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Dr. John Holdren, PCAST co-chair
Assistant to the President for Science and Technology
President's Council of Advisors on Science and Technology (PCAST)
Office of Science and Technology Policy
Eisenhower Executive Office Building
1650 Pennsylvania Avenue
Washington, DC 20504

Re: Report to the President on "Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods"

Dear Dr. Holdren,

I appreciate your Council's efforts to shore up the "science" in Forensic Science. I have a few comments on your Report.

1. CPI is a random number

The Combined Probability of Inclusion (CPI) method is less effective than you describe. This subjective way of interpreting DNA mixture data has not been validated, and gives inaccurate match statistics. A recent peer-reviewed article showed that CPI is simply a randomized count of tested loci [1].

2. Independent scientific validation

Science proceeds by empirical testing and peer-reviewed publication. Most peer-reviewed papers in science and technology have coauthors involved in method development or application. Lander writes about Lander's lab, not Botstein's; that is normal science. Independent peer-review, accepted by science and the courts (e.g., Daubert), helps mitigate conflicts of interest, such as funding sources (e.g., NIH grants or federal appropriation).

Forensic developmental validation usually includes a manufacturer in the study and publication (FBI QAS, Section 8). Such peer-reviewed studies often have an independent collaborator, such as a government laboratory. And crime labs conduct their own internal validations to confirm that their DNA technology works as advertised.

Your Report cannot unilaterally impose a novel notion of "independent authorship" for peer-review. That is not how peer-review operates in science and law. The "independence" of peer-review resides in the journals and reviewers, not in the authors.

3. Imposing arbitrary limits

TrueAllele[®] DNA mixture interpretation [2] has undergone over thirty validation studies. Seven of them are peer-reviewed publications [3-9]; the first one appeared in 2009. Courts have upheld the computer's reliability after ten challenges [10-19]. Defenders use TrueAllele to exonerate the innocent [20].

The objective TrueAllele process achieves your stated goals, and is backed by extensive validation. The defense can test the system for free. You properly decry the use of unfounded cutoffs and subjectivity in DNA interpretation. Yet you propose imposing such arbitrary limits (e.g., number of contributors) on a scientifically validated solution.

4. Remarks on Finding 3, paragraph 2

DNA analysis of complex-mixture samples, probabilistic genotyping

Objective analysis of complex DNA mixtures with probabilistic genotyping software is relatively new and promising approach.

> The TrueAllele approach is not new. The first methods paper was published fifteen years ago [2]. The system was first used in court seven years ago [21]. Over five hundred reports have been filed, in over two thirds of the states. Crime labs have been using their validated systems since 2014.

Before the method can be established as foundationally valid for a broad range of settings, more research is required appropriately to establish the capabilities and limitations of various approaches.

> Yes, scientific methods should "be established as foundationally valid" for their intended application. TrueAllele's capabilities and limitations are well established. "More research" is not required for using this system.

At present, published papers support the foundational validity of analysis, with some programs, of DNA mixtures of 3 individuals in which the contributor in question constitutes at least 20% of the intact DNA in the mixture.

> The published literature supports TrueAllele validity on mixtures of 4 or 5 individuals [5, 6], with fractions down to 1%. The exclusionary statistics needed to defend the innocent require this full range. Statistical inference shows the method is not limited to fixed limits [5]; as data complexity increases, match statistics shrink accordingly.

5. Access to CODIS database

The failure of CPI to interpret DNA mixtures [22] affects CODIS, the FBI's DNA database. CODIS is based on simplistic DNA analysis, imposing a CPI statistical threshold to block DNA mixtures. Most DNA evidence items are mixtures, and most mixtures are not uploaded to CODIS. The failure of CPI mixture interpretation translates into a failure of investigative DNA database search.

Police, defenders, courts and innocence groups share a common problem – FBI regulations prevent them from using CODIS to solve crime. When crime lab mixture interpretation fails, and outsiders produce scientifically validated DNA information, the FBI won't let the better science search CODIS. This is bad science and bad policy that impedes justice and harms innocent people. Your Report should recommend open access to CODIS.

6. Conclusion

Some have a dark view of your Report, seeing it as a partisan attempt to sideline legitimate forensic evidence, disrupt the court system, and pump money into undeserving agencies. The FBI is not a "leader" in forensic science; NIST lacks expertise in modern statistical analysis.

Regardless, your Report sheds light on important issues. Forensic feature-comparison needs more scientific foundation and empirical support. CPI for DNA mixtures has failed.

Fortunately, a decade of "probabilistic" genotyping software development has yielded statistical models of general applicability. Once again, DNA innovation and success point the way to better forensic science.

Sincerely,

Mark W. Perlin, PhD, MD, PhD
Chief Scientific and Executive Officer

References

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Peer-reviewed validation papers

   laboratory data

[3] Perlin MW, Sinelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE*. 2009;4(12):e8327.

[4] Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information. *Science & Justice*. 2013;52(2):103-14.

[5] Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences*. 2015; 60(4):857-868.

[6] Greenspoon SA, Schiermeier-Wood L, and Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276.

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[7] Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences*. 2011;56(6):1430-1447.

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[9] Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, and Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLoS ONE*. 2014:9(3):e92837.

Legal acceptance after challenge

[10] California trial court admitted TrueAllele into evidence in People v. Dupree Langston, Kern County, case number BF139247B, January 10, 2013. (Kelly-Frye)

[11] Indiana trial court admitted TrueAllele into evidence in State v. Dugniqio Forest, Vanderburgh County, case number 82D03-1501-F2-566, June 3, 2016. (Daubert)

[12] Indiana trial court admitted TrueAllele into evidence in State v. Malcolm Wade, Monroe County, case number 53C02-1411-F3-1042, August 3, 2016. (Daubert)

[13] Louisiana trial court admitted TrueAllele into evidence in State v. Chattley Chesterfield and Samuel Nicolas, Parish of East Baton Rouge, case 01-13-0316 (II), November 6, 2014. (Daubert)

[14] Massachusetts trial court admitted TrueAllele into evidence in Commonwealth v. Heidi Bartlett, Plymouth County, May 25, 2016. (Daubert)

[15] New York trial court admitted TrueAllele into evidence in People v. John Wakefield, Schenectady County, indictment number A-812-29, February 11, 2015. (Frye)

[16] Ohio trial court admitted TrueAllele into evidence in State v. Maurice Shaw, Cuyahoga County, case number CR-575691, October 10, 2014. (Daubert)

[17] Pennsylvania Superior Court affirmed TrueAllele admissibility ruling in Commonwealth v. Kevin Foley, Indiana County 2009 trial, establishing a statewide Pennsylvania precedent; 2012 PA Super 31, No. 2039 WDA 2009, filed February 15, 2012. (Frye)

[18] South Carolina trial court admitted TrueAllele into evidence in State v. Jaquard Aiken, Beaufort County, case number 20121212-683, October 27, 2015. (Jones)

[19] Virginia trial court admitted TrueAllele into evidence in Commonwealth v. Matthew Brady, Colonial Heights County, case number CR11000494, July 26, 2013. (Spencer-Frye)

[20] Guerra K. He went to prison for rape: proof of his innocence surfaced 25 years later. *Indianapolis Star*, July 17, 2016.

[21] Perlin MW. "The Blairsville slaying and the dawn of DNA computing," in *Death Needs Answers: The Cold-Blooded Murder of Dr. John Yelenic*, A. Niapas, Ed., New Kensington, PA: Grelin Press, 2013. https://www.cybgen.com/information/publication/2013/DNA/Perlin-The-Blairsville-slaying-and-the-dawn-of-DNA-computing/page.shtml

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