sequence the mtGenome of 283 individuals from 3 North American populations, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

667. Budowle, B. and Churchill, J.: Moving towards a validated high throughput sequencing solution for human identification: an evaluation of two SNP panels, autosomal STRs, and whole mitochondrial genomes, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

668. Thompson, L., King, J.L., Budowle, B. and LaRue, B.: Development of insertion-deletion (INDEL) marker panels for ancestral and individual identity genotyping, 25<sup>th</sup> International Symposium on Human Identification, Phoenix, AZ, 2014.

669. Budowle, B.: Bioterrorism and Microbial Forensics, Beto Lecture, Sam Houston State University, Huntsville, TX, 2014.

670. Budowle, B.: Development of DNA typing and forensic DNA databases in the US, Vietnam Forensic DNA Network 1<sup>st</sup> Annual Workshop, Hanoi, Vietnam, 2014.

671. Budowle, B.: Current approaches for the analysis of human remains, Vietnam Forensic DNA Network 1<sup>st</sup> Annual Workshop, Hanoi, Vietnam, 2014.

672. Budowle, B.: Methods to enhance the success of challenging samples, Vietnam Forensic DNA Network 1<sup>st</sup> Annual Workshop, Hanoi, Vietnam, 2014.

673. Budowle, B.: Bioterrorism and Microbial Forensics, Hjelt Lecture, University of Helsinki, Helsinki, Finland, 2014.

674. Budowle, B.: History of DNA databasing in the United States, Symposium on Human Identification DNA databasing in Peru, Lima, Peru, 2014.

675. Budowle, B.: Next generation sequencing for forensics, Symposium on Human Identification DNA databasing in Peru, Lima, Peru, 2014.

676. Budowle, B.: Current approaches for the analysis of human remains, Symposium on Human Identification DNA databasing in Peru, Lima, Peru, 2014.

677. Budowle, B.: The future of genetics and impact on forensic science, Symposium on Human Identification DNA databasing in Peru, Lima, Peru, 2014.

678. Budowle, B.: Perspectives on the Future of forensic genetics, Human Identification Solutions: Innovations and Perspectives, Madrid, Spain, 2015.

679. Budowle, B.: Ethics in the discipline of Forensic DNA, Bode Cellmark Forensics, 12th Annual DNA Technical Workshop - West, Coronado, CA, 2015.

680. Budowle, B.: Massively parallel sequencing: getting ready for forensic applications, Bode Cellmark Forensics, 12th Annual DNA Technical Workshop - West, Coronado, CA, 2015.

681. Budowle, B.: Forensic science - real world applied genomics, Genetics Graduate Student Association Spring Symposium on Applied Genomics, Texas A&M University, College Station, TX, 2015.

682. Budowle, B.: Overview of forensic genetics MPS, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

683. Budowle, B.: Forensic genetics MPS and Data Analysis Options, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

684. Schellberg, T. and Budowle, B.: Will NGS lead to significant expansion of the core loci? Identify benefits and policy/legal issues, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

685. Churchill, J.D., King, J.L., Chang, J., Wootten, S., Lagacé, R., and Budowle, B.: Chemistry and performance testing of forensically-relevant genetic marker systems within the Ion PGM™ System, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

686. Schellberg, T. and Budowle, B.: Implementation of NGS will ultimately lead to significant expansion of the core loci: An evaluation of the identity benefits and policy/legal issues? Identify benefits and policy/legal issues, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

687. Wiley, R., Sage, K., Sturm, S., King, J., Budowle, B., and LaRue, B.: An evaluation of a new Rapid DNA platform for field forward applications, 26th

Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

688. Vanek, D., Budowle, B., Dubska, J.: Factors influencing the reliability of the bone sample DNA typing results, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

689. Stoljarova, S., King, J., Churchill, J., Aaspollu, A., and Budowle, B.: Massively parallel sequencing of multiplex short amplicons of mtDNA for analysis of challenged forensic samples, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

690. Bottino, C.G., Budowle, B., King, J., Churchill, J., Silva, R., and Moura-Neto, R.S..: STR genotyping with Ion Torrent PGM and STR 10-plex system: highlights on performance and data interpretation, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

691. Vanek, D., Budowle, B., and Votrubova, J..: The collaborative exercise concept on DNA typing of bone samples, 26th Congress of the International Society of Forensic Genetics, Krakow, Poland, 2015.

692. Budowle, B.: Microbial forensics and its needs for standards and standardization, 2015 Rapid NGS Bioinformatic Pipelines for Enhanced Molecular Epidemiologic Investigation of Pathogens, American Society of Microbiology, Washington, D.C., 2015.

693. Harmon, R. and Budowle, B.: Recent developments: the illusion of quality through accreditation, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

694. Zeng, X., King, J., Hermanson, S., Patel, J., Storts, D.R., and Budowle, B.: An evaluation of the Powerseq<sup>™</sup> Auto System: a multiplex short tandem repeat marker kit compatible with massively parallel sequencing, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

695. Churchill, J., King, J.L., Schmedes, S.E., Novroski, N.M., Wendt, F., Ambers, A., and Budowle, B.: Power of the Illumina® Forenseq<sup>™</sup> DNA Signature Preparation Kit in human identity DNA typing, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

696. Novroski, N.M., Warshauer, D.H., King, J.L., Zeng, X., Churchill, J.D., and Budowle, B.: Detection of intra-allelic sequence variants in autosomal and X chromosome short tandem repeats using massively parallel sequencing, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

697. Wendt, F., Zeng, X., Churchill, J., King, J., and Budowle, B.: Analysis of single-source short tandem repeat (STR) and single nucleotide polymorphism (SNP) loci using a custom HaloPlex Target Enrichment System panel, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

698. Takahashi, M., King, J.L., Zeng, X., Churchill, J.D., and Budowle, B.: One amplification - two analyses: a combined CE and MPS workflow, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

699. Churchill, J., King, J.L., Chang, J., Wootton, S.C., Chang, C-W., Lagacé, R., and Budowle, B.: Evaluation of a short-amplicon multiplex for the mitochondrial genome on the Ion PGM™, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015. 700. Ambers, A., Gill-King, H., Dirkmaat, D., Benjamin, R., King, J., and Budowle, B.: Autosomal and Y-STR analysis of degraded DNA from the 120-yearold skeletal remains of Ezekiel Harper, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

701. Ambers, A., Churchill, J.D., King, J.L., Stoljarova, M., Gill-King, H., and Budowle, B.: Characterization of unidentified 140-year-old human skeletal remains using massively parallel DNA sequencing, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

702. Wiley, R., Sage, K., Budowle, B., LaRue, B.: An evaluation of a new rapid DNA platform for field forward applications, 26<sup>th</sup> International Symposium on Human Identification, Grapevine, TX, 2015.

703. Budowle, B.: Maturation of the field of microbial forensics, Ecology of Soil Microorganisms, Prague, Czech Republic, 20015.

704. Budowle, B.: Current approaches for the analysis of human remains, Bone Workshop and Conference 2015, Prague, Czech Republic, 2015.

705. Budowle, B.: Technology advances to enhance analysis of human remains: MPS, Bone Workshop and Conference 2015, Prague, Czech Republic, 2015.

706. Budowle, B.: How did DNA mixture interpretation become corrupted? Actual Innocence: Establishing Innocence or Guilt, Causes of and Solutions to Wrongful Convictions, The Center for American and International Law, Plano, TX, 2016.

707. Churchill, J.D., King, J., Chang, J.P., Wootton, S.C., Chang, C-W., Lagace, R., and Budowle, B.: Forensic application of massively parallel sequencing (MPS) with the Ion Torrent<sup>™</sup> Multiplex Mitochondrial Genome Panel and Hi-Q<sup>™</sup> sequencing chemistry, American Academy of Forensic Sciences, Las Vegas, NV, 2016.

708. Wiley, R.E., Sage K., Budowle, B., and LaRue, B.L.: An evaluation of a new Rapid DNA platform for field-forward applications, American Academy of Forensic Sciences, Las Vegas, NV, 2016.

709. Budowle, B., Churchill, J.D., King, J.L., Chang, J., Wootton, S.C., Chang, C-W., and Lagacé, R.: Forensic applications using the AmpliSeq<sup>™</sup> mtDNA whole genome panel and massively parallel sequencing, Human Identification Solutions Conference, Barcelona, Spain, 2016.

710. Budowle, B.: Massively parallel sequencing for human identification evaluating results of a mito panel for challenged samples. Innovations & Perspectives, Human Identification Solutions, Gurgaon, India, 2016.

711. Budowle, B.: Massively parallel sequencing for human identification evaluating results of Mixture ID panel and comparison with CE data. Innovations & Perspectives, Human Identification Solutions, Gurgaon, India, 2016.

712. Budowle, B.: Overview of CE data interpretation and mixture analysis. Innovations & Perspectives, Human Identification Solutions, Gurgaon, India, 2016.

713. Budowle, B.: Assessing novel multiplex kits and the Ion Torrent S5 system for casework applications, The  $8^{\rm th}$  AFSN Annual Meeting & Symposium, Bangkok, Thailand, 2016.

714. Novroski, N., Churchill, J., King, J., and Budowle, B.: What's hiding between the primers? Using massively parallel sequencing to capture STR repeat region and flanking region sequence variation,  $27^{\text{th}}$  International Symposium on Human Identification, Minneapolis, MN, 2016.

