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Microbial Diversity in Urban Environments: Concern for Antibiotic Resistance

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Abstract

Antibiotic resistance is a serious concern in the field of medicine as recent increase in antibiotic-resistant microbes can threaten infectious disease treatments. Overuse of antibiotics may lead to microbial resistance as bacteria exposed to various chemicals mutate enabling them to reduce or negate the effectiveness of antimicrobial drugs that are designed to kill them. Overuse of antimicrobial drugs in animal feed, crops and plants lead to increased concentration of antibiotics in our waters and soil. As bacteria mutate, they acquire new genetic elements contributing to antibiotic resistance. Soil being a large reservoir of environmental microbes, these elements find their way in soil bacteria. Therefore, we decided to identify the bacteria found in New York City's various soil environments and to determine their sensitivity (or resistance) to commonly used antibiotics. We identified bacterial isolates by Biolog system and tested their susceptibility to various antibiotics using Kirby-Baur method. Fortunately most of the bacteria isolated from different soil samples exhibited sensitivity to most of the antibiotics; however high percentage of isolates were found to be resistant to Penicillin. Resistance to Penicillin is plausible since Penicillin is one of the most widely used antibiotic. Awareness about microbial antibiotic resistance amongst general public is warranted.

Introduction

Antibiotic resistant bacteria pose a problem to human health. Since the discovery of antibiotics, most bacterial infections can be easily cured. The overuse and misuse of antibiotics, however, has caused some bacteria to become resistant and new antibiotics have had to be developed. The antibiotic resistance is polygenic trait controlled by various genes which can be transferred between bacteria and cause an antibiotic resistant population to grow (Blair and others 2016). The decline in biodiversity of microbes may be leading to the increase in allergies and a decrease in immunity against some microbes (Reese and others 2015). We expose ourselves to an unfathomable number of bacteria every day without our knowledge and sometimes certain types of bacteria can turn out to harmful to us. It has been seen that Streptococcus pneumoniae had increased resistance to the revolutionary drug penicillin shortly after twenty years from its discovery. The mutations in these microorganisms may occur in a relatively short amount of time and can spread quickly as well (Furuya and Loxy 2006). Local environments and human population presumably play a major role in determining the most frequent bacteria type you may encounter on a daily basis. To understand possible relationship between the highly populated environments and the types of bacteria present along with their antibiotic resistance, we will use DNA barcoding to isolate and identify the bacteria found at several public locations in and around New York City.

The purpose of this project is to identify the types of bacteria found in the various different locations and test for their antibiotic resistance. We hypothesize that the bacteria found in the areas with a larger flow of people such as public transportation and isolated area have different antibiotic resistant and have greater biodiversity. This will help us determine and understand any correlation between environment and the biodiversity of bacteria as well as their antibiotic resistance.

Materials & Methods

A total of 11 soil sediments from public areas and isolated locations were obtained. Locations were chosen on the presumption that higher flow of people and excessive contact with the surfaces may exhibit more antibiotic resistance in bacteria compared to that of preserved natural forests. The sediments suspended in sterile water and streaked on nutrient media to isolate and grow the bacteria. 58 colonies were picked and grown as pure cultures. The bacterial spp. identification was carried out using Biolog Test. A test of antibiotic resistance /susceptibility named Kirby-Baur test was conducted for 20 random samples out of the original 58 samples. Antibiotic discs were placed in each agar medium containing one of the 20 bacterial isolates and incubated at 37°C for 3 days. The 12 different antibiotics selected to test the resistance included some commonly used antibiotics such as Penicillin, Cipro, Ampicillin, gentamicin, Streptomycin etc.

