

# Investigation into the Microbiome of the Little Skate, *Leucoraja erinacea*, and its Intersection with Toxicity Metabolism of the Host

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Microbes that inhabit the intestines of host animals have significant effects on physiology, development, and signaling systems of the host, including those aspects involved in processing environmental toxins. The core microbiome of the little skate, *Leucoraja erinacea*, a cartilaginous fish related to sharks and rays and a model for effects of pollutants on marine animals, was characterized by sequencing the spiral valve intestine. Samples were prepared from 11 skates captured in environments that include a polluted test site and control site in New Haven Harbor and from animals held in a lab setting with water from Narragansett Bay. 16s rRNA amplicons were generated from DNA in microbial communities. Primers followed the Earth Microbiome Project protocol (515F/806R). Greengenes database mining was used in the QIIME pipeline to identify 16s rRNA gene homologs.

Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria were the most prevalent genera; the control sample had the greatest diversity at the genus level, and the polluted sample the least, dominated by Proteobacteria. The bioinformatics software package PICRUSt and the KEGG database were employed to predict metabolic activity of the samples, with focus on environmental toxins. Bray-Curtis and UniFrac analysis in QIIME showed similar community content in the individual animals from the laboratory-setting environment, though an individual from a polluted site clustered near to both. Clustered samples had similar numbers of PICRUSt-predicted functional sequences.

While a greater range of individual samples is needed to assess differences between skate gut microbiomes with respect to environment, the similarity in top genera for each sample demonstrated the first representation of a core microbiome for the little skate.