



B80 Streamlining the Analysis of Forensic DNA Testing: New Tools to Allow More Efficient Workflow From Processing to Final Result

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Attendees will gain an understanding of the tools available for DNA testing and utilizing these tools to make decisions during the processing of biological evidence.

This presentation will impact the forensic community and/or humanity by presenting an integrated system for DNA analysis.

This presentation will discuss new tools available for DNA testing that allow clear decisions to be made in the initial and final stages of processing DNA samples. These decisions include:

- Incorporating a screening mechanism to assess the need for further processing of DNA samples,
- Detecting the presence of mixtures of male and female DNA, in order to decide a path for extraction processing and subsequent amplification,
- Evaluating inhibition,
- Deciding a path for extraction processing of compromised DNA samples, and
- Determining if DNA results obtained from a sample meet the interpretation criteria set by the user.

Forensic scientists are often faced with making decisions about the best approach to take when analyzing DNA samples to obtain optimal results. However, often these decisions are made without prior knowledge of the nature of the sample.

The Quantifiler™ Human DNA Quantification Kit and the Quantifiler™ Y Human Male DNA Quantification Kit can be used to assess the need for further processing of DNA samples by incorporating these assays into the workflow as a screening mechanism. The utility of the Quantifiler Human and Quantifiler Y assays in detecting mixtures of human genomic DNA from male and female sources has been demonstrated. Experiments have been designed to simulate circumstances, such as a rape case investigation, in which a small minor component of male DNA must be discerned from a high background of female DNA have resulted in successful detection of the male donor. To this end, the ability to determine if a sample contains a mixture of female and male DNA and the ability to use these assays as a quantitative interpretational aid for DNA mixtures by determining the ratio of each contributor is a new and valuable tool available to analysts.

Additionally, since the Quantifiler kits allow preliminary determination of male:female mixture ratios this information will assist in selecting the appropriate method of extraction and genotyping of these samples. Further, the use of the Quantifiler kits in conjunction with the AmpF/STR® Yfiler™ PCR Amplification Kit, produces reliable and accurate Y-haplotypes and provides the forensic scientist with a robust set of tools for Y-chromosome analysis. Part of this set of tools is a valuable haplotype population database based on analysis of the 17-locus haplotype. The Y-STR database allows the forensic scientist to estimate the frequency of a Y-STR haplotype generated with the AmpF/STR® Yfiler™ PCR Amplification Kit.

Both the Quantifiler™ Human DNA Quantification Kit and the Quantifiler™ Y Human Male DNA Quantification Kits are useful assays not only for determining the amount of amplifiable DNA, but also for evaluating the degree of inhibition in the sample. Inhibitors can interfere with the reaction at several levels, leading to different degrees of PCR efficiency and even to complete inhibition. A wide variety of PCR inhibitors have been reported, particularly in DNA samples extracted from bloodstains. Data will be shown which demonstrate the utility of the Quantifiler™ Human DNA Quantification Kit and the Quantifiler™ Y Human Male DNA Quantification Kit.

Finally, until recently, genotyping projects required manual examination of all allele calls. GeneMapper® ID software minimizes this bottleneck by automating allele calling using a novel process component based quality values (PQVs) system that quickly assesses genotype quality and provides automated concordance checks. Further, for those labs that upload data to CODIS, projects can be exported into a CODIS compatible reporting format allowing easy data uploading.

DNA, Quantification, Y-STR