



B33 An Evaluation of DNA·VIEW® Mixture Solutions Beta Software with Two-, Three-, and Four-Person Mixtures for Forensic Applications

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After attending this presentation, attendees will have a basic understanding of how DNA·VIEW® Mixture Solutions can be utilized for forensic applications such as mixture analysis. Attendees will also understand the impact of this software on DNA mixture interpretation.

This presentation will impact the forensic science community by demonstrating the power, speed, and accuracy of DNA·VIEW® Mixture Solution as a possible tool for forensic mixtures interpretation.

DNA mixture interpretation is a rising issue in the field of forensic science and can be very challenging. Most current software used for forensic mixture interpretation are continuous models that use the Markov Chain Monte Carlo (MCMC) method to analyze mixtures and produce likelihood ratios. These also often require the user to input the number of assumed contributors prior to initiating the analysis of a mixture; a new analysis is required to test a different number of contributors. DNA·VIEW® Mixture Solution is new software that uses mathematical algorithms, rather than MCMC, to determine the probabilities of the evidence under various scenarios. The software calculates the probabilities for multiple prosecution hypotheses (Hp); for example, the probabilities of the evidence given that it includes the Person Of Interests (POI), perhaps a known victim, plus one, two, three, etc., unknown individuals. Similarly, it calculates the probabilities for multiple defense hypotheses (Hd). The probabilities of the most desirable Hp and Hd are then divided to obtain a fair likelihood ratio. The systematic exploration takes the place of guesswork regarding contributors and numbers of contributors.

Previously extracted DNA from four individuals from a Hispanic population was supplied by The George Washington University, Department of Forensic Science. The samples were quantified using the Quantifiler® Duo DNA Quantification Kit. Different volumes of these reference samples were then used to create two-, three-, and four-person mixtures with multiple ratios and diluted down to different DNA amounts for Polymerase Chain Reaction (PCR) reactions (2ng, 1ng, 500pg, 250pg, and 100pg). A total of 75 mixtures were created. The mixtures created ranged from simple to more complex with clear major contributors and the minor contributor remaining the same in all mixed samples. DNA samples, including single-source samples, were then amplified using AmpF/STR® Identifier® PCR Amplification Kit and detected on the 3130 Genetic Analyzer. Short Tandem Repeat (STR) profile analyses were performed with the Genemapper® ID-X version 1.4; a text file was created from each electropherogram data and imported into the latest DNA·VIEW® Mixture Solutions beta software version and interpreted. The software was analyzed on its ability to produce consistent likelihood ratios over several runs, its run time in the analysis of different mixtures, and its accuracy in determining the likelihood of a minor contributor being present in a mixture.

From the data, DNA·VIEW® Mixture Solutions provides consistent and repeatable results for all mixtures. DNA·VIEW® Mixture Solutions was also able to rapidly calculate and (if desired) deconvolve mixtures with times as low as a few seconds for simple two-person mixtures and ranging up to about one and one-half hours for more complex mixtures at low DNA concentrations, though such time may be affected by computational power of the instrument. Finally, the software seemed to accurately represent the compositions of the mixed samples for the most part as complex four-person mixtures with low DNA and would result in very little of the minor contributor being detected.

In conclusion, DNA·VIEW® Mixture Solution is an efficient, fast, consistent, repeatable, and intuitive program that has many potential applications in the field of forensic science and can assist in the efficiency of processing DNA mixtures.

DNA·VIEW®, Mixtures, DNA Contributors