Scientific Analysis on DNA Analysis Methods (SWGDAM) July 2013 Report

July 16-18, 2013

Federal Training Center in Dumfries, Virginia

I. **Agenda:**

Please see Attachment A.

II. **Meeting Synopsis:**

Tuesday, July 16, 2013
SWGDAM Chairman, Anthony Onorato, welcomed the attendees who introduced themselves. The Chair reviewed the agenda for the July 2013 meeting. In introducing the morning presentations, the Chair explained that the technical session would be devoted to a background on familial searching to include general and mathematical considerations as well as states and international experiences in familial searching culminating in a presentation and discussion on the recommendations of the Ad Hoc Working Group on Familial Searching.

 Ms. Dawn Herkenham provided a background on partial matches and familial searching beginning with the SWGDAM Ad Hoc Working Group on Partial Matches. With the approval of SWGDAM, this Group provided recommendations to the FBI Director on scientific recommendations for the FBI's Interim plan for the release of information in the event of a partial match at NDIS (available at http://www.fbi.gov/about-us/lab/forensic-science-communications/fsc/oct2009/standard_guidlines/swgdam.html). Ms. Herkenham reviewed state and federal legislative proposals to authorize familial searching as well as state laws prohibiting the use of familial searching. The FBI issued its Final Plan for the Release of Personally Identifiable Information in 2012 (Appendix G available at http://static.fbi.gov/docs/NDIS-Procedures-Manual-Final-1-31-2013-1.pdf). The FBI's CODIS Unit requested that SWGDAM provide scientific recommendations on familial searching relating to methodology, ranked lists and database size.

Dr. Douglas Hares followed with a presentation on database search strategies explaining how the national database is currently searched. Dr. Hares described how partial matches occur and how they differ from familial searching in that a partial match " is NOT an exact match of two profiles customarily used to infer the identity of the perpetrator; in a 'partial match' situation, a potential familial relationship may exist between the offender

and putative perpetrator; as the size of the database grows – the number of partial matches increases; and that the probability is low that a 'partial match' is due to a familial relationship." Familial searching, on the other hand, is a separate search of the database using specially designed software after the routine search of the database did not produce any candidate matches. Dr. Hares explained that the CODIS Unit is researching ways to improve searching of large databases to reduce the number of false candidate matches generated with moderate stringency searching; part of this project includes the separation of forensic unknowns (13 core loci single source), forensic mixtures and forensic partials.

Mr. Gary Sims explained general considerations for familial searching. Various approaches to familial searching include: looking for rare allele(s) running within a family; counting shared alleles (IBS); and use of likelihood ratio-based (LR) kinship analysis. Mr. Sims summarized the pros and cons of familial searching in noting that the goal is to strike an effective balance between privacy concerns and the need to provide information that may solve a violent crime or series of crimes. In finding the balance, Mr. Sims suggested that familial searching only be used in major violent crimes where there is a serious risk to public safety and all other investigative leads have been exhausted. For the genetic testing, the goal is to use procedures that are designed to detect a true relative but at the same time minimize the number of false relatives. As an example, Mr. Sims explained that in California, familial searching is only performed if the forensic unknown (crime scene) DNA profile is a single-source complete profile. Additionally, prior to the release of the name of the potentially related offender to the law enforcement agency, there should be a review of non-genetic information (metadata) bearing on relatedness; this non-invasive investigation may rely on public databases, law enforcement databases, vital records, etc., and may include geographic information. In California, there is a Familial Search Committee that reviews all of the information to determine if a name can be released to the submitting law enforcement agency. Mr. Sims stated that the fundamental limitation in familial searching is that a relative must be in the database in order to get a true familial hit. Among the additional challenges in familial searching, Mr. Sims noted that the larger the size of the database, the more difficult it becomes to find the relative, since there is a higher likelihood that more random sharing of alleles will occur and be detected in a larger pool.

Mr. Steven Myers explained that familial searching involves answering the question: "Are there relatives of person X found within database Y?" Use of the Likelihood Ratio (LR) allows the comparison of two probabilities: (1) How likely is it to see DNA profiles like these when the people are related; and (2) How likely is it to see DNA profiles like these when the people are unrelated. So, if option 1 is more likely than option 2, this LR provides support to the hypothesis that they are related. Mr. Myers explained how the

LR numerator relates to the first hypothesis and the LR denominator to the second. Mr. Myers described the California study and the study performed for the SWGDAM Familial Searching Group. Mr. Myers concluded with suggestions on what can be done to improve the ability to answer the question: type more loci or additional methodologies/technologies and/or use metadata (e.g., geography). A caution when using more loci because that means that there are also more chances for mutations and other genetic anomalies and there is a greater chance of the need to account for linkage disequilibrium between loci on the same arm of a chromosome.

