APPLICATION OF PRE-PCR SAMPLING STATISTICS TO Y-CHROMOSOME STR ANALYSIS WITH THE Yfiler® PLUS KIT

Sonja B. Klein, Mark D. Timken, Martin R. Buoncristiani, California Department of Justice Jan Bashinski DNA Laboratory

A recent study confirmed that stochastic effects (heterozygous peak-height ratios and allelic dropout frequencies) observed in autosomal STR profiles obtained from low-template amplifications of extracted DNA can be predicted using pre-PCR sampling statistics [1]. To test if the same predictions apply to Y-STR data, replicate amplifications of the NIST SRM® 2372A quantitation standard in a dilution series were performed using the Yfiler® Plus kit and detected on the LifeTech 3500 capillary electrophoretic instrument. Empirical dropout rates for each template amount in the dilution series were found to be in general agreement with the dropout rates predicted by the template-based Poisson distribution. Logistic regression analysis of the probability of dropout based on pre-PCR sampling statistics was also shown to predict the empirical dropout rates. Based on the results of this study, amplification of an accurate DNA standard to normalize RFU to template, combined with pre-PCR sampling predictions, may serve as a good starting point for establishing dropout probabilities for Yfiler® Plus amplifications of extracted DNA, and for setting stochastic threshold and peak-height ratio expectations for the multi-copy Y-STR loci referred to in the *SWGDAM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories* (January 2014).

[1] M. Timken, S. Klein, M. Buoncristiani, Stochastic sampling effects in STR typing: Implications for analysis and interpretation, *Forensic Sci. Int. Genet.* 11 (2014) 195-204.