



## Report on investigation into failing to consider allele sharing and improperly calculating combined probability of inclusion (CPI)

November 19, 2014

### Introduction

On 17 OCT 2014, the District of Columbia United States Attorneys Office (USAO) expressed specific concerns about “issues regarding the manner in which DFS has selected loci for CPI statistical analysis and major contributor RMP statistical analysis”.

### Background

A DNA sample is “mixed” when more than one contributor can be identified in the sample based on the apparent genetic profiles present. The amount of DNA contributed by the sources will vary and this may affect the interpretation of the results. The same alleles (variants of a gene at a particular location on the gene) from different contributors may overlap at the same position (locus) in the profile, making the significance of inclusion potentially problematic to interpret. These analyses are all conducted in the DFS Forensic Science Laboratory Division’s Forensic Biology Unit (“the Unit”). Three main statistical methods are used for determining the significance of including a person in the mixture, Combined Probability of Inclusion (CPI), Random Match Probability (RMP), or Likelihood Ratios (LR). The Department of Forensic Sciences (DFS) Forensic Science Laboratory Division uses the CPI method.

### Issues or allegation

On 17 OCT 2014, the USAO expressed specific concerns in a case pending before the court about “the manner in which DFS has selected loci for CPI statistical analysis and major contributor RMP statistical analysis” (Appendix A). The USAO engaged an outside expert to review specific reports from the Unit and, according to the USAO email, the expert claimed that the Unit had “failed to take into consideration the additive effects of shared alleles in mixtures” and that there were “case-specific examples where major contributor deconvolution may not be well supported”. The USAO clarified, stating, “...the problem identified by [the expert] is not with the protocol itself, but with the application of the protocol”. The USAO explicitly stated that they were not filing an allegation on this matter.

### Response

In an abundance of caution to determine if a systemic issue existed within the Unit, the DFS Director decided to treat the issues raised by the USAO as an allegation of a “testing error” and initiated an investigation in accordance with §5-1501.10 (a). Previously, the DFS Science Advisory Board (SAB) had agreed to review protocols based on broader interpretation concerns per §5-1501.12 (2) (see *Report on investigation into failing to consider allele sharing and improperly calculating combined probability of inclusion (CPI)*, available at [www.dfs.dc.gov](http://www.dfs.dc.gov)).

A conference call was held on 4 NOV 2014 with the USAO’s expert, USAO personnel, members of the SAB, and DFS personnel. The expert detailed his concerns. As a starting point, the expert acknowledged variation exists regarding interpretation of alleles and allele sharing *across* the forensic science community. He noted that variation in interpretation is “somewhat

acceptable". Additionally, he noted that variation in interpretations may occur *within* a laboratory system. Having reviewed the Unit's protocol the expert stated, "In my opinion, the [Unit's] protocols are scientifically sound." His concerns revolve around the Unit "not taking into consideration additive effects" of shared alleles and "at times, [the lab is] applying CPI without considering allele drop out." Further, during the call, the expert observed that the Unit was performing the CPI calculation correctly.

He and the USAO reiterated that neither of them believed a "testing error" had occurred in the case discussed; DFS concurred after reviewing the case file in light of the input up to that date.

### **Discussion**

After the conference call, it became clear that there was no concern about testing error, but rather a disagreement as to the methods and their application in mixture interpretation. The method the Unit uses to interpret mixtures had previously been brought to the SAB for review, pursuant to §5-1501.12 (2); see *Report on investigation into failing to consider allele sharing and improperly calculating combined probability of inclusion (CPI)*, available at [www.dfs.dc.gov](http://www.dfs.dc.gov).

### **Outcomes and Actions**

New protocols based on the SAB's recommendations are estimated to be in place by end of January 2015.

Any cases being reported by the Unit between the date of this report and the end of January 2015 will be issued under the current protocol. Cases scheduled for trial in that time frame may seek a request for continuance until the new protocol is in place; the reports will then be issued under the new protocol.

A non-exhaustive search of cases scheduled for trial by the end of January 2015 resulted in 27 cases being identified; of those, 7 had mixtures, and three had CPI statistics calculated; other cases may come to light. All of the 7 cases found were reviewed to determine if allele sharing had been taken into account; of the three with CPI calculations, only one was found to not have adequately taken allele sharing into account and an amended report will be issued. The appropriate stakeholders will be notified.

