OSAC Research Needs Assessment Form

Title of research need: Characterizing, designing and constructing integrated DNA mixture interpretation solutions

Keywords: Forensic DNA mixtures, signal processing, artifacts, DNA interpretation, low template DNA, complex DNA mixtures

Submitting subcommittee(s): BDIRC
(If SAC review identifies additional subcommittees, add them to the box above.)

Date Approved: 8/25/16

Background information:

1. Description of research need:

Despite recent advances in the development and construction of probabilistic interpretation systems for complex DNA mixtures, transitioning these systems into the forensic DNA pipeline is still a challenge. The solution to this barrier to transition still requires breakthroughs in signal analysis that come from innovative basic and applied research that looks beyond the analysis and interpretation schemes currently known.
In many cases the construction of current probabilistic systems includes algorithms that evaluate allele peak heights and stutter. However, DNA signal is complicated by additional elements such as pull-up, spikes, noise, incomplete adenylation, dye dissociation and raised baseline. These artifactual elements originate from a variety of sources, but in general, can be classified as PCR- or instrument- based artifacts. In order to create a DNA interpretation mechanism that is fully automated and objective, improvements in signal analysis and signal processing are required. Further, if artifacts continue to confound DNA signal then implementation of processes and algorithms that appropriately filter, or interpret, this signal is warranted.
An example of pioneering work in this area includes (1) where an integrated mathematical approach to model the data is developed. One major advantage of this method is the correction of raised baseline.
Other work has focused on implementing interpretation strategies that utilize the entire signal (2, 3).
Though there is evidence to suggest that the information gained –particularly for low-template DNA components- can be substantive (4, 5), a decrease in the analytical threshold exacerbates issues associated with artifact interpretation. Thus, as laboratories and researchers continue to explore the low signal regions of the evidence, improved mechanisms to analyze and interpret the signal are needed.

2. Key bibliographic references relating to this research need:

(1) Goor R., et al. A Mathematical Approach to the Analysis of Multiplex DNA Profiles. Bull Math Biol. 2011 Aug; 73(8): 1909-1931.
(2) Perlin M., et al. Linear Mixture Analysis: A Mathematical Approach to Resolving Mixed DNA Samples. J Forensic Sci. 2001; 46(6): 1372-1378.
(3) Swaminathan H., et al. CEESIt: A Computational Tool for the Interpretation of STR Mixtures. Forensic Sci Int: Genetics. 2016; 22: 149-160.
(4) Rakay CA., et al. Maximizing Allele Detection: Effect of analytical threshold and DNA levels on Rates of Allele and Locus Drop-out. Forensic Sci Int: Genetics. 2012; 6: 723-728.
(5) Taylor D., et al. Does the Use of Probabilistic Genotyping Change the Way We Should View Sub-threshold data? Australian J Forensic Sci. 2015; Dec.

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

Extensive research over the last two decades has yet to produce a fully objective and automated DNA interpretation system. Some systems rely upon the laboratory to apply a signal threshold during analysis, while others require artifact filtering, assumptions on the number of contributors, and/or inputs for allele drop-in or drop-out. Even in instances where the signal may be unencumbered by multiple contributors, degradation or low-template levels, DNA signal interpretation is still a necessity. Further, as the quantity of data continues to grow, automated signal interpretation and processing will become more of a necessity since signal noise and artifact will necessarily be present. Thus, mechanisms by which the signal can be evaluated in an objective manner will be required, regardless of platform.

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

As the level of DNA information generated by laboratories grows (i.e. additional loci, NGS data) manual interpretation of profiles containing noise, artifacts, and true signal will become more challenging. Thus, there is a need for DNA processing to approach automation. . Though there will, presumably, always be a need for laboratories to review the data, this research will allow for simultaneous improvements in signal detection and interpretation. If both detection and interpretation are normalized, then the rapidly developing science of DNA mixture interpretation can be effectively communicated to stakeholders alleviating concerns related to "black box" approaches.

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

This research will provide data and develop research products to examine and minimize variations that occur during mixture interpretation. If they are minimized, it is anticipated that this research can be transitioned more easily to the forensic laboratory, resulting in a standardized approach to mixture interpretation that can be effectively communicated to stakeholders.

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: 04/29/2016

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

SAC

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

2. Does the SAC agree with the status assessment? Yes X 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.)