F40 DNA Typing: Controls and Validation Updates to Support Current Testing

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After attending this presentation, attendees will learn that current controls and validation used for optimum amounts of DNA are lacking in establishing scientific practice for low amounts of DNA, which deters accuracy in obtaining and interpreting DNA typing results. Suggestions will be provided for controls and studies needed to augment current procedures.

This presentation will impact the forensic science community by providing information that will improve DNA typing accuracy. While DNA typing kits and analytical equipment have rapidly changed to allow typing of low quantities of DNA (Low Level DNA (LLD)), there has been no matching change in requirements for validation studies and controls to address additional problems that arise in typing LLD. The goal of this presentation is to present techniques and studies to strengthen current testing results.

Existing validation studies of two-person mixtures and sensitivity have demonstrated that LLD typing may exhibit known problems such as stochastic effect, founder effect, allelic dropout, and allelic drop-in. These issues become exacerbated with the use of current kits and analyzers that can operate with very low quantities of DNA, particularly when mixtures consist of more than two persons. Studies will be discussed that demonstrate that allele sharing can confuse interpretation of the number of contributors present; the data may look like two persons, but are actually three. Crime labs using data from LLD typing can address these issues through directed validation and controls. The existing validation studies do not address peak height imbalance due to allele sharing and investigation-borne contamination. Current controls do not address detection of contamination or stochastic effect in mixtures.

Currently, LLD typing is treated no differently than sufficient DNA samples with regard to testing controls. Existing controls are made up of sufficient DNA (positive amplification and Quality Control (QC)) or no DNA (negative control). LLD controls should be added, such as a low-level single-source known control and low-level mixture controls. It would be advantageous to add blind LLD mixture controls. Some labs currently set up a QC sample where the result is unknown to the analyst who then types the sample and provides the profile to the laboratory QC supervisor. It would be of minimal disruption to add an unknown LLD mixture sample.

LLD sample results are also more susceptible to contamination picked up during scene processing, during autopsies at coroner laboratories, from a victim requiring medical procedures, and during crime laboratory processing. Cases will be presented in which contamination was "proven" after the fact. Validation studies would help ascertain where conditions are poor and what steps can be taken in advance rather than in the aftermath. Mixture results are particularly problematic in determination of whether investigation-borne contamination is present and at what levels. Validation studies addressing this issue will be discussed.

Additional cleaning and testing procedures can be established at the DNA laboratory, coroner's autopsy rooms, and other potential evidence-handling locations to predetermine what contamination sources may exist. Suggestions will be made during the presentation on possible procedures to decrease contaminating DNA. Additional validation on pipetting accuracy will ensure more accurate results. LLD sample typing is more susceptible to amplification problems due to poor pipetting skills.

Validation, Contamination, Controls