B41 The Utility of the Precision ID Ancestry Panel for Predicting Ancestry From High-Quality and Forensic-Type Samples

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After attending this presentation, attendees will understand that a commercially available panel of Single Nucleotide Polymorphism (SNP) markers can be used to effectively predict the ancestry of known samples. Attendees will learn that genotype accuracy can be examined by testing congruence between the manufacturer's software and a third-party, well-accepted software. Attendees will also learn the impact of DNA degradation on ancestry predictions using this panel and the manufacturer's software.

This presentation will impact the forensic science community by providing the results of an initial assessment of the novel Precision ID Ancestry Panel for determining genotypes from samples of differing ancestry. This presentation will provide valuable information as to the applicability of the panel for forensic-type samples and the potential limitations of using this panel as tool for investigative leads.

Human individualization is typically accomplished by analyzing Short Tandem Repeats (STRs); however, in cases in which only a partial or incomplete STR profile is obtained, SNPs could provide valuable information to aid the investigation by providing information on biogeographic ancestry. Thermo Fisher Scientific, which developed the high-throughput Ion Torrent™ PGM™ sequencer, released the Precision ID Ancestry Panel, a 165-SNP panel for forensic ancestry prediction.

This study was directed at assessing the accuracy, reproducibility, and sensitivity of this novel panel and with the ability to provide accurate ancestry predictions for: (1) seven high-quality DNA samples that represent the three major ancestries of forensic interest in the United States (Hispanic, Caucasian, and African American); and, (2) forensic type samples, such as a toothbrush, bone, hair, shaving razor, cigarette butt, and nail clippings (*n*, 9). Libraries were prepared in triplicate using 0.2ng, 0.5ng, and 1.0 g DNA as input for the high-quality DNA samples (*n*, 63), and in duplicate where possible for the forensically relevant samples using 0.05ng–1.0ng of DNA (*n*, 39). Data was analyzed using the manufacturer's Human Identification (HID) SNP Genotyper plug-in (v.4.3.1) as well as CLC Genomics Workbench. Only 2% of all possible Quality Control (QC) flags were raised for the high-quality samples by the plug-in QC filter; 59% of these flags were due to the major allele frequency being outside the manufacturer's defined thresholds. A total of 9.8% of all possible flags were raised for the forensic type samples by the plug-in QC filter; 45% of the flags were due to locus drop-out.

A simulated degradation study was also conducted using the data generated from the seven high-quality samples prepared using 1.0ng of DNA. Data was divided into SNP subsets based on known amplicon lengths and commonly observed degradation lengths (i.e., SNPs with amplicon lengths <50bp, <75bp, <100bp, and <200bp), and ancestries subsequently predicted for each subset using the FROG-kb database (http://frog.med.yale.edu/FrogKB/). Incorrect ancestry predictions did occur in approximately 20% of the samples, primarily when Ancestry Informative Single Nucleotide Polymorphisms (AISNPs) with amplicon lengths <75bp were used in analyses. Even though the forensic type samples had more flagged SNPs than the high-quality DNAs, 72% of samples still had concordant ancestry predictions between replicates, demonstrating that this panel has the potential to be used in forensic casework with further testing.

SNP Typing, Ancestry, NGS

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