715. Wiley, R., Zeng, X., Larue, B., Greytak, E.M., Armentrout, S., and Budowle, B.: Blind testing and evaluation of a comprehensive DNA phenotyping system, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

716. Wiley, R., Sage, K., King, J., LaRue, B., and Budowle, B.: An evaluation of the RapidHIT<sup>®</sup> ID System for field forward applications, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

717. Ambers, A., Wiley, R., Novroski, N., Frey, B., MacInnis, A., King, J. and Budowle, B.: Improved Recovery of DNA with the 4N6FLOQSwab System and Nucleic Acid Optimizer (NAO) Baskets, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

718. Zeng, X., Warshauer, D.H., Davis, C.P., King, J.L., Churchill, J.D., Novroski, N., Wendt, F.R., Chakraborty, R., and Budowle, B.: Development of a comprehensive panel of short tandem repeat and single nucleotide polymorphism markers for human identification using massively parallel sequencing technology, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

719. Takahashi, M., King, J.L., and Budowle, B.: Identification of highly polymorphic Y-STRs based on underlying sequence variation,  $27^{th}$  International Symposium on Human Identification, Minneapolis, MN, 2016.

720. Churchill, J.D., King, J.L., and Budowle, B.: More and more markers: use of the Precision ID GlobalFiler Mixture ID Panel to analyze challenged and mixed samples, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

721. Churchill, J.D., King, J.L., and Budowle, B.: Completing the Circle: Forensic Analysis of the Entire Mitochondrial Genome on Ion Torrent MPS Platforms, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

722. Wendt, F.R., Churchill, J.D., Novroski, N.M., King, J.L., Ng, J., Oldt, R.F., McCulloh, K.L., Weise, J.A., Smith, D.G., Kanthaswamy, S., and Budowle, B.: STR and SNP genetic analysis of the Yavapai Native Americans using massively parallel sequencing, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

723. Wendt, F.R., Warshauer, D.H., Churchill, J.D., Novroski, N.M., Song, B., King, J.L., LaRue, B.L., and Budowle, B.: Sequencing of 68 Insertion/Deletion markers: motif and microhaplotypes, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

724. Wendt, F.R., King, J.L., and Budowle, B.: Analysis of massively parallel sequencing data using the STR allele identification tool - Razor (STRait Razor), 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

725. Budowle, B.: 4N6FLOQSwabs<sup>™</sup> and NAOBaskets<sup>™</sup>: innovative tools for recovering DNA from crime scene evidence, 27<sup>th</sup> International Symposium on Human Identification, Minneapolis, MN, 2016.

726. Budowle, B.: Enhancing forensic genetics capabilities by use of massively parallel sequencing, Japanese Association of Forensic Science and Technology, Tokyo, Japan, 2016.

727. Ambers, A., Wiley, R.E., Novroski, N.M., and Budowle, B.: Increasing DNA recovery with nylon flock swabs and one-step spin baskets, American Academy of Forensic Sciences, New Orleans, LA, 2017.

728. Novroski, N.M., Churchill, J.D., King, J. and Budowle, B.: The application of short tandem repeat (STR) sequence variation for the selection of novel STR markers to enhance DNA mixture deconvolution: what do we know and where are we headed?, American Academy of Forensic Sciences, New Orleans, LA, 2017.

729. Churchill, J.D., King, J., and Budowle, B.: Forensic analysis of the entire mitochondrial genome on Ion Torrent<sup>™</sup> massively parallel sequencing (MPS) platforms, American Academy of Forensic Sciences, New Orleans, LA, 2017.

730. Budowle, B.: Massively parallel sequencing can advance forensic genetics capabilities, 2<sup>nd</sup> Saudi International Conference of Forensic Medicine and Sciences, Riyadh, Saudi Arabia, 2017.

731. Budowle, B.: Massively parallel sequencing is NGS - that is now generation sequencing, 14th Annual DNA Conference - Bode West, Phoenix, AZ, 2016.

732. Budowle, B.: A review of the PCAST Report, 14th Annual DNA Conference - Bode West, Phoenix, AZ, 2016.

733. Budowle, B.: Advances in molecular biology, population genetics, and bioinformatics solve real world problems, Departmental Seminar, Department of Molecular Biology, University of Wyoming, Laramie, WY, 2017.

734. Budowle, B.: The adoption process of MPS into US forensic genetics laboratories: US perspective, Human Identification Solutions Conference, Vienna, Austria, 2017.

735. Budowle, B.: Microbial forensics for microbial and human identification in criminal and civil investigations, 10<sup>th</sup> International Society of Applied Biological Sciences Conference, Dubrovnik, Croatia, 2017.

736. Budowle, B.: DNA 101: The Science, National Attorneys General Training & Research Institute CEPI Forensic Science Symposium, Washington, DC, 2017.

737. Müller, P., Berger, B., Bodner, M., Alonso, A., Barrio, P., Martin, P., Köcher, S., Roewer, L., Willuweit, S., Budowle, B., The DNASEQEX Consortium, and Parson, W.: Systematic evaluation of massively parallel STR sequencing in the DNASeqEx Project, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

738. Budowle, B., Novroski, N., Wiley, R., and Ambers, A.: Micro sample swabbing for reduced sample consumption, increased sensitivity of detection and enhanced intelligence for processing biological evidence, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

739. Churchill, J., Peters, D., Strobl, C., Parson, W., and Budowle, B.: Massively parallel sequencing (MPS) can be considered NGS, i.e., now generation sequencing: implementation of whole genome mitochondrial DNA sequencing into routine casework, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

740. Churchill, J.D., Stoljarova, M., King, J.L., and Budowle, B.: Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

741. Peck, M.A., Didier, M.M., Zeng, X., Takahashi, M., King, J.L., Bennett, L., Falk, M.D., Sturk-Andreaggi, K., Marshall, C., Welti, S., McMahon, T.P., Holt, C., and Budowle, B.: Inter-laboratory validation study of the ForenSeq DNA Signature Prep Kit, MiSeq FGx Instrument, and ForenSeq Universal Analysis Software for length-based STR analysis, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

742. Votrubova, J., Ambers, A., Budowle, B., and Vanek, D.: Comparison of standard capillary electrophoresis based genotyping method and ForenSeq DNA Signature Prep kit (Illumina) on a set of challenging samples, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

743. Elwick, K., Zeng, X., King, J., Budowle, B., and Hughes-Stamm, S.: Comparative tolerance of two massively parallel sequencing platforms to common PCR inhibitors for missing persons cases, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

744. Guevara, E., Palo, J., King, J.L., Geppert, M., Wendt, F.R., Stoljarova, M., Guillen, S., Roewer, L., Budowle, B., and Sajantila, A.: Mitochondrial DNA and Y-chromosome diversity in the cloud forest area of northeastern Peru, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

745. Ambers, A., Votrubova, J., Vanek, D., Carbonaro, A., and Budowle, B.: What can we learn from ancient bones - Y-STR analysis of human skeletal remains from the American civil war, world war II, seven year's war, and the American old west, 27th Congress of the International Society of Forensic Genetics, Seoul, South Korea, 2017.

746. Budowle, B., Schmedes, S.E., and Woerner, A.E.: Microbial forensics and human identification, 9<sup>th</sup> Asian Forensic Sciences Network Annual Meeting and Symposium, Singapore, 2017.

747. Budowle, B.: Autosomal and Y STR typing of DNA from human skeletal remains and cadaver tissues, 9<sup>th</sup> Asian Forensic Sciences Network Annual Meeting and Symposium, Singapore, 2017.

748. Budowle, B.: Enhanced front end sample collection and extraction can improve DNA typing results and laboratory workflow, 9<sup>th</sup> Asian Forensic Sciences Network Annual Meeting and Symposium, Singapore, 2017.

749. Wendt, F.R., Sajantila, A., Chakraborty, R., Pathak, G., Woerner, A.E., Moura-Neto, R.S., and Budowle, B.: *In silico* evaluation of a more comprehensive pharmacogenetic profile for predicting opiate metabolizer phenotype, American Society of Human Genetics, Orlando, FL, 2017.

750. Wiley, R., King, J., and Budowle, B.: Typing highly degraded DNA using circularized molecules and target enrichment, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

751. Wendt, F.R., Rahikainen, A-L., Sajantila, A., and Budowle, B.: The future of the CYP2D6 molecular autopsy using tramadol-exposed individuals, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

752. Schmedes, S.E., Woerner, A.E., and Budowle, B.: Forensic human identification using targeted clade-specific markers from skin microbiomes with supervised learning classification, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

753. Woerner, A.E., King, J., and Budowle, B.: Quality scores in MPS data: what are they good for? 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

754. Churchill, J.D., Peters, D., Capt, C., Strobl, C., Parson, W., and Budowle, B.: The road to implementation, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

755. Budowle, B., Wiley, R., Novroski, N., and Ambers, A.: An alternate workflow for DNA analysis with increased sensitivity of detection and reduced consumption of evidence: casework and legal implications, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

756. Ambers, A., Votrubova, J., Vanek, D., Sajantila, A., and Budowle, B.: Improved Y-STR typing for disaster victim identification, missing persons investigations, and historical human remains, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

757. Takahashi, M., Peck, M.A., Didier, M., Zeng, X., King, J.L., Bennett, L., Falk, M.D., Sturk-Andreaggi, K., Marshall, C., Welti, S., McMahon, T.P., Holt, C., Smith, J., and Budowle, B.: Inter-laboratory internal validation study of the ForenSeq DNA Signature Prep Kit, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

758. Zeng, X., Elwick, K., King, J., Hughes-Stamm, S., and Budowle, B.: Assessment of impact of extraction methods on analysis of human remain samples on massively parallel sequencing success, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

759. Novroski, N., Woerner, A.E., King, J., and Budowle, B.: Upping the mixture game: newly-adopted STR markers for enhanced DNA mixture deconvolution, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

760. Moura-Neto, R., King, J., Mello, I., Dias, V., Budowle, B., and Silva, R.: Evaluation of Promega Powerseq<sup>™</sup> Auto/Y Systems Prototype an admixed sample of Rio de Janeiro, Brazil on Illumina MiSeq<sup>™</sup> sequences: Population data, sensitivity and mixtures studies, 28<sup>th</sup> International Symposium on Human Identification, Seattle, WA, 2017.

