

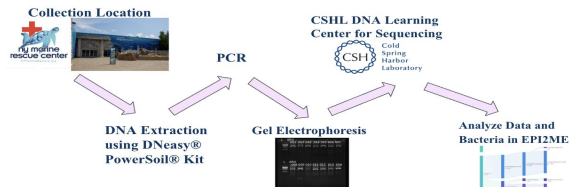
Abstract

This project intends to use Next Generation Sequencing (NGS) techniques to assess the gut microbial diversity of seals to understand how a GI condition, like cancer, can bring about changes in microbial species profiles. With cooperation from marine and zoological facilities from around the United States, microbial DNA will be extracted from a variety of seals, some potentially GI affected. We plan to analyze the microbes present to determine the presence of GI disease. Microbial species profiles will be developed using Illumina sequencing and data will be processed using the DNA Learning Center's Purple Line metabarcoding tool. As a practical application, it may be possible to use the information learned about seal gut microbiomes to develop a noninvasive assay useful for identifying cancers prior to animal death. Our results demonstrated a majority presence of microbes such as Firmicutes that indicate GI issues.

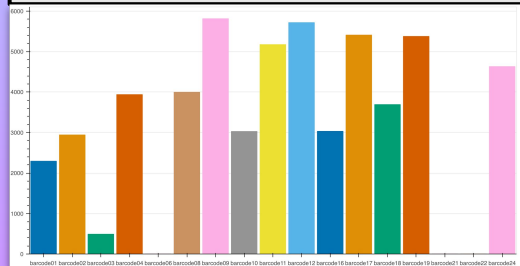
Introduction

By utilizing the interrelationship between gut microbes and cancers we can predict and detect cancers in seals by employing the research founded on the correlation between them. Each microbe performs functions that may affect the development of the cancer. Being able to identify these microbes can help us detect the possibility of this cancer earlier as well as understand how each one is affecting this cancer in seals. Seals excrete daily and they usually defecate on land, so it is easy to collect and it is easy to link the feces to a particular seal. It has been demonstrated that bacteria induce an immune response that activates particular host immune cell subtypes that identify and eliminate cancer cells as antigens. If we know how the microbiome changes in seals we can use it as an asset in future research. Because of the limited findings, we had to switch our hypothesis to compare microbes prevalent in seals versus sea lions, while including and analyzing our data collection of microbes in both species.

Methods and Materials



Results



Indices : barcode01 barcode02 barcode03 barcode04 barcode05 barcode06 barcode07 barcode08 barcode09 barcode10

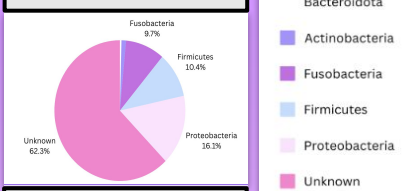
Simpson's index: 0.64 0.55 0.43 0.17 0.0 0.37 0.56 0.32

0 barcode11 barcode12 barcode16 barcode17 barcode18 barcode19 barcode21 barcode22 barcode24

0.36 0.43 0.42 0.72 0.83 0.42 0.0 0.0 0.7

Figure 2: Simpson's index - the closer the number is to 1, the more diverse the microbes. A number on the index is provided for each sample.

Seals



Sea Lions

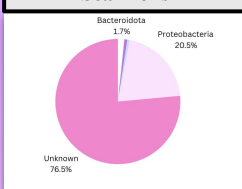


Figure 3: Ratio of microbes present in seals and sea lions

Seal: Java

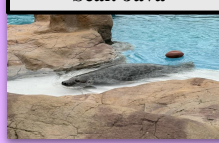


Figure 4: A picture of a Seal named Java. One of the specimen sample we analyzed.

Discussion

Healthy seals primarily had a higher prevalence of *Firmicutes* and *Bacteroidetes*. These bacteria are essential for digesting fibrous plant material, which aligns with the dietary habits observed in the controlled environments. However, the Sea Lions exhibited a slightly different microbial composition with a higher presence of *Proteobacteria* and *Actinobacteria*. This difference may be attributed to their varied diet and different environmental exposures compared to seals. These differences in microbial composition between seals and sea lions underscore the need to consider species-specific microbiomes when assessing gut health and disease potential. Drawing parallels from human studies, we can hypothesize the roles of these microbes in disease development. For example, *Fusobacteria* is consistently found in GI-affected individuals, suggesting its role in promoting inflammatory responses and cancer cell proliferation. Furthermore, for *Firmicutes*, their imbalance may contribute to metabolic disturbances, potentially exacerbating conditions like diabetes, which can indirectly influence cancer development.

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Research Paper and References

