B112 The Identification of Cadaver Liver Tissues Using Postmortem Transcriptome Biomarkers

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Learning Overview: After attending this presentation, attendees will have learned how to use postmortem messenger RNA (mRNA) transcripts in decomposing tissues to gain insight into the identification of tissue segments arising from organs collected from actual cadavers from ongoing criminal cases. Precisely, attendees will understand that RNA is stable in cadavers' liver tissues and is adequate for profiling gene expression and that gene expression signatures of mRNA exposed for up to 37 days of autolysis can be used to identify putative tissue fragments.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing information on the determination of internal organ sources from criminal casework that may assist in death investigations.

The human transcriptome is the complete expression of mRNA transcripts produced in all tissues. Approximately 10% of mRNA transcripts are encoded by tissue-enriched genes and a variety of genes are enhanced to a greater extent in one tissue type, some up to five times the maximum levels of all other tissues. RNA quality is contingent on tissue source; for example, liver and spleen are more abundant in ubiquitous RNases that degrade RNA molecules more rapidly and with a higher activity than less RNase-rich tissues (e.g., heart and muscle).

This study hypothesized that as a human body decays, mRNA profiles will permit organ identification using biomarkers on bona fide autopsy-derived sources. This study is the first of its kind to use actual cadaver tissue from ongoing criminal cases in a postmortem transcriptome identification assay. To test this hypothesis, total RNA was extracted and the approach was prioritized by performing targeted transcriptome analysis using RNA sequencing (RNA-Seq) in liver tissues obtained at autopsy from 30 criminal casework cadavers in Italy and the United States. Fifty nanograms of total RNA were converted to complementary DNA (cDNA) using reverse transcriptase and random primers. Targeted Oligonucleotide Pool (TOP) was hybridized to the cDNA on a streptavidin bead matrix. The resulting libraries were sequenced on the MiSeq® instrument. Percent contributions of liver biomarkers versus Postmortem Interval (PMI) for the overall set were determined and graphed. The results demonstrated that in each of the cadavers, the tissue was correctly identified as a liver sample. Furthermore, 98%–100% of the reads were attributable to liver biomarkers (e.g., AMBP, AHSG).

In conclusion, the results demonstrate as a proof of principle that a specific 8-biomarker liver assay is capable of identifying the original source of liver specimens from using cadaver tissue. The results also confirm that RNA molecules are stable in postmortem liver samples up to seven days, which makes RNA a sufficient molecule for gene expression studies. The design of this study validates a technique that will meet the demand for rapid and reproducible postmortem transcriptome methods to identify tissue fragments present in a variety of medicolegal investigations.

Criminal Cases, RNA Sequencing, Organ Tissue Identification

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