



B55 The DNA Mixture Conundrum: Sample Variation and Its Effects on Mixture Deconvolution Tools

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After attending this presentation, attendees will come to understand the need for stringent evaluation of mixture deconvolution tools and their applicability in solving DNA mixtures.

This presentation will impact the forensic community by illustrating that aid in DNA mixture interpretation may be found in DNA mixture deconvolution programs.

Learning Objectives: DNA mixture interpretation is often a dreaded and confounding task to many in the forensic community; however, it is important that reliable results are obtained when contributing mixture evidence to the criminal justice system. Without national guidelines on how to perform DNA mixture interpretation and statistical analysis, the possibility exists for inconsistency in mixture interpretation between laboratories across the United States. This study focuses on evaluating the DNA mixture deconvolution tools FSS-i³ i-STReam, Least-Square Deconvolution (LSD) and DNA_DataAnalysis and assesses if these programs may be used to aid forensic DNA analysts in solving two-person mixtures.

Materials and Methods: Several DNA mixture samples were created at different major and minor contributor ratios and amplified with various commercial STR kits. The samples were amplified in replicate in order to test the variation that exists within PCR and to observe how this variation affects the mixture deconvolution tool's ability to reliably solve DNA mixtures. The data was collected on a 3130xl and analyzed with GeneMapper ID v3.2 and i-STReam v4.1.3, LSD, or DNA_DataAnalysis v2.01.

Summary of Results: The deconvolution tools were evaluated based on if they made calls, if the calls were correct, and why incorrect calls were obtained. The variability between the replicates was also analyzed and this PCR variability was used to explain some of the different and/or incorrect calls that the mixture deconvolution tools obtained. Also, by performing this study at varying ratios, it can be illustrated that the reliability of the deconvolution tools is dependent on the ratios of the major and minor contributors. These ratios play directly into the mathematical formulas that the programs are using to solve the DNA mixtures. Furthermore, not only does the analyst need to be proficient in DNA mixture analysis, but optimization of various parameters within the programs is important to obtain the correct contributor profiles.

Conclusions: There are several DNA mixture deconvolution tools available to help analysts in deciphering these mixtures; not only do they bring more consistency to DNA mixture interpretation, but they also shorten analysis time and with appropriate tuning can prove to be fairly reliable. However, further analysis of these deconvolution tools is still needed before their applicability in the forensic community is established.

DNA Mixture Deconvolution, PCR Replicates, FSS-i³ i-STReam