B122 Human Identification Using the Skin Virome

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Learning Overview: After attending this presentation, attendees will have a better understanding of the potential for using viral DNA samples from humans' skin as an alternative genetic marker. This study presents data from research demonstrating that sufficient genetic diversity exists in a portion of the viral meta-populations residing on human skin to create a DNA profile that may be appropriate for forensic identification.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by describing some of the different types of viruses that are commonly detected on human skin and the processes required to collect those virome samples and derive patterns from them suitable for comparisons. The relative abundance of viral particles on human skin and the wide range of classification groups, as well as the stability of those characteristics, will be shown. This study will offer the forensic community a new tool to potentially identify biological samples when human DNA is not present in usable quantities.

The human bacterial microbiome has already been examined as an alternative method for postmortem interval determination and as a biological marker in cases involving soil samples. The human virome offers additional advantages, as viral genomes are even smaller than those of bacteria and thus are potentially more stable. They also have a variety of transcription strategies (for example, double- and single-stranded), increasing the possible number of discriminating markers; and are present throughout the human body, including the skin and body fluids, making them transferrable. The copy number of viral genomes in a given volume is substantially higher as well, compared to the copy number of human or bacterial genomes, increasing the likelihood of isolating a sufficient quantity for successful testing.

This study recruited 60 adult subjects (25 male and 35 female) for sample collections, including two sets of co-habitating couples. Direct samples of the skin virome were collected from each subject at five time points over the course of six months (baseline, two weeks, one month, three months, and six months) from each of their hands and their scalp. A pipeline was developed for viral isolation, amplification, and sequencing. This method used the inherent small size of viral particles to remove bacteria and other large cells (fungi, human, etc.) away from the viral particles by filtering with a 0.2 micron filter. The resulting viral particles were lysed and the DNA from viral particles extracted using the QIAamp® MinElute Virus Spin Kit. The resulting DNA was then amplified using Multiple Displacement Amplification (MDA) with the Sygnis TruePrime® WGA Kit and associated protocol to increase viral DNA yields. The amplified DNA was used for library preparation and sequencing on the Illumina® HiSeq platform. Library barcoding and preparation was performed using New England Biolab's NEBNext Ultra II library preparation kit. In addition to the virome samples collected from each study participant, metadata was collected with each sampling regarding use of hand sanitizers, hand and hair washing intervals, travel, and contact with domestic animals.

Quantitation of viral DNA and sequencing results show that the collection and preparation protocols developed in this study provided large amounts of testable virome DNA. Samples from every person and time point have been successfully processed, while human and bacterial sequences were filtered out, ensuring data quality. Analysis of the sequence information showed that virome patterns of specific viral groups can be clearly and easily differentiated among the study subjects, the majority of the virome pattern is the same between the different body parts, and each persons' virome pattern of these groups of interest did not demonstrate substantial changes between the first collection and the six-month collection.

Virome, DNA, Human Identification

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