Blue Devil Resistome Project

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Bass Connections in Information, Society & Culture

The Project

Antibiotic resistance has been called the biggest threat to modern medicine[1]. However, resistance has always been present in the environment[2]. The real problem is when resistance find its way into our food, homes, and hospitals where it can pair up with dangerous pathogens. This is where the Blue Devil Resistome project comes in.

Our Objectives

As Duke students, we asked three simple questions about the microbes and antibiotic resistances in our environment:

> **What are they?**
> **Where are they?**
> **When are they present?**

Only after learning more about the microbes around us and identifying areas at high risk for antibiotic resistance can we hope to stop its spread.

What We're Doing

Since summer 2017, we have been swabbing all over the Duke campus and measuring levels of antibiotic resistant microbes. By culturing swab samples on both broad and enteric media, we can estimate total microbial and potential pathogen load per site. We then isolate microbes of interest for follow-up whole-genome sequencing and resistance screening.
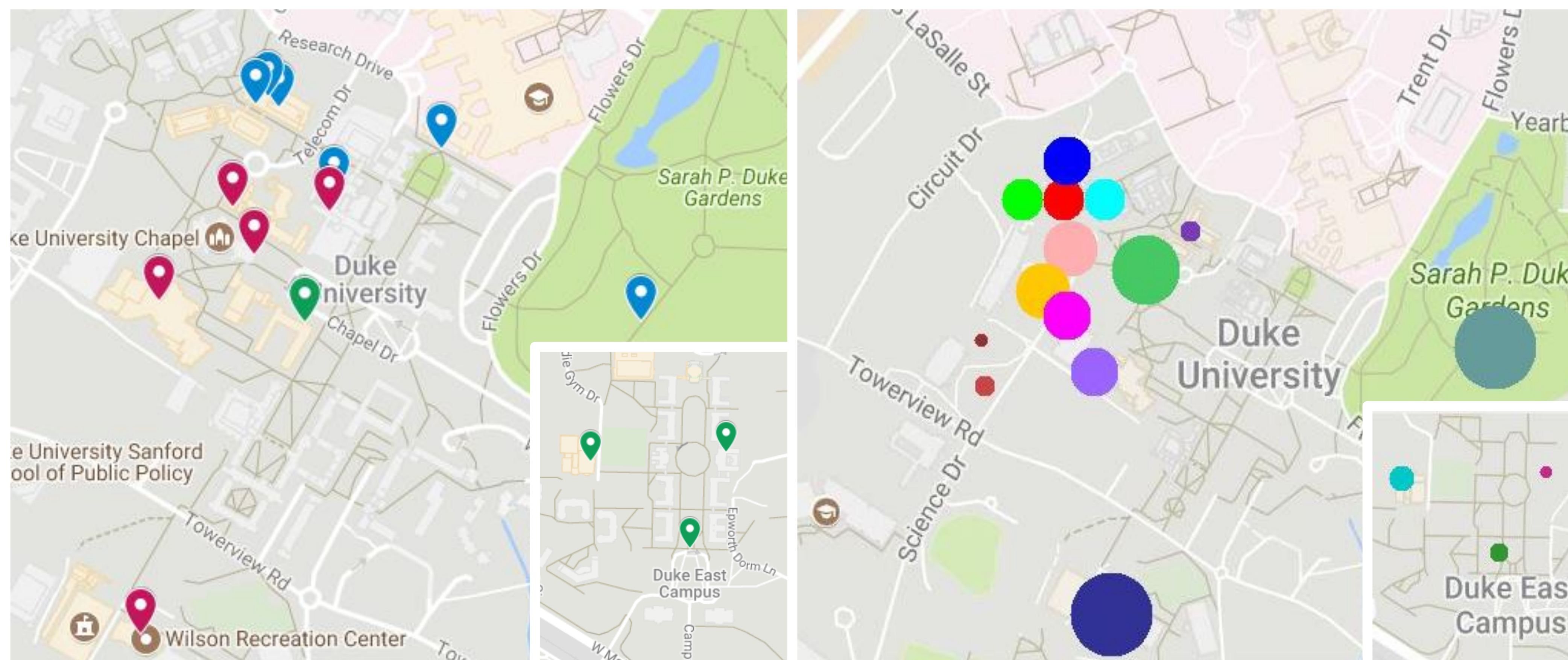

