H138 The Thanatotranscriptome: An Assessment of Messenger RNA (mRNA) Abundances in Cadaver Prostate Tissues

Sheree J. Finley, MS, Alabama State University, Forensic Science Program, 915 S Jackson Street, Montgomery, AL 36104; Mariah Tolbert, BSc, 611 Marlyn Drive, Prattville, AL 36067; Silvia D. Visona, MD, University of Pavia, Via Forlanini 12, Pavia 21100, ITALY; Antonio M.M. Osculati, MD, University of Pavia, Via Forlanini 12, Pavia 27100, ITALY; and Gulnaz T. Javan, PhD, Alabama State University, Forensic Science Program, 915 S Jackson Street, Montgomery, AL 36104*

After attending this presentation, attendees understand how to use the thanatotranscriptome of prostate tissues to gain further insight into apoptotic pathways after death. Precisely, attendees will understand that RNA is stable in cadavers' prostate tissues and is sufficient for profiling gene expression for up to 60 hours.

This presentation will impact the forensic science community by providing information on transcriptional mRNA abundance profiles of postmortem prostate tissues in which there is a paucity of previous studies.

Molecular autopsy has the potential to provide valuable information to establish the cause and manner of death in medicolegal investigations. Gene expression studies are well-established components of antemortem research with broad applications ranging from elucidating basic mechanisms responsible for physiological processes to ascertaining therapeutic targets in pathophysiological conditions; however, gene expression studies and their applications in the medicolegal field are still in their infancy. The thanatotranscriptome, or "transcriptome of death," involves the study of mRNA transcripts occurring in human tissues after death (*thanatos*, Greek for death). The identification of transcript abundances in human body tissues through mRNA-based profiling is potentially useful for forensic investigations.

It was hypothesized that there are detectable and significant disparities in transcript abundances in cadaver tissues from homicide and suicide victims compared to individuals who succumbed to natural causes. The intent of this study was to determine molecular markers (i.e., mRNAs) that provide accurate information regarding the cause and/or manner of death. This study investigated genetic studies involving organ- and manner-of-death-specific profiling of apoptosis gene expression panels through the application of Polymerase Chain Reaction (PCR). This procedure was performed using postmortem prostate tissues from actual criminal cases from the University of Pavia, Italy. Complementary DNA (cDNA) was synthesized and RNA concentrations were measured. The goal of this study was to provide detailed insight into expression of 84 key genes involved in complex apoptotic pathways from prostate tissues.

The results demonstrate that at 38hrs Postmortem Interval (PMI), most of the genes related to induction and positive regulation of apoptosis, Caspases, are upregulated more at 60hrs PMI. This finding suggests that apoptosis is upregulated compared to the control group. Several antiapoptotic genes, such as BCL2 and BCL2 A genes, are more expressed in 38hrs, but at 60hrs, they are drastically reduced in expression and, in some cases, to the insignificant fold-change level. These outcomes propose that initially, in the control group, cells fight with their antiapoptotic machinery; however, later, proapoptotic machinery takes over.

In conclusion, this study demonstrates that RNA molecules are stable in postmortem prostate samples, which makes RNA a sufficient molecule for gene expression studies. This study design validates a technique that will meet the demand for rapid and reproducible thanatotranscriptomic methods. These novel techniques will correlate apoptotic gene expression patterns as possible biomarkers compared to classic methods by expanding the capacity of molecular autopsy techniques.

Thanatotranscriptome, Prostate, RNA

*Presenting Author