Investigation Of Bacterial Communities Within the Microbiome of Tiger Sharks (Galeocerdo cuvier) in Biscayne Bay, Florida

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Introduction

• Every animal on Earth forms an association with microorganisms4
• The ocean contains the densest accumulation of microbes on Earth, therefore all marine organisms are exposed to a large and diverse group of microbes5
• Studies have provided much insight, but little is known about the interaction of microbes in shark health and immune defence and how it varies among different species and in diverse habitats.

Methods

• Sharks captured in South Florida via a circle-hook drumline system and then released once samples were obtained using a bacterial scraper.2
• Two cultures per sample were prepared, and incubated, then subcultured in the lab.
• DNA was extracted via Qiagen QIAmp DNA Mini Kit.
• Two cultures per sample were prepared, and incubated, then subcultured in the lab.
• DNA was extracted via Qiagen QIAmp DNA Mini Kit, and PCR was visualized using 6X TrackIT Cyan/Orange Loading buffer, and UV Transillumination in a Gel Doc system.
• Bacterial genus and families were identified via sequencing following PCR and the NCBI BLAST system.

Results

Abstract

Within Biscayne Bay, Florida, a preliminary study was completed on the tiger shark (G. cuvier) to create an understanding of the baseline bacterial makeup of the microbiome. Knowing the makeup of a healthy shark’s microbiome could lead to helpful insights to investigate microbial communities on various tissues of tiger sharks in the wild.

Figure 1. The ratio of gram-negative to gram-positive bacteria found in each of the tissue sites.

Figure 2. Cell Morphology Occurrences by Tissue Type. Bacillus, cocci and spirilla were quantified by absence or presence on the slides of tissue types skin, mouth, and gills.

Figure 3. Bacterial genus makeup of various tissue sites and water samples of G. cuvier. The number of occurrences present in the samples is documented in comparison to the tissue site.

Figure 4. Familial make-up of sample results. The percentage of each bacterial family found and identified on the tissue sites.

Table 1. Sample sites listed with specific family and genus plus observed gram stain results.

Discussion

• Investigating the relationships that exist in host tissues with bacterial communities may be important to understanding the health of the shark and its environment.6
• Tiger sharks exhibited both gram positive and gram negative bacteria.
• The mouth and skin samples contained the highest diversity of bacterial groups among tissue sites tested.
• Found in the mouth and gills, pseudalteromonas sp. mainly synthesizes biologically active molecules when present. It may provide the host with some protection from other microbes.
• Arthrobacter spp. have been shown to absorb heavy metals, behaving like an inorganic adsorbent. This bacterium was found in the mouth of tiger sharks 7
• Bacillus, which was found in mouth and skin samples, sometimes contains Bacillamide, an algicide that acts against a harmful dinoflagellate. This dinoflagellate is often responsible for many fish deaths during harmful algal blooms, making bacillus an important symbiont for animals living through these events 8
• Water samples had completely different bacterial families than any of the tissue sites, indicating that there may be limited horizontal transmission from surrounding water.

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References