

Beach vs Sewage Microbial Communities

Claire Borden and Clinton Charter, Dr. Lucia Carrau



Brooklyn Friends School and Uncommon Charter High School, Icahn School of Medicine at Mount Sinai

Abstract

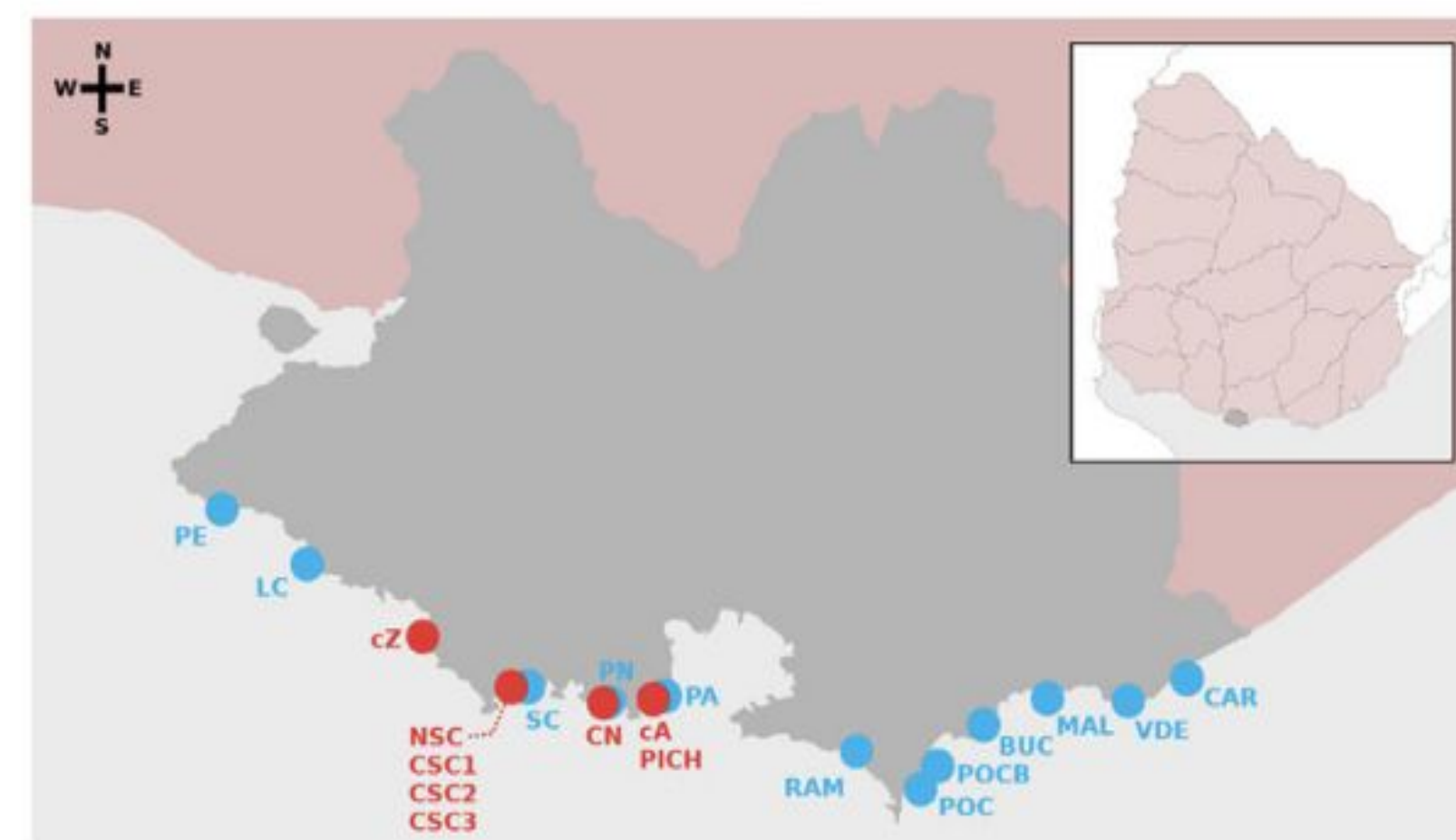
This project explored the similarities and differences between microbial communities (specifically looking at archaea, bacteria, and viruses) in different sewage and beach samples from Uruguay.

Introduction

We explored the question: What are the differences between the bacterial, viral, and archaeal families of microbial communities in different water environments, specifically in various sewage and beach environments in Uruguay? We wanted to learn about microbial communities and different microbes. This research is important to better understand the makeup of microbial communities and aquatic environments, specifically how they differ from one another.