Mr. Scott McWilliams, Mr. Brad Jenkins and Mr. Gary Sims discussed the experiences of Wyoming, Virginia and California, respectively, in familial searching. Mr. McWilliams noted that Wyoming uses in-house developed software and the Denver software to perform familial searching. Mr. McWilliams recommended that investigators have a concise goal and that there should be familial search association dispositioning on searches. Mr. Brad Jenkins noted that the following criteria are used in determining whether to accept a case for familial searching in Virginia: violent crime against a person; all investigative leads have been exhausted and critical public safety concerns remain; forensic unknown is a single-source complete or nearly complete DNA profile; the agency agrees to further investigation if potentially related individuals are identified; and additional sample remains for Y-STR's. Mr. Gary Sims reported that California had performed 61 familial searches as of July 2013 with most of these murder or sexual assault cases. Mr. Sims described the four cases in which familial searching was performed and the investigative lead information resulted in an arrest.

Mr Arnoud Kal from the Netherland Forensic Institute explained that legislation was passed in April 2012 to authorize kinship analysis in criminal cases. For passive kinship analysis, the DNA expert notes that two DNA profiles do not match but have a high degree of similarity and a statistical evaluation is performed. If the LR exceeds 100, the finding is reported to the prosecutor and reference material of family members is requested so additional analyses may be performed to confirm kinship. For the familial searching of the database; there are four stages: (1) pre-assessment; (2) familial search with Bonaparte software – longlist; (3) upgrades of database DNA-profiles – shortlist; and (4) communication of the shortlist to the prosecution.

Mr. Michael Chamberlain described legal issues and implications of familial searching. Mr. Chamberlain reviewed the potential 4th Amendment issues relating to the database search, the government conduct, the expectation of privacy, with respect to California, 9th Circuit and U.S. Supreme Court precedents. Mr. Chamberlin also discusssed report wording for the familial search results as well as obtaining a DNA sample for confirmatory analysis. Mr. Chamberlin discussed the 4th Amendment implications for

offenders and their relatives. The legal authorization for familial searching was reviewed (statutes, regulations, policy documents) as well as the necessity for such authorization. Mr. Chamberlin recounted the California successes with familial searching and offered the following suggestions: (1) err on the side of fewer leads, but higher quality; (2) before disclosure of lead(s), take all reasonable measures, consistent with implicated privacy interests, to confirm or dispel kinship hypothesis; (3) make familial searching the exception, not the rule; and (4) structure program to minimize intrusion into lives and relationships of family members, including database offenders.

Mr. Gary Sims and Mr. Steven Myers presented the draft recommendations of the SWGDAM Ad Hoc Working Group on Familial Searching and the study results, respectively. In gathering data to respond to the questions posed by the CODIS Unit, Mr. Sims described the three-part study that included familial searches of actual offender databases, as well as simulated searches of modeled databases. The study followed the assumptions provided to the Ad Hoc Working Group (13 CODIS core loci, single source, no Y-STR or additional genetic data). The study was designed to: (1) perform tests using actual databases to look for practical deviations from the models; (2) the tests described in #1 were replicated using the same set of 200 artificial evidence profiles searched against simulated 2.13 million person offender databases; and (3) tests were replicated using simulated 10 million person offender databases to more directly test searches of NDIS-size databases. Mr. Sims presented the recommendations to the questions as follows:

Is kinship matching (producing a ranked list of candidates based upon kinship statistics) more efficient at detecting relatives than counting the number of alleles shared? The Working Group determined that because the kinship LR approach takes into account the allele frequencies as well as the number of alleles that match, it is more effective in identifying the true relative than counting the number of shared alleles.

If the number of false positives generated prior to finding a true match is inversely related to the likelihood of sibship, does this suggest that many true siblings would not be found in large databases? If so, is there an optimal database size range for performing familial searching?

