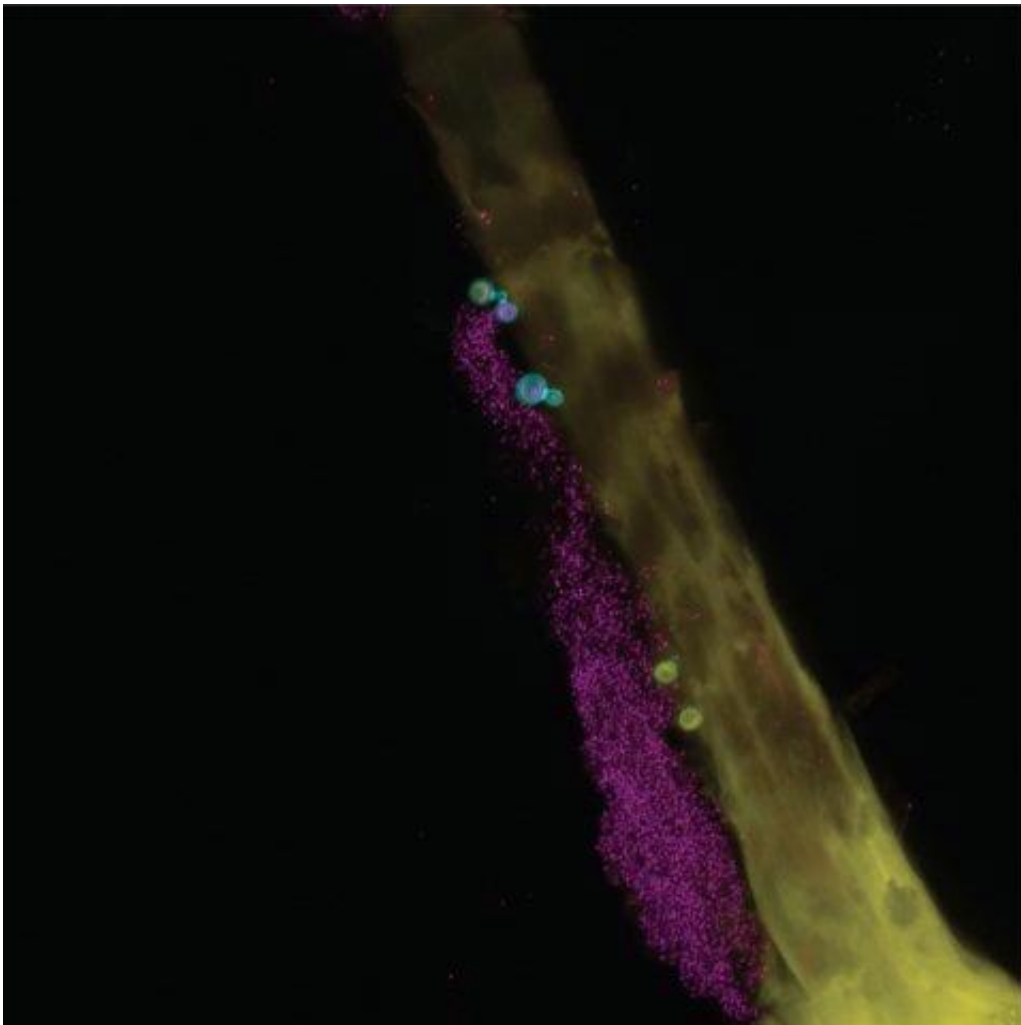


Researchers conduct first genomic survey of human skin fungal diversity

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Images show a hair follicle in the skin surrounded by bacteria and fungi under a fluorescent microscope. The samples were obtained from skin on the back of a study participant. Fungi appear blue-green, bacteria appear pink and skin cells and the hair shaft appear yellow. Credit: Alex Valm, NHGRI

While humans have harnessed the power of yeast to ferment bread and beer, the function of yeast or other types of fungi that live in and on the human body is not well understood. In the first study of human fungal skin diversity, National Institutes of Health researchers sequenced the DNA of fungi at skin sites of healthy adults to define the normal populations across the skin and to provide a framework for investigating fungal skin conditions.

Human [skin](#) surfaces are complex ecosystems for microorganisms, including [fungi](#), bacteria and viruses, which are known collectively as the skin microbiome. Although fungal infections of the skin affect about 29 million people in the United States, fungi can be slow and hard to grow in laboratories, complicating diagnosis and treatment of even the most common fungal skin conditions, such as toenail infections.

