

# The Effect of Susceptibility and Resistance Testing for Standard Antibiotic Treatment For Possible Unknown Gram Negative Bacterial species

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## ABSTRACT

The majority of studies on the movement of living or once-living materials through the atmosphere have focused on insect pest species. Over the past 10 years however, these studies have expanded to include investigations of the movement of fungal spores and pollen through the atmosphere, and a few have focused on bacterial species present in the air that we breathe. In this study, air samples were collected from February to August of 2007 on a biweekly basis, with a sampling filter apparatus was stationed on the South Main campus of Howard University in Washington, DC. The filter samples were collected mid week for a twelve-hour period beginning at 7:00 AM and concluding at 7:00 PM. Screening and analysis all 16S rDNA bacteria isolates was performed by cultural methods. The isolates were subjected to the standard antibiotic susceptibility and resistant testing.

A total of 24 isolates were identified to five Gram negative bacterial genera. Gram negative organisms have the potential to become pathogenic and cause disease. Based upon molecular analysis, it is suggestive that the species within the genera are new species. The distributions of the isolates are as follows: *Enterobacter* 11; *Yesinia* 3; *Escherichia* 4; *Pseudomonas* 2; *Pantoea* 4; 8 were resistant to Ampicillin, 1 was resistant to Gentamicin, 5 were resistant to Penicillin. Additionally, 4 microbials were found to be Intermediate to the antibiotics Ciprofloxacin, Tetracycline, Erythromycin, and Penicillin. The antibiotics tested are standard treated for diseases causes by these bacterial species. Although the isolates were not analyzed for possible virulence factors, the results provide critical insight of microbial biodiversity in the Washington DC, Metro Area, and the need to revise medical therapy and the development of new antibiotics to fight this family of possible new microorganisms. These microorganisms tested, have the potential for impacts on human respiratory health as well as other human disease conditions.

## INTRODUCTION

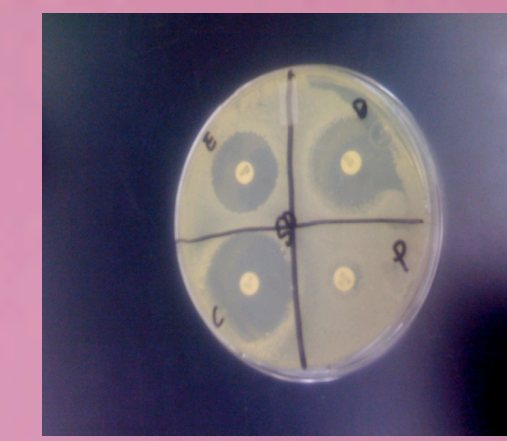
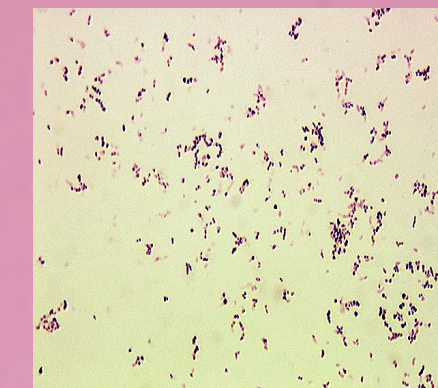
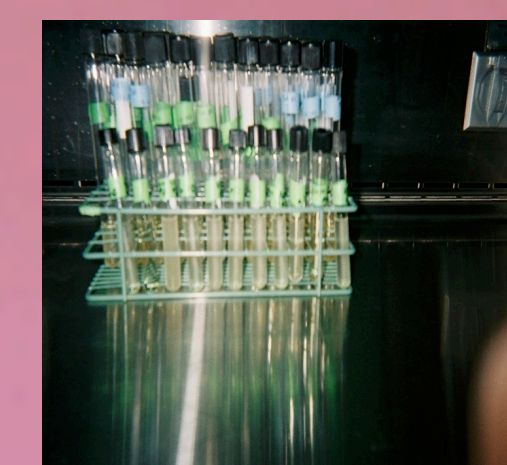
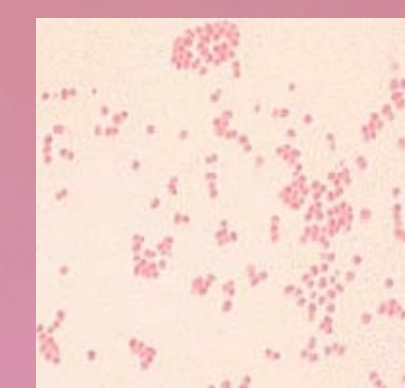
Microbial species dominate every environment. They are closely associated with the human body and from genomic studies little is revealed concerning our understanding about them. It is believed that airborne aerosols are carriers of several pathogenic microorganisms that may compound the causes of respiratory illness and childhood asthma.

