

The Identification of Resident Bacteria and the Comparison of the Gut and Skin Microbiome in Captive Bat Rays (*Myliobatis californica*)

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Background

Bat rays (Figure 1) are saltwater fish from the family Myliobatidae. They, like sharks, are elasmobranchs, meaning they are cartilaginous. Prior research on some species of stingrays has focused on the **mucus** of their skin and its **anti-microbial potential**.

A healthy microbiome is critical for the prevention of disease, and it also allows the rays to maintain **homeostasis**, both internally and externally. In order to maintain it, they **process urea** through their skin, producing an ammonia-like compound. It is unknown what effect this has on the resident microbiome, but it is theorized that this may have an **antimicrobial effect**.

This study aims to identify bacteria through swabs of the cloaca, as well as swabs of the wings. **Cloacal swabs** will be used to gain information about the digestive tract, while **wing swabs** will be used to describe the resident external bacteria and compare it to the environment.

Research Question

What microorganisms can be found in the microbiome of captive bat rays (*Myliobatis californica*) using epithelial and cloacal swabs?



Figure 1. Bat ray at the local aquatic facility where samples for analysis will be collected, photo courtesy of Emily Fleming

Methods

1. Three bat rays will be held for sampling using a plastic laundry basket and the help of animal attendants
2. 1 sterile swab per individual will be used to gently swab the cloaca (Figure 2)
3. The above procedure will be repeated using a separate swab on the animal's back (Figure 3)
4. These samples will be immediately plated on marine agar (Figure 5) along with a water and substrate sample
5. The samples will be allowed to culture for 2-3 days at or above 74 degrees F
6. Having obtained pure cultures, we will commence biochemical and genomic testing to identify the microbes present.
7. These results will be interpreted using a graph representing the unique microbial communities isolated from each swab (Figure 4).



Figure 2. Cloacal opening observed on the bat rays and location of swab site on the ventral side, photo courtesy of Emily Fleming



Figure 3. Top-down/dorsal view of a bat ray and location of swab site on the dorsal side, photo courtesy of Emily Fleming

Component Analysis of Microbial Communities Isolated from 3 *Myliobatis californicus* and their Environment

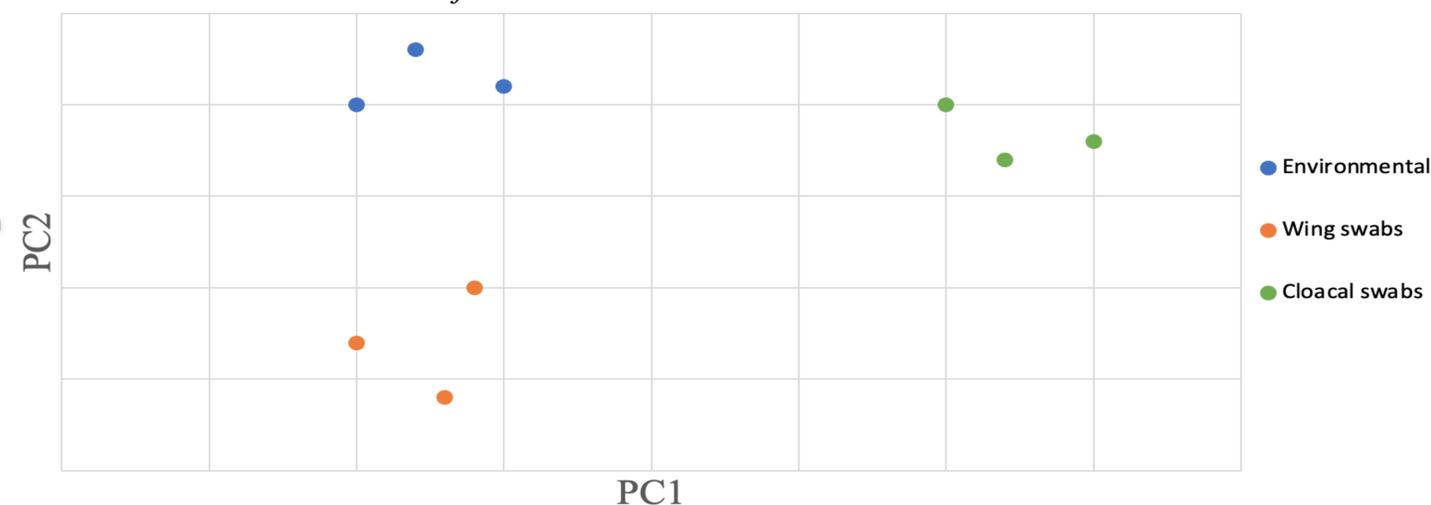


Figure 4. Example graph depicting the expected results of the experiment. It shows the bacterial communities and their similarities between individuals (Mb1, Mb2, and Mb3) and the environment (Ev1, Ev2, Ev3).

Expected Results

We expect to find a wide variety of bacterium types that differ between the skin and the cloacal opening (Figure 5). The cloacal opening is expected to feature obligate anaerobes that would have passed from the digestive tract, while the skin is expected to have its own unique microbes even compared to the environment (Kearns, et al). Despite the stingrays being touched by people frequently, we expect to find very few if any human microbes (Kearns, et al).

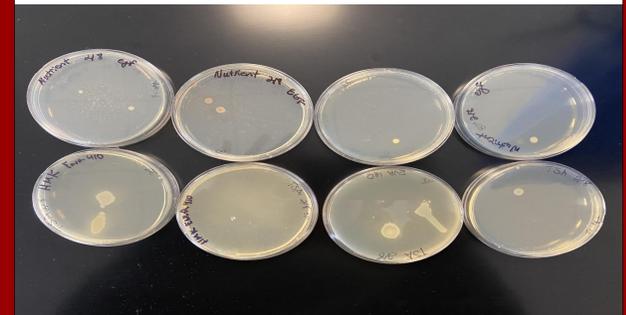


Figure 5. Sample agar plates used to isolate bacterial colonies from an environmental water sample, photo courtesy of Emily Fleming

Future Work

Further analysis of the microbiome of bat rays and research could not only lead to optimal captivity conditions, but also reveal the potential for antimicrobial compounds to be isolated from the bat rays' mucus, establishing a connection to the medical industry.

Acknowledgements and Work Cited

Kearns PJ, Bowen JL, Tlusty MF. 2017. The skin microbiome of cow-nose rays (*Rhinoptera bonasus*) in aquarium touch tank habitat. *Zoo biology* **36**: 226-230.

We would like to give a special thank you to Dr. Kyle Harris and Dr. Matthew Becker for their guidance during this project, as well as Ellisa Catahan for her invaluable guidance in the methods we used to undertake this study, and Jessica for knowledge of the species and aid in handling the bat rays during sample collection.

