TEXAS FORENSIC
SCIENCE COMMISSION
Justice Through Science

1700 North Congress Ave., Suite 445
Austin, Texas 78701

March 15, 2016

Via First Class Mail

Mr. Jason Spence
216 Seminole Drive #418
Huntsville, AL 35805

Re: Texas Forensic Science Commission File No. 15.18

Dear Mr. Spence:

At its February 12, 2016 meeting, the Commission considered your complaint. With respect to allegations of improper bite mark analysis testimony, the Commission will consider the testimony along with the other cases slated for review as part of its overall bite mark analysis review.

With respect to the DNA analysis, the Commission has no statutory authority to order DNA testing in any particular case, including the Melendez case, or to determine the status of testing at a particular time. However, we include a copy of DNA testing results provided by Walter Reaves as a courtesy. Any further inquiries regarding DNA testing should be directed to Mr. Reaves.

As with any statewide review conducted by the Commission, we expect the bite mark analysis case review will take considerable time. We will provide you a copy of any observations made regarding the bite mark analysis in question. However, please be aware the Commission does not comment upon the guilt or innocence of any individual and its reports are not admissible in civil or criminal actions.

If you have any further questions, please feel free to contact our office.

Sincerely,

Leigh M. Tomlin

Leigh M. Tomlin
by MKA w/permission

encl.

FORENSIC BIOLOGY
LABORATORY REPORT

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TO: The Law Office of Walter M. Reaves Jr., P.C.
Attention: Walter M. Reaves Jr.
100 North Sixth Street
Suite 802
Waco, Texas 76701

REPORT DATE: 11/09/15
NMS LABS' WORK ORDER NUMBER: 14324440
AGENCY NUMBER: 83-553C2/83-557-CT

SUBJECT(S): Harper, Terry Lee
Melendez, Anthony
Spence, David
Spence, Steve
Wilkens, Derwin
Wilkens, John David

ITEM(S) SELECTED for EXAMINATION and/or ANALYSIS

The following item(s) was/were selected for examination and/or analysis by NMS Labs' Criminalistics Department. Any item(s) submitted to NMS Labs but not listed in the following Summary Table was/were not examined at this time.

Summary Table: Item(s) Selected for Examination and/or Analysis*

NMS Number	**Submitted as** NMS analyst description	**Forwarded for Analysis**	*Derived from Agency Item #*
ITEM 1	**Outer envelope** containing 19 envelopes	*See Below*	*None Provided*
EX01-1	**Envelope #1** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-2	**Envelope #2** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-3	**Envelope #3** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-4	**Envelope #4** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-5	**Envelope #5** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-6	**Envelope #6** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-7	**Envelope #7** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-8	**Stamp #1 from Envelope #7** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-9	**Stamp #2 from Envelope #7** Two fiber-tipped swabs	*DNA*	*None Provided*
EX01-10	**Stamp #3 from Envelope #7** Two fiber-tipped swabs	*DNA*	*None Provided*
ITEM 2	**Reference sample from Steve Spence**	*See Below*	*None Provided*
EX02-1	One buccal swab	*DNA*	*None Provided*

NMS Number	Submitted as NMS analyst description	Forwarded for Analysis	Derived from Agency Item #
ITEM 3	**Reference sample from Anthony Melendez**	*See Below*	*None Provided*
EX03-1	Two fiber-tipped swabs	*DNA*	*None Provided*
ITEM 4	**Reference sample from Terry Lee Harper**	*See Below*	*None Provided*
EX04-1	Cutting from fabric bearing bloodstain	*DNA*	*None Provided*
ITEM 5	**Reference sample from Derwin Wilkens**	*See Below*	*None Provided*
EX05-1	One fiber-tipped swab	*DNA*	*None Provided*
ITEM 6	**Reference sample from John David Wilkens**	*See Below*	*None Provided*
EX06-1	Cutting from paper bearing bloodstain	*DNA*	*None Provided*

***IMPORTANT NOTE:** Please see Addendum 1 at the end of this report for the definitions of "examination" and "analysis" and an explanation of the techniques used for the detection of possible biological material on an evidentiary item.

