A113 Likelihood Ratio Statistics for DNA Mixtures Allowing for Drop-Out

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After attending this presentation, attendees will understand how the likelihood ratio can be used to assign statistical weight to comparisons between DNA evidence profiles and profiles from known individuals. This method is appropriate for low or high template samples, for single source samples or mixtures, for degraded or pristine DNA, and for single, duplicate, or triplicate measures.

This presentation will impact the forensic science community as the analytic method presented allows quantitative comparison between evidence and exemplar profiles when degradation and/or allelic drop-out may have occurred.

The standard statistic calculated when evidentiary and exemplar STR profiles are identical is the random match probability (RMP). The RMP can be used for single source evidentiary profiles and for mixtures when individual contributors' profiles can be deconvoluted (deduced). Two methods, Random Man Not Excluded (RMNE) and likelihood ratio (LR), are commonly used to quantify the statistical weight of mixed DNA profiles when contributors cannot be deduced. The DNA commission of

the International Society of Forensic Genetics recommends the LR (Gill *et al*. Forens Sci Int 2006 160:90-101),[1] as it uses more of the available data than RMNE and parameters for allelic drop-out and drop-in can be incorporated into the LR. A likelihood ratio method and software for analysis of single source or mixed low template or high template evidence samples has been developed and validated. This method, the Forensic Statistical Tool (FST), is modeled after existing methods (Curran *et al*. Forens Sci Int 2005 148:47-53; Gill *et al*. Forens Sci Int 2007 166:128-

138).[2,3]

The method incorporates drop-out and drop-in parameters in the LR calculated by FST, using empirically determined rates from single source buccal swab samples containing 6.25 pg to 500 pg of template DNA and from mixtures of two or three contributors containing a total of 25 pg to 500 pg of template DNA.

FST computes the LR for pairs of prosecutor and defense hypotheses and for sample characteristics specified by the user. The user must select the number of contributors to the sample and then upload or enter an evidence profile and comparison sample profile(s), such as those from suspect(s) and victim(s). In addition, the amount of template DNA used for each amplification must be specified. Evidence profile data from up to three amplifications may be considered simultaneously. Finally, if the evidence profile represents a mixture of DNA from two or more contributors, the user must specify whether or not the profile of the major contributor can be deduced. FST calculates the LR according to the sample specifics and generates a PDF file that includes the LR, as well as the evidence and comparison profiles and the sample characteristics entered by the user. The LR is computed using allele frequency estimates in four New York City populations: Asian, Hispanic, Caucasian, and Black. These are the same samples that the Office of Chief Medical Examiner of the City of New York uses to calculate random match probabilities for single source or deduced sample profiles.

FST can also compute the LR using each individual in a LabTypes database as the test sample, rather than a profile from a comparison sample, to check for evidence sample contamination. This capability and a database of over 1,200 population samples were used to develop a null distribution for the LR for single source, two-contributor, and three- contributor scenarios. The main objective of this exercise was to determine the range of LR values that can be expected when the calculation is performed using individuals who did not contribute to the evidence sample. This will help to ensure that use of the program will not result in fortuitous matches between evidence profiles and non- contributors to the sample.

The performance of the program was evaluated with hundreds of profiles generated from a variety of sample types, including blood and buccal samples, purposefully degraded buccal samples, and touched items with one, two, three, and four known contributors. In this presentation, the analytical strategy and validation of the software will be presented.

References:

1. Curran JM, Gill P, Bill MR (2005) Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure. *Forens Sci Int* 148:47-53
2. Gill P, Brenner CH, Buckleton JS, Carracedo A, Krawczak M, Mayr WR, Morling N, Prinz M, Schneider PM, Weir BS (2006) DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forens Sci Int* 160:90-101
3. Gill P, Kirkham A, Curran J (2007) LoComatioN: a software tool for the analysis of low copy

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number DNA profiles. *Forens Sci Int* 166:128-138

DNA Mixtures, Likelihood Ratio, Allelic Drop-Out

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