## H32 Postmortem Hair Microbiome and Its Forensic Applications

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**Learning Overview:** After attending this presentation, attendees will better understand bacteria associated with human hair samples collected after death.

**Impact on the Forensic Science Community:** This presentation will impact the forensic science community by helping forensic scientists find new ways for analysis of hair evidence during death investigation.

Human hair is often encountered at crime scenes. However, those hairs most often found don't often contain nuclear DNA needed for the current human DNA workflow. This survey of the microbiome associated with human hair can aid researchers in determining whether hair can be useful in Postmortem Interval (PMI) estimation as well as in determining whether the area from which the hair is collected is important. This analysis was performed as part of an ongoing investigation into the microbiome of hair samples. Previous research has shown that in living humans, bacteria associated with scalp hair are significantly different from those bacteria associated with pubic hair in both sexes. We also know that bacteria associated with pubic hair of males are significantly different than those bacteria associated with pubic hair of females. One question that remains unanswered is how hair microbiome is affected after death, and whether the scalp hair microbiome changes depending on the area of the scalp it is collected from. To understand this, scalp and pubic hair samples were collected from ten human cadavers from the United States (Office of the Chief Medical Examiner, Richmond, VA) and from 25 human cadavers from Europe (Medicolegal Institute of Paris, France). For the European population, scalp hair samples were collected from frontal, occipital, left and right parietal, and vertex regions of the scalp, whereas for the American population, scalp hair samples were collected from a single location. Pubic hair samples were collected from a single location in the pubic area in both populations. All samples were stored at -80°C. DNA was extracted from approximately one inch of finely cut hair samples using the Tridico et al. method with the addition of zirconium bead beating.[1] Samples were then amplified using dual-index 16SrDNA MiSeq® sequencing using the protocol as described by Kozich et al.[2] Sequences were then analyzed using mothur version 1.39.4, and statistical analysis was performed using R version 3.4.0.[3,4]

Preliminary results indicate that the bacterial structures associated with scalp hair are significantly different from those associated with pubic samples. The majority of bacteria found in scalp and pubic hair samples belong to the phyla Cyanobacteria, Proteobacteria, Spriochaetes, and BRC1, varying only in their relative abundances. When comparing the genera, pubic hair samples show much higher relative abundance of *Staphylococcus*, where scalp hair showed a higher relative abundance of *Selenomonas, Vagococcus,* and *Streptococcus*. However, initial tests did not indicate significant variation between male and female pubic or scalp hair samples. As the majority of samples were obtained from Caucasian donors, no determination was made on whether race impacted the microbiome of hair samples.

In conclusion, this ongoing study provides information on the bacterial communities associated with hair samples collected from human remains. This information will help provide better understanding of the usefulness and utility of hair associated microbial communities in forensic investigations.

**Reference(s):**

1. Tridico, S.R., Murray, D.C., Addison, J., Kirkbride, K.P., and Bunce, M. (2014). Metagenomic Analyses of Bacteria on Human Hairs: A Qualitative Assessment for Applications in Forensic Science. *Investigative Genetics*, 5(1), 16. https://doi.org/10.1186/s13323-014-0016-5.
2. Kozich, J.J., Westcott, S.L., Baxter, N.T., Highlander, S.K., and Schloss, P.D. (2013). Development of a Dual-Index Sequencing Strategy and Curation Pipeline for Analyzing Amplicon Sequence Data on the MiSeq Illumina Sequencing Platform. *Applied and Environmental Microbiology*, *79*(17), 5112–5120. http://doi.org/10.1128/AEM.01043-13.
3. Schloss, P.D. et al. Introducing Mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. *Appl. Environ. Microbiol.* 75, 7537-7541, doi:10.1128/AEM.01541-09AEM.01541- 09 [pii] (2009).
4. *R: A Language and Environment for Statistical Computing.* (R Foundation for Statistical Computing, http://www.R-project.org, Vienna, Austria., 2011).

**Hair Microbiome, Necrobiome, 16S rDNA**