B70 "The Sexome": Identifying Unique Microbial Signatures in Male and Female Pairings

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Learning Overview: The goal of this presentation is to inform attendees of sexual assault case relevance and confidence in the determination of a sexual act.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by developing scientific confidence in sexual assault case reports in determining that a sexual act has occurred, even without the presence of spermatozoa. This could also prove fundamental to sexual assault research to cases in children who are subject to frequent assault by family members.

Sexual assault casework typically involves analysis following the collection of a vaginal sample. The presence of spermatozoa in a vaginal sample exhibits as viable proof that a sexual act has occurred. Resulting analyses may also indicate the identity of the assailant by means of profiling the biological DNA present in a sample. However, the presence of spermatozoa can deteriorate over time or be completely absent from a mixed sample due to a number of factors such as the assailant is aware that the deposit of seminal fluids can implicate in a possible profile. Another factor to consider is that there may be, by chance, a complete absence of spermatozoa in the seminal sample due to a possible vasectomy or a condition of azoospermia or oligospermia. Ultimately, each circumstance would likely result in a profile that is unable to be determined. Current research methods are examining the human microbiome as a means of profiling by the identification of unique bacterial signatures in specific areas of the body. Recent studies are attempting to determine the typical bacteria in the urogenital microbiome for means of identifying male- and female-specific species of bacteria. The aim of this particular study is to examine the urogenital microbiome of male-female pairings to identify unique bacterial signatures, and if these signatures transmit following intercourse.

There were 10 consensual heterosexual couples who participated in the study (20 participants in total). Each couple were instructionally directed to sample their own genitalia prior to and following intercourse. Pre-coital samples were sampled three to four days post-menses (for females). Post-coital samples were collected approximately two to six hours following intercourse to best replicate typical reporting periods for sexual assault victims. These samples where extracted using a PureLink™ Microbiome DNA Purification Kit and subsequently sequenced by the 16S Ribosomal RNA Gene Amplicons for the Illumina® MiSeq® System to identify sex-independent, unique bacterial signatures in males and females and subsequent transmission. Sequenced data was analyzed by the MiSeq® Reporter software for classifications of organisms from the V3 and V4 amplicon via a 16S rRNA database. This classification is based on the Greengenes database and the output was read at each taxonomic level to identify unique bacteria in the male and female microflora.

While human microbiome research is in its relative infancy, future studies should be conducted to understand and discriminate the male and female microbiomes. In particular, examining the unique microflora of their urogenital microbiome. It would develop the scientific confidence in sexual assault cases to determine that the sexual act has occurred. Additionally, future studies could improve the capability of detection of male bacteria in female sexual assault victims, ultimately resulting in enhanced profiling methods and confidence for females in reporting sexual assaults. This particular research would also serve well for sexual assault cases where male DNA fractions are not detected via typical analyses. It could also prove fundamental to sexual assault research to cases in children who are subject to frequent assault by family members.

Sexual Assault, Microbiome, Bacteria