INTERPRETATION OF A COMPLEX DNA MIXTURE WITH GENOPROOF MIXTURE V3.1

A.M. Pflugbeil, H. Schönborn, V. Borsdorf, A. Jede, B. Schotten
qualitype GmbH

An ongoing challenge evaluating DNA evidence is the interpretation of difficult STR typing results. The presence of several contributors in DNA mixtures, specific phenomena like allele drop-in or dropout, occurring due to low quality and quantity of the extracted DNA, can result in weak match probabilities. As a result, the evidential weight decreases and no biostatistically assured statement is possible when binary or threshold based models are employed. Therefore, current research in the field of DNA interpretation methods moves fast towards continuous interpretation strategies. Common probabilistic genotyping approaches, such as the application of fully continuous models, incorporate empirically determined biological models and enable the use of more detailed DNA profile information (biological core parameters) in order to reduce subjectivity in the interpretation of results.

We designed a comprehensive framework and implemented an algorithm for interpretation of complex DNA mixtures according to a fully-continuous model.

GenoProof Mixure 3.1 covers the entire evaluation process from raw data analysis, genotype deconvolution and statistic calculations of likelihood ratios (*LRs*). In this work we will present the new face of version 3.1 of GenoProof Mixture and the complexity of our expert software by evaluation a real case scenario. We analyzed a complex four-person mixture taking two PCR replicates of two different STR kits into account and calculated the likelihood ratio for the inclusion of one suspect in the hypothesis of prosecution. Furthermore a deconvolution of the mixture was carried out and evaluated. In order to exclude a related person to the suspect *LRs* were also calculated for each possible degree of kinship. The resulted *LR* confirmed the hypothesis of prosecution significant. All results were summarized in a report.

Keywords: DNA mixtures, STR, Likelihood Ratios, Probabilistic genotyping software