OSAC Research Needs Assessment Form

Title of research need: Assessment of specific classes of evidence types to determine the necessity to quantify DNA before amplification of human autosomal STR loci

Keywords: DNA quantitation, trace DNA, direct PCR,

Submitting subcommittee(s): BDRIC **Date Approved:** 8/25/16

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

Background information:

1. Description of research need:

The current quality assurance standard (QAS) for forensic testing laboratories requires that human DNA quantitation is attempted for all forensic unknowns. This requirement poses a problem for evidence types expected to yield low amounts of DNA such as DNA swabs from cartridge casings, other touched objects, or single fingermarks. It has been shown that direct PCR amplification without prior DNA extraction can improve the DNA typing success rate, for example for touched fabric and fired cartridge cases. In the example of fired cartridge cases, rarely, if ever, will greater than 1ng of DNA be recovered. However, due to the QAS requirements, an extraction is performed solely to be able to perform the quantitation step prior. At this point, the entire extract typically will be concentrated and the entire volume used during the amplification. Unfortunately, it has been demonstrated numerous times that a significant portion of DNA is lost during DNA extraction and concentration. If there is no value to performing the extraction and quantitation, it would seem logical to avoid steps that waste DNA, and increase the handling of a sample which increases the risk of contamination/laboratory error. Furthermore, the quantitation results obtained for DNA from these types of samples are often not predictive of the quality of the profile generated after amplification. If a sample is subjected to DNA extraction, it can also be advantageous to not consume additional extract for the mandatory quantitation step. It should be possible to establish categories of biological evidence where the DNA yield is expected to be within a certain range and robust STR amplification results can be obtained without quantitation data.

Since there is a wide body of literature regarding direct PCR and/or the correlation between evidence type and amplification success, we emphasize that this research may take the form of a literature survey that compiles existing data and defines the desired categories based on combined findings from independent studies.

2. Key bibliographic references relating to this research need:

Garvin, AM and Fritsch A. (2013), Purifying and Concentrating Genomic DNA from Mock Forensic Samples Using Millipore Amicon Filters. J Forensic Sci, 58: S173–S175.
Holland M, Wendt F. (2015) Evaluation of the RapidHITTM 200, an automated human identification system for STR analysis of single source samples. Forensic Sci Int Genet 14:76–85.
Lee SB, McCord B, Buel E (2014) Advances in forensic DNA quantification: a review. Electrophoresis 35:3044-3052.
Linacre A, Pekarek V, Swaran YC, Tobe SS (2010) Generation of DNA profiles from fabrics without DNA extraction. Forensic Sci. Int.: Genet 4:137-141.
Phipps M, Petricevic S (2007) The tendency of individuals to transfer DNA to handled items. Forensic Sci. Int. 168:162-168.
Templeton JEL, Linacre A (2014) DNA profiles from fingermarks. BioTechniques S7:259-266.
Templeton JEL, Taylor D, Handt O, Skuza P, Linacre A (2015) Direct PCR Improves the Recovery of DNA from Various Substrates. JFS 60(6): 1558-1562.
Mapes AA, Kloosterman AD, et al. Knowledge on DNA Success Rates to Optimize the DNA Analysis Process: From Crime Scene to Laboratory. Journal of Forensic Sciences. 61:1055-1061

3a. In what ways would the research results improve current laboratory capabilities?

Establishing a category of evidence where the results are not compromised after omitting human DNA quantitation will result in faster turn around time for evidence testing, higher throughput and conservation of DNA extracts. In addition to having a positive effect on laboratory capacity, this would also enable laboratories to adopt direct PCR techniques, which could lead to increased STR typing success rates.

3b. In what ways would the research results improve understanding of the scientific basis for the subcommittee(s)?

In recent years DNA testing has been expanded to many types of biological evidence such as touched objects known to generally yield low amounts of DNA. There is no systematic study categorizing touch evidence sample types based on yield, and then using this information to proceed to STR amplification and result interpretation without having specific quantitation data for each sample. This research is also needed to provide a safe mechanism to divide biological evidence prior to applying single device DNA testing techniques.

3c. In what ways would the research results improve services to the criminal justice system?

Being allowed to omit the mandatory DNA quantitation step for certain categories of biological evidence would decrease turnaround times, and increase laboratory throughput. This would improve case resolution, support the identification of repeat offenders, and help victims and victims' families. It is also feasible that the implementation of direct PCR for certain sample types will increase the STR success rate and thus result in more conclusive results such as positive associations and/or more exonerations.

4. 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.

Subcommittee Approval date: 4/29/2016

(Approval is by majority vote of subcommittee. Once approved, forward to SAC.)

SAC

1. Does the SAC agree with the research need? Yes ⓧ No ◯

2. Does the SAC agree with the status assessment? Yes ⓧ No ◯

If no, what is the status assessment of the SAC:

Approval date: 08/24/2016

(Approval is by majority vote of SAC. Once approved, forward to NIST for posting.)