



Report on investigation regarding DNA interpretation issues at the Department of Forensic Sciences

January 29, 2015

Introduction

On January 22, 2015, the Department of Forensic Sciences (DFS) was made aware of disclosure that was provided to the Public Defender Service by the District of Columbia's United States Attorney's Office (USAO). This disclosure contained information and a summary statement outlining issues identified from the review of six cases that had been processed, analyzed, and reported by the DFS Forensic Biology Unit ("the Unit"). The summary from the USAO's retained expert panel, comprised of Dr. Bruce Budowle, Dr. Frederick Bieber, and Ms. Lisa Brewer, was dated December 30, 2014.

Background

The interpretation of DNA mixtures in forensic DNA analysis has been a long-standing issue within the forensic community. Several textbooks, professional journals, presentations, workshops, and web-based information sources have been devoted to this issue.^{1,2,3,4,5,6} To date, a universally accepted methodology within the forensic DNA community for mixture interpretation remains unresolved. At the national level, no standards have been put forward by the Scientific Working Group for DNA Analysis Methods (SWGDM) for DNA mixture interpretation⁷, neither has the recently formed Organization of Scientific Area Committees (OSAC) on DNA Analysis yet to issue any guidelines.⁸ As a result of lack of external guidance, forensic DNA laboratories have been left to develop and implement mixture interpretation protocols on their own accord. In doing so, forensic laboratories have based such internal protocols on the expertise, understanding, and interpretation of general DNA analysis guidelines that best fit the needs and scope of the laboratories. This has led to a wide variety of

¹ Butler, John. *Fundamentals of Forensic DNA Typing*. Elsevier, 2010. Print.

² Butler, John. *Advanced Topics in Forensic DNA Typing: Methodology*. Elsevier, 2011. Print.

³ Various authors. Special edition- "Analysis and Biostatistical Interpretation of Complex and Low Template DNA Samples" *Forensic Science International: Genetics*. Ed- John Butler. Vol. 6, Issue 6. December 2012. Online- [http://www.fsigenetics.com/issue/S1872-4973\(12\)X0006-1](http://www.fsigenetics.com/issue/S1872-4973(12)X0006-1).

⁴ Budowle, Bruce. "Mixtures DFS Interpretation Issues" UNT Health Science Center PowerPoint, created 02/05/2007, modified 10/22/2014.

⁵ Coble, Mike. "MIX 13- Mixture Interpretation Interlaboratory Challenge" NIST Applied Genetics PowerPoint, created 7/23/2013, modified 8/1/2013.

⁶ Online- "Information on DNA Mixture Interpretation", National Institute of Standards and Technology, STRBase, 2014. <http://www.cstl.nist.gov/strbase/mixture.htm>

⁷ Online- "SWGDM Mixture Committee Resource Page", <http://swgdam.org/resources.html> 2015.

⁸ Online- "Organization of Scientific Area Committees", <http://www.nist.gov/forensics/osac/index.cfm> 2015.



interpretation methods in the forensic DNA field.⁹ The current technologies and chemistries utilized in forensic DNA analysis have increased in throughput and sensitivity. As a direct result of this, more mixed DNA profiles i.e. profiles containing DNA from more than one person, are being developed in forensic casework than ever before. In order to properly interpret these mixtures, the standards developed independently within each laboratory must be applied.¹⁰

Issues or allegations

The six cases under issue appear to have been selected by the USAO as part of a review of Combined Probability of Inclusion (CPI) calculations; however issues above and beyond CPI were reported for all six cases. The expert panel from the USAO outlined five “thematic issues of concern” in regards to the cases: the limitation of CPI calculations, the application of CPI calculations, the appropriateness of DNA mixture deconvolution, the definition of “intimate samples”, and the use of a stochastic threshold when interpreting DNA mixtures.

Response

All of the reported issues fall under the general category concerning the DNA mixture interpretation guidelines within the Unit. On January 27, 2015, the reported issues and related cases were reviewed in depth by DFS personnel. The general finding of the review were ultimately seen as a difference of opinion between experts in regards to all five of the noted issues. The arguments and criticisms raised in the USAO report were not found to be persuasive. In all cases, it was seen that the Unit personnel issuing the reports adhered to the Unit’s DNA mixture interpretation guidelines that were in place at the time the work was performed on the cases.