The research team from the National [Human Genome Research](#) Institute (NHGRI) and the [National Cancer Institute](#) (NCI), both parts of NIH, extended their recent genome sequencing study of skin bacteria, using DNA sequencing techniques optimized for identifying fungi. The study appears in the May 22, 2013 early online issue of *Nature*.

The researchers found that a single type of fungus, belonging to the genus *Malassezia*, is predominant on the head and trunk. Hands, which harbor a great diversity of bacteria, are home for relatively few types of fungi. In contrast, feet, including toenails, heels and toe webs contain tremendous diversity.

"Applying DNA sequencing to a study of the skin's fungi is the natural progression in understanding [microbial life](#) that co-exists on our bodies," said NHGRI Scientific Director Daniel Kastner, M.D., Ph.D. "Along with recent genome sequencing to define [bacterial diversity](#), this analysis of fungal diversity provides a more complete human microbiome picture."

"Fungal communities occupy complex niches, even on the human body," said Heidi Kong, M.D., co-senior author and an investigator in the dermatology branch of NCI's Center for Cancer Research. "By gaining a more complete awareness of the fungal and bacterial ecosystems, we can better address associated skin diseases, including skin conditions which can be related to cancer treatments."

The researchers collected samples at 14 body sites from 10 healthy adults. DNA sequencing of the fungi in the samples identified fragments of DNA, called phylogenetic markers, which can be counted and used to distinguish one type of fungus from another. The sequencing efforts generated more than 5 million markers, from the samples, representing more than 80 fungal types, or genera. In contrast, traditional culturing methods produced 130 colonies of fungi that represented only 18 fungal genera.

In 20 percent of the study participants, the researchers observed problems such as heel and toe web scaling or toenail changes consistent with possible fungal infections. From genome sequencing analysis, the researchers found that different individuals with heel site infections have common fungal communities at that site, while those with toenail infections display tremendously different fungal communities.

"DNA sequencing reveals the great diversity of fungi, even those that are hard to grow in culture," said Julie Segre, Ph.D., co-senior author and senior investigator, NHGRI Genetics and Molecular Biology Branch. Her expertise is the development of microbial DNA sequencing technology. "DNA sequencing enabled us to learn immeasurably more about where fungi predominate as a part of the human skin microbiome."

The researchers identified fungi from two phyla, Ascomycetes and Basidiomycetes, as part of the normal fungal census at the 14 skin sites.

The most common genus *Malassezia* was present in 11 of 14 sites sampled on the body. The researchers found *Malassezia* fungus on every skin surface of healthy volunteers, whether on the back of the head, behind the ears, in nostrils and on the heels. Heels were also home to many additional fungi, including the genera *Aspergillus*, *Cryptococcus*, *Rhodotorula*, and *Epicoccum*.

"DNA sequence-based methods of identification enabled us to differentiate among species of fungi and to conclude that the diversity of fungi is highly dependent on the body site rather than the person who is sampled," said Dr. Kong. A dermatologist, Dr. Kong explained why these sites were selected for exploration: "Our study focused on areas of the skin where we commonly find skin diseases that have been associated with fungi."

The most complex site, the heel, is home to about 80 genus-level types of fungi. The researchers found about 60 types in toenail swab samples and 40 types in samples from the webs of the toes. Sites with moderate fungal diversity are inside the bend of the arm, inside of the forearm and palm, with each location supporting 18 to 32 genera of fungi. Surprisingly, head and trunk body sites—including the back, back of the neck, inside the ears, behind the ears, and between the eyebrows—have far fewer fungi types, with just two to 10 genera each.

The research team compared fungal diversity data with the [skin bacteria](#) on the same healthy adults. They found that while arms have high measures of bacterial diversity, they have lower fungal diversity. They found the reverse to be true for sites on the feet. Core body sites had neither a high bacterial diversity nor a high fungal diversity. The researchers had previously shown that bacterial diversity can be predicted by whether skin is moist, dry or oily. Fungal diversity, instead, seems to depend upon where a particular skin site is on the body.

The researchers observed, in addition, that there is greater similarity in the fungal community structure on the left and right sides of the same person's body compared to the same body parts on any two individuals. Fungal communities also appear to be quite stable over time, with little change when tested on two separate occasions, up to three months apart.

"The data from our study gives us a baseline about normal individuals that we never had before," Dr. Segre said. "The bottom line is your feet are teeming with fungal diversity, so wear your flip flops in locker rooms if you don't want to mix your foot fungi with someone else's fungi."

More information: [dx.doi.org/10.1038/nature12171](https://doi.org/10.1038/nature12171)

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