Identification of Archaea Associated with Recovery from Antibiotic Exposure

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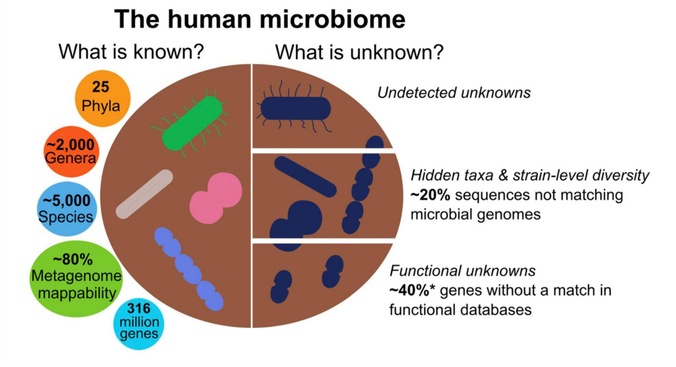
ABSTRACT

Dysbiosis, or a microbial imbalance, of the human gut microbiome has been associated with numerous immunological and neurological disorders. Antibiotic exposure, among others, is one of the leading causes of gut dysbiosis, and can lead to increased risk of health issues if the gut microbiome does not recover after exposure. However, there may be microbiota normally present that aid in recovery from antibiotic-exposure, including fungi and archaeal species. This study focused on determining if there are fungi or archaea associated with gut recovery by comparing the detected presence of archaea in hosts that have recovered and not recovered from antibiotic exposure. The results indicate that there are no fungal or archaeal species associated with recovery from antibiotic-exposure.

INTRODUCTION



GMFH Editing Team GMFH Editing Team. (2020, March 24). The knowns and unknowns of the human microbiome. Retrieved May 11, 2021, from https://www.gutmicrobiotaforhealth.com/the-knowns-and-unknowns-of-the-human-microbiome/

The Human Microbiome

The human microbiome is a complex system of microorganisms unique to each individual that plays an important role in maintaining host health(1). An imbalance in this microbial community is called dysbiosis. In the human gut microbiome, dysbiosis has been associated with a multitude of disorders, diseases and immune dysfunction(2)(3)(4).

Antibiotic Use and Gut Dysbiosis

One major cause of gut dysbiosis is the usage of antibiotics. Antibiotic use disrupts the levels of pathogenic and commensal microbes, allowing for the formation of empty niches that can be filled by pathogens or an overgrowth of normal flora(5). Studies have suggested that the long-term effects of antibiotic usage may include increased risk of infection(6) and metabolic disease(7).

Fungi in Gut Microbiome

The role of bacteria and its interaction with antibiotics in the gut microbiome has been extensively studied, but the role of fungi in the gut microbiome has not. Just under 280 fungal species have been identified in the gut microbiome(8), but dysbiosis of the fungal communities has been associated with diseases such as Type 2 diabetes mellitus(9) and bacterial keratitis(10). Fungi appear to play an important role in host health, and the loss of normal bacteria may cause issues from fungal overgrowth.

HYPOTHESIS

There are fungal species associated with gut microbiome recovery from cefprozil.

METHODOLOGY

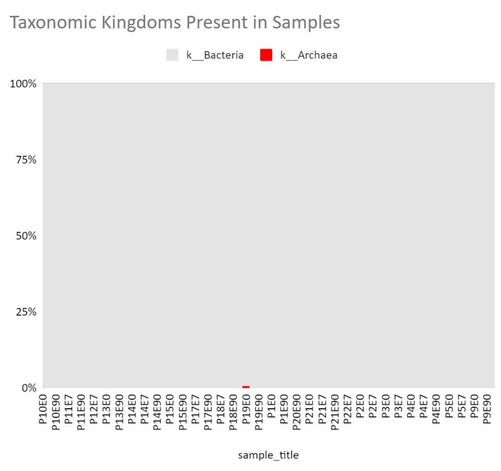
Data Accession and Analysis:
- Data uploaded to Qiita[11] from "The initial state of the human gut microbiome determines its reshaping by antibiotics"[12]

Identification of Gut Microbiota:
- Gut microbiota determined through kingdom and species level barplots

Recovery Determination:
- Diversity levels across three time points (Day 0, 7, and 90: pre-, during-, and post-exposure respectively) determined using Simpson's Diversity Test
- Recoverers: similar or higher diversity at Day 90 as seen at Day 0
- Non-Recoverers: lower diversity at Day 90 as seen as Day 0

Identification of Recovery-Associated Archaea:
- Two-tailed student *t*-test performed between recoverers, non-recoverers at each timepoint
- Hypotheses used were H_0: $\mu_1=\mu_2$ and H_A: $\mu_1\neq\mu_2$, alpha level of 0.1.

