

Scientific Working Group on DNA Analysis Methods (SWGDM) July 2021 Report

July 13 - 15, 2021

Virtual Meeting

I. Agenda:

Please see Attachment 1.

II. Meeting Synopsis:

Tuesday, July 13, 2021

The SWGDAM Chair, Anthony Onorato, acknowledged Ms. Tiffany Thoren from the Federal Bureau of Investigation's (FBI) CODIS Unit for her assistance with the virtual meeting. The Chair congratulated new members Dorothy Catella and Bill Hudlow and welcomed new invited guests Tiffany Vasquez, Ben Knowles and Heather Parrish. The Chair informed attendees of the passing of Barbara Koons, a researcher at the FBI Laboratory known to many of the attendees. Tamyra Moretti and Jack Ballantyne shared their memories of Barbara as a fantastic scientist and great person. The Chair also congratulated Taylor Scott on his retirement from the FBI and Dr. Jenifer Smith on her retirement from the D.C. Department of Forensic Sciences.

TECHNICAL SESSION

The Chair introduced the Technical Session on Y STRs.

Brandon Letts, a member of the SWGDAM Lineage Marker Committee presented his Committee's update and the survey data related to discrete Laplace and the use of YHRD. He reported that a total of 77 responses were received from the CODIS laboratories surveyed. Mr. Letts noted that those using match probabilities were using theta with a few using discrete Laplace. Approximately 30% of the respondents noted that it would be of benefit to calculate match probabilities with discrete Laplace through YHRD. YHRD has offered to develop a standalone for the purpose of calculating discrete Laplace match probabilities with the U.S. Y STR data.

Steven Myers presented on Y STR Statistics. Mr. Myers offered that this exercise was previously done without the inclusion of discrete Laplace and the majority approach was

to use the counting method to respond to the question of how likely is it that a randomly selected man would have this haplotype. He explained the approach favored by ISFG is $(x + 1)/(n + 1)$ where $X \neq 0$. He also explained a number of complicating factors for taking sample frequencies and using them as surrogates for a probability (i.e., concentrations of patrilineal relatives, Y STR haplotypes seen only once in the database, etc.). Mr. Myers reviewed the Clopper Pearson process, theta (Balding Nichols), SWGDAM theta values, the Kappa approach favored by Charles Brenner, and the Omega approach.

Sascha Willuweit presented on discrete Laplace, YHRD and the U.S. subpopulations. Mr. Willuweit discussed the concept of discrete Laplace in that there are different allele distributions by population data and allele distributions are not random and observations in detail. He explored whether current subpopulations are a feasible partition. Mr. Willuweit provided an online demonstration using YHRD.

Lutz Roewer presented an update on YHRD. Established in 2000, it now has 337,449 haplotypes (100,000 more than in 2018). Data relating to these haplotypes are included in over 680 publications. Recently, inquiries have been made on whether some specific populations gave free, informed consent when providing their samples/data and he will keep SWGDAM updated on this. Dr. Roewer explained that the discrete Laplace calculated frequency values for 17 Y STRs. He also reviewed the ISHI report he presented with Mr. Willuweit in May, 2021.

Walther Parson presented an ISFG/EMPOP update. Dr. Parson announced that the next meeting will be in August/September in Washington, D.C. He also expanded upon the recent ethical issues relating to the possible inclusion of persons who have not given free consent, noting that data has been and will be removed from YHRD if the associated publications are retracted by the authors. Dr. Parson reiterated that it is important that the data is scientifically published in a peer-reviewed journal. He noted that it is increasingly difficult to find publishers for this data because it is not viewed as new or novel. He suggested that FSI: Reports may be a suitable journal for publishing population data. Dr. Parson acknowledged that the YHRD database has turned into a routine tool being used by the forensic community and that there is a lot of work involved in curating the database.

Michael Coble presented on the Application of Probabilistic Genotyping to Y Haplotypes. Dr. Coble provided an update on the use of probabilistic genotyping systems in the U.S. with a total of 75 laboratories that have implemented either STRmix or TrueAllele. He explained the benefits of probabilistic genotyping systems as it expands the type of mixtures that can be interpreted, and it can help to identify non-suspect

genotypes for database searches. With respect to probabilistic genotyping systems for Y's, Dr. Coble noted that the California Department of Justice has an in-house program and the SWGDAM Lineage Marker Committee had worked on a semi-continuous tool but while there is no firm release date on another 'haplotype-centered' tool, he expects that probabilistic genotyping for Y STRs is coming soon.

