

DETERMINING CONTRIBUTOR PROFILES FROM DNA MIXTURES OF VARYING RATIOS

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Mixtures exist whenever more than one individual contributes biological material to a DNA sample. Mixtures, which are commonly seen in evidentiary samples (typically with two or three contributors), are more challenging to interpret compared to single source DNA samples that come from known references. Deciphering mixtures to determine the individual contributor profiles can be a time-consuming task for a forensic DNA analyst that requires training and experience. Over the past decade, our group at the National Institute of Standards and Technology (NIST) has conducted several interlaboratory studies involving mixture interpretation with short tandem repeat (STR) markers in order to better characterize issues that arise when trying to decipher the contributors to a DNA mixture result [1].

Computer software tools to aid STR mixture interpretation (e.g., [2]) have become available in recent years. We have evaluated several software programs for DNA mixture deconvolution including the i-STReam portion of FSS-i3 v4.1.3 (Promega Corporation, Madison, WI), the Web-based Least Squares Deconvolution (Web-LSD) available at <https://lsd.lit.net/>, and an Excel-based program developed at the U.S. Army Criminal Investigation Laboratory (USACIL) entitled DNA_DataAnalysis v2.1.3. Multiple mixture data sets (either from previous NIST interlaboratory studies, collaborators, or new in-house generated sample sets) have been evaluated with these software programs to explore the impact of contributor ratios and STR allele peak height ratios on the ability to determine the contributors' DNA profiles. Mixture ratios ranging from 1:1 to 1:30 were examined as well as two and three person mixtures. The results of this research will be described in the context of the International Society of Forensic Genetics (ISFG) mixture interpretation recommendations [3].

References

¹Interlaboratory Studies on DNA: <http://www.cstl.nist.gov/biotech/strbase/interlab.htm>

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