B78   Evaluating Likelihood Ratio Variability of Major Component DNA Profiles in Complex Mixtures

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Learning Overview: The goals of this presentation are: (1) to determine the robustness of likelihood ratios of major component DNA profiles in complex mixtures with an uncertain number of contributors, and (2) to develop a quantitative method for determining when a major component DNA profile can be confidently deconvolved using probabilistic genotyping.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by offering one method that can be used to quantitatively determine a major component DNA profile in a complex mixture, and to bring consensus on how uncertainty can and should be evaluated.

Validation and implementation of Applied Biosystems[TM] Globalfiler[TM] PCR amplification kit at the Bureau of Alcohol, Tobacco, Firearms and Explosives (ATF) forensic science laboratory has resulted in an increase in the observation of complex DNA profiles. Often, these DNA profiles consist of perceived major components along with an indeterminate number of minor contributors. Deconvolution of DNA profiles using probabilistic genotyping software STRmix requires the user to provide the assumed number of contributors present in the DNA profile. Accurate determination of number of contributors to a mixture is not always possible and, in these instances, the DNA profile should not be used for comparison or statistical analysis. Complex DNA profiles with robust major components may be an exception. In this study, fourteen artificially created three, four, and five-person complex mixtures including major components were amplified using the Applied Biosystems[TM] Globalfiler[TM] PCR amplification kit at concentrations of 500pg and 1.0ng, with an additional subset being amplified at 250pg. The resulting DNA profiles were deconvolved using STRmix with the correct number of contributors and with reasonable variation to the number of contributors. All deconvolutions were compared to a database consisting of known contributors and 1,000 known non-contributors to evaluate the effect of number of contributors on calculated likelihood ratios. Deconvolution resulted in consistent characterization of the major component, and minimal variation in calculated likelihood ratios at all assumed number of contributors. As expected, reduction in the number of contributors often resulted in the exclusion of known contributors to the minor component as well as known non-contributors. Mixture proportions determined during deconvolution under varied number of contributors were analyzed and indicated that a major component is suitable for comparison if the ratio of the major proportion to the sum of the minor proportions is greater than 2:1. It is the hope of the authors that this study is viewed by the forensic DNA community as one method that can be used to quantitatively determine a major component DNA profile in a complex mixture. Additionally, it is hoped that this study will spark discussion within the community and lead to consensus on how uncertainty can and should be evaluated.

Mixture, Major Component, Probabilistic Genotyping