



A43 Large-Scale Evaluation of ArmedXpert™ for 2 - 4 Person DNA Mixture Analysis

Lashon Stephens, BS, 1 Innovation Dr, North Charleston, SC 29419; Roman Aranda, PhD, FBI, 2501 Investigation Pkwy, Quantico, VA 22135; Lawrence A. Presley, MS, USACIL, 4930 N 31st St, Forest Park, GA 30927-5205; and Brigid O'Brien, PhD, USACIL, 4930 N 31st St, Bldg 925-S, Forest Park, GA 30297*

After attending this presentation, attendees will understand the effectiveness of ArmedXpert's™ ability to deconvolute Short Tandem Repeat (STR) DNA mixture data.

This presentation will impact the forensic science community by demonstrating the accuracy, effectiveness, and limits of the ArmedXpert™ program.

ArmedXpert™ is an Excel-based software program created with the purpose of assisting DNA analysts in deconvoluting two-, three- and four-person DNA mixtures. This software program uses Short Tandem Repeats (STR) and Y-STR DNA profiles, and displays the possible combinations for the various contributor scenarios. The effectiveness of this program relies on statistical probabilities and subjective interpretation from the user. The main goal of this research is to determine how accurate and effective ArmedXpert™ is at assisting forensic scientists to deconvolute DNA mixtures under varying concentrations and conditions.

In this study, two-, three-, and four-person DNA mixtures were generated and initially profiled by the Boston University School of Medicine. This pilot study evaluates the examiners' ability to interpret a DNA mixture profile from a mixture data set. The Boston University study contains over 2,000 mixture combinations, which were generated with various contributor numbers, concentrations, injection volumes, and amplification kits. The effectiveness of ArmedXpert™ was determined by analyzing the examiners' ability to use the software to correctly identify allele calls, determine the major, minor, and number of contributors, and the statistical random match probability (RMP) of each contributor when compared to the known Boston University data set. The examiners' input was entered into an spreadsheet-based macro program that calculates the partial genotype accuracy, residual frequency of the known and calculated RMPs, and the failure rate of missed allele calls. This spreadsheet macro will also determine if the calculated allele calls from the DNA analyst match the alleles from the Boston University data set, and if an incorrect allele was called. The partial genotype accuracy calculates the DNA analysts' ability to call the correct alleles when compared to the known DNA mixture profile. An average of these metrics will be calculated to determine the extent that ArmedXpert™ assists DNA analysts at mixture interpretation when compared to analysts that deconvolute without software assistance. Mixture interpretations with incorrect allele calls will be averaged separately from the correct allele calls. Statistical analysis, such as a chi-squared test, will be performed on the overall results to determine how effective ArmedXpert™ is at assisting DNA analysts at deconvoluting DNA mixtures.

In the future, a large-scale study of DNA examiners will be conducted to determine the overall metrics of the mixture evaluations. These metrics will be used to determine if ArmedXpert™ can effectively assist DNA analysts in interpreting DNA mixture analysis. Because there is no universal standard for analysis of DNA mixture, the results from the study may vary depending on the experience of the DNA analyst. The effectiveness of ArmedXpert™ may be influenced by the DNA analysts' familiarity with the software program and their ability to determine the major, minor, and number of contributors.

The opinions or assertions contained herein are the private views of the author and are not to be construed as official or reflecting the views of the Department of the Army, the Department of the Navy, or the Department of Defense.

ArmedXpert™, DNA Mixtures, Error Rates