

OSAC RESEARCH NEEDS ASSESSMENT FORM



Title of research need:

SNP panel development and genotyping methods that are practical for wildlife forensics

Describe the need:

Development of SNP panels for species of forensic interest would be highly valuable, as would associated genotyping methods that are practical for wildlife forensic laboratories and practitioners to implement. The use of SNP panels in wildlife forensics can increase the genetic discrimination between individuals, hybrids, and phylogenetically close taxa (1, 2, 3, 4, 5). SNP genotyping methods include array-based hybridization, PCR-based strategies (TaqMan assay, Melt-MAMA, RNA-DNA hybrid primers), or sequencing (Sanger or next generation). Further research is required to develop SNP panels for direct application to wildlife forensic casework and to build databases, workflow methodologies, and protocols for the respective genotyping methods.

Keyword(s):

SNP panel, wildlife, genotyping, database

Submitting subcommittee(s):

Wildlife Forensic Biology

Date Approved:

10/7/2022

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)

ANSI/ASB Standard O48, Wildlife Forensic DNA Standard Procedures, states that “4.4.1 Protocols shall exist for all analysis and interpretation methods routinely used in the laboratory, and these protocols shall include defined data quality indicators.”

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)?

SNP panels are being developed for species of conservation or management interest on a regular basis, but rarely are they evaluated for the same validation criteria required of forensic databases. As a result, there is a lag in the published literature for forensic applications.

3. Key bibliographic references relating to this research need: (ex.: Toll, L., Standifer, K. M., Massotte, D., eds. (2019). Current Topics in Opioid Research. Lausanne: Frontiers Media SA. doi: 10.3389/978-2-88963-180-3)

1. King, J. L., Churchill, J. D., Novroski, N., Zeng, X., Warshauer, D. H., Seah, L. H., & Budowle, B. (2018). Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeq™ DNA Signature Prep Kit. Forensic Science International. Genetics, 36, 60–76.

2. Lorenzini, R., Fanelli, R., Tancredi, F., Siclari, A., & Garofalo, L. (2020). Matching STR and SNP genotyping to discriminate between wild boar, domestic pigs and their recent hybrids for forensic purposes. *Scientific Reports*, 10(1), 3188.
3. Ogden, R., Gharbi, K., Mugue, N., Martinsohn, J., Senn, H., Davey, J. W., Pourkazemi, M., McEwing, R., Eland, C., Vidotto, M., Sergeev, A., & Congiu, L. (2013). Sturgeon conservation genomics: SNP discovery and validation using RAD sequencing. *Molecular Ecology*, 22(11), 3112–3123.
4. Carroll, E. L., Bruford, M. W., DeWoody, J. A., Leroy, G., Strand, A., Waits, L., & Wang, J. (2018). Genetic and genomic monitoring with minimally invasive sampling methods. *Evolutionary Applications*, 11(7), 1094–1119.
5. von Thaden, A., Cocchiararo, B., Jarausch, A., Jüngling, H., Karamanlidis, A. A., Tiesmeyer, A., Nowak, C., & Muñoz-Fuentes, V. (2017). Assessing SNP genotyping of noninvasively collected wildlife samples using microfluidic arrays. *Scientific Reports*, 7(1), 10768.
6. Scientific Working Group for DNA Analysis Methods (SWGDM) Revised Validation Guidelines. *Forensic Science Communications*. July 2004, 6(4).

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?

Forensic Biology/DNA, Scientific Research, Increased information about the discriminatory power and sensitivity of alternate biological analyses (e.g., proteomics, microbiome, plants, animals) to associate individuals with crime scene evidence.

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

Genetic marker panel development that incorporates forensic validation criteria would reduce the need to replicate published research to provide a forensically useful database. If standard validation criteria were followed, databases could be adopted and shared across multiple laboratories more efficiently.

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

The availability of SNP panels for various species, hybrids, and phylogenetically close taxa is limited and requires further research and validation to be practical for wildlife forensic casework use. The increased power of SNP data, and similar high-resolution data, would enable wildlife forensic laboratories to incorporate analysis of more complex species identifications that involve hybrids and subspecies.

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

The ability to provide objective, scientific information pertinent to regulations allows the criminal justice system to determine if a violation has occurred. With this information, true violators can be prosecuted, and non-violators can be dismissed, thus informing effective enforcement of laws and regulations. Without the ability to identify evidentiary materials that are potentially illegal or criminal violations, these cases cannot be made using scientific- or forensic-based evidence.

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

I

	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.