Results

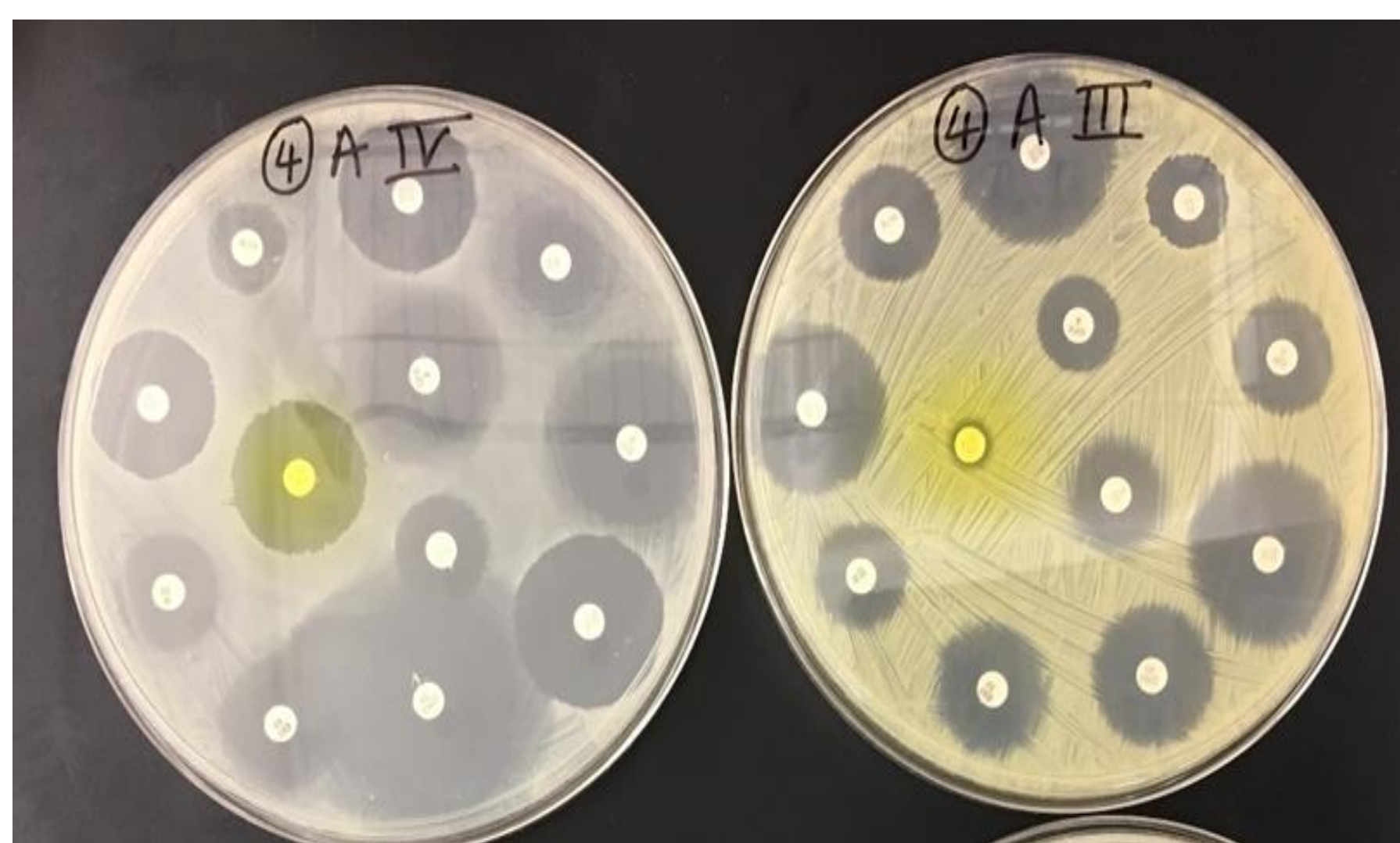


Figure 1 Some of the bacterial isolates, such as (4) AIII, (4) AIV, (4) BII were found to be susceptible to most, if not all, of the tested antibiotics and (4) BI recorded to have some resistance to some tested antibiotics. The 11 sediments samples obtained showed much diversity of microbial population among the different locations as well as within the same location. As for the 20 random bacteria isolates we picked to perform the Kirby-Baur test, the results were intriguing. About 27% of the 58 bacteria were resistant whereas about 63% of the bacterial isolates were susceptible to the 12 commonly used antibiotics. Some bacteria tested intermediate resistant or susceptible to the antibiotics tested but overall most were sensitive.

