

Characterization of the human skin resistome and two microbiota cutotypes

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Abstract

Skin microbes play fundamental roles in maintaining balance in the skin. An imbalance – microbial dysbiosis – is associated with the onset and progression of many common skin diseases. To better understand the functions of skin microbes, a recent study aimed to develop a catalog of skin microbiome reference genes. Using a sample of 822 skin samples from Han Chinese individuals, combined with 538 previously obtained North American samples, researchers constructed the integrated Human Skin Microbial Gene Catalog, or iHSMGC, comprising over 10 million genes. Using the catalog, they found that skin commensals such as *Staphylococcus* are an important reservoir of antibiotic resistance genes (ARGs). Microbe- and skin site-specific ARG signatures were identified, as were differences between populations. Two patterns of microbial networks – “cutotypes” – were identified in the newly analyzed samples, with *Moraxella osloensis* and *Cutibacterium acnes* serving as markers of the cutotypes. Distinct patterns of marker genes, functional modules, and host skin properties were observed, suggesting that host-dependent factors might underlie their development. The development of the iHSMGC will facilitate further studies of the human skin microbiome, and the present findings contribute to better understanding of the interpersonal complexity of our skin microbes.