UPDATE SESSION

Andrea Borchardt presented an update for the Bureau of Justice Assistance and their forensic suite of programs. She explained that there have been changes in the grants and the period of performance will now coincide with the Federal Fiscal Year and begin October 1st and run for 24 to 36 months. Ms. Borchardt noted that performance reporting is required and accreditation may be required. She distinguished the Policy, Program office and Performance Metrics team. Ms. Borchardt described the following grant programs and their status: Coverdell, CEBR, Prosecuting Cold Cases, SAFE-ITR, Post-conviction DNA, Strengthening ME/Coroner Systems, and SAKI Testing. She also provided updates on BJA's National Training and Technical Assistance Center and the FFY 2022 President's Budget.

TECHNICAL SESSION

Brandon Letts reviewed revisions to the draft SWGDAM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories and the Supplemental Information (FAQ) document as a result of the comments received from the SWGDAM review. There was further discussion and suggested revisions that will be reviewed by the Lineage Marker Committee.

Wednesday, July 14, 2021

Committees and Working Groups held scheduled meetings.

UPDATE SESSION

The following Committees and Working Groups provided updates: Autosomal STR, CODIS, Investigative Genetic Genealogy, Quality Assurance, Next Generation Sequencing and Rapid DNA. The new Chair of the Rapid DNA Committee is Douglas Hares. See <https://www.swgdam.org/committees> (bottom of page) for update slides.

ROUND TABLE

The Round Table for the July meeting was a presentation by John Butler, Special Assistant to the Director of the National Institute of Standards and Technology (NIST). Dr. Butler presented an update on the draft DNA Mixture Interpretation: A NIST Scientific Foundation Review; which is currently posted for public comment. He explained that there will be a webinar the following week, a closed review at the end of the month and a presentation at ISHI in September. Dr. Butler indicated that Congress has asked for this review and he provided a summary brief review of the Report highlighting key takeaways.

Following Dr. Butler's presentation, he was available for a Q&A session which included the following discussions: Has NIST answered the question of whether there is foundational validity for the ways we analyze evidence? And the follow-up question to Key Takeaway 4.3, is there no data to support this? Dr. Butler responded that they believe that there is data out there but it is not publicly available. There was a suggestion that federal funding used to fund these foundational reviews may be better used in funding the foundational research, if needed. There was also a comment that forensic laboratories are not considered sufficiently unbiased so how can they do a validation that will ever be considered "suitable" for these purposes. It was noted that a similar comment was made in a GAO Report. Dr. Butler noted that NIST has performed a 2021 study examining discrimination performance and LR values for two different LRs using the PROVEDIt dataset.

In response to an inquiry concerning how to respond to courts that have accepted peer-reviewed validations, Dr. Butler said that they are only addressing scientific acceptability. He explained that labs have different challenges and the issue is how well can you do it and have it assessed externally. The question was raised why the QAS audit process is not sufficient? And what will be enough? Dr. Butler indicated that there is no threshold or criteria that address this and stated that someone has to establish the threshold and cited the World Trade Center as an example.

There was further discussion concerning the threshold of reliability and Dr. Butler responded that that was the whole point of 4.4 and the need to draw a line at some point. When questioned as to what would satisfy that threshold, Dr. Butler stated that everyone is making that decision now and deciding that they can go on-line – that decision is being made by the technical leader. When it was pointed out that it appears that there must be some criteria that is used in 4.3, Dr. Butler explained that there is not enough data to make that decision. In response to a request to determine if there is foundational validity, Dr. Butler stated that the labs make their data available. And, upon further questioning if 2 person mixtures are acceptable, Dr. Butler responded sure. There were concerns

raised that if there was not a statement relating to the foundational validity of simple mixtures, that this NIST foundational review would be used in support of challenges to those mixture cases as well.

When asked for a discipline that could serve as an example, Dr. Butler noted that digital PCR could be such an example.