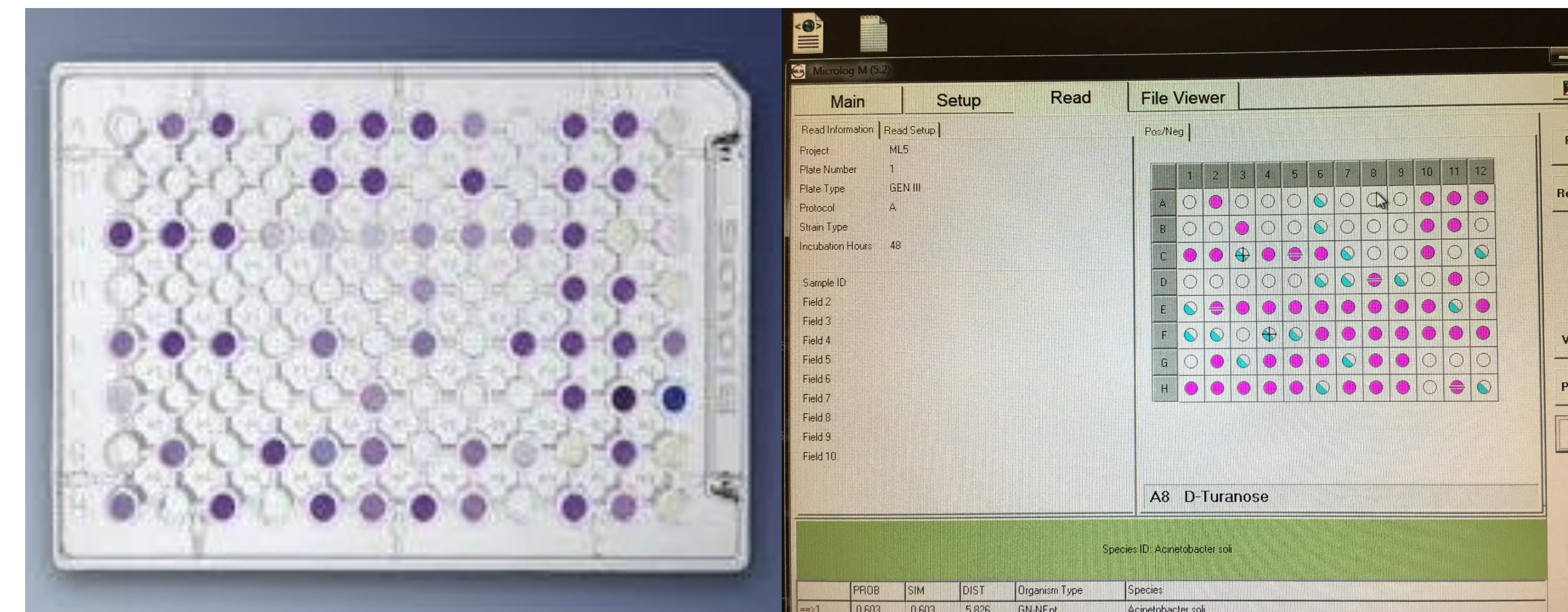
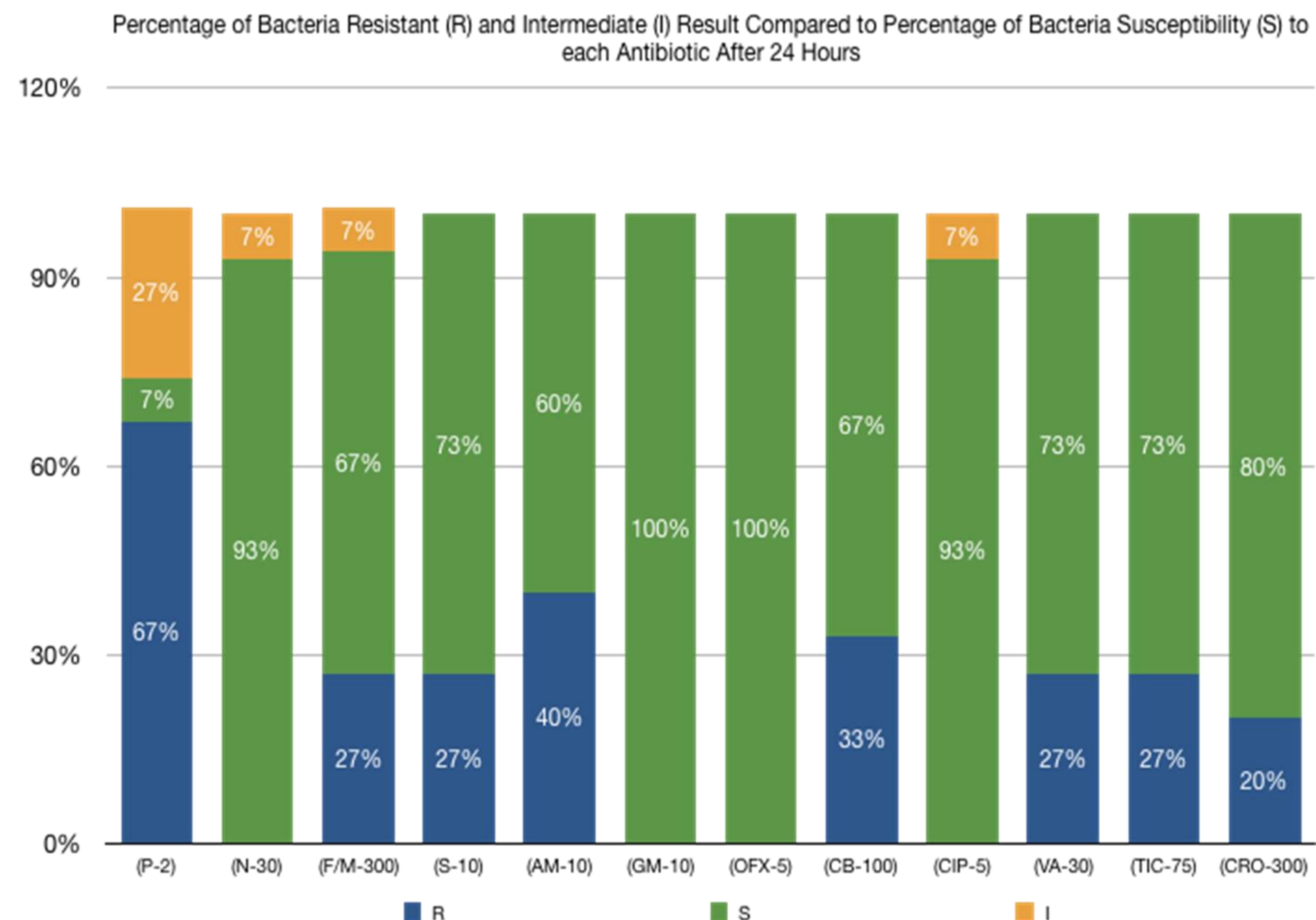


Figure 2 Biolog test for Identification of bacteria spp. *Escherichia Coli* and *Bttiauxella Gavinae* were identified in some of the sediment samples analyzed.

Discussion

Our results were encouraging. As hypothesized the locations with a presumably greater influx of people showed greater diversity of microorganisms. This indicates the vast number of bacterial species we come into contact with every day without knowing it. The test for antibiotic resistance/ susceptibility showed that most bacterial species were susceptible rather than resistant countering our hypothesis. This is a positive outcome providing some relief, that these bacteria can be successfully treated with common antibiotics if need be. The chosen locations included crowded urban, Queens garden and preserved natural Forest which are inevitably used by a large number of people and although our intuition said that this would mean that the bacteria would be more antibiotic resistant, the results showed the contrary. Some antibiotics seem to be incredibly stronger than others, but overall the bacteria are more susceptible to the antibiotics. Our results may have been more interesting if all the bacteria existing at these locations were identified- i.e. if we could study the microbiome by using next generation sequencing. And testing antibiotic resistance of each individual microbial species would be great. These ideas would lead to new and exciting data which could begin to connect our world to the microbial world.

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