Materials & Methods

We used raw data from “Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters” (Fresia et al. “Urban Metagenomics Uncover Antibiotic Resistance Reservoirs in Coastal Beach and Sewage Waters.” Microbiome, 2019). The data was collected, DNA extracted and Illumina sequenced.



The Number of Archaeal, Bacterial, and Viral Families in All of the Beach and All of the Sewage Samples

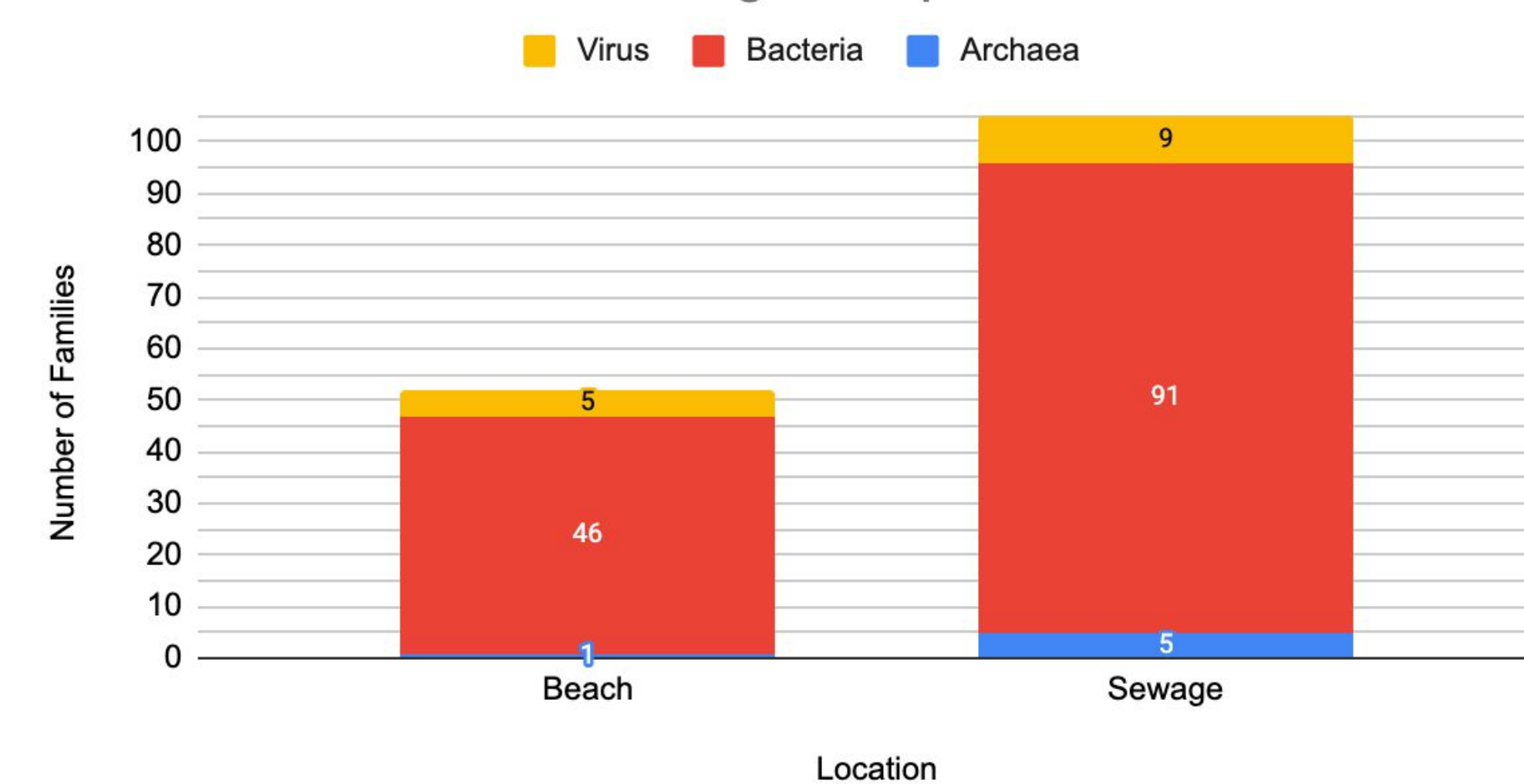


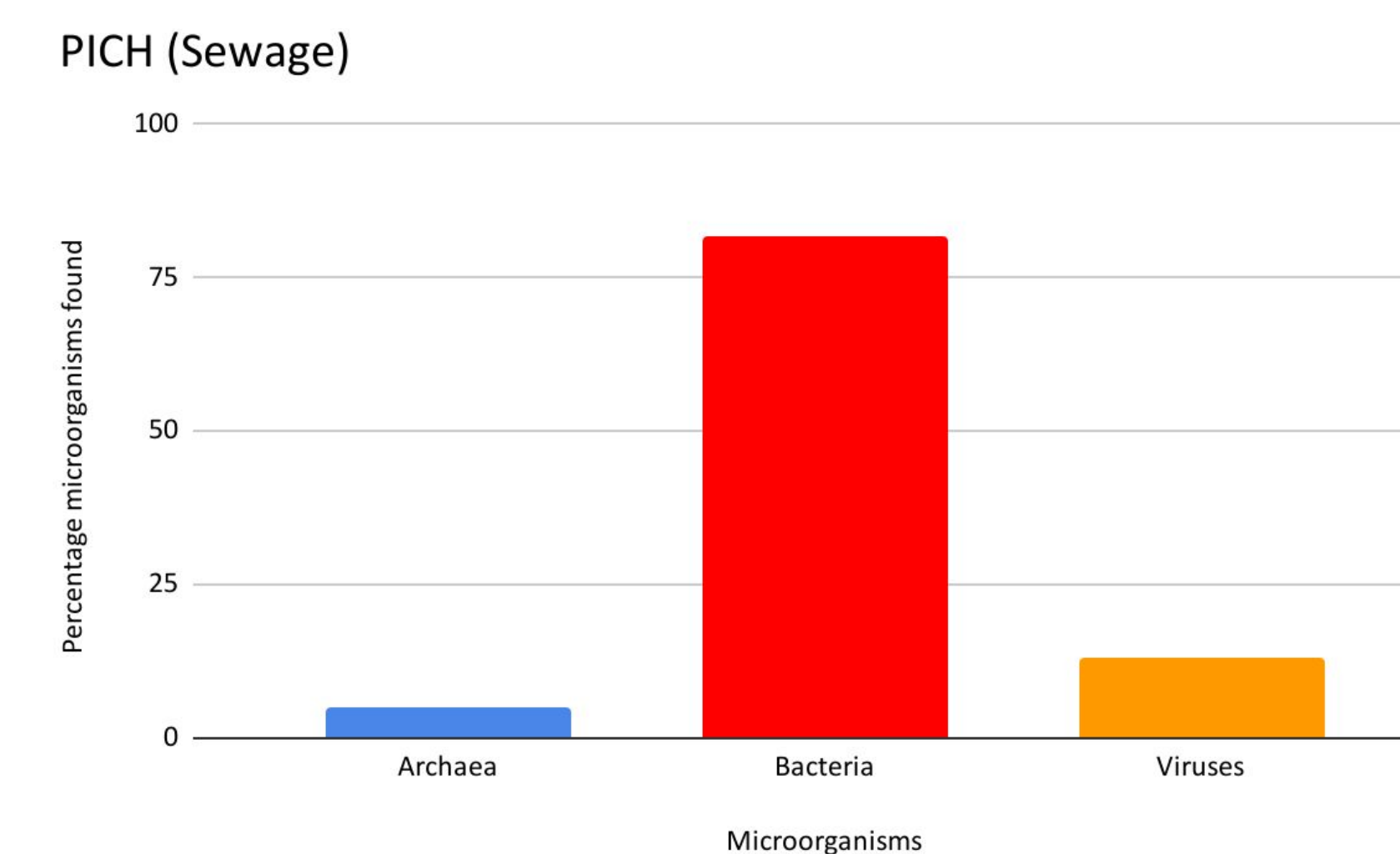
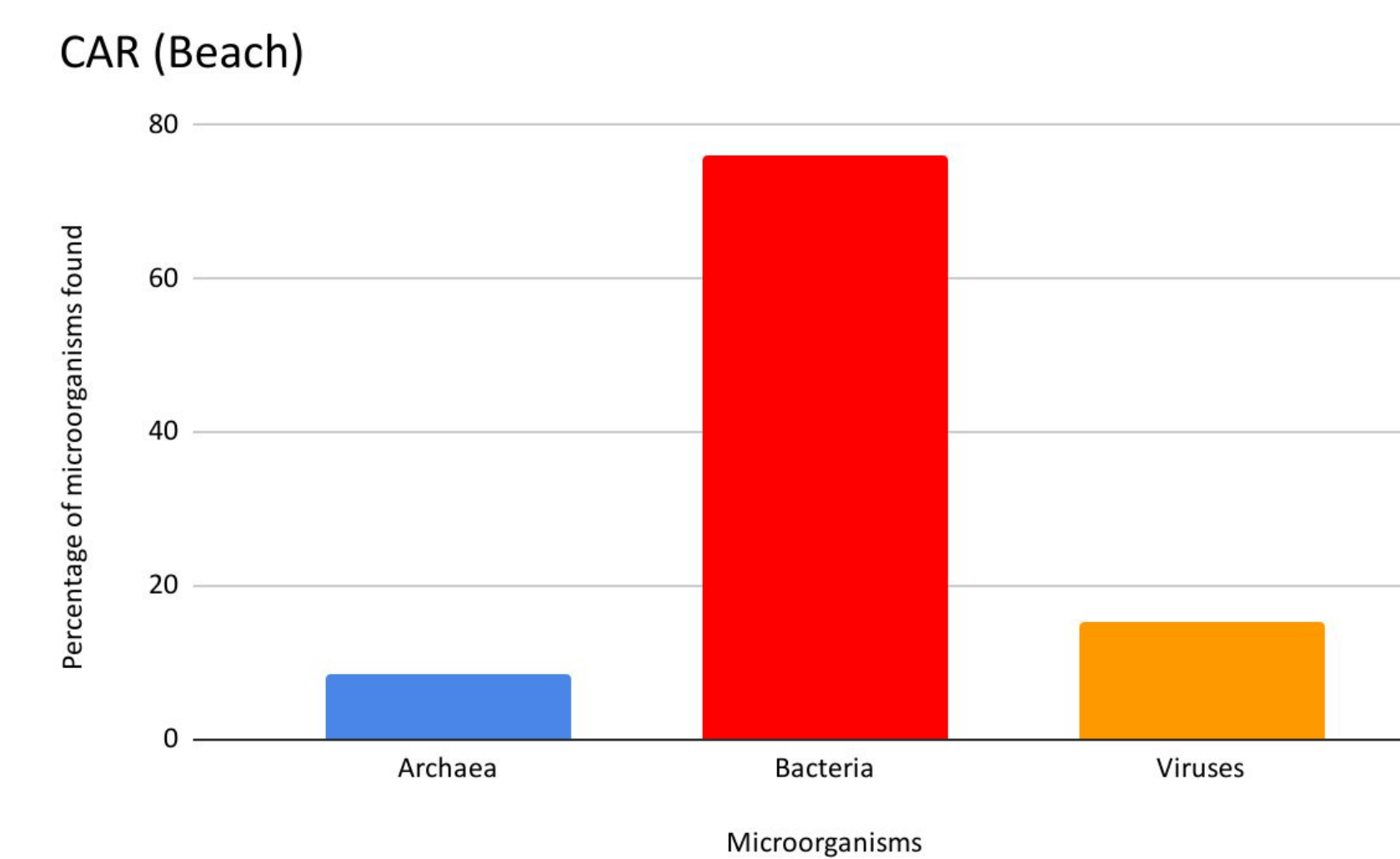
Table of the Ratio of Each Microorganism Type in All Beach and All Sewage Locations