**Appendix A: Email communication to DFS from DC USAO, dated 17 OCT 2014**

On Oct 17, 2014, at 3:26 PM, Ambrosino, Michael (USADC) <[Michael.Ambrosino@usdoj.gov](mailto:Michael.Ambrosino@usdoj.gov)> wrote:

Max,

I'm following up with you on the issues relating to DFS's selection of loci for mixture analysis and statistical calculations that has arisen in [case title and citation]. As previously discussed with you and members of your management team, Dr. Bruce Budowle was initially retained by the United States to conduct a likelihood ratio calculation with respect to a particular piece of evidence in this case. In the course of his review, it has come to light that there are issues regarding the manner in which DFS has selected loci for CPI statistical analysis and major contributor RMP statistical analysis. I'm resending the 4 disclosures that have been made in connection with this case to defense counsel outlining Dr. Budowle's review of the work done by DFS and areas where Dr. Budowle reached different interpretations of potential allele dropout regarding mixture calculations and interpretation of major contributors at some loci. I'm also attaching a Power Point prepared by Dr. Budowle discussing the issues that have arisen.

Based on the protocols set forth on DFS's website, it would appear that DFS is endeavoring to comport with principles set forth in a number of peer-reviewed publications relating to mixture interpretation, such as those stated in Budowle, B., Onorato, A.J., Callaghan, T.F., Della Manna, A., Gross, A.M., Guerrieri, R.A., Luttmann, 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. Although the concepts outlined in publications such as this one are sound, Dr. Budowle has identified problems that have arisen in the manner in which DFS has *implemented* these principles, including the following:

#### 1. Additive Effects of Shared Alleles

The DFS protocols exclude loci from statistical analysis when any one of their peaks is below the 200 RFU stochastic threshold. See FBS 18 Population Statistics 7.5.1.4. This is a perfectly acceptable interpretation practice. However, according to Dr. Budowle, DFS has failed to take into consideration the additive effects of shared alleles in mixtures. Therefore, a peak above 200, in and by itself, may not represent solely an allele from a single individual. It is possible under the DFS general protocol that the allele may be comprised of two individuals or more and, depending upon the case-specific context, each or one of the contributors to that allele may be below 200 RFU. Thus, stochastic effect thresholds may still apply. For example, if an allele peak height was 280 RFU and it was a mixture of two individuals, one contributing 190 RFU and the other contributing 90 RFU, then the partner alleles of each contributor could have potentially dropped out. It would appear that this scenario is not being accounted for in current CPI calculation practices. This same issue applies to additive effects of alleles and stutter.

#### 2. Major Contributor Deconvolution When Peak Height Signal is Relatively Low

According to Dr. Budowle, there have been case-specific examples where major contributor deconvolution may not be well supported. One scenario where this issue has arisen is where a major component of a mixture shows signs of substantial degradation and the minor component does not reveal substantial degradation.

### 3. Combining Single Source and CPI Calculations into One Final Statistic

There were examples where one locus was calculated using CPI and another locus was calculated using RMP. According to Dr. Budowle, these two calculations should not have been combined into one statistical value.

As you are aware, Dr. Budowle is the most highly published forensic DNA expert in the world. In fact, Dr. Budowle is the most frequently cited DNA authority in DFS's protocols. The U.S. Attorney's Office has turned to Dr. Budowle for the past 20 years for guidance on virtually each and every important DNA issue that has arisen. Clearly, these issues raised by Dr. Budowle cannot go unaddressed. I am hopeful that our two offices can work together to ensure that the statistical calculations produced by DFS are sound.

To date, DFS has responded by taking the position that it has a protocol in place and followed that protocol. However, Dr. Budowle's evaluation of the evidence raises the concern that DFS did not follow its own protocol. To be clear, the problem identified by Dr. Budowle is not with the protocol itself, but with the application of the protocol. To date, no one from DFS has explained whether the agency agrees or disagrees with the particular analysis conducted on each of the items of evidence in this case. I am requesting that DFS take such a position.

Because of the importance of this issue to the litigation of pending criminal cases, it must be resolved expeditiously. Two felony cases have already gone forward without the use of available DNA evidence. This issue potentially impacts every case in which DFS has conducted a CPI mixture calculation or conducted a major contributor calculation.

Our offices must work together to resolve this issue so that we can take corrective action before any more cases proceed to trial. Moreover, we need to expeditiously develop a plan to evaluate all cases in which DFS has issued a report with a CPI mixture statistic or a major contributor statistic. When I requested a list of cases that contain CPI mixture calculations or mixtures from which a major contributor calculation was conducted, your General Counsel responded that "the determination as to what files may be affected rest squarely with your attorneys." To be clear, all files where CPI or major contributor calculations have been calculated may be affected. We need the lab to identify the universe of cases where CPI calculations or major contributor calculations have been performed so that we can determine which cases may be affected.

Dr. Budowle is flying to China tomorrow. However, he will be back the week of October 27<sup>th</sup>. I would like to schedule a meeting with members of our offices and Dr. Budowle to see if we can have a meeting of the minds on this issue and a plan for moving forward.

Regards,

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