761. Sherier, A.J., Ambers, A., Wiley, R.E., Novroski, N. M., and Budowle, B.: Increasing DNA typing success with improved front-end processing and alternate workflow strategies, American Academy of Forensic Sciences, Seattle, WA, 2018. 762. Scmedes, S.E., Woerner, A. E., and Budowle, B.: Candidates of Skin Microbiomes for Human Identification, NIJ R&D Symposium, American Academy of Forensic Sciences, Seattle, WA, 2018.

763. Jeanguenat A.M., Budowle, B., and Dror, I.: Practical ways to address cognitive bias in forensic DNA decision making, American Academy of Forensic Sciences, Seattle, WA, 2018.

764. Budowle, B., King, J.L., Novroski, N.M.M., Takahashi, M., Wendt, F.R., and Woerner, A.E.: The research and development progress of enhancing mixture interpretation with highly informative STRs, National Institute of Justice Forensic Science Research & Development Symposium, Pittcon, Orlando, FL, 2018.

765. Budowle, B.: Criteria for selecting a DNA databasing workflow, 24<sup>th</sup> All India Forensic Science Conference, Ahmedabad, India, 2018.

766. Budowle, B.: University of North Texas (UNT) efforts on missing and trafficked persons, Central America Regional Forensic Conference, San Jose, Costa Rica, 2018.

767. Budowle, B.: UNT Center for Human Identification's missing persons program, 2018 Missing Mrigrant Program Summit, Edinburg, TX, 2018.

768. Churchill, J.D., King, J.L., and Budowle, B.: Application of the Precision ID GlobalFiler NGS STR Panel, Human Identification Solutions Conference, Rome, Italy, 2018.
#### FUNDING

PI; Improved Tools and Interpretation Guidelines for Examining Limited Low Copy Number DNA Obtained from Degraded Single Source Samples: Bones, Teeth, and Hairs; Awarded by the National Institute of Justice; Award Number: 2009-DN-BX-K188; 10/01/2009 - 9/30/2011; Total: \$935,992.00.

Co-PI; Development of an Expert System for Automated Forensic mtDNA Data Analysis; Awarded by the National Institute of Justice; Award Number: 2009-DN-BX-K171; 10/01/2009 - 03/31/2011; Total: \$353,857.00.

Co-PI; Establishing the quantitative basis for sufficiency: threshold and metrics for friction ridge pattern detail quality and foundation for a standard; Awarded by Virginia Tech subcontract; the National Institute of Justice; Award Number: 2009-DN-BX-K229; 10/01/2009 - 09/30/2011; Total: \$854,907.00; Subcontract: \$123,120.00.

PI; Addressing Quality and Quantity; the Role of DNA Repair and Whole Genome Amplification in Forensically Relevant Samples; Awarded by the National Institute of Justice; Award Number: 2010-DN-BX-K227; 10/01/2010 - 09/30/2012. Total: \$363,613.00

PI; Identity, Lineage, and Phenotypic SNP Identification, Assay Development, and Data Interpretation; Awarded by the 2010 Intelligence Community Postdoctoral Research Fellowship Program; Award Number: 2010\*0937130\*000; 09/01/2010 - 08/31/2010; Total: \$239,076.00.

PI; Indel Study; Awarded by Life Technologies; Project ID RP0060; 10/18/2010 -04/01/2011; Total: \$30,000.00.

PI; Research Collaboration; Awarded by Promega Corporation; 10/01/2010 - 09/30/2012; Total: \$142,006.28

Co-PI; Comprehensive Training Program in Forensic DNA Interpretation and Statistics; Awarded by National Institute of Justice; Award number: NIJ-2010-93494, 2010-DN-BX-K239; 10/01/10-09/30/12; Total: \$999,481.00.

PI; Microbial Forensics Technical and Scientific Process; Awarded by Signature Science; Award number: 2012-030-0002; 02/01/2012-01/31/2013; Total: \$131,164.98.

Co-PI; Testing, Evaluation and Demonstration of New Technologies; Awarded by RTI International subcontract; Awarded by the National Institute of Justice; Award number: 2011-DN-BX-K564; 10/01/2011 - 09/30/2012; Total: \$375,000.00.

PI; Development of Reference Sample DNA Profiling for Databases Using Next Generation Sequencing Technologies; Awarded by the National Institute of Justice; Award Number: 2012-DN-BX-K033; 10/01/2012 - 6/30/2014; Total: \$747,797.00.

PI; NIJ Ph.D. Graduate Research Fellowship Program FY 2012; Awarded by the National Institute of Justice; Award Number: Award 2012-IJ-CX-0016; 10/01/2012 - 09/30/2013; Total: \$24,988.00.

PI; Validation of Rapid DNA Typing System; Awarded by Department of Defense; Contract Number: HQ0034-13-P-0002; 1/28/2013 - 01/27/2014; Total: \$32,659.80. PI; Microbial Forensics Technical and Scientific Process; Awarded by Signature Science; Renewal of Award number: 2012-030-0002; 02/01/2013-01/31/2014; Total: \$131,164.98.

Co-PI; Testing, Development of Improved Insertion-Deletion Assays for Human and Ancestral Identifications from Degraded Samples; Awarded by the National Institute of Justice; Award number: 2013-DN-BX-K036; 10/01/2013 - 09/30/2015; Total: \$336,282.96.

PI; Microbial Forensics Technical and Scientific Process; Awarded by Signature Science; Renewal of Award number: 2012-030-0002; 02/01/2014-01/31/2015; Total: \$131,164.98.

PI; Deadwood Project, Historic Preservation Archives Department Deadwood, South Dakota; 09/01/2014-12/31/2014; Total: \$3000.00.

PI; Familial Searching; Awarded by RTI International subcontract; 09/05/2014-12/31/2014; Total: \$ \$71,550.77.

PI; Novel Collection Device for Enhanced DNA Recovery and Release from Biological Stain Samples; Awarded by the National Institute of Justice; Award Number: 2014-DN-11X-K031; 01/01/2015 - 12/31/2016; Total: \$487,884.00.

PI; Human Microbiome Species and Genes for Human Identification; Awarded by the National Institute of Justice; Award Number: 2015-NE-BX-K006; 01/01/2016 - 12/31/2017; Total: \$589,701.00.

PI; Enhancing Mixture Interpretation with Highly Informative STRs; Awarded by the National Institute of Justice; Award Number: 2015-DN-BX-K067; 01/01/2016 - 12/31/2017; Total: \$585,415.00.

Co-PI; Enhanced Sample Preparation and Data Interpretation Strategies for Massively Parallel Sequencing for Human Identification in Missing Persons and DVI Casework; Awarded by the National Institute of Justice; Award Number: 2015-DN-BX-K067; 01/01/2016 - 12/31/2017; \$294,805.59.

PI; DNA Capacity Enhancement and Backlog Reduction Program, FY15, Awarded by the National Institute of Justice; Award Number: 2015-DN-BX-0057, 01/01/2016 - 12/32/2017; \$507,165.00.

PI; Using DNA Technology to Identify the Missing, FY15, Awarded by the National Institute of Justice; Award Number: 2015-DN-BX-K070; 01/01/2016 to 12/31/2017; \$2,238,750.00.

PI; Management and Support of the National and Missing Persons System, FY15, Awarded by the National Institute of Justice; Award Number: 2011-MU-BX-K063; 10/01/2016 to 09/30/2017; \$5,866,325.85.

PI; DNA Analysis of Sexual Assault Evidence, Interagency Agreement Texas Department of Public Safety, 09/01/2016 - 12/31/2016; \$192,990.00.

PI; Typing Highly Degraded DNA Using Circularized Molecules and Target Enrichment; Awarded by the National Institute of Justice; Award Number: 2016-DN-BX-0154; 01/01/2017 - 12/31/2018; \$682,474.00.

PI; Application for Funding to Support the National Missing and Unidentified Persons System (NamUs); Awarded by the National Institute of Justice; Award Number: 2016-MU-BX-K007; 10/01/2016 - 09/30/2017; \$4,700,000.00.

PI; FY 2016 DNA Capacity Enhancement and Backlog Reduction Program; Awarded by the National Institute of Justice; Award Number: 2016-DN-BX-0114; 01/01/2017 - 12/31/2018; \$473,465.00.

PI; Evaluation and Implementation of High Throughput Second Generation Sequencing for Mitochondrial DNA Testing in Missing Persons and Forensic Casework at the UNT Center for Human Identification; Awarded by the National Institute of Justice; Award Number: 2016-DN-BX-K001; 01/01/2017 - 12/31/2018; \$727,072.00.

