A168 The Analysis of Defined Data Sets of Mixture STR Profiles Using Several Mixture Deconvolution Tools

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The goal of this presentation is to take a defined data set of simulated STR mixtures and process the data through several mixture deconvolution tools available to the forensic community.

This presentation will impact the forensic community by providing a survey of additional tools available to the forensic scientist for the evaluation of mixed STR DNA profiles.

Mixture deconvolution tools, also known as fancy calculators, have been designed by several programmers/companies to assist forensic scientists in mixture interpretation of casework STR data. Mixture results pose an additional challenge in case interpretation and can be quite time- consuming, even for the experienced forensic scientist. Cases involving sexual assault, homicide, and touch DNA often have a mixture of two or more DNA profiles. As advances are being made in the forensic community with expert systems for single source DNA interpretation, more and more focus is being directed at other software tools that can assist the forensic examiner in interpretation of mixed STR profiles.

Controlled mixture studies were conducted to produce two data sets; each data set used a different pair of male and female DNA samples. The design of the mixture samples included varying ratios of the male and female DNA at 30:1, 10:1, 3:1, 1:1, 1:3, 1:10, and 1:30 with various DNA input levels. The different amounts of DNA added to each amplification (i.e., 1.5X, 1.0X, 0.5X, and 0.25X) were based on the manufacturers' published recommendations. These varying ratios and varying input quantities of DNA were amplified with PowerPlex® 16 System (Promega Corporation, Madison, Wisconsin) and AmpFℓSTR Identifiler®, Profiler Plus®, COfiler®, and SGM Plus® PCR Amplification Kits (Applied Biosystems, Foster City, California). All samples were run on multi- capillary electrophoresis instruments.

The raw data were analyzed using several mixture deconvolution tools and calculator packages. These include but are not limited to: DNA_DataAnalysis Software (United States Army Criminal Investigative Laboratory, Fort Gillem, Georgia); FSS-i3™ Expert Systems Software version 4.1.3 (Promega Corporation) in conjunction with GeneMapper® *ID* Software version 3.2 (Applied Biosystems); GeneMapper® *ID-X* Software (Applied Biosystems); and, TrueAllele® Casework System Package (Cybergenetics, Pittsburgh, Pennsylvania). The results of these studies demonstrate that fancy calculators can positively identify a partial profile of a minor contributor even at low ratios amplified with 0.25 ng total DNA. All of these tools can evaluate two-person DNA mixtures and produce best-fit major profiles and others can provide invaluable assistance with three-person mixed profiles. Each of the mixture deconvolution tools interprets the mixed data using mathematical modeling and algorithms from output peak definition and peak height information for each of the amplifications. Some of the software packages report weighted ratios whereas others report proportions. It is clear from this evaluation that the different mixture deconvolution tools address stutter differently and ask very different questions of the data. For example, the knowledge base of one software program uses no *a priori* information regarding the mixtures, whereas another software program allows the user to define one reference, for example the victim, in its interpretation. One critical observation is that the software packages perform the calculations in the same manner every time producing unbiased and reproducible results. These comparisons and the results from the different software packages will be discussed.

The focus of this presentation is to share information about the different mixture deconvolution tools that are available to the forensic community, both commercially and as freeware. Through surveying the different mixture deconvolution tools, it is clear that the knowledge base of each software program is different and that they are each querying different parameters. It is the intent of this presentation to share the advances made with each software program and their respective limitations.

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Mixture Profiles, Deconvolution Tools, Software