REFINING LABORATORY SOPS FOR ENHANCED CONSISTENCY THROUGH INCORPORATION OF SWGDAM'S GUIDELINES FOR AUTOSOMAL STR TYPING

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Advancements in technology and instrumentation have expanded the variety and complexity of samples typically encountered in a forensic DNA laboratory. As a result of these improvements, analysts are increasingly confronted with challenging profiles arising from poor DNA quality/quantity and complex mixtures. Standard Operating Procedures (SOPs) for DNA mixture interpretation may harbor vague language to accommodate the widest variety of casework scenarios, relying heavily on the individual analyst's experience and training. Although affording flexibility, these generalized SOPs can lead to interpretation differences among analysts.

In January 2010, The Scientific Working Group on DNA Analysis Methods (SWGDAM) approved guidelines for the interpretation of autosomal STR typing to provide direction to the forensic community. Built upon a solid foundation of validation studies, these guidelines serve as a decision making framework within a laboratory's well-defined SOP. It is impractical to establish a guideline for every scenario; however, a well-defined SOP containing scenario-specific structure will consistently direct interpretation toward reproducible conclusions. As a result, any individuals adhering to the same SOPs should ultimately arrive at the same conclusion.

Three mock casework scenarios were prepared with non-probative DNA samples to specifically challenge mixture interpretation consistency among analysts. Using these scenarios, we illustrate where potential discrepancies are more likely to occur due to ambiguously written SOPs. By using SWGDAM's Interpretation Guidelines for Autosomal STR Typing to strengthen SOPs, analysts will interpret data more consistently within laboratories and ultimately foster confidence in the reproducibility of complex sample interpretation.