PI; FY17 Graduate Research Fellowship in Science, Technology, Engineering, and Mathematics; Awarded by the National Institute of Justice; Award Number: Award 2017-IJ-CX-0010; 08/01/2017 - 07/31/2018; Total: \$46,155.00.

PI; Reducing Human Trafficking Through Forensics in Central America; Awarded by the U.S. Department of State; Award Number: S-INLEC-17-GR-1013; 09/20/2017 - 09/20/2018; \$3,301,122.48.

PI; Development of a Mitochondrial Mixture Database and Interpretation Tool; Awarded by the National Institute of Justice; Award Number: 2017-DN-BX-0134; 01/01/2018 - 12/31/2019; Total: \$556,910.00.

PI; Application for Funding to Support the National Missing and Unidentified Persons System (NamUs); Awarded by the National Institute of Justice; Award Number: 2016-MU-BX-K007 (continuation); 10/01/2017 - 09/30/2018; \$7,455,832.00.

PI; FY 2017 DNA Capacity Enhancement and Backlog Reduction Program; Awarded by the National Institute of Justice; Award Number: 2016-DN-BX-0114; 01/01/2018 - 12/31/2019; \$494,555.00.

#### GRADUATED STUDENTS

#### Masters

Shamika Kelley, Masters, Thesis Practicum: Assessment of DNA transfer events involving routine human behavior, May 2010.

David Warshauer, Masters, Thesis Practicum: An evaluation of saliva-based DNA transfer, August 2011.

Alyssa Koehn, Masters Thesis: Identification of unknown PCR products generated during STR analysis of bone samples, May 2013.

Andrea Moore, Masters Thesis: STR typing of reference samples with rapid DNA technology, May 2014.

Lisa Skandalis, Masters Thesis: Population variances in the whole mitochondrial genome impacting capture for human identification, May 2015.

Allison Conway, Masters Thesis: A validation of STRmix for forensic casework, May 2017.

Doctoral Pamela Marshall, Doctoral Dissertation: Improved tools for the robust analysis of low copy number and challenged DNA samples, May 2014.

David Warshauer, Doctoral Dissertation: Development of a comprehensive massively parallel sequencing panel of single nucleotide polymorphism and short tandem repeat markers for human identification, August 2015.

Xiangpei Zeng, Doctoral Dissertation: Selection of Highly Informative Markers for Apportionment of Ancestry and Population Affiliation, May 2016.

Sarah Schmedes, Doctoral Dissertation: Genetic Profiling of Skin Microbiomes for Forensic Human Identification, September 2017.

#### POST-DOCTORAL FELLOWS

Meredith Turnbough 2010-2011

Bobby Larue 2010-2012

Seung Bum Seo 2012-2014

Jennifer Churchill 2014-2018

Angela Ambers 2015-2018

Maiko Takahashi 2015-present

Xiangpei Zeng 2016-2017

August Woerner 2016-2017

Magdalena Bus 2018 - present

Sheree Hughes-Stamm, PhD Assistant Professor of Forensic Science Director of Graduate Programs Department of Forensic Science College of Criminal Justice Sam Houston State University

#### **Degrees Earned**

Ph.D., 2012, Forensic Genetics, Health Science & Medicine, Bond University, Gold Coast, AUSTRALIA. Forensic DNA typing of highly degraded samples

BSc., 1997, (Hons Eq.) Human Anatomy & Physiology, University of Queensland, Brisbane, AUSTRALIA

# Professional Licensure and Certifications

N/A

# Peer-Review Publications and Artistic Performances/Exhibitions

#### Articles

Amanda Wheeler, Natalia Czado, David Gangitano, Meredith Turnbough, Sheree Hughes-Stamm. (2016) Comparison of DNA Yield and STR Success Rate from Different Tissues in Embalmed Bodies. International Journal of Legal Medicine (in press, June 2016)

Amy Sorensen, Elizabeth Rahman, Cassandra Canela, David Gangitano, Sheree Hughes-Stamm. (2016) Preservation and Rapid Purification of DNA from Decomposing Human Tissue Samples. Forensic Science International;Genetics (in press, Feb 2016)

Sheree Hughes-Stamm, Frauke Warnke, Angela van Daal. (2015) An alternate method for extracting DNA from environmentally challenged teeth for improved DNA analysis. Legal Medicine, 18, 31 - 36

Rachel Houston, Matthew Birck, Sheree Hughes-Stamm, David Gangitano. (2015) Evaluation of a 13loci STR multiplex system for Cannabis sativa genetic identification. International Journal of Legal Medicine, 130(3):635-47

Cassandra Schield, Cassandra Campelli, Jennifer Sycalik, Christopher Randle, Sheree Hughes-Stamm, David Gangitano<sup>.</sup> (2016) Identification and persistence of Pinus pollen DNA on cotton fabrics: A forensic application. Science & Justice, 56(1):29-34

Amy Sorensen, Clare Berry, David Bruce, Michelle Gahan, Sheree Hughes-Stamm, Dennis McNevin. (2015) Direct-to-PCR tissue preservation for DNA profiling. International Journal of Legal Medicine, 130 (3):607 – 13

James White, Sheree Hughes-Stamm, David Gangitano. (2015) Development and validation of a rapid PCR method for the PowerPlex<sup>®</sup> 16 HS system for forensic DNA identification. International Journal of Legal Medicine, 129(4):715-23

Sarah Bahlmann, Sheree Hughes-Stamm, David Gangitano. (2014) Development and Evaluation of a Rapid PCR Method for the PowerPlex<sup>®</sup>S5 System for Forensic DNA Profiling. Leg Medicine, 16(4):227-33

P Noseda, M Hernandez, B Gonzalez, S Hughes---Stamm, D Gangitano. (2013) Genetic Study of Three Closely Linked X chromosome STR Markers in an Argentinian Population. J Forensic Investigation. 1(2): 4

Sheree Hughes-Stamm, Mark Barash, Kelly Grisedale, Angela van Daal (2013) Initial evaluation of a 96-plex GoldenGate<sup>®</sup> Genotyping SNP assay with suboptimal and whole genome amplified samples. Journal of Forensic Investigations. 1 (1); 8-16

S.R. Hughes-Stamm, K.A. Ashton, A. van Daal. (2011) Assessment of DNA Degradation and the Genotyping Success of Highly Degraded Samples. International Journal of Legal Medicine. 125(3):341-8

M.K. Jones, S.R. Hughes-Stamm, T.H. Cribb. (2000) Ultrastructure of the digestive tract of Gyliauchen nahaensis (Platyhelminthes, Digenea), an inhabitant of the hind---gut of herbivorous fishes. Journal of Morphology 246 (3):198-211

S.R. Hughes-Stamm, T.H. Cribb & M.K. Jones. (1999) Structure of the tegument of Gyliauchen nahaensis (Digenea: Gyliauchenidae), with observations on tegument-associated microorganisms. Journal of Parasitology 85:1047-1052

Wen Yang, Malcolm Jones, Jinjiang Fan, Sheree Hughes-Stamm, Donald McManus. (1999) Characterisation of a family of Schistosoma japonicum proteins related to dynein light chains. Biochimica et Biophysica Acta 1432: 13-26

# Books

N/A

# Chapters

N/A

# Proceedings

Amy Sorensen, MS, David Gangitano, PhD, Sheree Hughes---Stamm, PhD. 2014. DNA Preservation and Rapid Purification of Decomposing Human Tissue Samples; A DVI Application. Association of Forensic DNA Analysts and Administrators (AFDAA). 2014 Summer Meeting. Houston, TX

Bodies, Bones and Bombs; Human Identification. 2016. *Esiri Tasker, Charity Beherec, Rachel Houston, Sheree Hughes-Stamm* 2<sup>nd</sup> Human Identification Solutions (HIDS) Conference. Barcelona, Spain.

Artistic Performances N/A

Artistic Exhibitions N/A

## **Research Monographs and Technical Reports**

Final Technical Report - US National Institute of Justice (NIJ) Award #2013---DN---BX---K034

## **Funded External Grants**

US National Institute of Justice (NIJ) Award #2015-DN-BX-K066 (for Jan 2016-Dec 2017) Principal Investigator. Funded for \$725,000 Enhanced Sample Preparation and Data Interpretation Strategies for Massively Parallel Sequencing for Human Identification in Missing Persons and DVI Casework PI: Sheree Hughes-Stamm, Co.PI: Bruce Budowle, Co-Inv: David Gangitano

US National Institute of Justice (NIJ) Award #2013-DN-BX-K034 (for Jan 2014-Dec 2014) Principal Investigator. Funded for \$170,000 Preservation of high throughput methods for Human Tissue Samples in Tropical Climates. PI: Sheree Hughes---Stamm, Co.PI: David Gangitano

SHSU Enhancement Research Grant (ERG) \$15,000 (2015) Forensic Next Generation DNA tools for decomposed tissues. Co-PIs: Sheree Hughes-Stamm and David Gangitano

SHSU Enhancement Research Grant (ERG) \$10,000 (2014)
Biological and environmental factors related to stalking.
PI: Danielle Boisvert
Co.Inv: Todd Armstrong, Matt Nobles, Brian Boutwell, David Gangitano, Sheree Hughes-Stamm

Bond University Faculty of Health Science & Medicine Research Grants (two grants in 2008) \$15,000 each

Bond University Research and Consultancy Services (BURCS/BUGSR) Student Support Scheme Grants (2009 and 2011) \$3000 each.

