B77   A Logistic Regression Approach for Combining Likelihood Ratio (LR) in the Field of DNA Mixture Interpretation

Eugenio Alladio, PhD*, Department of Chemistry, University of Torino, Torino 10125, ITALY; Monica Omedei, PhD, Centro Regionale Antidoping "A. Bertinaria", Orbassano 10043, ITALY; Selena Cisana, PhD, Centro Regionale Antidoping A Bertinaria, Orbassano 10043, ITALY; Denise Caneparo, MS, Orbassano , ITALY; Paolo Garofano, MD, PhD, Laboratorio Genetica Forense - CAD, Orbassano (TO) 10043, ITALY; Tereza Neocleous, PhD, School of Mathematics and Statistics, Glasgow G12 8QQ, UNITED KINGDOM

Learning Overview: After attending this presentation, attendees will understand the critical role DNA typing interpretation plays in courtrooms and how the outcome can change dramatically if the evidence collected at a crime scene is considered as a single item instead of different parts of a whole, and therefore offering different degrees of reliability.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by showing that logistic regression could act as a valuable tool for the combination of likelihood ratios (LRs) provided by various biostatistical software and approaches. It returns a unique LR value that eases the interpretation process and allows combination of the various LR results with parameters such as the degradation index and the overall amount of DNA to be amplified.

Due to different interpretation procedures, Low-Template DNA (LT-DNA) mixture profiles obtained from the crime scene represent the most challenging situation for the DNA analyst. Their interpretation may prove very difficult, especially if several variables are present. These variables may be of different nature (e.g., random sample degradation, contamination, etc.). Furthermore, another source of complexity to interpretation of DNA mixtures is the fact that there are three main models that can be used when interpreting data obtained from electropherograms (epg): the binary approach (currently obsolete), the semi-continuous approach, and the fully-continuous approach. These models present different degrees of difficulty in terms of application and interpretation. Despite the forensic community having proposed several recommendations over the past few years, a standardized, "universal," and rigorous approach to LT-DNA mixture analyses has still to be defined.

The main aim of this study is to build a generalized, comprehensive approach to combine the likelihood ratio (LR) results that are provided by the different probabilistic approaches (and corresponding different software) for DNA mixture interpretation.

Several *ad hoc* DNA 2- and 3-person mixtures (already employed for validation purposes) were analyzed at the Laboratory of Forensic Genetics of the Regional Antidoping and Toxicology Center "A. Bertinaria" (Orbassano, Italy) by means of different probabilistic software involving both the semi-continuous (or qualitative) and the fully-continuous (or quantitative) models. In particular, software such as LRmix Studio, Lab Retriever, DNA•VIEW®, EuroForMix and STRmix™ were employed in this study, but the developed approach can be extended to an unlimited number and kind of different software. Logistic regression approaches were used to combine the different LR values, together with the degradation index and DNA quantification parameters. Furthermore, a simple R Shiy app has been developed to allow analysts to deal with this kind of data.

DNA Mixtures Interpretation, Logistic Regression, Likelihood Ratio