A new method for extracting skin microbes allows metagenomic analysis of whole-deep skin

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In the last decade, an extensive effort has been made to characterize the human microbiota, due to its clinical and economic interests. However, a metagenomic approach to the skin microbiota is hampered by the high proportion of host DNA that is recovered. In contrast with the burgeoning field of gut metagenomics, skin metagenomics has been hindered by the absence of an efficient method to avoid sequencing the host DNA. We present here a method for recovering microbial DNA from skin samples, based on a combination of molecular techniques. We have applied this method to mouse skin, and have validated it by standard, quantitative PCR and amplicon sequencing of 16S rRNA. The taxonomic diversity recovered was not altered by this new method, as proved by comparing the phylogenetic structure revealed by 16S rRNA sequencing in untreated vs. treated samples. As proof of concept, we also present the first two mouse skin metagenomes, which allowed discovering new taxa (not only prokaryotes but also viruses and eukaryots) not reachable by 16S rRNA sequencing, as well as to characterize the skin microbiome functional landscape. Our method paves the way for the development of skin metagenomics, which will allow a much deeper knowledge of the skin microbiome and its relationship with the host, both in a healthy state and in relation to disease.
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