Communicating Forensic Findings Workshop: Current Practices and Future Directions

Session 2: Communicating Results in Forensic Reports and Testimony

Clinton Hughes – Brooklyn Defender Services
Question 1 – Fantasy Island

If we took all your advice and suggestions today on how to communicate results effectively – what would that look like tomorrow in lab reports or in court testimony?
Can you discuss more of the cultural divide between scientists and their use of language vs. what those reading the reports or hearing the testimony want/need? (scientific language and precision vs layman’s terminology)
Assumption – the greatest danger of assigning false support for a non-contributor in Forensic DNA Mixture Analysis occurs when relative(s) of the person mixture are contributors to a crime scene sample.
“Likelihood Ratio (LR): A measure of the relative strength of support that particular findings give to one proposition against a stated alternative. . .” (xix)
We define error as the failure of a system to achieve its intended goal or outcome.” (16)

“Outcome Error: An error in the final opinion or result.” (xix)
Q. So your testimony is that the only false positives with STRmix come from misidentifying the number of contributors.

A. In addition to limit artefacts. Meaning when we're doing edits and removing artefacts, we didn't remove the artefacts. And multiple artefacts are actually aligning with alleles with that person of interest that we are comparing with the mixture. That may lead to false positives.
Q. False inclusion of values can also occur because of allele sharing between true contributors and noncontributors, correct?

A. Not necessarily.

Q. That's not my question, right?

False inclusions can occur because allele sharing between true contributors and noncontributors, correct?

A. The answer is no.
Workshop Description – Day 1

“From the presentations and discussions, we are looking to examine any knowledge gaps that may impact an end user’s understanding of the findings.”
February 2021

AMERICAN ACADEMY OF FORENSIC SCIENCES

73rd AAFS ANNUAL SCIENTIFIC MEETING

ONE ACADEMY

PURSUITING JUSTICE THROUGH TRUTH IN EVIDENCE
The False Inclusion of Non-Contributors in DNA Mixtures Cases
Marie Semaan, MS*; Sarah Abbas, MS; Issam Mansour, PhD
(FSF Emerging Forensic Scientist Award Oral Presentation)
The American University of Science and Technology attended the 21st triennial meeting of the International Association of Forensic Sciences IAFS 2017 that was held in Toronto, Canada; on August 21-25 2017. Two graduate students from the Faculty of Health Sciences, Ms. Marie Semaan and Mrs. Sarah Abbas, presented part of the research work conducted at AUST in the field of Forensic Science (DNA Analysis), under the supervision of Dr. Issam Mansour.

Ms. Semaan presented her Master's research in an oral presentation entitled “DNA Mixture Analysis in inbred Lebanese communities. Assessment of expert DNA mixture software”. Whereas, Mrs. Abbas' communication entitled “Inbreeding effect on forensic investigations involving DNA mixtures: The Lebanese population case” was presented as part of her PhD research work conducted in collaboration with the University of Lausanne - Switzerland.

Forensic Science experts, professional organizations and delegates from around the world were available in this meeting to share information, new practices and advancements in the field. Among the audience were Professor Frederick Bieber, Professor Pierre Margot, Dr. Michael Pollanen, world leaders in the field of Forensic Science and decision makers in forensic investigative strategies.

The meeting served as a unique opportunity for the AUST community to reassure their pivotal role in the advancement of forensic sciences in the Middle-East and North Africa region, introduce themselves to new trends in the scientific community and establish strategic partnerships with other international organizations.
A Mixed DNA Profile Controversy

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A mixed DNA profile controversy revisited

Tim Kalafut PhD¹ | Simone Pugh MS² | Peter Gill PhD³,⁴ | Sarah Abbas MSc⁵,⁶ |
Marie Semaan MSc⁵ | Issam Mansour PhD⁵ | James Curran PhD⁷ | Jo-Anne Bright PhD⁸ |
Tacha Hicks PhD⁹,¹⁰ | Richard Wivell BSc (hons)⁸ | John Buckleton DSc⁷,⁸
A mixed DNA profile controversy revisited

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|        |     |     |     |     |     |     |     |     |
| **LR_{ij/ju}** |     |     |     |     |     |     |     |     |
| STRmix™ (GlobalFiler 21 loci) |     |     |     |     |     |     |     |     |
| 1:1    | 0   | 0   | 0   | 1.43×10^{28} | 0   | 0   | 2.43×10^{27} | 0   |
| 3:1    | 0   | 0   | 0   | 1.53×10^{28} | 0   | 0   | 2.33×10^{27} | 0   |
A mixed DNA profile controversy revisited

TABLE 6 Unconditioned LRs for Experiment 4 (4:1 low-level mixture) using STRmix™ and data from El Andari et al. (6) and $\theta = 0.01$

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<td>$\text{LR}_{ja/uu}$</td>
<td>$1.46 \times 10^{10}$</td>
<td>$9.14 \times 10^{11}$</td>
<td>$5.86 \times 10^{23}$</td>
<td>$1.58 \times 10^{11}$</td>
<td>$7.40 \times 10^8$</td>
<td>$4.61 \times 10^{11}$</td>
<td>$1.80 \times 10^{10}$</td>
<td>$4.07 \times 10^{12}$</td>
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Note: All eight references give values that support the first proposition compared to the alternative when no conditioning profiles are used.
“Most software deal with dyadic relationships, that is relationships between two individuals. . .”
“Neither STRmix™ nor LRmix deal with triadic situations or higher, although DBLR™ does [22].”
“Neither LRmix nor any other software or interpretation method can claim that the rate of false support is zero.”
“. . .there will always be uncertainty about the source of the DNA, as we cannot know who left the DNA trace.”
“. . . this explains why DNA (or any evidence) should not be solely relied upon to reach a conclusion, but instead must be considered in combination with the other elements of the case.”
“Empirical work has previously been reported assessing the risk of false support to a non-donor who is related to the true donor(s) (see for example [4]).”
“Empirical work has previously been reported assessing the risk of false support to a non-donor who is related to the true donor(s) (see for example [4]).”

“An important missing element from many validation studies is the degree of allele sharing that has been tested.” (86)
“If validation studies are conducted using mixtures that do not explore the complexity induced by allele sharing, the user may inadvertently extrapolate validation results and apply methods beyond the limits of the validation studies conducted.” (89)
The analysis of the in vitro and in silico mixtures assuming NoC = 3 with no use of a conditioning profile or with the use of a conditioning profile but without informed priors on the mixture proportions (Mx priors) was ineffective.
Workshop Description – Day 1

“From the presentations and discussions, we are looking to examine . . . any knowledge gaps that may impact an end user’s understanding of the findings.”
Thank you –
Dr. Sandra Koch,
Donna Ramkissoon,
and all the other folks at NIST!