"THE DEVELOPMENT OF A COMPLETELY ROBOTIC HIGH-THROUGH-PUT SYSTEM FOR STR TYPING OF MODERATELY CHALLENGED ORAL SWABS"

Theodore D. Anderson, Demris A. Lee, Timothy P. McMahon, <u>Tracey L. Johnson</u>, James P Ross and Brion C. Smith *Armed Forces DNA Identification Laboratory, Rockville, MD*

The Armed Forces DNA Identification Laboratory was challenged with the development of a system to expedite the analysis of several thousand oral swabs collected on various substrates, without standard procedures, and warehoused under unknown storage conditions for as long as two and half years. Due to the varied history of these samples it was necessary to anticipate a wide range of DNA yields and quality. Robotic platforms were validated for extraction. amplification and analysis. These included the Qiagen 9604, the Corbett Robotics CAS-1200 and the AB 3100. In advance of a lab-wide transition from AmpFLSTR® Profiler Plus® and AmpFLSTR® COfiler® to a single multiplex, we also validated PowerPlex® 16. Additionally, because a high-through-put formatted quantification system did not exist in-house, the system was intentionally designed without quantification or subsequent normalization steps. To assist with data management and data review we employed the use of LISA v. 7.02.1, an information management system designed and developed by Future Technologies, Inc. and the expert system TrueAllele® v. 2.6.30 designed and developed by Cybergenetics. Profile success, data quality considerations, validation parameters, data management strategies and disconcordant results will be discussed.