#### **Peer-Review Presentations/Posters**

Amanda Wheeler, Natalia Czado, David Gangitano, and Sheree Hughes-Stamm. Comparison of DNA Yield & STR Success Rates from Various Tissues in Embalmed Bodies. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Amy Sorensen, Clare Berry, David Bruce, Michelle Gahan, Sheree Hughes-Stamm, and Dennis McNevin. Tissue Preservation with Direct-to-PCR for DNA Profiling: An Alternative DVI Approach. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Carrie Mayes and Sheree Hughes-Stamm. Development and Initial Evaluation of a miRNA System for Forensically Relevant Body Fluids Using Capillary Electrophoresis. Proceedings of the Gordon Research Conference; Forensic Analysis of Human DNA (June 2016).

Esirioghene Tasker, Bobby LaRue, David Gangitano, and Sheree Hughes-Stamm. Analysis of DNA from Postblast Fragments for Identification and Determination of Ancestry. Proceedings of the Gordon Research Conference; Forensic Analysis of Human DNA (June 2016). Daniela Anane-Bediakoh, Martin Lopez, Holly Whillock, Sheree Hughes-Stamm, and Amy Castillo. Can DNA Data Be Used to Establish a Cut-Off Time for Juvenile Sexual Assault Exams. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Kyleen Elwick, Sheree Hughes-Stamm, Kimberly Andreaggi, and Michelle Peck. Optimization and Validation of the ForensicGEM Rapid Extraction Method for High-throughput Processing of Cotton Buccal Swabs. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Natalia Czado, Bobby LaRue, Jr., Amanda Wheeler, Rachel Houston, Amy Sorensen, David Gangitano, and Sheree Hughes-Stamm. The Effectiveness of Various Strategies to Improve DNA Analysis of Formaldehyde-Damaged Tissues From Embalmed Cadavers for Human Identification (HID) Purposes. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Rachel Houston, Sheree Hughes-Stamm, and David Gangitano. Evaluation of a 13-Loci Short Tandem Repeat (STR) Multiplex System for *Cannabis sativa* Genetic Identification. Proceedings of the American Academy of Forensic Sciences (Feb 2016).

Rachel Houston, Sheree Hughes-Stamm, David Gangitano. 2015. Evaluation of a 13-loci STR multiplex system for *Cannabis sativa* genetic identification. The 26<sup>th</sup> International Symposium on Human Identification. Grapevine, TX.

Elizabeth Rahman, David Gangitano, Gabriel Boselli, Sheree Hughes-Stamm . 2015. Evaluation of a One-Step DNA Extraction Method for "touch" Samples. The 26<sup>th</sup> International Symposium on Human Identification. Grapevine, TX.

A. Sorensen, C. Berry, D. Bruce, M. Gahan, S. Hughes-Stamm and D. McNevin. 2015. Direct-to-PCR Tissue Preservation for DNA Profiling. The 26<sup>th</sup> International Symposium on Human Identification. Grapevine, TX.

Amy Sorensen, MS, Elizabeth Rahman, BSc, Cassandra Schield, MS, James White, MS, David Gangitano, PhD, Sheree Hughes---Stamm, PhD. 2015. Room Temperature DNA Preservation and Rapid Purification of Decomposing Human Tissue Samples; An Alternative DVI Approach. AAFS 67th Annual Scientific Meeting, Orlando, FL

Amy Sorensen, MS, David Gangitano, PhD, Sheree Hughes---Stamm, PhD. 2014. Room Temperature DNA Preservation and High---Throughput Purification of Decomposing Human Tissue Samples; An Improved DVI Approach. The 22nd International Symposium on the Forensic Sciences. The Australian and New Zealand Forensic Science Society. Adelaide, Australia

Amy Sorensen, MS, David Gangitano, PhD, Sheree Hughes---Stamm, PhD. 2014. Room Temperature DNA Preservation and Rapid Purification of Decomposing Human Tissue Samples; A DVI Application. The 25th International Symposium on Human Identification. Phoenix, AZ.

James White, B.S.\*; Sarah Bahlmann, M.S.; Sheree Hughes---Stamm, Ph.D.; David Gangitano, Ph.D. 2014. Development and Evaluation of a Rapid PCR Method for a Commercially Available MiniSTR Kit for Human Identification. AAFS 66th Annual Scientific Meeting, Seattle, WA

Elizabeth Rahman, B.S.\*; Sheree Hughes---Stamm, Ph.D. 2014. Preservation of Human Tissue Samples in Tropical Climates. AAFS 66th Annual Scientific Meeting, Seattle, WA

Kourtni Woods, B.S.\*, Frank Warnke, DDS, Sheree Hughes---Stamm, Ph.D. 2014. An Improved Method of DNA Extraction From Environmentally Challenged Teeth AAFS 66th Annual Scientific Meeting, Seattle, WA

Sarah Bahlmann, Sheree Hughes---Stamm, David Gangitano. 2013. Development and Evaluation of a Rapid PCR Method for the Powerplex<sup>®</sup>S5 System for Forensic DNA Profiling. The 23rd International Symposium on Human Identification, Atlanta, USA

S.R. Hughes---Stamm. 2012. The 200 year---old HMS Pandora shipwreck: Combined Forensic Anthropology and Genetic Analysis of the Skeletal Remains Recovered. Australian and New Zealand Forensic Science Society (ANZFSS) Symposium. Hobart, AUSTRALIA

Sheree Hughes---Stamm, Kevin Ashton, Angela van Daal. 2011. STR Genotyping of Environmentally Challenged Skeletal Samples. The 22nd International Symposium on Human Identification, Washington DC, USA

Mark Barash, Wenji Liu, Sheree Hughes---Stamm, Angela van Daal. 2011 Identification of Single Nucleotide Polymorphisms (SNPs) Involved in the Determination of Physical Appearance. The 22nd International Symposium on Human Identification, Washington DC, USA

Sheree Hughes---Stamm, Kevin Ashton, Angela van Daal . 2010. Assessment of DNA Degradation and the Predictive Genotyping Success of Highly Degraded Samples. The 21st International Symposium on Human Identification, San Antonio, TX, USA

S.R. Hughes---Stamm, K.A. Ashton, A. van Daal. 2009. Assessment of DNA Degradation and the Genotyping Success of Highly Degraded Samples.

6th International Society of Applied Biological Sciences (ISABS) Conference Human Genome Project Based Applications in Forensic Science, Anthropology and Individualized Medicine. Split, Croatia.

S.R. Hughes---Stamm, K.A. Ashton, A. van Daal. 2008. Measures of DNA Degradation and the Presumptive Genotyping Success of Highly Degraded Samples. Australian and New Zealand Forensic Science Society (ANZFSS) Symposium. Melbourne, AUSTRALIA

M.K. Jones , S.R. Hughes---Stamm, T.H. Cribb. (2000) Morphology of the digestive system of the digenean trematode Gyliauchen nahaensis --- An endocommensal flatworm with a herbivorous diet. New Zealand Society for Parasitology/ Australian Society for Parasitology. Wellington, NZ

Pantaleon M., Hughes---Stamm S.R., Kaye P.L. 1999. Glucose is essential for GLUT3 expression and blastocyst formation in the mouse.

Australian Society for Biochemistry and Molecular Biology Incorporated (ASBMB) Australian and New Zealand Society for Cell & Developmental Biology Incorporated Combined Conference Abstracts. Sym---35---05 (Abstract)

M. Pantaleon, S.R. Hughes---Stamm, P.L.Kaye. 1998. A role for glucose in cleavage stage mouse development. Australian Society for Reproductive Biology. Pg.43

# Work or Professional Experiences

Assistant Professor, Forensic Science (2012-current) Director of Graduate Programs, Department of Forensic Science Forensic Science Department, Sam Houston State University, Huntsville, TX. Senior Teaching Fellow (2006-2012) Faculty of Health Sciences and Medicine, Bond University, Gold Coast, Australia

Teaching Fellow (2002-2006) School of Physiotherapy and Exercise Science, Griffith University, Gold Coast, Australia Postgraduate Tutor (2000---2001) Department of Anatomical Sciences, University of QLD, Brisbane, Australia

Research Assistant (1999) Department of Anatomical Sciences, University of QLD, Brisbane, Australia

Laboratory Technician (1998) Science Department, University of the Sunshine Coast, Australia

Research Assistant (1997-1998) Department of Physiology and Pharmacology, University of QLD, Brisbane, Australia Center for Microscopy and Microanalysis, University of QLD, Brisbane, Australia

Anatomy Tutor (1996) Department of Anatomical Sciences, University of QLD, Brisbane, Australia

## **Honors and Awards**

Australian and New Zealand Forensic Science Society (ANZFSS) National Award, 2012 Bond University Alumni Student Opportunity Award, 2011 Bond University Open Day Graduate Poster Prize, 2009 Australian and New Zealand Forensic Science Society (ANZFSS) Allan Hodda Memorial Award, 2009 Australian Postgraduate Award (APA), 2008 Australian Federation of University Women Fellowship Award, 2001 Australian Society of Reproductive Biology Serono Junior Scientist Award, 1997 Science Faculty Commendation for High Achievement, UQ (GPA>6.0), 1996 & 1997 Golden Key National Honour Society Member For outstanding scholastic achievement (UQ)

# **Other Competencies**

Texas Forensic Science Commissioner, 2014-current Walker County Voluntary Organizations Active in Disaster (VOAD) (2013- current) American Academy of Forensic Sciences, Trainee Affiliate (2012- current) American Academy of Forensic Sciences, Student Affiliate (2011- 2012)

Australian & New Zealand Forensic Science Society (QLD Branch, Steering Committee) 2008---2012 Bond University Women's Network (Steering Committee) (2009-2012)

Australian Federation of University Women (1997-2000) Advanced Pathology Training Course (1997)

# D. JODY KOEHLER

1700 N Congress Avenue, Austin, TX 78701 | 512-936-0729 | jody.koehler@fsc.texas.gov

EDUCA	TION
-------	------

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 periorini use job duries that are required or menn, serving as the Quanty Mangel and DNA Technical Leader, and approving expenditures required to operate the laboratory.	
reeninear beauer, and approving experiences required to operate the faboratory	

#### Texas Department of Public Safety Crime Laboratory DNA Section Supervisor II/III, Austin Laboratory 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**

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

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

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

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.