In response to a question relating to how to protect the privacy of the data while making it publicly available, Dr. Butler noted that that issue is discussed in the report and that when the defense looks at the internal validation, they are looking at whether it is sufficient. When asked for clarification on that, Dr. Butler responded the user is to determine if the data is valid and reliable. It was questioned what responsibility is on the user to be knowledgeable on probabilistic genotyping? It was stated that there are a lot of burdens put on the provider but not anything on the user to which Dr. Butler noted that the user does have to have access to use that data.

In response to a specific inquiry on what other study is needed for example to support probabilistic genotyping for 2 person mixtures? Dr. Butler noted that he would not be addressing anything in a legal context. There was additional discussion on this issue and the PCAST Report as well as the responsibility to acknowledge that this foundational review is already being used in a legal context. It was noted that there is no recognition of all of the data and are looking for something constructive that can be pulled out of the report to assist forensic DNA laboratories to which Dr. Butler explained that they are trying to address that issue in Box 4.1. When asked what is to be gained by putting that additional information out there and if there is some metric that can be used, Dr. Butler added that allele sharing needs to be studied more. In response to an inquiry if they had reached out to labs and asked to look at their data, Dr. Butler stated that they did but were told no, that he could FOIA it. There was further discussion that the review of the data at a laboratory would not be sufficient since this foundational review suggests that it must be publicly available. It was further questioned why they could not visit the laboratories to review the data as auditors review this data during their audits without requiring it to be publicly available. Dr. Butler referred the attendees to line 2404 of the report. The comment was made that the laboratories thought this was accomplished with the validation summaries.

There were additional inquiries that there is no independent body to review this information and no specific standard to meet and Dr. Butler responded that was not accurate as how you share the information with someone else is their perspective. The question was posed if all labs release their data, will it be looked at and Dr. Butler said that it would not. In response to whether it is the intent that this report is not used as a weapon, Dr. Butler referred to page 1.

There were additional questions relating to the independent review panel and Dr. Butler noted that they are not saying that you need to have a panel. In questioning the point of a foundational review and to define thresholds, it was asked how could we have satisfied this process to which Dr. Butler referred to Pete's study and Box 4.1.

On behalf of SWGDAM, the Vice Chair, Russell Vossbrink, thanked Dr. Butler for presenting their report and engaging in the discussion.

Thursday, July 15, 2021

Tracey Johnson and Lucas Zarwell with the Office of Investigative and Forensic Sciences with the National Institute of Justice (NIJ) presented an update on NIJ activities. Ms. Johnson joined NIJ in January and shared her observations with the attendees: forensic biology is undergoing expansion toward alternative markers and/or new technology; phenotypic methods that avoid the need for comparisons to large databases; methods that prevent the need for mixture interpretation; development and evaluation of tools that assist with analysis and interpretation; more robust foundational understanding; shift towards the analysis of proteins or DNA modification; R&D plans that recognize the need for efficiency and scalability; and examination of non-human DNA. She also provided an update on the Forensic Science Public Labs Program (solicitation closed on June 10, 2021), the Forensic Science R&D Program (which also closed on June 10, 2021), the Forensic Technology Center of Excellence (FTCoE), and requested support for DNAmix 2021. Office Director Lucas Zarwell updated attendees on the NamUs program with award of the contract to RTI in April and NIJ focusing resources to eliminate the backlog of MU casework. He expects that NamUs will be taking submissions in September.

TECHNICAL REVIEW SESSION

Document review of the draft SWGDAM Validation Guidelines for the Use of an Expert System with Forensic Samples by Amy McGuckian, Chair of the Forensic DNA Casework Expert System Working Group. Ms. McGuckian noted that the Working Group provided an update to the CODIS State Administrators at their May meeting and will continue to meet to adjudicate the technical review comments received from SWGDAM members and invited guests. Ms. McGuckian reviewed a number of the comments that they have addressed in the draft relating to clarifying internal validation, interpretation software and additional terminology. There was also a discussion of the terms should and shall and the most appropriate term for use in a guidance document.

Brandon Letts reviewed additional revisions to the draft SWGDAM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories and the

Supplemental Information (FAQ) document that were raised during Tuesday's discussion. Wording was suggested to include that the YHRD is frequently changed so the version used should be saved. The following additional language was also recommended for inclusion in SWGDAM guidance documents: "absent any other directive, the use of the term 'shall' or 'must' is not intended to transform these guidelines into standards."

