Genome Biology

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Skin microbiome in health and disease

Julie A Segre[1*], Elizabeth A Grice[1], Heidi H Kong[2], Sean Conlan[1], Evan Snitkin[1], Lilia Mijares[3], Patrick Murray[3], Eric D Green[1], Maria L Turner[2]

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Human skin serves as the first line of defense against pathogenic bacteria, while also providing a home to billions of symbiotic bacteria. By sequencing the DNA of bacteria collected from the skin of humans and mouse models of human disease, we investigated how these bacteria contribute to health and, conversely, how changes in the bacterial community structure might contribute to chronic skin disorders.

Our analysis of 16S ribosomal RNA gene sequences obtained from 20 distinct skin sites of healthy humans revealed that physiologically comparable sites harbor similar bacterial communities and provides a baseline for studies that examine the role of bacterial communities in disease states and the microbial inter-dependencies required to maintain healthy skin. We explored the selective shift in the microbiota observed in skin disorders commonly treated with antimicrobial agents such as eczema and diabetic wound healing. For example, we show that a longitudinal selective shift in wound microbiota coincides with impaired healing in diabetic mice. We demonstrate a parallel shift in longitudinal gene expression that occurs in a cluster of genes related to the immune response. Furthermore, we establish a correlation between relative abundance of *Staphylococcus* spp. and the expression of cutaneous defense response genes. These data demonstrate that integrating two types of global data sets lends a better understanding to the dynamics governing host-microbe interactions. Clinical management of these disorders requires better biomarkers to realize the therapeutic potential of manipulating the microbiome. Targeted therapies to maintain healthy skin might require not only inhibiting the growth of pathogenic bacteria, but also promoting the growth of symbiotic bacteria. Microbiome studies show the power of bridging genomics and clinical medicine to gain valuable insight into the human body as a complex super-organism.

Author details
[1]NISC Comparative Sequencing Program, NHGRI, NIH, Bethesda, MD 0892-4442, USA. [2]Department of Dermatology, CCR, NCI, NIH, Bethesda, MD, USA. [3]Department of Laboratory Microbiology, NIH Clinical Center, NIH, Bethesda, MD 20892-751 1, USA.

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[1]NISC Comparative Sequencing Program, NHGRI, NIH, Bethesda, MD 0892-4442, USA
Full list of author information is available at the end of the article