November 2006 – March 2017

May 2004 – November 2006

August 2002-August 2003

November 1996-July 2001

December 1994-November 1996

## D. JODY KOEHLER

#### 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



# INTEROFFICE MEMO

То:	Quality Case Record for CARs/IRs: 2016-007, 2016-008, 2016-009, 2016-010, 2016-011, 2016-012, 2016-013, 2016-024, 2016-026, 2016-027, 2016-029, 2016-033, 2016-037, 2016-038, 2016-055, 2016-058, 2016-059, 2016-060, 2016-062, 2016-063, 2016-066, 2016-070, 2016-071, 2016-073, 2016-074, 2016-078, 2016-080, 2016-082
Cc:	Lloyd Halsell III, Acting Technical Leader (October 10, 2015 to July 1, 2016) SA 1-14-16 Robin Guidry, DNA Technical Leader (96 11) 1016 Jennifer O'Callaghan, Forensic Biology Manager 111016200 Irma Rios, Forensic Analysis Division Director The River 11-18-16 Lori Wilson, Quality Director Sulfam 1110/2016
From:	Aimee Grimaldi, Quality Specialist Annue grimalde 11/10/2014 Paula Evans, Quality Specialist Paula Evane 11/10/16
Date:	November 4, 2016
Re:	Root Cause Analysis for 2016 First and Second Quarter Contamination Events

Between January and July 2016, multiple instances of contamination were reported to the Quality Division as required by Biology Section SOPs. Contamination is the unintentional introduction of exogenous DNA into a DNA sample or PCR reaction. The Biology Section has quality control measures in place to detect possible contamination and ensure the integrity of DNA results obtained from evidence samples. One such quality control measure is the use of a reagent blank during the extraction process. The reagent blank is a control sample that contains no DNA and is used to monitor for contamination from reagents used during the extraction process. In addition, this control is treated as and run in parallel to the casework samples on the batch. For this reason, the reagent blank can also detect contamination introduced during the processing of casework samples.

In accordance with the FBI QAS standard 9.7, the Biology Section has and follows a policy for the detection and control of contamination. Reviewing controls for contamination, including reagent blanks, is part of the DNA analysis process. The detection of contamination is a confirmation that the quality system is robust and is working. When contamination is reported to the Quality Division, each occurrence is investigated by the Biology Section and the Quality Division in an attempt to determine the source of the contamination, analytical step at which the contamination occurred, amount of activity present (number of peaks above and below threshold), and if the contamination can be resolved by reprocessing. In addition to investigating the source of contamination, the Biology Section and the Quality Division ensure that results and statements written in the report are clear, accurate, and transparent. Additional items the Quality Division considers during root cause analysis are: date of occurrence, number of contamination events in a given time frame, amplification kit used, batch number, and automated vs manual processes.

There were instances during the first and second quarters of calendar year 2016 in which possible contamination was reported to the Quality Division and, through the meeting step (the first step of the Quality Incident/Corrective Action Process) or the investigation itself, determined to not be contamination. This memo is intended to address only those situations where contamination was determined to be present.

Potential sources of DNA contamination include but are not limited to contamination between samples during processing, human genomic DNA from the environment, the analyst processing the samples, a vendor maintaining the equipment, or an unknown source. Because DNA testing is sensitive to minute quantities of DNA, it is not always possible to determine the source of exogenous DNA introduced to the reagent blank.

Members of the Biology Section and Quality Division worked together to troubleshoot these instances of contamination. The first step was performing a lab decontamination, which was done on March 28, 2016. On April 8, 2016 the Acting Technical Leader instructed the Forensic Biology Section to perform lab decontamination on a weekly basis. Additional PPE requirements were also implemented for lab staff and visitors to prevent contamination. Lab coat, gloves, hair coverings and face masks are required during screening, extraction, quantification, and amplification. In the post-amplification laboratory, gloves and a lab coat are required. This PPE is not optional and anyone entering the areas where these procedures are performed must abide by these requirements. These preventive measures were put in place in order to minimize the risk of contamination. Since completely eliminating all contamination is unlikely due to the sensitivity of DNA technology, HFSC instituted a DNA Profile Policy on June 23, 2016. This policy requires all HFSC staff members, regardless of position, to submit their DNA for inclusion in the staff DNA database. This allows for a better means to source contamination if it presents itself. Cleaning tube racks and other plasticware with a bleach bath before use was considered but has not been implemented.

When compared to 2015, more contamination events were reported to the Quality Division during the first half of 2016. However, this was partially due to biology SOP changes, increased production, and a change in technical leaders. Seven contamination events that were reported in the first half of 2016 would not have been reported in 2015 because the SOP did not require contamination that was resolved with reamplification to be reported to the Quality Division. For the time period of September 1, 2014 to May 05, 2016, the DNA SOP 2 - Quality Assurance stated the following:

Confirmed contamination events will be summarized in a CAPA that will document the details of the contamination event, including the cases involved, the date of detection, the investigative actions taken, the source of the contamination, if known, and any corrective actions taken.

Unacceptable activity in a reagent blank or negative control that cannot be readily attributed to an artifact must be investigated to determine if it is reproducible contamination. The first course of action is to re-inject the sample on the genetic analyzer to determine if the activity is in the amplified DNA product or if it was perhaps introduced during post-amplification sample set-up. If not reproduced upon re-injection, the data from samples associated with the reagent blank or amplification negative control may be used for interpretation. If reproduced upon re-injection, the reagent blank is then re-amplified to determine if the activity is in the DNA extract or if it was introduced during the amplification set-up. If reproduced upon re-injection, the samples associated with the amplification negative control must be re-amplified. If not reproduced upon re-amplification, the data from samples associated with the reagent blank may be used for interpretation. If reproduced upon re-amplification, the data from samples associated with the reagent blank may be used for interpretation. If reproduced upon re-amplification, the data from samples associated with the reagent blank may be used for interpretation. If reproduced upon re-amplification, the data from samples associated with the reagent blank may be used for interpretation. If reproduced upon re-amplification, the DNA activity is determined to be in the DNA extract and all samples associated with the contaminated reagent blank must be re-extracted because the data from samples associated with that reagent blank may not be used for interpretation due to unacceptable quality controls.

It is recommended that any steps taken to investigate potential contamination are performed by a  $2^{na}$  technician to establish a transparent exploration.

Therefore, only confirmed contamination was reported to the Quality Division in calendar year 2015. The Acting Technical Leader informed the Forensic Biology Section on February 16, 2016 that activity, including possible contamination which is resolved, must be reported to the Quality Division so that trends can be evaluated. The DNA SOP was then updated to include the new requirements and issued May 06, 2016. The current SOP states:

Unacceptable activity in a reagent blank or negative control that cannot be readily attributed to an artifact must be investigated to determine if it is reproducible contamination. Unacceptable activity includes a pattern of data that can be differentiated from background. A single activity point may not be evidence of contamination. The Technical Leader shall have sole discretion in determining if a single point is acceptable or if it requires further processing.

The first course of action is to re-inject the sample on the genetic analyzer to determine if the activity is in the amplified DNA product or if it was perhaps introduced during post-amplification sample set-up. The reinject plate may be set up again or re-injected from the same plate. If not reproduced upon re-injection, the data from samples associated with the reagent blank or amplification negative control may be used for interpretation.

If reproduced upon re-injection, the reagent blank is then re-amplified to determine if the activity is in the DNA extract or if it was introduced during the amplification set-up. If the activity is in the amplification negative control and re-produced upon re-injection the samples associated with the amplification negative control must be re-amplified. If activity in a reagent blank is not reproduced upon re-amplification, the data from samples associated with the reagent blank may be used for interpretation. If reproduced upon re-amplification, the contaminated reagent blank must be re-extracted because the data from samples associated with that reagent blank must be used for interpretation.

Activity that is resolved with re-injections shall be tracked with a contamination log. Activity that is resolved by re-amplification shall be tracked with an HFSC Incident form. Activity that is reproduced upon re-amplification shall be tracked with an HFSC Corrective Action Report form. These tracking measures are guidelines only and can be amended by the Technical Leader or HFSC Quality Division.

In addition to the preventative measures already described, the Quality Division requested that the Forensic Biology Section run a series of tests to gather more data in order to eliminate some possible contributors to contamination. Multiple blanks were run through the entire DNA process to eliminate consumables (e.g. plasticware, trays, tubes) as possible contributors. The data indicated that consumables are not a likely cause of the contamination. However, it should be noted that plasticware contamination could be sporadic and not seen in every tube or plate in a given lot. In addition, the Quality Division spoke with the Biology Section about pursuing options to add quality control measures to the analysis process (e.g., looking at ways to create a database or spreadsheet that had the ability to compare profiles generated by the lab to each other and to crosscheck contamination against multiple batches).