Lisa Schiermeier-Wood, Chair of the Laboratory Operations Committee reviewed the draft SWGDAM Validation Guidelines for DNA Analysis Methods: Overview Document and the draft Modified Rapid DNA Internal Validation Guidance Module for Single Source Samples. Ms. Schiermeier-Wood explained that the plan is to release the Overview Validation document first and link the module-specific documents to the Overview document. Glossary definitions will be left to the Quality Assurance Standards and not repeated in these documents. There was an inquiry about leaving in the NGS-specific information until the NGS module is issued and Ms. Schiermeier-Wood responded that she will raise that issue with the Committee for discussion. Lilly Moreno described the draft Modified Rapid DNA Module revisions. Ms. Schiermeier-Wood also provided a Committee Update on their progress and future documents (quant and Y STR).

UPDATE SESSION

Carl Soberalski presented an update on the Organization of Scientific Area Committees (OSAC). He noted that the documents now have a more streamlined process for review and he identified the documents currently out for comment. He noted that the two DNA-related Committees - the Human Forensic and Wildlife Forensic Biology - work closely with their subcommittees and task groups in identifying needed standards and developing those standards. He also reviewed the standards currently proceeding through the Registry process. There was an inquiry concerning implementation and compliance and it was noted that a task group is evaluating the use of an audit checklist.

Dawn Herkenham provided a Legislative Update. She reviewed pending Federal legislation with potential impact and/or funding for the forensic DNA community. Ms. Herkenham also reviewed 2021 pending and passed legislation related to forensic genetic genealogy and genetic information as well as other DNA-related legislation. She reviewed recent DNA cases (confrontation clause, novel DNA testing) and probabilistic genotyping admissibility decisions.

Peter Vallone with the National Institute of Standards and Technology (NIST) provided an update on the following NIST activities: SRM 2391d; CE concordance studies; Y SNP Typing Interlaboratory Study; support for Genetically Variant Peptides (GVPs); recent manuscript examining discriminating performance and likelihood ratios using STRmix

2.6 and EurForMix 2.10; and their Sequencing projects. Dr. Vallone also described that they have several papers in development, as well as updates on the activities of the NIJ/NIST Expert Working Group on Human Factors and the Scientific Foundation Review on DNA Mixtures. He noted that there is a request for participation in DNAmix 2021 (being run by Noblis and Bode as part of a 4-phase study).

The SWGDAM Chair provided his report which included the following: correction to a subpopulation formula in the Autosomal STR Interpretation Guidelines (available at www.swgdam.org); a new Databasing emphasis convened within the CODIS Committee to share information related to the high-throughput processing of DNA reference samples; a new Committee of Correspondence on Missing Person Casework, chaired by Ann Gross; and QAS coordination activities for which he encouraged the submission of suggestions.

The Chair noted that the January 2022 Technical Session may include education issues and include a FEPAC presentation, a forensic science degree program, a presentation by the DNA Efficiency Training Group on training and hiring; and possibly a panel discussion.

The Chair kicked off the SWGDAM Bylaws Review. They were last updated in 2014 and he will provide a copy of the 2014 Bylaws in addition to the proposed revisions for discussion at the January 2022 SWGDAM meeting. The proposed revisions cover acknowledgment of the ad hoc groups, expediting work products, foregoing public comment for non-guidelines/standards documents, as appropriate, and membership, with a focus on maintaining forensic DNA practitioners.

The Chair noted that the consensus of the membership and invited guests are to provide comments on the NIST Scientific Foundation Review on Mixtures. Comments may be provided to SWGDAM to submit as a body and members/invited guests are also welcome to submit individual comments.

The next SWGDAM meeting will be January 11-13, 2022.

III. Attendees:

Please see Attachment 2.

IV. Next Meeting:

The next meeting will be held January 11-13, 2022.