Figure 1. Maps of Duke campus with (a) sample site locations and (b) their relative microbial loads.
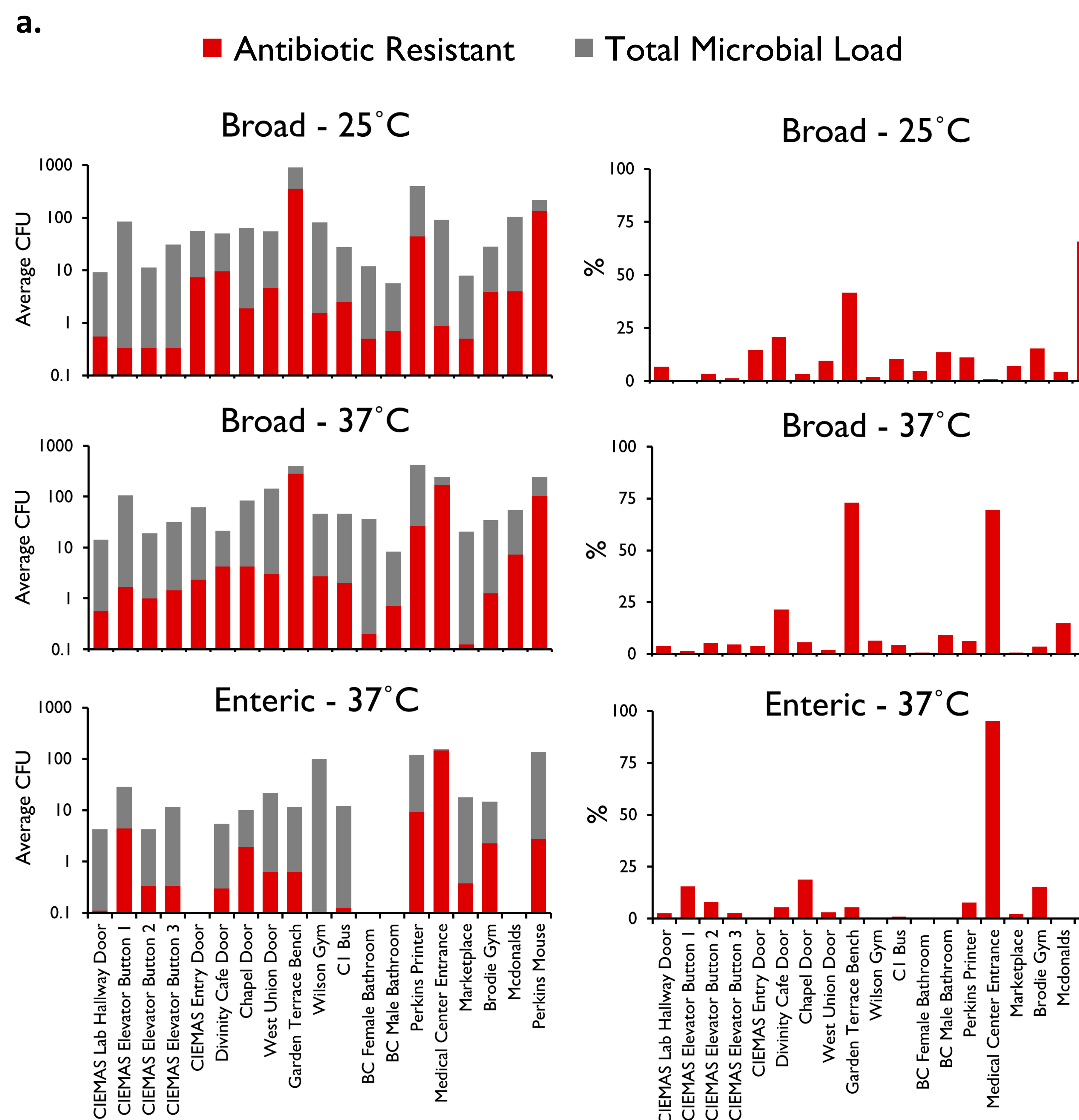

Figure 2. (a) Sample site colony forming units (CFU) and percent antibiotic resistant normalized by total microbial load. (b) Noteworthy pictures of plates during the course of the project.

Database Development

In parallel with experimental aspects of the project, we are developing a database integrated with a website to present our data and methodology. We hope to incorporate machine learning algorithms to more fully characterize the isolates we have collected in the future.

Figure 3. Using a SQL server for the database, updates of our progress can be found at http://bluedevilresistome.python anywhere.com/

Our Findings

We have already made a number of discoveries from our first two semesters of sampling. For example, sites with greater microbial loads generally exhibited a higher percent antibiotic resistant. While percent resistant remained consistent throughout the year, enteric microbial load displayed seasonal dependence. Moving forward, we aim to incorporate 16S rRNA and whole genome sequencing results to study bacterial diversity and track the epidemiological spread of antibiotic resistance. Once we've collected sufficient samples for this exploratory phase, we hope to examine the effect of social and/or sanitary interventions on microbial load, antibiotic resistance, and human behavior.

References

1. United Nations General Assembly (2016) **2.** Allen HK et al. (2010) Call of the wild: antibiotic resistance genes in natural environments. *Nature Reviews Microbiology*, *8*(4), 251–259.