A76 Weight of Evidence for DNA Profiles From Degraded Samples: Low Template Samples and Mixtures

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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 scenarios with multiple sets of results for the same sample.

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 generation of DNA profiles from small amounts of skin cells or degraded body fluids was historically not feasible. However, with the advent of more sensitive molecular technologies, it is now possible to obtain genotypes from these samples. The generation of STR profiles from low-template or degraded DNA samples may be accomplished by several methods, such as increased PCR cycle numbers (Findlay et al. 1997; Gill et al. 2000),[1,2] nested PCR (Taberlet et al. 1996),[3] and purification of PCR product (Smith and Ballantyne 2007).[4] Using increased PCR cycle numbers, full STR profiles can reliably be obtained from 25 – 50 pg of DNA; partial profiles may be obtained from even lower quantities of starting DNA (Prinz et al. 2006; Caragine et al. 2009).[5,6].

While these advances have expanded the range of case types for which DNA evidence is useful, they have also introduced new analytic challenges. The comparison of known DNA profiles to evidence samples containing small amounts of DNA or degraded DNA can be challenging, as many of the results produce mixtures and/or partial DNA profiles. Alleles from known contributors may be absent or, conversely, extraneous alleles that cannot be attributed to known contributors may be present. These phenomena are commonly known as allelic drop-out or drop-in, respectively. Due to a higher occurrence of allelic drop-out and drop-in with low template or degraded samples, relative to high template or robust samples, the DNA Commission of the International Society of Forensic Genetics (ISFG) cautions that standard STR analysis methods may not be appropriate for low template samples (Gill et al. 2006)[7].

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 ISFG recommends the LR (Gill et al. 2006),[7] as it uses more of the available data and parameters for allelic drop-out and drop-in can be incorporated. That said, RMNE does not require specification of the number of contributors to a mixture and the calculation is more intuitive; therefore, RMNE is easier than the LR to explain to a jury. However, RMNE cannot be used if any of the exemplar profile alleles are missing from the evidence profile.

An analytic method has been developed for the comparison of evidence profiles from small or compromised DNA samples to known profiles while accounting for the probability of allelic drop-out and drop-in, starting with a framework similar to that presented in Curran et al (2005).[8] The method compares the probability of the evidence profile data under two competing hypotheses via a likelihood ratio. Specification of the hypotheses is flexible and the method can include data from multiple replicates of an evidence profile. Drop-out and drop-in parameters were estimated empirically in single source samples and in mixtures of DNA from two to four contributors with 6.25 pg to 500 pg of starting DNA. Estimates were obtained from purposefully degraded samples and from non-degraded samples.

The method has been implemented in a web-based software application. In this presentation, the analytical strategy will be presented and the software's performance will be demonstrated using mock casework profiles.

References:

1 Findlay I, Taylor A, Quirke P, Frazier R, Urquhart A (1997) DNA fingerprinting from single cells. *Nature* 389:555-556

2 Gill P, Whitaker J, Flaxman C, Brown N, Buckleton J (2000) An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. *Forens Sci Int* 112:17-40

3 Taberlet P, Griffin S, Goossens B, Questiau S, Manceau V, Escaravage N, Waits LP, Bouvet J (1996)

 ** Presenting Author*

Reliable genotyping of samples with very low DNA quantities using PCR. *Nucleic Acids Res* 24:3189-3194

4 Smith PJ and Ballantyne J (2007) Simplified low-copy-number DNA analysis by post-PCR purification. *J Forens Sci* 52:820-829

5 Prinz M, Schiffner L, Sebestyen JA, Bajda E, Tamariz J, Shaler RC, Baum H, Caragine T (2006) Maximization of STR DNA typing success for touched objects. *Int Congress Series* 1288:651-653

6 Caragine T, Mikulasovich R, Tamariz J, Bajda E, Sebestyen J, Baum H, Prinz M (2009) Validation of testing and interpretation protocols for low template DNA samples using AmpFlSTR Identifiler. *Croat Med J* 50:250-267

7 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

8 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

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