SCIENTIFIC WORKING GROUP

DNA ANALYSIS METHODS

SWGDM VIRTUAL REGULAR MEETING

July 13 - 15, 2021

AGENDA

Monday, July 12, 2021

SPECIAL COMMITTEE AND WORKING GROUP MEETINGS

Scheduling at Committee and Working Group Discretion

Tuesday, July 13, 2021

1:00 PM – 6:00 PM

TECHNICAL SESSION: QUANTITATIVE Y-STR GENETICS

YSTR Survey Results – Brandon Letts
Reporting Forensic Y Haplotype Statistics – Steven Myers
Y Haplotype Math– Sasha Willuweit
YHRD Update – Lutz Roewer
ISFG/EMPOP – Walther Parson
Applications of Probabilistic Genotyping – Michael Coble

PARTNER AGENCY UPDATE SESSION

Bureau of Justice Assistance

COMMITTEE OF THE WHOLE SESSION

Review of the proposed revisions to the *SWGDM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories* and new *YSTR Supplemental Information (FAQs)* – Lineage Marker Committee



SCIENTIFIC WORKING GROUP

DNA ANALYSIS METHODS

Wednesday, July 14, 2021

COMMITTEE AND WORKING GROUP BREAKOUT SESSION

Scheduling at Committee and Working Group Discretion

3:00 PM – 6:00 PM

COMMITTEE/WORKING GROUP UPDATE SESSION

ROUND TABLE SESSION

Thursday, July 15, 2021

1:00 PM – 6:00 PM

PARTNER AGENCY UPDATE SESSION

National Institute of Justice

COMMITTEE OF THE WHOLE SESSION

Review of the new proposed *SWGDM Validation Guidelines for the Use of an Expert System with Forensic Samples* – Forensic DNA Casework Expert System Working Group

Review of the proposed revisions to the *SWGDM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories* and new *YSTR Supplemental Information (FAQs)* – Lineage Marker Committee

Review of the proposed revisions to the *SWGDM Validation Guidelines for DNA Analysis Methods* and new *Modified Rapid DNA Internal Validation Guidance Module for Single Source Samples* – Laboratory Operations Committee

PARTNER AGENCY UPDATE SESSION

Biology SAC

Legislative Update

National Institute of Standards and Technology

COMMITTEE OF THE WHOLE SESSION

Kick-off of 2014 SWGDM Bylaw Review & ADJOURNMENT

Chair Anthony J. Onorato | ajonorato@fbi.gov | SWGDM.org

Attachment 2 - Attendees

**SWGDM July 2021 Meeting
July 13-15, 2021
Attendees**

SWGDM Chair
Anthony Onorato

SWGDM Vice Chair
Russell Vossbrink

SWGDM Executive Secretary
Dawn Herkenham

SWGDM Attendees

Chris Askew
Jack Ballantyne
Suzanne Barritt-Ross
Tiffany Bazazzadegan
Todd Bille
Thomas Callaghan
Jocelyn Carlson
Chris Carney
Amber Carr
Dorothy Catella
Michael Coble
Jerrilyn Conway
James Corcoran
Jennifer Coursey
Brenda Danosky
Neil Fernandopulle
Connie Fisher
Russell Gettig
Ann Marie Gross
Lisa Grossweiler
Jessica Hanna
Douglas Hares
Brian Harmon
Bruce Heidebrecht
Joseph Hof
Bill Hudlow
Deedra Hughes
Ted Hunt

Jodi Irwin
Jessica James
Elizabeth Johnson
Tracey Johnson
Kristy Kadash
Marla Kaplan
Susannah Kehl
Debbie Kennedy
Ben Knoch
Jason Kokoszka
Brandon Letts
George Li
Eugene Lien
Lauren Lu
Beth Ann Marne
Justin Maxwell
Barbara McCarty
Amy McGuckian
Scott McWilliams
Gary Molina
Shawn Montpetit
Lilly Moreno
Tamyra Moretti
Steven Myers
Vanessa Nelson
Mary Lou Nicholson
Jeff Nye
Darrel Oubre
Heather Parrish
Walther Parson
Evelyn Ridgley
Lutz Roewer
Juliet Rolando
Erica Romsos
Lisa Schiermeier-Wood
Alyssandra Shaffer
Phillip Simmers
Rhalie Simmons
Christie Smith
Mark Smith
Carl Sobieralski
Melissa Suddeth

SWGDM July 2021 Report

Joel Sutton
Tiffany Thoren
Peter Vallone
Jeanette Wallin
Susan Welti
Ray Wickenheiser
Sascha Willuweit
Richard Wilson
Tiffany Vasquez

*Please note that attendance above is for
7/13/2021 only.