EXAMINING PARTITION EFFICIENCY OF CELL TYPES FOLLOWING QIACUBE/EZ1® ADVANCED XL DIFFERENTIAL EXTRACTION

Badiah Hannon[1,2], M.S.; Rachel Houston[1], Ph.D.; Tim Kalafut[1], Ph.D.
[1]Department of Forensics, Sam Houston State University
[2]Houston Forensic Science Center

Forensic laboratories are experiencing high demand to analyze sexual assault samples due to the increasing backlog of sexual assault kits (SAKs). To combat the ever-growing backlog, laboratories are encouraged to employ a direct to DNA (DTD) approach. This approach eliminates serology or screening of swabs contained in the kits. The most common serological tests for semen are the acid phosphatase (AP) color change test, antigen-based tests for semenogelin and the prostate specific antigen (PSA/p30), and the microscopic identification of spermatozoa.

While these serology tests are useful in screening biological evidence, they sometimes fail to identify semen and have various false positive reactions. Based on the condition of the evidence, influenced by storage conditions and passage of time, sometimes these tests are not as sensitive as the PCR process used for quantifying male DNA and/or the actual genetic typing. In addition, these serology steps require additional time, and consume or destroy part of the evidence. However, without this serological testing, or when these tests give mixed results, there may be much uncertainty about the nature of the biological source of the male DNA.

Differential extraction was developed to isolate male sperm from mixtures containing male and female cells following sexual assault. This process results in two fractions, the first is designed to recover DNA from non-sperm cells (F1, epithelial, or non-sperm fraction), and the second is designed to be enriched for male DNA from sperm cells (F2 or sperm fraction). In this study, the fractionation of male DNA from various body fluids following differential extraction was examined. The amount of male DNA present in the non-sperm and sperm fractions for each fluid was observed. Based on this data, we were able to determine a difference in fractionation between samples containing sperm and samples not containing sperm.

This data supports the suggestion that sperm partitions differently in the differential extraction compared to non-sperm samples. Given this different fractionation pattern, it may be possible to give an opinion about the male cell type present in the sperm fraction even with no – or ambiguous – serology results. We suggest that laboratories evaluate the male DNA partitioning in their differential extraction process. This would allow an evaluation of the DNA results given the male DNA comes from sperm cells rather than some other cell type.