According to the Asthma and Allergy Foundation, one in ten adults and children suffer from asthma in Washington DC, and the American Lung Association has rated Washington, DC as one of the top five most challenging places for people with asthma to live, particularly in the summer months. The bacterial populations that are present in the air may be related to the increases in certain diseases such as asthma, community acquired pneumonias, and other diseases observed in the District of Columbia public health records. The observed microbial biodiversity is associated with meteorological parameters.

Therefore, there is reasonable suspicion to believe that the outdoor air we are breathing in the Washington, DC area contain microbials that have the potential to be harmful and pathogenic. Therefore, microbiological, molecular, and phylogenetic analysis may prove to be an asset in characterizing and identifying airborne microbials.

## MATERIALS & METHODS

Sampling Culturing  
PCR of 16S rDNA Sequencing  
Antibiotic tests



## RESULTS

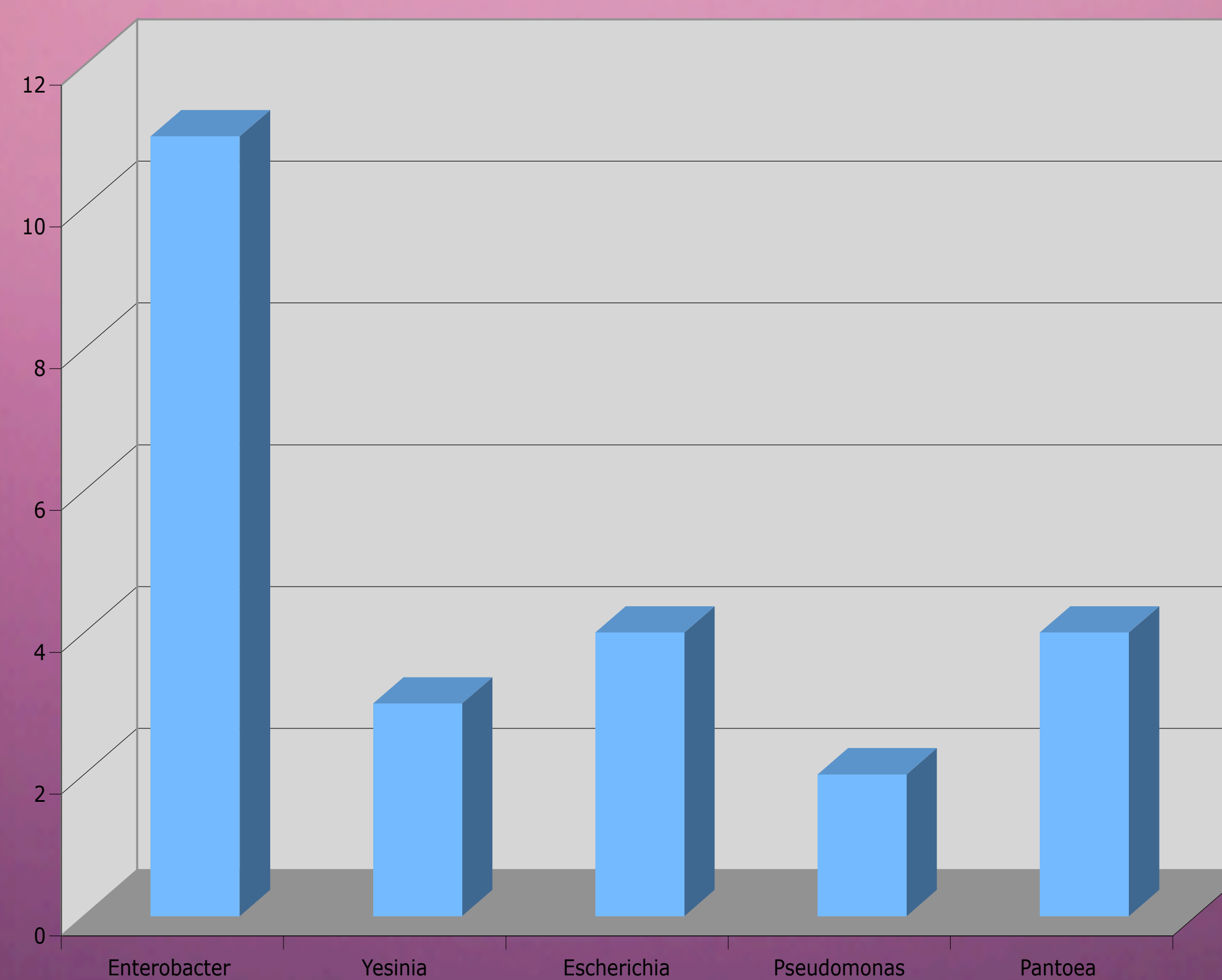


Figure 1. Total number of Gram negative isolates by genera

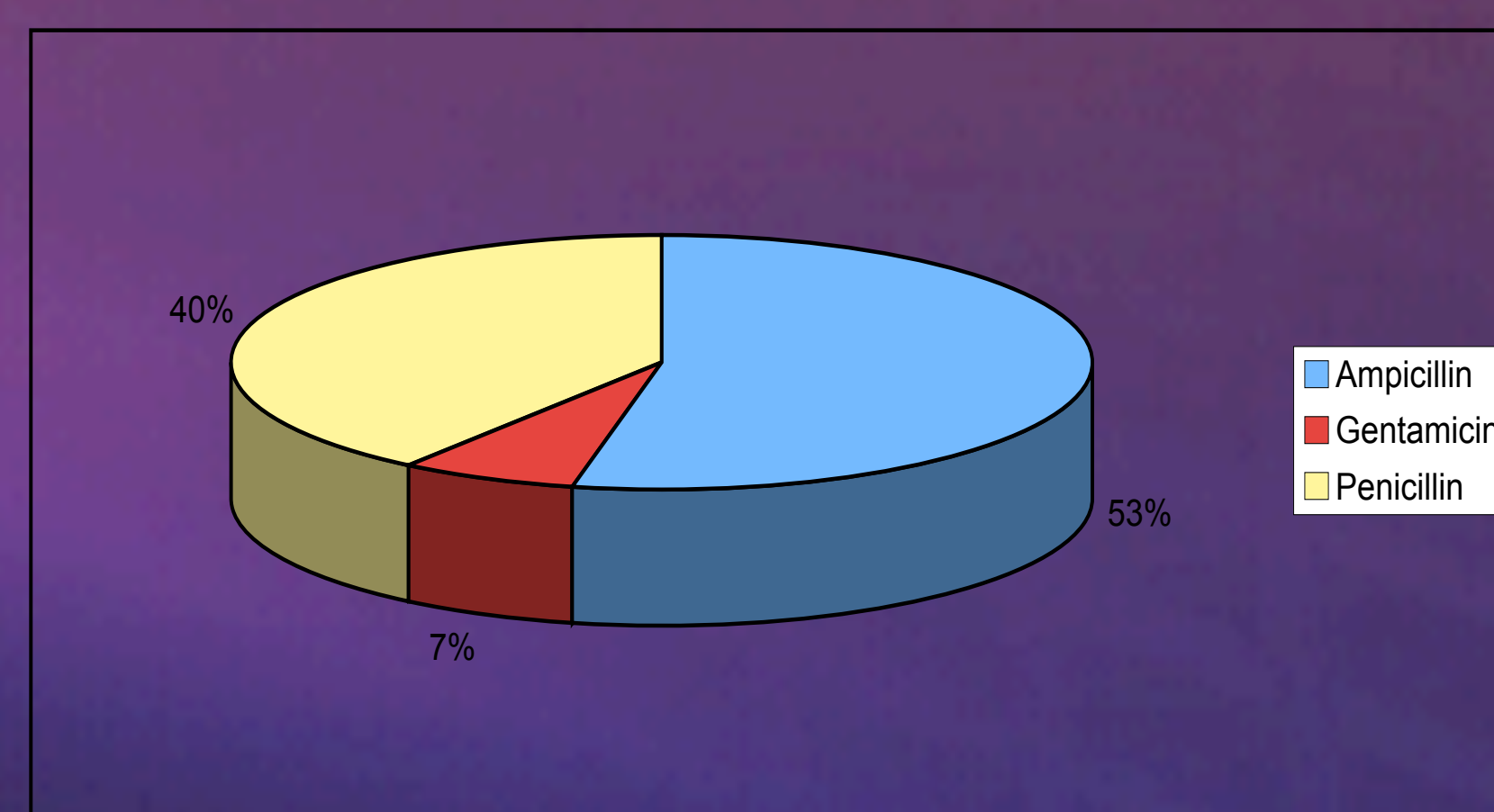


Figure 2. Percent of total resistant by antibiotic

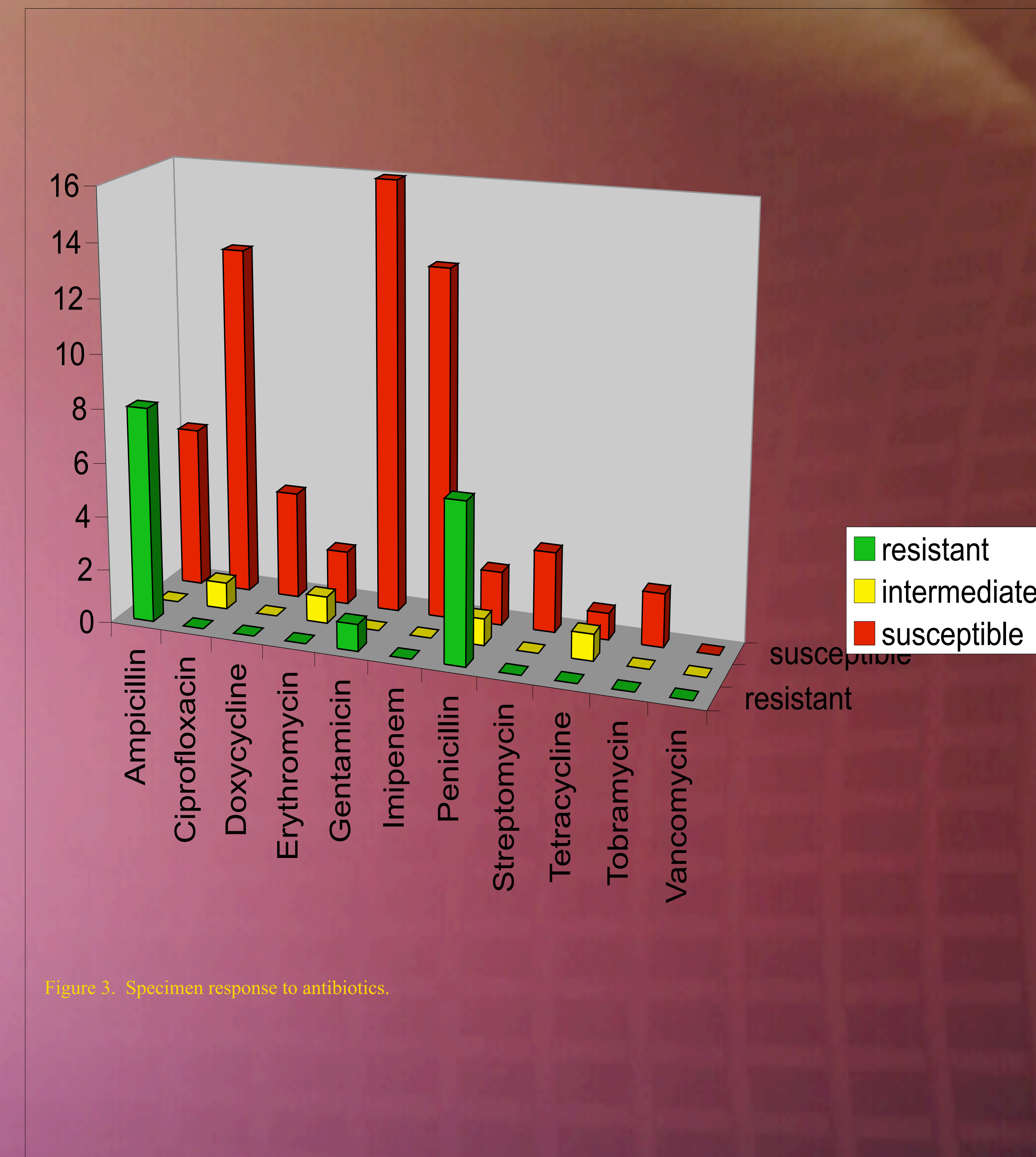


Figure 3. Specimen response to antibiotics.

## CONCLUSIONS

- Several opportunistic pathogenic species that may infect immunocompromised, elderly, and young individual humans were identified. Out of the three hundred and twenty one isolates collected between February and July of 2007, 76 were identified to have a positive identification of 98% or less match with the National Institute of Health with organisms previously deposited in Genbank, indicating possible new species.

- Twenty four of the organisms were from five Gram negative genera, *Enterobacter*, *Yesinia*, *Escherichia*, *Pseudomonas*, and *Pantoea*. Fifteen were found to be resistant to antibiotics used for standard treatment.

- Four were found to have an intermediate response to the antibiotics. For these organisms new drug therapies should be investigated. Although the isolates were not analyzed for possible virulence factors, the results provide critical insight of microbial biodiversity in the Washington DC, Metro Area as well as proper antibiotic treatment for the microorganisms identified.

- Additional tests will be performed to determine virulence factors, and impact on daily human living. There are six additional months of air collections that will be subjected to microbiological and molecular test to establish identification and characterization, susceptibility and resistance, and virulence. Organisms that preliminarily display characteristics of new species and new genus will be subject to species and genus identification tests. Gene expression for the microbials that display the greatest similarity for pathogenesis and potential for human harm will be subjected to gene expression panels. Hopefully, this future work will assist in the genesis for antibiotic production.

## Acknowledgements

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