RESULTS

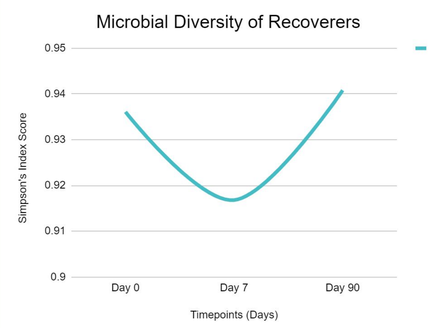


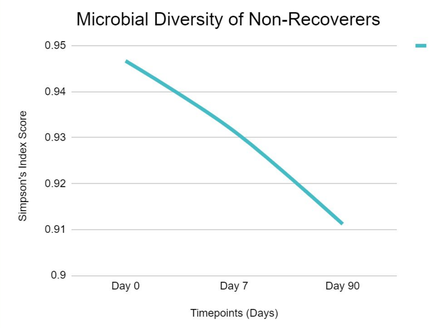
Microbiota

The only two kingdoms found to be present in the samples were Bacteria (99% to 100% of the sample depending on the sample) and Archaea (0% to 1% of the sample depending on the sample). No Fungi were detected in any samples.

Microbial Diversity

Using the data from the Simpson's Diversity Index, the samples were sorted into recoverers and non-recoverers. Recoverers showed a similar or higher diversity after exposure as they showed prior to exposure (P2, P9, P10, P11, P12, P13, P17, P21, P22). Non-recoverers showed a lower diversity after exposure compared to prior to exposure (P1, P5, P15, P18, P19, P20).





Day 0 Results

Top five most prevalent species: *M. smithii, M. smithii CAG:186, M. millerae, M. mazei, M. archeon Phil4* (recoverer-specific), and *M. archeon Methan_05* (non-recoverer-specific).
The respective p-values :0.55, 0.55, 0.58, 0.39, 0.52, and 0.36.

Day 7 Results

The top five most prevalent species:*M. smithii, M. smithii CAG:186, M. mazei, M. archeon Phil4, M. millerae* (recoverer-specific),and *M. archeon Methan_05* (non-recoverer-specific).
The respective p-values: 0.96, 0.95, 0.52, 0.48, 0.82, and 0.36.

Day 90 Results

The top five most prevalent species: *M. smithii, M. smithii CAG:186, M. mazei, M. archeon Phil4, S. acidocaldarius* (recoverer-specific) and *M. archeon Methan_05* (non-recoverer-specific).
The respective p-values:0.94, 0.92, 0.42, 0.90, 0.32, and 0.47.

DISCUSSION

Lack of Fungal Presence

As expected, the majority of the samples were made up of bacterial species. However, there was no fungal presence detected in any of the samples, suggesting that the original hypothesis is not supported. However, for there to be no fungal species found in any of the samples is strange. There are a few possible explanations:

1. Fungi are not a normal gut microbiota
2. The fungal species present were not able to be classified by the Qiita software.
3. The sequencing process that produced the data was mislabelled as metagenomic, when it should have been 16S (eukaryotes do not have 16S rRNA)

Archaeal Association with Recovery

While there was no detected fungal presence, there were archaeal species detected, and the focus of the study shifted to determining how archaea are associated with recovery. Though the differences between each of the top five species of non-recoverers and recoverers for each time point seemed significant, all student t-tests resulted in p-values much greater than the alpha level of 0.1. As such, the null hypothesis that the mean values of the five species are not different between recoverers and non-recoverers must be accepted. This suggests that there are no archaeal species associated with recovery from antibiotic exposure.

CONCLUSION

- Hypothesis not supported: no fungi present in any sample, no fungi associated with recovery from antibiotics
- No archaeal species that appear to be associated with recovery from antibiotics
- Future work: look at more samples for fungal presence and look at split between archaeal and bacterial diversity

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