

Accepted Manuscript

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PII: S1872-4973(18)30022-X
DOI: <https://doi.org/10.1016/j.fsigen.2018.06.020>
Reference: FSIGEN 1918

To appear in: *Forensic Science International: Genetics*

Received date: 18-1-2018
Revised date: 1-6-2018
Accepted date: 28-6-2018

Please cite this article as: Quaak FCA, van Duijn T, Hoogenboom J, Kloosterman AD, Kuiper I, Human-associated microbial populations as evidence in forensic casework, *Forensic Science International: Genetics* (2018), <https://doi.org/10.1016/j.fsigen.2018.06.020>

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Human-associated microbial populations as evidence in forensic casework

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Highlights

- Forensically relevant body sites harbor diverse microbial populations
- Microbial targets can be used for human cell type identification
- Microbial population analysis has proven to be more valuable than looking for indicator organisms
- Human DNA profiling and microbial population analysis can be performed on the same DNA extract

Abstract

In forensic investigations involving human biological traces, cell type identification is often required. Identifying the cell type from which a human STR profile has originated can assist in verifying scenarios. Several techniques have been developed for this purpose, most of which focus on molecular characteristics of human cells. Here we present a microarray method focusing on the microbial populations that are associated with human cell material. A microarray with 863 probes targeting (sets of) species, specific genera, groups of genera or families was designed for this study and evaluated with samples from different body sites: hand, foot, groin, penis, vagina, mouth and faeces. In total 175 samples from healthy individuals were analysed. Next to human faeces, 15 feline and 15 canine faeces samples were also included. Both clustering and classification analysis were used for data analysis. Faecal and oral samples could clearly be distinguished from vaginal and skin samples, and also canine and feline faeces could be differentiated from human faeces. Some penis samples showed high similarity to vaginal samples, others to skin samples. Discriminating between skin samples from different skin sites proved to be challenging. As a proof of principle, twenty-one mock case samples were analysed with the

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