OSAC RESEARCH NEEDS ASSESSMENT FORM

Title of research need: Methods in Forensic Genealogy

Describe the need: Forensic Genealogy is the combination of genetic DNA analyses with traditional record-based family tree genealogy. A familial genetic connection is generated from a crime scene sample with individual(s) from a database of genetic records that are then tied via records from births, deaths, marriages etc., with the intention of intelligence identification. Close family relationships may be inferred from STR data using familial searching of STR databases, depending on the country/states legislation, however more distant relationships can be found using SNP data generated using multiple methods (SNP array genotyping or sequencing) and searching non CODIS databases such as GEDmatch. A more thorough comparison of both STR and SNP approaches, including standards on how the data is generated, order of operations, calculation of error due to decreased sample quality, mixtures, loss of SNPs etc. to name a few, should be explored. The development of standards and training material, including training programs is needed as there are several aspects to this field. These trainings can be broken down into 1. SNP data generation standards and approaches like those used in STR DNA profiling. 2. Statistical approaches to infer a potential familial match (e.g., LR or IBS/IBD measures), including court-ready reporting statistics in the absence of STR data should be explored. 3. Standards and approaches in the genealogy portion of this field and the generation of non-genetic family trees, including order of operations/rules on how to prove identity (given multiple family trees are generated) from intelligence information.

Keyword(s): SNPs, STRs, Massive Parallel Sequencing, SNP array, Genotyping

Submitting subcommittee(s): Human Biology **Date Approved:** 10/05/2021

(If SAC review identifies additional subcommittees, add them to the box above.)

Background Information:

1. Does this research need address a gap(s) in a current or planned standard? (ex.: Field identification system for on scene opioid detection and confirmation)

Yes, in the use of Forensic Genealogy for casework.

2. Are you aware of any ongoing research that may address this research need that has not yet been published (e.g., research presented in conference proceedings, studies that you or a colleague have participated in but have yet to be published)?

Yes , but not enough in detail.

3. Key bibliographic references relating to this research need:

1) Kling D, Phillips C, Kennett D, Tillmar A. Investigative genetic genealogy: Current methods, knowledge and practice. *Forensic Sci Int Genet*. 2021;52:103474.
2) Tillmar A, Fagerholm S.A, Staaf J, Sjölund P, Ansell R. Getting the conclusive lead with investigative genetic genealogy – A successful case study of a 16 year old double murder in Sweden. *Forensic Sci Int Genet.* 2021;53:102525.
3) Galván-Femenía, I., Barceló-Vidal, C., Sumoy, L. *et al.* A likelihood ratio approach for identifying three-quarter siblings in genetic databases. *Heredity.* 2021;126, 537–547.
4) Kling D, Tillmar A. Forensic genealogy—A comparison of methods to infer distant relationships based on dense SNP data. *Forensic Sci Int Genet.* 2019;42:113-124.
5) Thomson J, Clayton T, Cleary J, Gleeson M, Kennett D, Leonard M, Rutherford D. An empirical investigation into the effectiveness of genetic genealogy to identify individuals in the UK. Forensic Sci Int Genet. 2020;46:102263.

4. Review the annual operational/research needs published by the National Institute of Justice (NIJ) at https://nij.ojp.gov/topics/articles/forensic-science-research-and-development-technology-working-group-operational#latest? Is your research need identified by NIJ?

Yes, "Development of genetic genealogy testing procedures for use by the crime labs".

5. In what ways would the research results improve current laboratory capabilities?

The whole field needs standardization and rules that are transparent and can be shared internationally.

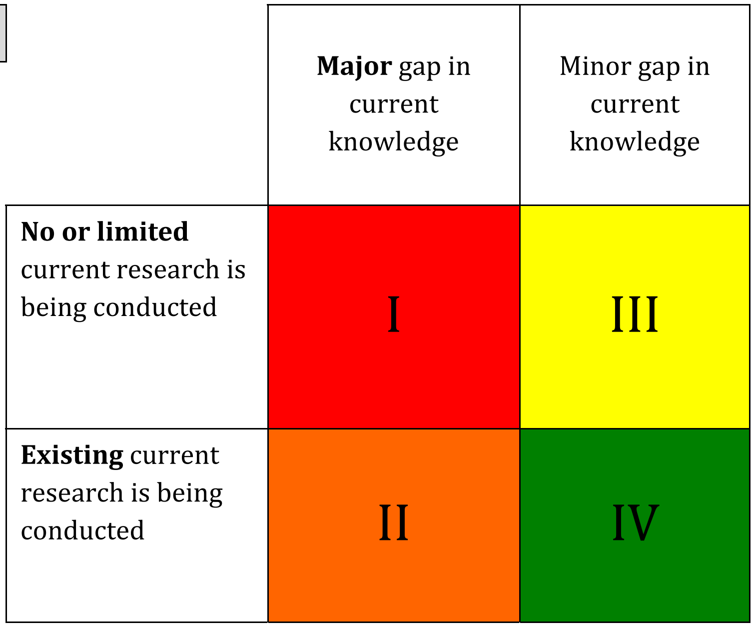
6. In what ways would the research results improve understanding of the scientific basis for the subcommittee(s)?

Better exploration of the caveats of bad samples/data and minimum requirements for accurate identification using FGG on all populations (not just Europeans for which many of the SNP databases available only consist).

7. In what ways would the research results improve services to the criminal justice system?

It will provide standards and rules for future implementation of FGG in all forensic capable laboratories that is akin to accepted STR profiling protocols.

8. Status assessment (I, II, III, or IV): II



	Major gap in current knowledge	Minor gap in current knowledge
No or limited current research is being conducted	I	III
Existing current research is being conducted	II	IV

This research need has been identified by one or more subcommittees of OSAC and is being provided as an informational resource to the community.