Using the Ion S5™ and MiSeq FGx™ Systems to Identify Challenging Human Remains

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Missing persons' cases, unidentified human remains, and mass disasters are problems faced not only within the United States, but also many other countries worldwide. An overwhelming number of migrants and refugees have died or gone missing in their efforts to cross borders or seas. Routinely in missing persons' cases, challenging skeletal remains (bone and teeth) are the only samples available for DNA analysis. However, some samples are more challenging to process than others because of their biological composition, environmental exposure (humidity, temperature, UV light, and microorganisms), DNA damage and/or degradation, the presence of inhibitors, and the possibility of contamination or comingled remains.

This study evaluates the comparative performance of the two most common forensic sequencing chemistries and platforms used within the community for identifying extremely challenging biological samples. Bone samples and teeth (N = 24) from 14 cadavers that were subjected to a range of environmental insults (cremation, embalming, decomposition, and fire). Samples were extracted in triplicate using a total demineralization protocol. DNA was prepared and sequenced using an early access Degradation panel with Precision ID chemistry on the Ion S5™ System (Thermo Fisher Scientific) in parallel with the ForenSeq™ DNA Signature Prep Kit (Primer Mix A) on the MiSeq FGx™ (Illumina). Samples were also genotyped traditionally using a capillary electrophoresis (CE) based STR amplification kit.

Overall, the results of this study demonstrate that both platforms were able to successfully sequence a variety of challenging samples. The sequencing data also showed higher success rates and greater powers of discrimination than CE-based STR typing with these challenging and low template skeletal samples. More in-depth results and the comparative performance metrics for the two chemistries will be discussed during our presentation.