Next, the Forensic Biology Section ran samples in an arrangement (sample, blank, sample, blank) on instrumentation in order to eliminate equipment as a possible contributor to the contamination events. Nine blanks were processed in this fashion. Two of the blanks produced peaks that needed to be evaluated for contamination. After further review, the blanks were deemed acceptable by the Acting Technical Leader. The data gathered from this test indicated that the equipment was not a likely cause of the contamination.

Lastly, the Forensic Biology Section ran contamination-free autosomal samples through the YSTR process to determine the sensitivity of YSTR data. The same nine blanks from above were processed for YSTRs. Three blanks

produced peaks that were distinct from background noise and required examination. The Acting Technical Leader examined the data from this test. Upon examination and secondary processing, two of the peaks were deemed acceptable. However, the third contained a labeled peak that was confirmed contamination. The data suggests that activity may be seen during YSTR analysis that was not originally seen in autosomal analysis. This may be due to the fact that YSTR PCR includes two additional cycles. Two additional cycles make YSTR analysis more sensitive which could increase the potential of developing low-level DNA. Even with the data from this test, most of the possible contamination events were not able to be sourced due to too little information. Too little information means that the partial profile developed could not be sourced to a person, object, consumable, etc.

The amount of samples processed was also considered. During April, May, and June, the Forensic Biology Section performed 8,629 extractions. This was almost a 180% increase when compared to the amount of extractions performed during the first quarter of 2016. Figure 1 below shows the contamination events reported to the Quality Division each month of Quarters 1 & 2. This graph shows a large decrease between March and April. Some of this could be attributed to the additional PPE requirements that were put in place and the additional lab cleaning that was implemented. The initial high volume in February and March may be attributed to a "February push" in which production expectations were increased. However, in May there was a large increase in reporting which is most likely due to the increase in production between the first and second quarters. As the Forensic Biology Section began adjusting to a large increase in production, it appears the contamination began to decrease.







The Quality Division will continue to analyze and monitor corrective action and incident data. The possible causes listed above have all been considered. Unfortunately, the root cause for many of the contamination events is unknown. This is not unusual due to the nature of DNA analysis. Many of the contaminated reagent blanks yielded too little information to conclude the source of the contamination. Recommendations that have been discussed that have not been implemented at the time of this memo are bleach baths for plasticware and the implementation of a system to compare unknown profiles seen in contamination to profiles obtained within a batch or multiple batches. Recently the Quality Division was informed that the weekly decontamination had been discontinued after the SAK project. However, the Biology Section has decided to reinstate the decontamination of

the laboratory on a monthly basis as a preventive measure to reduce the risk of contamination. As of the date of this memo, monthly decontamination had not been implemented.

The incidents/corrective actions that were reported to the Quality Division between January and July 2016 remained open for root cause analysis investigation and trending purposes. This memo documents the measures taken to determine the source(s) of the contamination events and is used to close-out the Quality Division incidents/corrective actions.



# THIS FORM IS FOR BIOLOGY/DNA REPORTING ONLY

Quality Division Use Only			
Quality Tracking #:	2017-075	Date Quality Division Notified:	9/27/2017
Non-Conformance Level:	Class I	Date Submitted to Management for Review:	1/29/2018
		1	
Date Submitted to Quality	1/29/2018	Date Closed:	1/29/2018
for Review:			
Date of Discovery:     7/1/2017     Division:     Biology/DNA Division			

· ·		,	
Date of Incident:	7/1/2017	Section:	Biology/DNA

Forensic Case Number(s), if applicable:	Agency Case Number(s), if applicable:
A. 2017-066: 2017-14042, 2017-11029	A. 2017-066: 091007517, 071212917
A. 2017-079: 2017-14996, 2017-14994	A. 2017-079: 097525717, 097528717
A. 2017-081: 2017-15186, 2017-15129, 2017-15141	A. 2017-081: 098112917, 099946217, 097738817
B. 2017-063: 2017-12708, 2017-12590	B. 2017-063: 079049317, 081430717
B. 2017-082: 2017-15188, 2017-14998, 2017-15145,	B. 2017-082: 090406017, 096686517, 099700717,
2017-15022	099388117
C. 2017-056: 2017-11708, 2017-09791, 2017-12202,	C. 2017-056: 075066217, 063002017, 076796717,
2017-10259, 2017-10495	066645717, 068070317
C. 2017-067: 2017-13146, 2017-12577, 2017-12999	C. 2017-067: 085132817, 080809517, 083380517
C. 2017-073: 2017-10200, 2017-10893, 2016-24547	C. 2017-073: 063767017, 069848317, 162829816
D. 2017-071: 2017-13512, 2017-14768	D. 2017-071: 082865217, 096766317
E. 2017-062: 2017-13035, 2017-13340	E. 2017-062: 083798517, 084925717
The first column indicates the assigned Quality Division	The first column indicates the assigned Quality Division
incident number.	incident number.



Corrective Action Report Form – Biology Only Quality Division

# Description of Discrepancy/Non-conformance. Do not include analysts' names unless otherwise instructed by the Section Manager or Division Director(s):

There were twenty-two possible contamination events reported within the months of July, August and September, 2017. Of the twenty-two reported events, twelve had DNA activity which was resolved upon re-amplification and the other ten require re-extraction. As is required by the DNA SOP, all twenty-two events were reported to the DNA Technical Leader and/or the Quality Division and subsequently the ten events which require re-extraction were assigned the following incident numbers: 2017-056 (type C), 2017-062 (type E), 2017-063 (type B), 2017-066 (type A), 2017-067 (type C), 2017-071 (type D), 2017-073 (type C), 2017-079 (type A), 2017-081 (type A) and 2017-082 (type B). The other twelve events that were resolved upon re-amplification were not assigned incident numbers but are tracked in Qualtrax for tracking and trending purposes. Results were not reported in any of the affected cases until each contamination event was resolved. If resolution was not possible, the results were not reported.

During this time, the contamination rate was calculated and the observed rate of contamination was above the historical threshold. The rate of contamination is calculated by dividing the number of contamination events in a given month by the number of samples processed (per extraction or amplification process). This rise in the contamination rate triggered the Quality Division to initiate this corrective action and the contamination events were analyzed in an attempt to determine the root cause(s) of this spike.

When analyzed, the contamination events were categorized in six ways:

- A. sourced to Client Services/Case Management (CS/CM) Specialist
- B. sourced to Forensic Biology staff who did not perform work in the case
- C. sourced to another sample in the same batch
- D. sourced to Forensic Biology staff member who performed work in the case
- E. interpretable but not sourced
- F. inconclusive

# **Actions Taken:**

Several actions were taken to educate staff on the importance of preventing contamination, proper use of personal protective equipment (PPE) and good laboratory practices. Contamination prevention was discussed with the entire Forensic Biology staff at the August 23, 2017, technical meeting. At the September 13 section-wide production meeting, management discussed the use of PPE at all times when handling evidence, reagents, and equipment in the laboratory, including computer keyboards. A meeting with the DNA Technical Leader, laboratory staff who perform extraction, quantification, amplification and/or capillary electrophoresis preparation, and a Quality Division Specialist was held on September 19 to solicit and discuss best practices while performing bench-work analysis.

The laboratory implemented several global measures to help prevent contamination. These measures included: regularly scheduled deep cleaning followed by swipe tests to measure effectiveness; revising the monthly clean-up checklist to more clearly define the expectations of a "deep clean"; and reformatting the checklist to effectively convey analyst accountability. Automation instrumentation is now decontaminated prior to and after each use,

Corrective Action Report Form – Biology Only Issued By: Quality Director Uncontrolled When Printed Document ID: 10723 Issue Date: 01/31/2017 Page 2 of 6



Corrective Action Report Form – Biology Only Quality Division

rather than only before use. Several physical changes were made inside the Forensic Biology laboratory space to further prevent contamination. PPE gowning stations were created outside of laboratory spaces so that gowning takes place prior to entering extraction rooms or the screening bench area. The laboratory entrance door adjacent to an extraction room was transitioned to an emergency exit-only door to further minimize traffic in the extraction area. Badge access was terminated at that portal. All staff must now enter the laboratory using the main laboratory entrance. The reagent preparation balance was moved out of the area where cleaning/drying racks and autoclaving occurs in order to minimize traffic in that area. Keyboard covers were purchased to ease the decontamination of computer keyboards.

The DNA SOP was enhanced to include more language and discussion surrounding the unintentional introduction of DNA to samples and controls.

Actions taken for each of the six categories of contamination are as follows:

A. As a direct result of the contamination events, the CS/CM Specialist was provided supplemental instruction on proper PPE donning and tube/supply handling. As a result of this instruction, the Specialist continues to don proper PPE while performing all laboratory functions but now has a greater understanding of the potential for unintentional DNA transfer. Specific laboratory space has been designated for the Specialist to perform her job duties (such as autoclaving tubes and cleaning tube racks). Staff were told to not enter this area unless necessary. If staff must enter this area, proper PPE is required. The Specialist continues to minimize her time in any laboratory areas that are undergoing active bench-work which in turn limits her direct contact with casework samples. In addition, because her DNA was detected in reagent blank controls, she is exercising more precaution when stocking consumables and handling tubes for the autoclave process. This greater awareness of the possibility of unintentional DNA transfer is expected to minimize the detection of her DNA on consumables.

