B72 The Evaluation of Degraded Human DNA Samples Using the Illumina® Global Screening Array

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Learning Overview: After attending this presentation, attendees will better understand the analysis limitations of genome-wide Single Nucleotide Polymorphism (SNP) genotyping data from low-quantity and degraded forensic samples.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing results for considering alternative data metrics for assessing the accuracy potential in downstream analyses and forensic genealogical investigations as it applies to degraded DNA.

Forensic Genetic Genealogy (FGG) applies enhanced genetic processing techniques (array-based genome-wide SNP genotyping) coupled with traditional genealogical research techniques to generate new investigative leads. Application of FGG technology can be most useful in cases that have gone cold or where traditional investigative means have been exhausted. The use of this technology in investigative forensics has skyrocketed since the 2018 arrest of Joseph DeAngelo as the Golden State Killer.

The Infinium™ assay workflow is a genome-wide microarray genotyping assay that utilizes the BeadChip platform.[1] This accurate and flexible microarray technology allows for the ability to interrogate a large number of SNPs through unlimited loci multiplexing.[2-4] However, overcoming the 200ng standard input for this assay is essential for forensic genomics, as it is rare to obtain DNA at such high quantities from forensic samples. Previous work to optimize sensitivity of the assay demonstrated a total DNA input <1.0ng successfully generated high-quality genotyping data.

An additional challenge this method faces with forensic samples, other than DNA quantity, is the quality. For SNP genotyping analysis, the quality of the data is critical. The goal of the degradation study is to evaluate how the severity of DNA degradation affects the quality of the SNP data.

The severity of DNA degradation in traditional Short Tandem Repeat (STR) analysis can be visualized as it presents an identifiable sloped pattern demonstrating the interruption of the polymerase during amplification. As the amplification chemistries are fundamentally different between STR and SNP typing, it is hypothesized that the form of DNA degradation could have less of an impact on the genotyping data.

For this study, genomic DNA was experimentally degraded using Ultraviolet C (UV-C) light at defined intervals up to 1.®J/cm^2. Samples were quantified pre- and post-treatments and typed using GlobalFiler® to confirm degradation. The STR profiles coupled with the Degradation Index (DI) from the quant method demonstrated that as the dosage increased, so too did the amount of degradation (quantified via visual pattern in the profile and increase in DI). Five samples expressing specific degradation patterns based on STR results were selected for genome-wide SNP genotyping, in duplicate, on the iScan to evaluate the performance of the Infinium™ Global Screening Array in its ability to accurately type Low-Copy Number (LCN) degraded DNA sample types.

Analysis of the SNP data showed similar trends in most aspects. Concordance of the degraded samples did trend down as the dosage amount increased. Concordance was performed between treated samples and a control sample run alongside. One metric used to evaluate the performance of the assay is the call rate, which is a percentage of the total number of SNPs genotyped over the total number of SNP targets in the assay. When evaluating the samples using this metric, the trend was unexpectedly parabolic. As the dosage level increased, the curve trended down, then re-bounded and began increasing, resulting in the 0.0mJ/cm^2 and the 1.0J/cm^2 samples having very similar call rates.

Reference(s):

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SNP Genotyping, Forensic Genetic Genealogy, DNA Degradation