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Correcting Forensic DNA Errors

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Highlights:

DNA mixture interpretation can produce opposing conclusions by qualified forensic analysts, even within the same laboratory. The long-delayed publication of the National Institutes of Standards and Technology (NIST) study of 109 North American crime laboratories in this journal demonstrates this most clearly. This latest study supports earlier work that shows common methods such as the Combined Probability of Inclusion (CPI) have wrongly included innocent people as contributors to DNA mixtures. The 2016 President's Council of Advisors on Science and Technology report concluded, "In summary, the interpretation of complex DNA mixtures with the CPI statistic has been an inadequately specified—and thus inappropriately subjective—method. As such, the method is clearly not foundationally valid." The adoption of probabilistic genotyping by many laboratories will certainly prevent some of these errors from occurring in the future, but the same laboratories that produced past errors can also now review old cases with their new software—without additional bench work. It is critical that laboratories adopt procedures and policies to do this.

Correcting Forensic DNA Errors

To Err is human, to correct error is responsible science. Butler et. al recently published the results of Mix13, the largest and most thorough assessment of North American forensic DNA labs [1]. Some of us have publicly quarreled about how their striking results were delayed and downplayed by an unprecedented attempt at disclaimers [1,2,3]. The reason for our concern is not a desire to expose flaws, but rather the fear that we may lose an historic opportunity to correct errors, and restore freedom to those wrongfully convicted by incorrect DNA mixture analysis.

Inspired by Mix13, my laboratory contracted with statistical software company Cybergenetics to review post conviction claims of innocence where DNA mixtures figured prominently. This collaboration has already resulted in overturning 5 wrongful convictions in cases where earlier DNA methods failed [4,5,6].

Butler and the team at NIST did exactly what many of us in the field had requested: conduct an interlaboratory study that used challenging examples and included contextual information. They constructed 5 scenarios, and the fifth was the most challenging: a ski mask from a bank robbery with a complex DNA mixture of at least three contributors. The labs were given three suspects (A, B, and C) to compare to that mixture. According to the authors, the purpose of this test was to determine, "How many labs would consider this mixture as too complex to interpret?" In essence, they were testing the labs' ability to recognize the limits of their techniques. However, the study also measured the false positive rate across the system. In this case, a false positive was the wrongful inclusion of a person in a DNA mixture with an accompanying match statistic. This is equivalent to an innocent person being wrongly tied to a crime by DNA. The results show that 68% of the 108 accredited labs did just this--included the innocent "suspect C." Remember that the point of the exercise was to see how many labs thought it was too complex to interpret. The conclusion: 27 (25%) of the labs deemed the mixture inconclusive, 7 (6%) correctly excluded the suspect, but the majority--74 (68%) wrongly included an innocent suspect and supplied a match statistic. It is a chilling conclusion. Just as perplexing are the match statistics reported by labs in the Mix13 study, which varied over 14 logs. While the authors point out that NIST used DNA mixtures created in the laboratory, the results support a 2010 study [2] conducted with actual case data. In that study, 17 analysts at an out of state laboratory were asked to reanalyze a complex DNA mixture from a Georgia case where the analyst had included a suspect. Only 1 of the 17 analysts agreed with the Georgia analyst's original conclusion, 13 excluded the suspect, and 3 found the mixture inconclusive. The man implicated by that dubious original interpretation is still in prison. These studies of complex DNA mixtures show that the Combined Probability of Inclusion (CPI) and other manual methods can wrongly include innocent people as potential contributors to DNA mixtures. The 2016 President's Council of Advisors on Science and Technology report concluded, "In summary, the interpretation of complex DNA mixtures with the CPI statistic has been an inadequately specified—and thus inappropriately subjective—method. As such, the method is clearly not foundationally valid' [8].

The good news is that the only lab that used probabilistic genotyping software (TrueAllele by Cybergenetics) in the NIST study, got the right answer and excluded suspect C. Since these programs have been recommended by international commissions [9] most labs are adopting them, and many potential errors will be prevented. But what is our retrospective responsibility? If we had learned that a particular lab chemical caused false positives, we would certainly reprocess those cases with a more trustworthy reagent. Likewise, if an expert system was found to cause nationwide errors, we would re-run our data with alternate software. Our responsibility is no different in cases where the error was human. We must go back, detect and correct our mistakes. In 2013, the Virginia Department of Forensic Science did just this, and published its results [10]. While this study was not looking specifically for wrongful convictions, it shows the value and relative ease of reanalyzing old mixture cases with new software. In the Virginia study, 144 old cases were reviewed using TrueAllele. Most of the new analyses just boosted match statistics beyond the CPI calculations. However, in 5 cases, TrueAllele excluded the known profile where manual CPI had included them. When analysts re-checked their work in light of these results, they changed their conclusions. This demonstrated that TrueAllele could reverse erroneous matches, and produce more convincing true matches—facilitating convictions in languishing cases, and avoiding wrongful imprisonment. This can all be done without any new wet lab work.

Prosecutors from Boston to Houston have created Conviction Integrity Units that are overturning wrongful convictions--70 in 2016 alone [11]. There is now an opportunity (I would argue a responsibility) for crime labs to set up Conclusion Integrity Units. Such groups could decide how best to review old cases, and develop mechanisms to effectively deal with requests for reevaluation from lawyers and prisoners. These reviews will produce new suspects for prosecution, and reverse wrongful inclusions like those exposed by the NIST study and others.

A large part of my casework is people who claim wrongful conviction. Probabilistic genotyping can often tell if their claims are true. This has been established both by science (see the VA and NIST studies above cited above), and by the courts through exonerations. In our most recent case (2019), Johnnie Lee Gates who served 44 years in prison for murder (and had been on death row) was granted a new trial [11]. Unfortunately, the innocence claims that we handle through post conviction court procedures can take years because getting access to data files often requires time-consuming and expensive litigation. But in-house reviews by crime laboratories, like the one in Virginia, can be done expeditiously. We would be happy to share the lessons we have learned with any laboratories considering similar programs.

do not necessarily represent the official position or policies of the U.S. Department of Justice.

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