OSAC RESEARCH NEEDS ASSESSMENT FORM

Title of research need: Establishing the value and designing a process for including flanking region SNPs in MPS based STR casework

Describe the need: Massive parallel sequencing (MPS) reveals not only repeat sequence substructure but also single nucleotide polymorphisms in the flanking region [1,2]. These additional polymorphisms will distinguish otherwise identical STR alleles and increase the power of discrimination, but data processing and allele nomenclature are an unresolved issue [3,4]. Some software approaches deliberately focus on the STR region omitting the flanking region [3,5]. Flanking region SNPs may also aid in the interpretation of DNA mixtures [6]. More research is needed to determine how much value flanking region SNPs add to forensic MPS data, and if these SNPs should be included in data analysis and reporting. Research should focus on universal allele calling, building databases, establishing the relevant power of discrimination, and validating these polymorphisms for casework.

Keyword(s): Massive parallel sequencing, SNP alleles

Submitting subcommittee(s): Human Biology **Date Approved:** 05/04/2021

(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 MPS sequencing for forensic analyses

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

3. Key bibliographic references relating to this research need:

1) Gettings KB, Aponte RA, Vallone PM, Butler JM. STR allele sequence variation: Current knowledge and future issues. *Forensic Sci Int Genet*. 2015;18:118-130.
2) van der Gaag KJ, de Leeuw RH, Hoogenboom J, et al. Massively Parallel Sequencing of Short Tandem Repeats—Population data and mixture analysis results for the PowerSeq™ system. *Forensic Sci Int Genet*. 2016;24:86-96.
3) Wendt FR, King JL, Novroski NMM, et al. Flanking region variation of ForenSeq™ DNA Signature Prep Kit STR and SNP loci in Yavapai Native Americans. *Forensic Sci Int Genet*. 2017;28:146-154.

4) Parson W, Ballard D, Budowle B, et al. Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. *Forensic Sci Int Genet*. 2016;22:54-63.

5) King JL, Churchill JD, Novroski MM, et al. Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeqTM DNA Signature Prep Kit. *Forensic Sci Int Genet*. 2018;36:60-76.

6) Warshauer DH, Lin D, Hari K, et al. STRait Razor: A length-based forensic STR allele-calling tool for use with second generation sequencing data. *Forensic Sci Int Genet*. 2013;7(4):409-417.

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?

No

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

This research is needed to ensure any future implementations of MPS based STR typing use the full potential of this new method. It is critical to establish nomenclature/SNP designations and database frequencies prior to any implementation in forensic case work. A common international language for these new allele variations will aid in sharing and comparison of data across laboratories.

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

More data on population frequencies and power of discrimination of sequence based STR allele calling incorporating flanking region SNPs will provide a better basis for understanding and implementing these human DNA polymorphisms.

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

In many cases DNA mixture contributors share STR alleles, which complicates data interpretation. Incorporating flanking region SNPs may distinguish between same length STR alleles and will aid in the interpretation and resolution of mixed DNA testing results. Having this additional information should further decrease the occurrence of fortuitous matches and false positives. This benefit is more likely to take effect for STR loci with little internal sequence structure variation.

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

	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.