

IT RUNS IN THE FAMILY OR DOES IT? – USING PROBABILISTIC GENOTYPING TO EVALUATE POSSIBLE FAMILIAL RELATIONSHIPS IN COMPLEX MIXTURES

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Over the past few years, probabilistic genotyping and familial searching have been widely discussed topics in the forensic science community. While at times these topics may seem unrelated, probabilistic genotyping software can help to determine the possibility that a family member of a suspect may have contributed to a mixture instead of the suspect themselves. Additionally, some probabilistic genotyping software, such as STRmix™, have familial searching options. In 2016, STRmix™ was validated at DNA Labs International (DLI) for use with the Applied Biosystems AmpFLSTR® Identifiler® Plus PCR amplification kit. With the expansion of the new core CODIS STR loci, STRmix™ was validated at DNA Labs International for use with the Applied Biosystems Globalfiler™ and Promega PowerPlex® Fusion 6C PCR amplification kits at the beginning of 2017.

STRmix™ can be used to assist in deconvoluting mixtures that would otherwise be too complex for DNA analysts to resolve without the use of probability genotyping software. After evaluating the sample with the software, a likelihood ratio is generated, which compares two alternate hypotheses. Although DLI reports the stratified likelihood ratio, a series of likelihood ratios evaluating different factors are calculated and available for the analyst to examine. This includes several types of relationship likelihood ratios include sibling, parent/child, half siblings, uncle/aunt/niece/nephew and first cousins. These relationship likelihood ratios are calculated by comparing the proposition that the person of interest is a contributor to the mixture versus the proposition that a relative of the person of interest is a contributor to the mixture.

Typically, a high value for the likelihood ratio indicates extremely strong support that an individual contributed to a mixture. However, if the calculated relationship likelihood ratios are low, then the possibility that a relative contributed to the mixture should be considered. Since STRmix™ was first implemented at DLI, hundreds of analyses have been performed using this software. In some cases, another family member was suggested to be a part of the mixture based on the evaluation of these relationship likelihood ratios. Case examples evaluating the possibility of familial relationships occurring in mixture samples and how these instances were managed will be discussed.