Outcomes and Actions

All of the noted issues from the retained experts for the USAO are currently being addressed through the development and implementation of new mixture interpretation protocols, statistical calculation protocols, and report writing guidelines stemming from prior issues/allegations raised by the USAO at the end of 2014.^{11,12} The outcome of

⁹ Butler, John. “Mixture Interpretation Issues & Insights” NIST Applied Genetics PowerPoint, presented 1/10/2007. Online- http://www.cstl.nist.gov/strbase/pub_pres/SWGDAM_Jan2007_MixtureInterpretation.pdf

¹⁰ Dror, Itiel E. and Hampikian, Greg, Subjectivity and bias in forensic DNA mixture interpretation, *Science & Justice* 51 (2011) 204-8.

¹¹ D.C. Department of Forensic Sciences “Report on investigation regarding general concerns about DNA mixture interpretation.” November 19, 2014. Online- http://dfs.dc.gov/sites/default/files/dc/sites/dfs/page_content/attachments/Report%20on%20DNA%20mixture%20interpretation.pdf



these prior investigations, which included a review and recommendation from the DFS Scientific Advisory Board, called for enhancements to the scientific approach the Unit was using in DNA mixture interpretation. As a result, new protocols and guidelines have been developed and the members of the unit are currently undergoing detailed training in the new mixture interpretation methodology, which to date has been independently observed and favorably reviewed by Dr. Frederick Bieber (Appendix A).

Dr Bieber made suggestions for ongoing study of Dr Word's training material; this is part of the planned activities during the current training sessions. DFS will, of course, make the revised protocols and worksheets, and the training materials available to Dr Bieber.

Specifically, the proposed changes to the mixture interpretation protocols will address all of the issues raised by the scientific panel appointed by the USAO and by the DFS' Scientific Advisory Board. These protocols will include the documented justification of mixture identification, mixture deconvolution, and the determination of the number of potential contributors to a DNA mixture. The statistic calculation protocols will address the statistical inclusion or exclusion of individuals within a DNA mixture based on Combined Probability of Inclusion (CPI) methodologies, and when CPI should be applied as a calculation.

The changes to the analytical guidelines will reinforce the need for explicit documentation of the justification of the mixture identification, define and clarify the role of the stochastic and analytical thresholds, and address the definition of, and analytical approach used, for intimate samples.

¹² D.C. Department of Forensic Sciences "Report on investigation into failing to consider allele sharing and improperly calculating combined probability of inclusion (CPI)." November 19th, 2014. Online-
http://dfs.dc.gov/sites/default/files/dc/sites/dfs/page_content/attachments/Report%20on%20CPI.pdf



APPENDIX A-

E-mail exchange between Dr. Frederick Bieber and DFS Deputy Director Dr. Chris Maguire-

From: Bieber, Frederick R., Ph.D.

Date: January 27, 2015 at 6:11:02 PM EST

To: Maguire, Christopher (DFS)

Subject: DFS lecture by Dr. Word 1/27/2015

Dear Chris, et al.

Many thanks for making it possible for me to "sit in" on today's lecture by Dr. Word from a distance, as foul weather dashed any air travel from Boston. The computer connection was just fine, though some of the audio of the lively Q/A was not very clear at times.

The day's training seemed to go quite well. Dr. Word's presentation emphasized many of the key elements relating to identification of alleles and genotypes in both straightforward and in complex DNA mixtures. Dr. Word carefully emphasized the need to document any/all assumptions about alleles present, assumptions made (about drop-out, stochastic effects, number of contributors), and the need to evaluate the "evidence" without relying on the "knowns".

As the seminar started a bit late (~11:00AM) Dr. Word needed to skip over or pass quickly over many important slides in her presentation.

Chris, it would be key, in my opinion, for your DNA team to study Dr. Word's handout carefully, in a group, to assure understanding of the many important points.

Dr. Coble made some key comments throughout the day but made no formal presentation. Perhaps this is scheduled? Going forward it would seem important to have Dr. Coble (or Dr. Word) return to DFS for a very thorough session or two on the actual statistical aspects of DNA mixture reporting.

During the seminar, reference was made several times to a "new" worksheet being put into place for documentation. If you are willing/able to send me a copy of this, along with a copy of Dr. Word's presentation, that would be helpful. In the meantime I will think carefully about Ideas for any further recommendations for continuing ed for your group.

Best regards,
Fred B.

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