B128 Validation of the Roche Linear Array Mitochondrial DNA HVI/HVII Region-Sequence Typing Kit

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After attending this presentation, attendees will learn that the Roche Linear Array Mitochondrial DNA HVI/HVII Region-Sequence Typing Kit is validated for use as a screening method in forensic casework.

This presentation will impact the forensic community and/or humanity by demonstrating the use of the Roche Linear Array mtDNA sequence typing kit that will decrease casework turnaround time by quickly screening for exclusions, thereby allowing the analyst to focus on more probative samples.

Mitochondrial DNA (mtDNA) typing is a useful tool in the forensic biology laboratory due to the high mtDNA copy number per cell, high degree of polymorphism, and maternal inheritance. MtDNA typing is often successful in yielding profiles in cases where there is an insufficient amount or quality of DNA for nuclear STR DNA testing. While direct DNA sequencing is commonly used to determine mtDNA sequence variation, the Linear Array assay is a more simple and rapid method (e.g. the procedure can be done in about 2 hours versus several days for DNA sequencing) that can be used as a screening technique in mtDNA casework.

This presentation will demonstrate that the Roche Linear Array strips are a specific, sensitive, and robust method for the detection of sequence variation in hypervariable regions I and II (HVI/HVII) of the mtDNA control region. During the course of the validation for the new mtDNA laboratory at the NYC Office of Chief Medical Examiner, several different studies were performed on the Linear Array strips to meet the current SWGDAM guidelines for DNA analysis.

Sensitivity studies revealed that the most favorable banding and intensity patterns were achieved with approximately 75ng of amplified DNA. Mixture studies revealed that minor components could be seen at a 50:1 ratio, indicating that the array is highly sensitive. Non-probative samples from different tissue types, including, hair, muscle, and bone, were also typed with the Linear Array strips and were found to be in agreement with typing results from direct DNA sequencing. Typing of all laboratory staff was also performed to maintain an in-house database to rule out possible contamination concerns. Lastly, decontamination procedures, such as cleansing gloves in bleach, were employed to minimize the number of failed negative controls.

mtDNA, Linear Array, Validation

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