B137 Multiple Factors Influencing Probabilistic DNA Mixture Interpretation of Highly Challenging Samples: The Relevance of Deep Validation Studies to Ensure Quality Assurance Requirements in Actual Casework

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After attending this presentation, attendees will better understand how important deep validation studies and Quality Assurance (QA) are in order to establish the limits and the capabilities of laboratories and experts, and how protocols, kits, instruments, and probabilistic software choices may influence the statistical results.

This presentation will impact the forensic science community by providing the ability to establish robust and reliable lab protocols useful when approaching actual casework samples.

DNA mixture probabilistic interpretation is undoubtedly one of the most challenging tasks in forensic genetics.[1,2] In the past ten years, new statistical models and software have been developed in this field to perform more sophisticated calculations to include or exclude a suspect from a complex DNA profile; but can we ever determine that we have enough information, and the right information, to accomplish this?

Multiple factors may affect DNA mixture interpretation and this is obviously due to one-by-one contributor template concentration and integrity, but also to systematic protocols chosen during sample processing. For these reasons, DNA extraction and quantitation methods, typing kits, and Capillary Electrophoresis (CE) instruments play a fundamental role in information used for probabilistic interpretation; results will only be as close to reality as the data used for calculation is reliable.[3,4] Semi-continuous and fully continuous methods play a key role as they take into account different aspects of DNA mixture profiles in qualitative terms, such as quantitative data used for statistics.[5] Therefore, QA processes, for both analysis and probabilistic calculations, can guarantee results' robustness and permit understanding laboratory performances when approaching complex DNA profile interpretation such as Low Template DNA (LT DNA) mixtures derived from trace evidence collected at the crime scene.

The detailed knowledge of each step of the entire validated method from trace evidence to interpreting a DNA mixture profile is certainly the crux to solving the most complicated problems in forensic genetics and, even more importantly, to understanding if laboratories and experts have all the puzzle pieces to accomplish this.

Multiple quantitation kits, typing kits, instruments, and probabilistic software results will be presented in order to underline their characteristics and differences, revealing what expectations experts may have for each of them during the interpretation of actual casework.

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