MRNA PROFILING OF BODY FLUIDS; STABILITY WITH EXPOSURE TO RAIN

Mara L. Lennard Richard[1,3], Vivian Y. Chu[1,3], Barbara W. Koons[1], Rhonda L. Craig[2], Richard Guerrieri[2], James M. Robertson[1]
[1]Counterterrorism and Forensic Science Research Unit, FBI Academy, Quantico, VA
[2]DNA Unit 1, FBI Laboratory Division, Quantico, VA
[3]Oak Ridge Institute for Science and Education, Oak Ridge, TN

Novel molecular techniques for analyzing gene expression profiles within a tissue or cell type through messenger RNA (mRNA) may offer advantages when compared with existing conventional serological testing, especially in the areas of sample size and analysis time. Due to compatibility with current DNA extraction methods, mRNA based analysis has the potential for co-extraction of both nucleic acids from one sample. While it has been suggested that mRNA is inherently unstable and is rapidly degraded by ubiquitous RNases, it has been documented that high quality RNA can be recovered from body fluid stains stored at room temperature for up to 15 years. For forensic samples, the stability of RNA within body fluid stains after exposure to various environmental conditions, including the effects of rainfall, must be considered. To address this issue, a small scale study was designed to expose 72 samples of semen, saliva, and blood to the environment and rainfall conditions. The samples were placed on cotton sheeting, blue jeans or cotton swabs. One set of samples was harvested after the first heavy rainfall and a second set that was exposed to the environment the entire time was harvested after a one month time period. Serological tests were also preformed on the samples at both time points. Additionally, RNA was extracted and the samples were then transcribed to cDNA for mRNA profiling. The study indicated that for all three materials more RNA was isolated from the samples subjected to one month's exposure than those harvested after the first heavy rainfall. However, once transcribed to cDNA, the pattern was reversed meaning more cDNA was detected in the first heavy rainfall samples. This observation could be due to the accumulation of contaminating RNA from fungi or pollen, or to an increasing amount of sample degradation resulting in partial cDNA transcription in the one month samples. The mRNA profiling results were analyzed for the expression of a housekeeping gene and body fluid specific markers. The results of the serological analysis were then compared to the mRNA profiling results.