Microorganism	Sewage	Beach
Archaea	2.20747375	3.292274167
Bacteria	94.03936625	94.19681
Virus	3.75316	2.739179091

Results

- Bacteria were the most abundant among the microbes
- Sewage water was more diverse than beach water
- PICH was the most diverse sewage, and CAR was the most diverse beach
- Four microbial families (in last table) were in every sample

Tables & Figures



Family	Beach			Sewage		
	100%	≥75%	Exclusive	100%	≥75%	Exclusive
Mycoplasmataceae						
Pseudomonadaceae						
Enterobacteriaceae						
Comamonadaceae						
Nitrosopumilaceae						
Moraxellaceae						
Iridoviridae						cZ
Parvoviridae						CSC2

Discussion

Despite our challenge of losing our original samples, the data we used allowed us to our original topics of interest: aquatic microbial communities and microbes. For our observations, we found bacteria is the most abundant in aquatic locations than archaea or viruses. Also, since more microbial families and individuals were found in sewage water, it has more biodiversity than beach water.

References

Fresia, Pablo, et al. “Urban Metagenomics Uncover Antibiotic Resistance Reservoirs in Coastal Beach and Sewage Waters.” Microbiome, 2019.

Acknowledgements

Thank you, Dr. Maria Carrau, for being our research mentor and gathering data for our project