DNA ANALYSIS

Test samples were analyzed by deoxyribonucleic acid (DNA) analysis of short tandem repeats (STRs) using polymerase chain reaction (PCR) and capillary electrophoresis (CE) technology. The raw analytical data are available upon request.

Statistical analyses of autosomal-STR DNA profiles obtained using Applied Biosystems™' Identifiler Plus® kit are based on results from up to fifteen loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA). These include the thirteen core CODIS loci specified by the FBI.

Statistical analyses of Y-STR DNA profiles (not applicable to females) obtained using Promega™'s PowerPlex® Y23 kit are based on up to twenty-two male-specific loci (DYS576, DYS389I, DYS448, DYS389II, DYS19, DYS391, DYS481, DYS549, DYS533, DYS438, DYS437, DYS570, DYS635, DYS390, DYS439, DYS392, DYS643, DYS393, DYS458, DYS385, DYS456 and Y GATA H4). Y-STR profile frequencies are based on a 95% upper confidence interval.

DNA INTERPRETATION AND CONCLUSIONS

Reference/Exemplar DNA Samples

- The sample identified as EX01-1 (reference/exemplar sample from Envelope #1) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-2 (reference/exemplar sample from Envelope #2) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-3 (reference/exemplar sample from Envelope #3) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-4 (reference/exemplar sample from Envelope #4) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-5 (reference/exemplar sample from Envelope #5) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-6 (reference/exemplar sample from Envelope #6) failed to produce an autosomal-STR DNA profile suitable for comparison.
- The sample identified as EX01-7 (reference/exemplar sample from Envelope #7) failed to produce a human DNA quantification value.
- The sample identified as EX01-8 (reference/exemplar sample from Stamp #1) failed to produce a human DNA quantification value.
- The sample identified as EX01-9 (reference/exemplar sample from Stamp #2) failed to produce a human DNA quantification value.

- The sample identified as EX01-10 (reference/exemplar sample from Stamp #3) failed to produce a human DNA quantification value
- The sample identified as EX02-1 (reference/exemplar sample from Steve Spence) produced a full autosomal-STR DNA profile.
- The sample identified as EX02-1 (reference/exemplar sample from Steve Spence) produced a full Y-STR DNA profile.
- The sample identified as EX03-1 (reference/exemplar sample from Anthony Melendez) produced a full autosomal-STR DNA profile.
- The sample identified as EX03-1 (reference/exemplar sample from Anthony Melendez) produced a full Y-STR DNA profile.
- The sample identified as EX04-1 (reference/exemplar sample from Terry Lee Harper) produced a full Y-STR DNA profile.
- The sample identified as EX05-1 (reference/exemplar sample from Derwin Wilkens) produced a partial Y-STR DNA profile.
- The sample identified as EX06-1 (reference/exemplar sample from John David Wilkens) failed to produce an Y-STR DNA profile suitable for comparison.

CLOSING REMARKS

The submitted item(s) and associated exhibit(s) will be retained until further disposition. Sufficient quantities of reference/exemplar samples remain for reanalysis, depending upon the type of DNA profiling system used.

This analysis was performed under chain-of-custody. The chain-of-custody documentation is on file at NMS Labs.

Positive and negative controls at each stage of analysis of this case performed as expected.

Analysis performed by:

Jennifer K. Sears, B.S.
Forensic Biologist

Review performed by:

Britton Morin, M.S.F.S.
Forensic Biologist

******* END OF REPORT *******

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

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

Definitions

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

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

Examination Techniques for Detecting Possible Biological Material

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

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

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

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

Serological Tests and Result Interpretation

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

Blood

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

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

Seminal Fluid

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

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

Sperm Cells / Spermatozoa

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

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

Saliva

RSID Saliva (RS) Test:

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

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Urine

Combined Urea/Creatinine Test:

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

Fecal Matter

Urobilinogen Test:

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

Species Group Identification

Ouchterlony Double Immunodiffusion Test:

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

DNA Tests and Result Interpretation

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

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

General Categories of Testing Conclusions

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

Additional Cautionary Notes

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

General Categories of Statistical Conclusions

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