B75 Laboratory Quality and Efficiency Without Robotic Dependency

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After attending this presentation, attendees will have learned how to manage a high-throughput laboratory without robotics.

This presentation will impact the forensic community and/or humanity by demonstrating how to improve laboratory management and sample processing.

Elimination of errors while maintaining a high volume of throughput is a goal of any forensic laboratory, and the mitochondrial DNA (mtDNA) section of the Armed Forces DNA Identification Laboratory (AFDIL) is no exception. In order to meet increasing output demands while maintaining forensic laboratory standards, the mtDNA section has developed several novel practices and non-robotic procedures for storing, handling, and processing DNA sequencing samples.

All samples entering the AFDIL are registered in the in-house network application: Laboratory Information Systems Application (LISA). LISA facilitates the generation of forms for all scientific procedures in a step-wise fashion. LISA has been programmed to arrange selected samples on forms in such a way as to optimize the use of reagents and machine time. The scientist processing the samples indicated must sign off each form upon completion. This creates individual responsibility for sample processing and storage. LISA also stores the electronic forms indefinitely, enabling scientists to view the processing history of a sample and reprint any forms they wish.

The mtDNA section is comprised of seven teams: six responsible for amplification and analysis and one responsible for sequencing. This compartmentalization allows for more efficient use of time and equipment as samples progress through amplification, sequencing, and analysis in assembly line fashion. With ever-increasing numbers of samples at various stages of processing, keeping track of them and maintaining order in storage freezers has become increasingly difficult. In lieu of an expensive barcode tracking system, a system of color coding and designated shelving has been developed to facilitate organization of samples.

One of the more difficult challenges to maintaining error-free output has been the transition from sequencing using individual 0.2 mL tubes to sequencing using 96-well plates. Individual tubes could be labeled, capped, and moved; therefore, it was easier to verify the extent to which each sample had been processed. Innovative steps have been taken to create a similar arrangement for the 96-well plates, involving a system of color-coding, labeling, and verifying. Ancient DNA samples are processed with different volumes of template based upon the resulting band intensities on ethidium-stained 2% agarose gels. Since it is tedious to program robots to process 96-well plates with different volume requirements in each well, manual set up of sequencing plates is the viable option. The use of multi-channel and electronic pipettes has reduced the number of sample transfers and shortened the set up time of sequencing reactions. Since implementing this system, output has more than tripled, from 430 sequencing samples in June 2005 to an average of just under 1500 samples per month in the next five months.

Another step that has been taken to insure the expeditiousness of sample processing is the switch from using labor intensive Centricon® column purifications to ExoSAPit to eliminate unincorporated dNTPs and primers from amplification reactions. This switch provided a doubling of output capabilities to an average of 2800 samples per month over the next six months.

The above practices along with a strong dedication to the mission of identifying and repatriating the remains of America's military men and women enable the AFDIL to process approximately 800 ancient remains specimens and 2000 family reference samples per year with great efficiency.

The views expressed herein are those of the authors and not necessarily those of the Armed Forces Institute of Pathology, the U.S. Army Surgeon General, nor the U.S. Department of Defense.

DNA, High-Throughput, Contamination

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