Can we establish the number of ranked candidates (kinship matching) that would require investigation in order to ascertain a "true" relative when searching a database with over 10 million DNA profiles? If so, what is that number? The Working Group observed that the familial searches for the study were performed with a relative present in the database and therefore those results represented the most positive outcome for such searches. Additionally, the Group cautioned that, unlike the Working

Group's studies which deliberately placed one or more relatives in the database, a real-life perpetrator may **not** have a relative in the actual SDIS or NDIS databases. If the percentages reported by the U.S. Bureau of Justice Statistics for inmates are representative of current offender databases, there will be a close (first order) relative in the database approximately half of the time. The Working Group's study results demonstrated that the size of the database searched has an impact on the rankings. For example, Wyoming, with the smallest number of unique profiles in this study (19,300), was able to identify the full sibling in the #1 ranked position approximately 56.8% of the time while California, having the largest number of unique profiles (1,780,000) was able to identify the full sibling in the #1 ranked position approximately 22.8% of the time. As a practical matter, since the true relative is not always ranked as the #1 candidate in familial searches, especially as the size of the database being searched increases, the Working Group noted that ranked lists of offenders would have to be reviewed. To the extent that additional filters (analysis of additional STRs/Y-STRs or review of metadata) or thresholds are available, these lists can be further distilled to reduce the number of false positives. Accordingly, at NDIS with an offender database well over 10 million DNA records and without the additional filters of metadata and geography, it would be difficult to establish a reasonable threshold for the review of ranked lists.

The SWGDAM Executive Board met Tuesday evening.

Wednesday, July 17, 2013

The following Committee meetings were held during the day:
Autosomal STR Committee
CODIS Committee
Enhanced Detection Methods and Interpretation Committee
Missing Person and Mass Disaster Committee
MtDNA Committee
Quality Assurance Committee
Rapid DNA Committee
Y-STR Committee
Ad Hoc Working Group on Familial Searching

A round table discussion was held Wednesday evening that included the following issues: DNA transfer between two unrelated cases; reporting matches, statistics and experts; sample consumption when working with touch DNA cases; confrontation clause issues when the DNA analyst is no longer available for testimony; safeguarding the employee's

DNA record under GINA; and the use of expert systems for single source evidence samples.

Thursday, January 17, 2013

The Committees continued their individual meetings until noon on Thursday.

The Chair opened the Thursday session with Committee Updates. During the MtDNA Committee Update, Mr. Pokorak reviewed revisions to the DRAFT Guidelines document that was distributed to the membership and invited guests for the technical review. A motion was made to approve the Guidelines as revised and the document was approved (with one abstention).

At the conclusion of the Committee Updates, the session resumed with a legislative update from Ms. Herkenham. Ms. Herkenham provided a brief review of State arrestee provisions to include the newest addition: Nevada. Nevada enacted arrestee legislation in May 2013 and it requires probable cause (in the form of a warrant or a probable cause hearing) before submission of the DNA sample from the felony arrestee for analysis. With the addition of Nevada, 29 states, the Federal government, the Department of Defense and Puerto Rico have enacted laws to authorize the collection of DNA samples from certain categories of arrestees. The sunset provision for Maryland's arrestee provision (set to expire in December 2013) was repealed. Additionally, Ms. Herkenham updated attendees on Federal legislation, such as the Katie Sepich Enhanced DNA Collection Act (effective January 2013) and the Sexual Assault Forensic Evidence Reporting (SAFER) Act of 2013. Ms. Herkenham also reviewed sexual assault evidence processing and reporting legislation enacted in Colorado, Illinois and Texas.

Dr. Douglas Hares provided an update on the progress of the CODIS Core Loci Working Group. Dr. Hares presented updated NDIS statistics, noting that there have been over 204,000 investigations aided by CODIS as of June 2013. Dr. Hares mentioned that the NDIS Operational Procedures Manual is available on the FBI's Internet site at www.fbi.gov/about-us/lab/biometric-analysis/codis. Dr. Hares explained that the core loci database validation began in December 2012. The casework validation is expected to begin in July 2013. Once all the data is compiled and reviewed, the selection of new core is anticipated for early 2014 with implementation of the additional core loci expected to occur 24 months after selection. Dr. Hares acknowledged the efforts of the National Institute of Standards and Technology (NIST) in performing data analysis of the

database validation studies completed thus far and reviewed some examples from that data.

