W15 STR Wars: The Rise of Sequencing

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Learning Overview: After attending this presentation, attendees will have been introduced to forensic DNA sequencing methods that are currently being adopted for the analysis of Combined DNA Index System (CODIS) core Short Tandem Repeat (STR) loci, mitochondrial DNA, autosomal Single Nucleotide Polymorphisms (SNPs), and other non-traditional markers.

Impact on the Forensic Science Community: This workshop will impact the forensic science community by showcasing the innovative sequencing strategies that international forensic laboratories are implementing to improve their approach to forensic casework.

The foundation of modern forensic DNA analysis is STR typing on Capillary Electrophoresis (CE) technology. Using one- to two-dozen highly polymorphic loci in a multiplexed amplification, DNA profiles from any two random individuals can be discriminated with high certainty. STR data are numerically recorded and simple to store in electronic databases. This has positioned STR typing at the center of DNA databasing efforts (e.g., the National DNA Index System [NDIS] and International Criminal Police Organization [INTERPOL]) that bridge law enforcement and government agencies to solve forensic cases. The advent of probabilistic genotyping for STR mixture deconvolution has solidified its role in criminal casework.

Despite the robustness of STR typing, it has fundamental drawbacks that preclude its use from becoming ubiquitous. STR typing with CE technology requires intact nuclear DNA fragments of several hundred base pairs for successful amplification. Therefore, it has limited use for degraded DNA that may be found in aged remains, burned material, or hair shafts. Additionally, the core STR loci are randomly segregating and not revealing of linkage blocks that facilitate extended kinship analysis. As a result, traditional autosomal STR markers limit kinship assessments to close relatives, such as those in a nuclear family.

The gaps in forensic DNA testing that were left by STR typing on CE platforms have been filled in with sequence-based analyses of other genomic targets such as mitochondrial DNA (mtDNA) and nuclear Single Nucleotide Polymorphism (SNP) markers. The detection of these markers allows for identity, ancestry, and phenotype predictions, as well as kinship analyses. Furthermore, the implementation of Massively Parallel Sequencing (MPS) methodologies into forensic laboratories has opened the door to feasible protocols for sequencing large number of these loci. Commercial MPS kits targeting STRs as well as SNPs and the entire mtDNA genome are now available and have been implemented in forensic laboratories for casework. Prototype SNP panels are being developed by the International Commission on Missing Persons and the Visible Attributes Through Genomics (VISAGE) Consortium for kinship assessment and DNA phenotyping, respectively. The increase of the fundamental knowledge on new traits such as facial shape may be incorporated into these newly developed MPS tools. High-density SNP generation through microarray testing and MPS allow for extended kinship analysis and genetic genealogy. However, these advancements cannot be implemented without considering the ethical and legal implications. Issues with method validity, data management, genetic privacy, and lack of regulations/standards must be examined as the field of forensics continues to envelop this powerful technology. Yet, MPS technologies continue to evolve at a rapid pace, and soon the value of MPS may eclipse that of the longstanding CE technology.

DNA, Sequencing, Human Identification