B154 The Utility of the Human Hair Microbiome in the Forensic Analysis of Human Hairs

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Learning Overview: After attending this presentation, attendees will gain a better understanding on bacteria associated with human hair and its temporal stability.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing a foundation about the human hair microbiome and its potential use in casework.

Hair is among the most commonly found pieces of evidence at a crime scene, yet it doesn't contain much probative value unless the root is present. Previous research has explored the hair microbiome to unlock evidentiary hair's full probative potential, but they used small sample sizes. The main goals of this study were to identify the core bacterial taxa associated in human pubic and scalp hairs in both sexes and examine the temporal stability of the hair microbiome at room temperature. To accomplish these goals, pubic hair (n=58; 33 female and 25 male), and scalp hair (n=65; 40 female and 25 male) sample were collected and stored at 25°C for zero week (Baseline), six weeks, and twelve weeks in an incubator. DNA extraction was performed within a day after collection for baseline samples and after six and twelve weeks for other samples. 16S ribosomal DNA (16S rDNA) high-throughput sequencing was performed on all samples using dual-index strategy on Illumina MiSeq FGx sequencing platform. Data analysis was performed in mothur and in SPSS. Firmicutes, Actinobacteria, Proteobacteria, and Bacteroidetes constitute almost 97% of all bacteria associated with human hairs. In both sexes, bacterial diversity of pubic hair was much higher than bacterial diversity of scalp hair. Significant difference in bacterial structure was observed between pubic hair and scalp hair. This difference was mainly because of high relative abundance of Proteobacteria in scalp hair. Bacterial structure was also significantly different between male and female pubic hairs. This difference was mainly because of high relative abundance of *Lactobacillus, Prevotella,* and *Gardnerella* in female pubic hair. Although, bacterial structure associated with female scalp hair was significantly different than bacterial structure associated with male scalp hair in Chi square test, the same was not true in analysis of molecular variance (AMOVA). In both pubic and scalp hair, bacterial diversity decreased with increase in storage time at room temperature. Bacterial structure associated with baseline samples were significantly different than bacterial structure associated with twelve weeks samples, and this difference was mainly because of increase in relative abundance of Betaproteobacteria with storage time. In conclusion, the study provides evidence that time, origin on body, and sex all play a role in the hair microbiome and understanding these variables provides a foundation for using hair in future forensic analysis of hair.

Human Hair, Bacteria, 16s rDNA