B35 Unique Solutions to Addressing the Backlog of Criminal Casework

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By attending this presentation, attendees will learn of solutions developed to effectively address the backlog of cases requiring DNA analysis.

This presentation will impact the forensic community and/or humanity by demonstrating the combination of a growing backlog of cases requiring DNA analysis and the severe budget constraints that states are facing requires novel approaches to the analysis of casework. The authors want to share with the community the processes developed to help address this problem.

Crime labs across the country face a growing backlog of cases requiring DNA analysis. This includes not only an increased demand for DNA-testing on current cases but also the testing of older cases which were either never submitted due to the lack of a suspect or were tested prior to the adoption of the 13 CODIS STR loci. This has left many crime labs with hundreds of 'no-suspect' cases requiring analysis but no increase in the number of analysts available to do the work. New York City alone had a backlog of greater than 15,000 no-suspect sexual assault kits. From October 2000 to July 2003, we analyzed over 6000 of these kits for the New York City Police Department. During this time, we initiated work with many other crime labs with different requirements requiring customized solutions to their problems. In order to process these cases in the most efficient manner and meet the demands of various users, we have developed processes addressing the primary bottlenecks encountered during the analysis of these cases. The primary areas covered here include 1) the screening of the kit to identify male component DNA, 2) quantitation of DNA extracts and 3) final generation of a CMF file and a court-ready allele table.

One of the primary bottlenecks to the analysis of sexual assault cases is the initial screening of a case for the presence of seminal fluid. Typically, this entails a combination of Acid Phosphatase (AP) screening, microscopic searches for spermatozoa and/or P30 testing. In a typical sexual assault evidence collection kit containing multiple vaginal, anal, oral and various body swabs, it can take over an hour to screen a single kit. Rather than use a traditional serology approach to screening, we have developed a DNA-based procedure in which we differentially extract one sample of each type without any pre-screening. Following DNA extraction of case samples, we employ a Y-Marker Screen (YMS) to screen samples for the presence of male DNA. The YMS test gives a greater level of profile sensitivity than the STR multiplexes used for DNA analysis, so false negative results are eliminated. The YMS test consists of the Amelogenin primers as a control to ensure that either X-chromosome or both X and Y-chromosome DNA are identified (if only X-chromosome DNA is observed, then only female DNA is present). Primers for two monomorphic Y-Sequence Tagged Sites (STS) are co-amplified with the Amelogenin primers. The STS's are only diagnostic for the presence of Y-DNA, and do not require STR-like analysis. As a result, quantification is not required prior to YMS-amplification. Additionally, the amplitude of the STS product is diagnostic for the approximate quantity of male DNA in the sample extract, providing value to the scientist when attempting to troubleshoot complex STR analysis results. Given these characteristics, the YMS test provides a simple and efficient way to determine if male DNA is present and if an STR profile can be generated from a sample. Samples that test negative for the presence of male DNA at this point can be reported as negative and not processed further. This system has been used on over 3500 cases and our data suggests that it has resulted in a higher percentage of foreign profiles for eventual CODIS upload than traditional screening approaches.

Once positives have been determined, all samples must be quantified using a primate-specific assay. Rather than using a traditional approach such as a hybridization assay, we have developed a PCR-based assay which amplifies a defined region of the human TH01 locus with subsequent detection using PicoGreen on a fluourometer. This gives a precise representation of human DNA present in the sample in an output format (Microsoft Excel) that allows for rapid calculation of dilutions before amplification. Equally important, because the system uses simple commercially-available primers and a low-cost detection system, the cost for quantitation is much lower than other commercially available methods. To date, the method has been used successfully on more than 30,000 samples.

The ultimate goal of no-suspect cases differs from traditional casework. Rather than the generation of a profile for comparison to known individuals, profiles are generated primarily for upload to CODIS. While Genotyper is well-equipped for reference samples to export data in a CMF-ready format, evidentiary samples often contain mixtures that must be interpreted or partial profiles that must be analyzed locus by locus and across numerous amplifications. Following analysis of STR data by two independent reads and final review, the data is traditionally summarized by the hand-entering of an allele table in a report or the hand-entry of a profile for upload to CODIS. This allows for potential transcriptional errors and, in the process, creates a tremendous review burden for the crime lab. To address this problem, we have written a program for generating CMF files and allele tables which converts Genotyper table data into both a court-ready allele table (in Microsoft Word format) and a CMF file (in Microsoft Excel format) for upload to CODIS. It is customized to the individual laboratory to meet their review and upload requirements.

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The backlog of no-suspect cases across the country is currently estimated at over 300,000 and growing. As states face increasing budget constraints, the time required to train more analysts will delay our ability to solve these crimes. By addressing existing bottlenecks in the processing of cases with effective high-throughput solutions, we have successfully increased the overall efficiency of the laboratory while also increasing the quality of the work. The processes outlined above will be discussed.

DNA Backlog, No-Suspect Casework, CODIS

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