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Effects on the Human Microbiome: Antibiotics and other Chemicals

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Abstract

With skin being the largest organ of the human body, there is a very large surface area for a microbiome to form and live. The human microbiome is composed of different types of bacteria, fungi, and archaea, in different locations of the body. This layer can be greatly affected by daily practices including, hygiene habits, exercise, and antibiotic uses. The major objective of this study is to identify species of the human microbiome from various body sites and test their resistance to major chemicals. To achieve this objective, the mouth, ear, axillary area, hand, belly button, and foot of several individuals will be swabbed, and the resulting microbial growth will be tested for resistance against several antibiotics and household chemicals. The results of this study will help with the understanding of antibiotic resistance and other mechanisms for resistance across the human body. These results could also help in the future by preventing the spread of disease and potentially preventing further antibiotic resistance.

Introduction

We as humans have a natural microbiome composed of thousands of bacterial species that act as a first line of defense over the surface of our skin. Every individual has a unique composition of their microbiome based on where they live, hygiene habits, gender, and other varying factors. There is a lot of current research being done on the human microbiome. Some bacteria, good or bad, have begun developing resistance to antibiotics or other chemicals as they are being frequently exposed to them. This has led scientists to study and understand how some bacteria can become resistant to chemicals that once would have killed them.

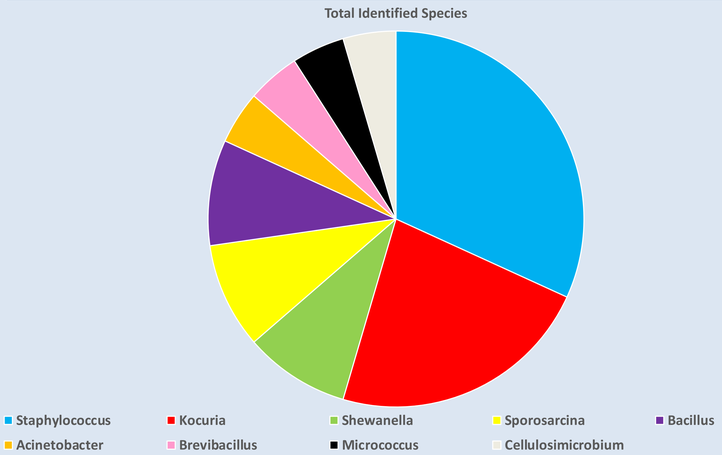

Figure 2. Total Identified Species on Human Body Samples Collected

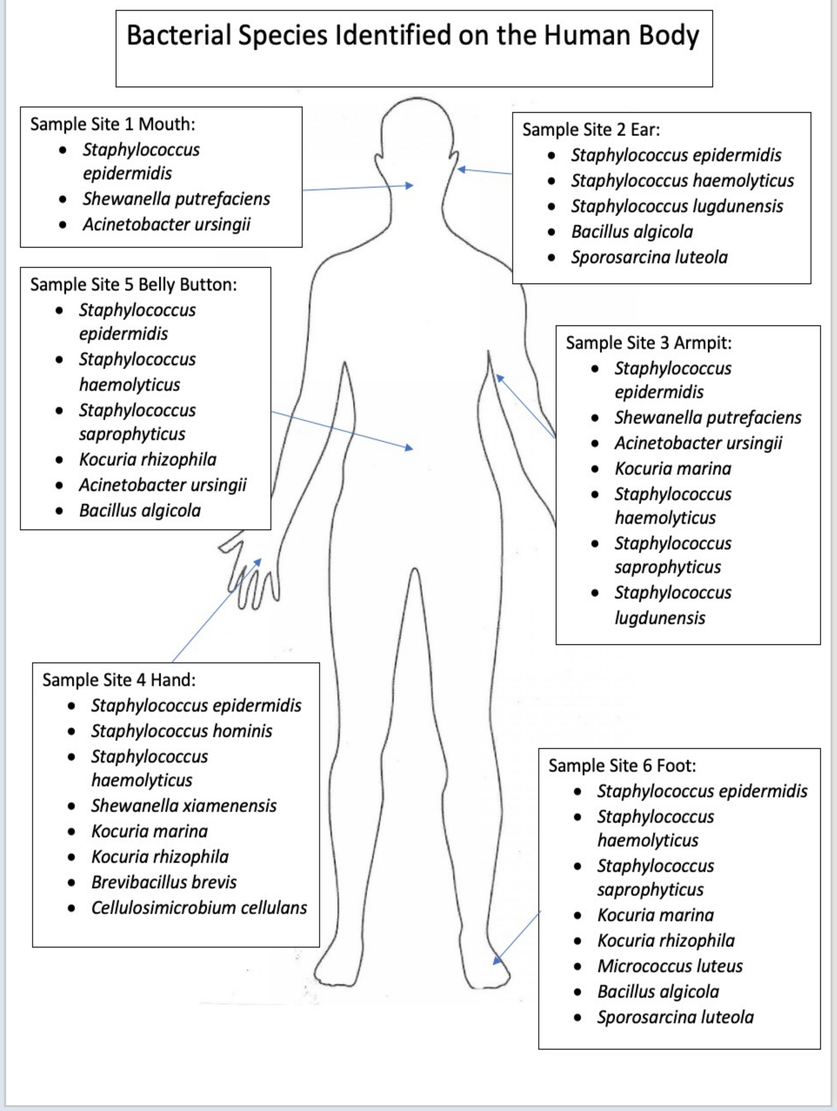

Figure 1. Bacterial Species Identified from volunteer samples

Methods

- Samples were collected from the mouth, ear, axillary area, hand, belly button, and foot of 11 individuals. These individuals were all students from the University of Southern Maine.
- Samples were spread and grown on agar petri dishes
- Colonies were then isolated
- PCR was run on 37 of the different species found from the 66 total samples collected

<u>Still to come:</u>

- Antibiotics will be tested on the known species
- Household chemicals will be tested (i.e.. hand soap, deodorant etc.)

Objective

The objective of this study was to identify bacterial species found in various locations on the body and test for antibiotic resistance or inhibitions from other chemicals.

Results

Of the 66 samples from volunteers, 37 bacterial species were isolated, and PCR identified the genera and species of most of them. We were able to confirm 18 of those belonged to the genera: *Staphylococcus, Kocuria, Shewanella, Actinobacter, Bacillus, Sporosarcina, Brevibacillus, Cellulosismicrobium, Micrococcus*. The species types are listed in the locations they were found in Figure 1. You can see the proportion of how many bacterial species were found in Figure 2.

Some trends already noted, based on the amount of colony growth, indicated that antiperspirant or deodorant played a large role in the volume of bacterial growth present. People who wore deodorant had little to no growth and people without deodorant had a wider variety of species present.

Discussion

So far, we have successfully isolated and identified 18 species from the samples collected. The next step is to begin antibiotic tests on the confirmed species types and look for antibiotic resistance trends. This will help the goal of the research, seeing how the microbiome can be affected by antibiotics and other household chemicals. Already there has been a noticeable difference in bacterial growth in people who wear or do not wear a deodorant or antiperspirant.

The genera listed above do agree with other scientific research as they are commonly found on the human body. Some samples came from soil or marine life, and this could play a role in the environment in which these samples were collected. Other factors that could affect the microbiome are gender, hygiene habits etc.

Acknowledgements

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