Dr. Thomas Callaghan provided an introduction to Next Generation Sequencing. Dr. Callaghan explained the Sänger method of sequencing. Next Generation Sequencing is designed to sequence millions of molecules; on multiple, non-identical templates; use special chemistry – platform specific; and include bioinformatics. Dr. Callaghan reviewed the chemistry and technology used in Next Generation Sequencing specific to several instruments. In determining whether Next Generation Sequencing (NGS) is suitable for human identification, Dr. Callaghan raised the following questions: (1) Can NGS technology increase sensitivity of analysis on limited and/or degraded samples (crime scene application)? (2) Can NGS produce mtDNA and STR data that matches today's quality and reliability?; and (3) When the person of interest is not in the DNA database, can we take advantage of advances in genetic analysis to provide investigative leads on the person of interest?

The Chair introduced Dr. John Butler and Dr. Peter Vallone to provide an update on NIST activities. Dr. Butler updated the participants on his new position at NIST as Special Assistant to the Director for Forensic Science; a position within the Office of Special Programs. Dr. Butler explained that NIST and DOJ announced plans in February 2013 to establish a National Commission on Forensic Science, as recommended in the National Academy of Sciences Report entitled " Strengthening Forensic Science in the United States: A Path Forward." It is expected that the National Commission will have its first meeting in Fall of 2013. Dr. Butler noted that the Biological Evidence Preservation Handbook and Forensic Science Laboratory Facilities Handbook are now available. Additionally, a DNA Technical Leaders Summit is being planned in conjunction with the Annual CODIS Conference (subject to funding approval).

Dr. Peter Vallone provided an update on the following items: NIST SRM 2372 was returned to sale in January, 2013 with the next generation SRM being certified for copy/target number; NIST continues to test Rapid DNA instruments and provide feedback to vendors; planning of an interlaboratory mixture study to assess how laboratories are applying the SWGDAM recommendations; working on an agreement to test a new 27 Y-STR multiplex kit; pilot study for SRMs for next-generation sequencing; working with the FBI on a consortium validation project to determine how well new loci perform in the new multiplex kits; sequencing of variant alleles (sequencing of SRM 2391c to further characterize and determine interesting genomic characteristics within STR fragments in support of Next Generation Sequencing); completion of mass spectrometry work; and assessing DNA extraction efficiency.

III. **<u>Attendees:</u>**

Please see Attachment B.

IV. **<u>Next Meeting:</u>**

The next meeting will be held January 14-16, 2014.

SWGDAM REGULAR MEETING

July 16 - 18, 2013

AGENDA

Tuesday, July 16, 2013

7:00 AM	Chair and Vice Chair Meeting
8:00 AM	Welcome and Business Matters

TECHNICAL SESSION: FAMIAL SEARCHING

8:15 AM	SWGDAM History of Partial Matches and Familial Searching – Dawn Herkenham
9:00 AM	Database Searching Strategies and Return Assessment – Doug Hares
9:45 AM	BREAK
10:00 AM	General Familial Searching Considerations – Gary Sims
10:45 AM	Mathematical Familial Searching Considerations – Steven Myers
11:30 AM	Practical Familial Searching Experiences: Wyoming – Scott McWilliams
12:15 PM	LUNCH
1:15 PM	Practical Familial Searching Experiences: Virginia and California – Brad Jenkins and Gary Sims
2:00 PM	Practical Familial Searching Experiences: The Netherlands – Arnoud Kal
3:00 PM	BREAK
3:15 PM	Legal History of Familial Searching in California – Michael Chamberlain Committee of the Whole Session:

