ANALYSIS OF DNA FROM POST-BLAST PIPE BOMB FRAGMENTS FOR IDENTIFICATION AND DETERMINATION OF ANCESTRY

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Improvised explosive devices (IEDs) are weapons used to detrimentally affect people and communities. Recently, a brand of exploding targets called Tannerite® (Tannerite® Sports, LLC) was identified as a potential material for abuse as an explosive in pipe bombs.
While it is possible to recover DNA from post-blast fragments using short tandem repeat markers (STRs), genotyping success can be negatively affected by low quantities of DNA, heat degradation, and/or PCR inhibitors. Alternative markers such as insertion/null polymorphisms (INNULs) and single nucleotide polymorphisms (SNPs) are bi-allelic markers that can potentially yield smaller amplicons than STRs, which are more likely to resist degradation. Genetic markers may also be analyzed using massively parallel sequencing (MPS), which has shown some initial success with sequencing degraded and low-level DNA samples.

In this study, we created 10 pipe bombs spiked with known amounts of biological material to: 1) recover “touch” DNA from the surface of the device, and 2) recover traces of blood from the ends of wires (simulated finger prick). The bombs were detonated with the binary explosive Tannerite® using double-base smokeless powder to initiate the reaction.

The Quantifiler® Trio DNA Quantification Kit (Thermo Fisher Scientific) was used to assess the quantity and quality of the DNA extracts. STR analysis was conducted using the GlobalFiler® Amplification Kit (Thermo Fisher Scientific), INNULs were amplified using an early-access version of the InnoTyper™ 21 Kit (Innogenomics Technologies, LLC), and SNP analysis via MPS was performed using the HID-Ion Ampliseq™ Identity Panel using the Ion Chef and Ion PGM™ sequencing system (Thermo Fisher Scientific). In addition, SNP analysis using the HID-Ion Ampliseq™ Ancestry Panel (Thermo Fisher Scientific) on PGM was conducted to explore the success of predicting ancestry from the blood recovered from wires post-blast.

The results of this study demonstrated that INNUL markers resulted in more complete genetic profiles on average when compared to STR profiles. However, the random match probabilities calculated for samples using INNULs were lower than with STRs until more than 14 STR alleles were reported. These results suggest that INNUL analysis may be well suited to supplement failed STR analysis from post-blast IED fragments.

Human identification using SNP analysis via MPS showed variable success with low-level post-blast samples in this study. However, 5 out of 6 blood samples resulted in correct ancestry predictions.