B. The laboratory took specific measures to address contamination sourced to Forensic Biology staff who did not perform work on the case. Several of these measures addressed the laboratory's decontamination practices. The autoclaving process was defined with a written procedure and was modified to allow for a longer autoclave time. Tube racks were previously washed only with Liquinox detergent which resulted in them being "clean" but there was no expectation for them to be DNA-free/decontaminated. Now, in addition to Liquinox, tube racks are stored in bleach "baths" after use and until cleaning, and bleach is also used as a decontaminant in the washing process. Tube racks were then set out to dry in an area of the lab where PPE was not required. Staff is now discouraged from unnecessarily entering this area. If staff must enter this area, proper PPE is required. Several other measures addressed best practices for PPE use and sample handling. PPE gowning stations have been created outside of laboratory spaces so that all types of PPE (glove, labcoats, hair nets, masks, etc.) are in one convenient location so that gowning takes place prior to entering extraction rooms or the screening bench area. In addition, staff is now required to wear gloves when using any laboratory keyboard. The laboratory was utilizing an entrance door that was adjacent to an extraction room. This door has now been transitioned to an emergency exit-only door to further minimize traffic in the DNA extraction area. Badge access was terminated at that portal thereby forcing all staff to enter the laboratory via the main laboratory entrance. Finally, daily team huddles were relocated from an office space within the laboratory to an office space that is completely independent of the laboratory (on a separate floor).

Corrective Action Report Form – Biology Only Issued By: Quality Director Uncontrolled When Printed Document ID: 10723 Issue Date: 01/31/2017 Page 3 of 6



Corrective Action Report Form – Biology Only Quality Division

C. Measures taken to address contamination sourced to another sample in the same batch included reinforcing good laboratory practices and clean techniques while performing bench-work through discussion, sharing of best practices, and an enhanced training program. The training program has been modified so that it will impart these techniques onto all new staff, not just technicians. The Evidence Handling Laboratory Skills Worksheet was created and is a required training document that will ensure trainees can prepare an appropriate bleach solution, properly clean laboratory equipment, handle and label sample tubes in a manner that minimizes the potential for contamination, and operate a pipette in a manner that minimizes potential contamination.

D. Action taken to address contamination sourced to a Biology staff member who perform work in the case included reinforcing good laboratory practices and clean techniques while performing bench-work through discussion, sharing of best practices, and an enhanced training program.

E. The laboratory took specific measures to address contamination that was interpretable but not sourced (meaning there was enough DNA activity for comparison purposes but the DNA activity does not match any of the samples in our staff database or any of the casework samples that were being processed at or around the same time). These measures included: continuing to search and upload unsourced but comparable profiles to the Local DNA Index System (LDIS) and the GeneMapper ID-X comparison tool; continuing to search International Commission on Missing Persons' (ICMP) Online DNA Elimination Database; providing DNA profiles to vendors for searching in their staff databases; continuing to autoclave sample tubes that can be autoclaved; and a decontamination experiment with HFSC's Research and Development Division. This experimental plan will help to better understand our decontamination practices by examining factors such as different cleaning reagents, time the cleaning reagent is in contact with the surface before wiping, and DNA-free versus sterile swabs.

F. While no actions were taken to specifically address the contamination that was inconclusive, the aforementioned actions are expected to minimize this type of contamination as well. Lastly, the Quality Division conducted interviews, observations and a series of Voice of Customer interviews with limited groups of staff members. These groups were selected according to laboratory job function: screeners, technicians, report writers/analysts and management. Pareto charts were created to summarize the aggregated responses and aid in root cause analysis. The results of the analysis showed the increase of awareness in all interview groups regarding contamination and outlined the steps taken to prevent contamination in the laboratory as mentioned above.

# Summary of Root Cause Analysis:

Several causes were identified as contributing to these contamination events: the CS/CM Specialist's laboratory technique, laboratory facilities, training program, and cleaning culture.

The Specialist's responsibilities have evolved over time from transporting evidence to and from the DNA laboratory and the Houston Police Department Property Room to responsibilities that are solely within the laboratory (ie. decontaminating racks and autoclaving tubes). She never entered into the laboratory's formal training program in which she would have been exposed to proper PPE expectations, gained knowledge regarding best laboratory practices and been given a more overall concept of the sensitivity of current day DNA testing. As a result of this recent instruction, she now has a greater awareness regarding the possibility of unintentional DNA transfer.

Corrective Action Report Form – Biology Only Issued By: Quality Director Uncontrolled When Printed Document ID: 10723 Issue Date: 01/31/2017 Page 4 of 6



# Houston Forensic Science Center Corrective Action Report Form – Biology Only

Quality Division

There are shortcomings in the laboratory's facility. Because of the limitations within the laboratory's physical space, there has historically been a blurred line as to what was considered laboratory space and what was considered office space. While colored tape now outlines the areas of the laboratory in which PPE is required, the laboratory's facilities are still limited in the sense that there is laboratory space and office space abutting one another. HFSC is aware of these facility shortcomings and, although the facility itself cannot be changed, the laboratory has identified environmental risks and, in response to these risks, has heightened awareness regarding workflow, access to PPE and minimizing traffic through designated laboratory space.

The laboratory's training program was identified as needing improvement. Historically the training program lacked clear ownership, lacked instruction for the trainers and did not replicate batch sizes that were comparable to that of casework. All of those concerns have now been addressed. The training program is now facilitated by the Operations and Training Supervisor and emphasis has been placed on good laboratory practices and clean techniques while actively performing bench-work. One staff member was involved in five of the contamination events: one in which her profile was found in a reagent blank of an extraction she did not perform (type B), two in which the contamination was sourced to another sample in the same batch (type C), one in which she was the technician who performed the extraction in the case (type D) and one in which the data was interpretable but not sourced (type E). This staff member was authorized for extraction on April 27, 2017. When this trend was observed, the staff member received supplemental instruction from the Technical Leader and was observed by a more experienced staff member and no concerns were noted.

The laboratory's cleaning culture was not as strong as it needed to be. The laboratory has always participated in weekly cleaning, however lab-wide, monthly deep cleans began in direct response to this spike in contamination events. The Biology laboratory now acknowledges the importance of having a strong cleaning culture especially when there is an increased demand in production. During these monthly deep cleans, production is halted, tasks are evenly distributed among staff and if a staff member completes his assigned task, the expectation for him to then help fellow staff complete their assigned tasks has been clearly communicated by management. Management is also demonstrating the importance of the deep cleans by actively monitoring each clean. Swipe tests have been implemented as a tool to measure the effectiveness of these cleans. Moreover, the cleaning culture of the laboratory has evolved significantly.

# Additional Information/Follow-Up:

During evaluation of these contamination events, several potential root causes were considered as contributing factors but ultimately eliminated. These included manual versus robotic procedures, the increased sensitivity of the GlobalFiler amplification kit, the QIACube differential extraction procedure and poor amplification technique.

The amplification procedure allows for both the use of robotics and a manual option. The data does not support the theory that contamination events are more likely to occur in procedures that are performed manually than those done with the aid of robotics. The procedure is only performed manually on a limited basis and the contamination events were not isolated to that subset of amplifications. The laboratory's extraction procedures all rely on robotics, which even further discredits this theory.

Corrective Action Report Form – Biology Only Issued By: Quality Director Uncontrolled When Printed Document ID: 10723 Issue Date: 01/31/2017 Page 5 of 6



# Houston Forensic Science Center Corrective Action Report Form – Biology Only

Quality Division

The data does not support the theory that the contamination events were directly correlated to the laboratory's implementation of the GlobalFiler amplification kit. This amplification kit has a higher sensitivity than the previous amplification kit and was implemented in casework in January 2017. If the transition to GlobalFiler was a contributing factor, the expectation would have been an increase in contamination events at or around this time frame. However, the spike in contamination events occurred much later in the year, thereby discrediting this theory.

While there was a noted increase in contamination of the reagent blanks that are created as part of the QIAcube differential procedure, this increase has been categorized as correlation and possible causation. The laboratory had an increased amount of differential procedures being performed in the months in which the spike occurred, however there is no evidence that the extraction procedure inherently lends itself to increased contamination. The differential procedure was not modified at or around the time of the spike. Therefore, if the procedure itself inherently caused increased contamination events, a spike would have been expected when the procedure was brought online initially. There were no laboratory contamination events for the months of October, November and December 2017 and the differential procedure is still being performed consistently.

The data does not support the theory that the contamination events that ultimately resolved upon re-amplification were due to poor technique in the original amplification. Upon review of the data, it was not possible to identify a particular staff member whose technique could have been contributing to the contamination events. The activity observed prior to re-amplification was generally low level in nature. Seventy five percent of the events involved less than or equal to one peak above the analytical threshold; ninety percent involved less than or equal to two peaks above the analytical threshold. Lastly, for each of these twelve events, the DNA activity was resolved upon re-amplification and there were no concerns when the amplification procedure was observed.

Section Manager:	Courtney Head	Date:	1/29/2018
<b>Technical Leader:</b>	Robin Guidry	Date:	1/29/2018
CODIS Administrator:	Jennifer Clay	Date:	1/29/2018
<b>Division Director:</b>	Amy Castillo	Date:	1/29/2018

Quality Director: Lori Wilson

Date: 1/29/2018