4:15 PM   Review of the Familial Searching Working Group's Document – FSWG

5:30 PM   ADJOURNMENT

7:00 PM   Executive Board Meeting

Wednesday, July 17, 2013

8:00 AM   Committee Sessions

Autosomal STR – John Butler

CODIS – Doug Hares

Enhanced Detection Methods – Eugene Lien

mtDNA – Cathy Knutson

Missing Persons/Mass Disaster – John Tonkyn

QA – Jodi Dahl

Rapid DNA – Jennifer Wendel

Y-STR – Tamyra Moretti

ROUND TABLE SESSION

6:00 PM   TBD - Moderator: Russell Vossbrink

Thursday, July 18, 2013

8:30 AM   Committee Sessions

12:00 PM   LUNCH

1:00 PM   Committee Session Updates

Autosomal STR – John Butler

CODIS – Douglas Hares

Enhanced Detection Methods – Eugene Lien

Mass Spectrometry/mtDNAU – Cathy Knutson

Missing Person/Mass Disaster – John Tonkyn

Quality Assurance – Jodi Dahl

Rapid DNA – Jennifer Wendel

Y-STR – Tamyra Moretti

UPDATE SESSION

1:30 PM   Legislative Update – Dawn Herkenham

2:30 PM   CODIS Core Loci Expansion Update – Douglas Hares

3:00 PM   BREAK

3:15 PM   Rapid DNA/Next Generation Sequencing Update – Thomas Callaghan

3:45 PM   NIST Update – John Butler/Peter Vallone

CLOSING BUSINESS SESSION

4:15 PM   Chair Report – Tony Onorato

5:00 PM   ADJOURNMENT

SWGDAM July 2013 Meeting
Members and Invited Guests (IG)
Attendance

<u>SWGDAM Chair</u>

Anthony Onorato
FBI Laboratory

<u>SWGDAM Vice Chair</u>

Russell Vossbrink
Scottsdale Police Department

<u>SWGDAM Executive Board</u>

Eric Pokorak
FBI Laboratory

Margaret (Peg) Schwartz
Vermont Forensic Laboratory

Taylor Scott
Illinois State Police

Gary Sims
California Department of Justice

Dawn Herkenham (IG)
SAIC

<u>SWGDAM Members & Invited Guests</u>

Jack Ballantyne (IG)
University of Central Florida

Todd Bille (IG)
Bureau of Alcohol, Tobacco and Firearms

John Butler (IG)
National Institute of Standards and
Technology

Amber Carr (IG)
FBI Laboratory

Chris Carney (IG)
FDLE – DNA Database

Michael Chamberlain (IG)
California Department of Justice

Ranajit Chakraborty (IG)
University of North Texas Health Science
Center

Jerrilyn Conway (IG)
FBI Laboratory

James Corcoran (IG)
FBI Laboratory

Rhonda Craig (IG)
FBI Laboratory

Jodi Dahl (IG)
FBI Laboratory

Tina Delgado (IG)
FBI Laboratory

Neil Fernandopulle (IG)
Centre of Forensic Sciences

Connie Fisher (IG)
FBI Laboratory

Russell Gettig (IG)
NY State Police Forensic Investigation
Center

Ann Marie Gross
MN Bureau of Criminal Apprehension

Richard Guerrieri
FBI Laboratory

Douglas Hares (IG)
FBI Laboratory

Bruce Heidebrecht
Maryland State Police

Brian Hoey
Missouri State Highway Patrol

Deedra Hughes
Mississippi Crime Laboratory

Clark Jaw (IG)
FBI Laboratory

Brad Jenkins (IG)
Virginia Department of Forensic Science

Elizabeth Johnson (IG)
U.S. Army Crime Lab

Catherine Knutson (IG)
MN Bureau of Criminal Apprehension

Ken Konzak
California Department of Justice

Sylvain Lalonde (IG)
Royal Canadian Mounted Police

George Li
Virginia Department of Forensic Science

Eugene Lien
NYC Office of the Chief Medical Examiner

Beth Ann Marne
Pennsylvania State Police

Cathy McCord
Texas Department of Public Safety

Amy McGuckian
Palm Beach County Sheriff's Office

Scott McWilliams (IG)
Wyoming State Crime Laboratory

Jeff Modler (IG)
RCMP Forensic Science & Identification
Services

Gary Molina (IG)
Texas Department of Public Safety Crime
Laboratory

Tamyra Moretti (IG)
FBI Laboratory

Steven Myers
California Department of Justice

Nicole Nicklow (IG)
FBI Laboratory

Jeffrey Nye (IG)
Michigan State Police

Dixie Peters (IG)
University of North Texas Health Science
Center

John Planz
University of North Texas Health Science
Center

Juliet Rolando (IG)
FBI Laboratory

Joel Sutton (IG)
USA CIL

John Tonkyn
California Department of Justice

Peter Vallone (IG)
National Institute of Standards and
Technology

Stacy Warnecke (IG)
Kentucky State Police

Jennifer Wendel
FBI Laboratory

Ray Wickenheiser (IG)
Montgomery County Police Crime
Laboratory

Tim Zolandz (IG)
FBI Laboratory