



Criminalistics Section – 2004

B23 Whole Genome Amplification of Limited Quantity Samples

Nana Yaa S. Lamouse-Smith, BA, MS, Robin L. McDowell, MFS*, Robert E. Wenk, MD, and Francis A. Chiafari, MS*, BRT Laboratories, Inc., 400 West Franklin Street, Baltimore, MD 21201*

After attending this presentation, attendees will learn about a new technique they may want to incorporate into their SOPs for handling limited biological samples.

This presentation will impact the forensic community and/or humanity by describing the technique which can be used on challenging samples to obtain DNA profiles. This may help to obtain DNA profiles (either complete or partial) from limited samples where before this may have not been feasible or results achieved did not provide enough information.

This study investigated the utility of Whole Genome Amplification (WGA) as a method to enhance the sensitivity of current STR technology for samples with limited cell quantity. WGA uses Phi29 DNA polymerase and random hexamer primers to amplify eucharomatic DNA by highly processive strand displacement. Our initial experiments involved determining the minimum number of cells necessary to yield successful WGA, followed by phenotyping with Profiler Plus and Cofiler to measure fidelity. Epithelial cells were collected, counted, and lysed prior to WGA, with the yield determined by Pico Green. Serial dilutions with as few as 10 total cells yielded WGA product, and produced accurate profiles with Profiler Plus and Cofiler. Initial experiments indicate that this technology may improve the production of profiles from minimal samples in a cost-effective manner. Applications of this technology to mock and non-probative samples will be discussed.

Whole Genome Amplification, Limited Sample, DNA