Effects of Human Activity Level on Antibiotic Resistance in Bacteria

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Background

- Antibiotic resistance is a growing public health concern that reduces the effectiveness of infection treatments
- Soil bacteria naturally produce antimicrobial compounds to compete with neighboring microbes
- Environmental bacteria may carry antibiotic resistance-related traits that could impact human health
- Human activity and pollution may influence microbial diversity and bacterial competition in soil environments
- This study investigated antibiotic-producing soil bacteria collected from NYC environments with different levels of human activity

Methods

- Collected 1-2 g soil samples from NYC locations with varying human activity levels
- Suspended soil in deionized water and performed serial dilutions (up to 10^{-4})
- Spread samples onto nutrient agar and isolated morphologically distinct colonies
- Screened isolates for antimicrobial activity using *E. coli* lawns
- Extracted genomic DNA from isolates with inhibition zones
- Amplified 16S rRNA genes using PCR
- Confirmed PCR products with gel electrophoresis
- Sent PCR products for Sanger sequencing
- Analyzed sequences using DNA Subway and BLAST

Refer to the QR code for references and a detailed methods procedure

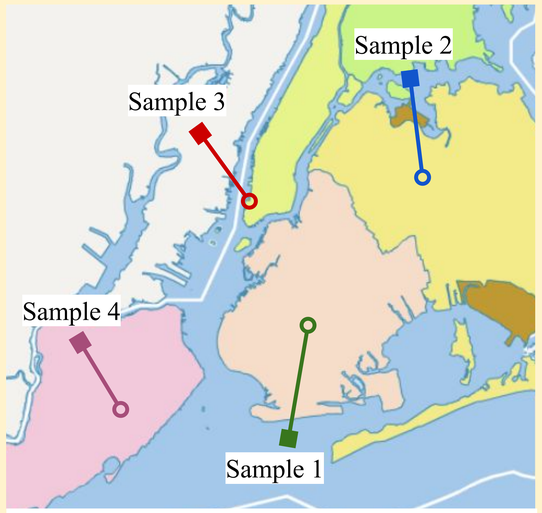

Figure 1: Map of sampling sites

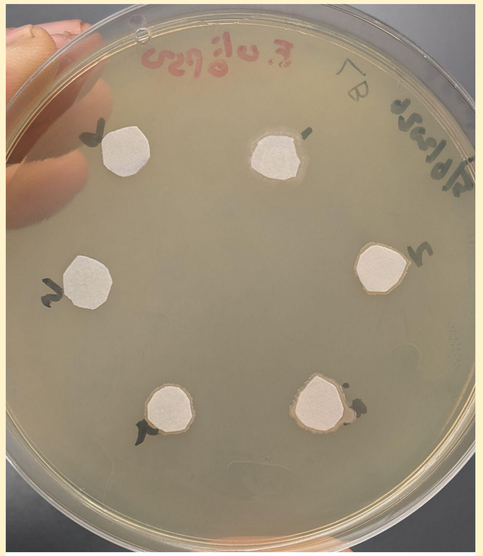

Figure 2: Sample 3 E. coli plate

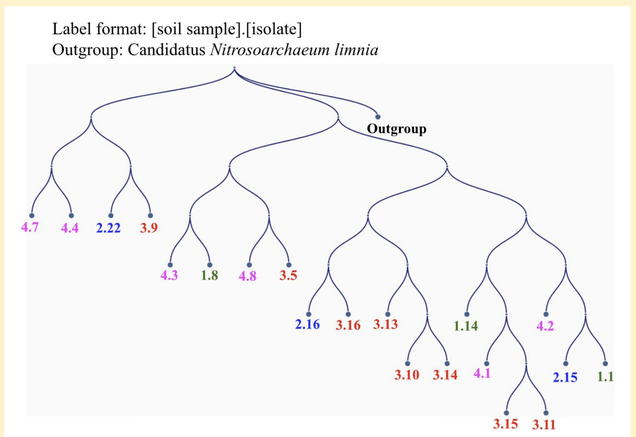

Figure 3: Phylogenetic tree of results

Soil sample	Coordinates	Isolate #	Identity
Sample 1	40.62961, -73.96322	1	Bacillus megaterium strain TAUC4
Sample 1	BROOKLYN	8	Lysinibacillus cavernae strain CAU 1677
Sample 1		14	Bacillus sp. PPB17
Sample 2	40.7088346, -73.8584327	15	Priestia megaterium strain SOTI05
Sample 2	QUEENS	16	Staphylococcus hominis strain F1
Sample 2		22	Pseudomonas fluorescens
Sample 3	40.7182846, -74.0162079	5	Lysinibacillus sp. 2008723339
Sample 3	MANHATTAN	9	Pseudomonas putida strain CPO 16.110
Sample 3		10	Staphylococcus sp. strain H34
Sample 3		11	Bacillus cereus strain CZIV-1068
Sample 3		13	Uncultured bacterium clone nck277d08c1
Sample 3		14	Staphylococcus epidermidis strain PgBE265
Sample 3		15	Bacillus cereus strain 6-3
Sample 3		16	Staphylococcus haemolyticus strain KJ1-5-97
Sample 4	40.567883, -74.117146	1	Bacillus mobilis strain ROA036
Sample 4	STATEN ISLAND	2	Bacillus stratosphericus strain YKCM-AS-4B
Sample 4		3	Lysinibacillus fusiformis strain NBRC 15717 (T)
Sample 4		4	Pantoea sp. strain 58-1
Sample 4		7	Pantoea sp. strain WY5
Sample 4		8	Lysinibacillus xylanilyticus strain LonMTB_3

Table 1: Results of DNA barcoding of all soil isolates

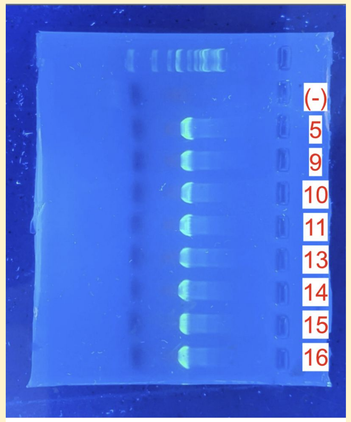

Figure 4: Gel electrophoresis of soil Sample 3 isolates

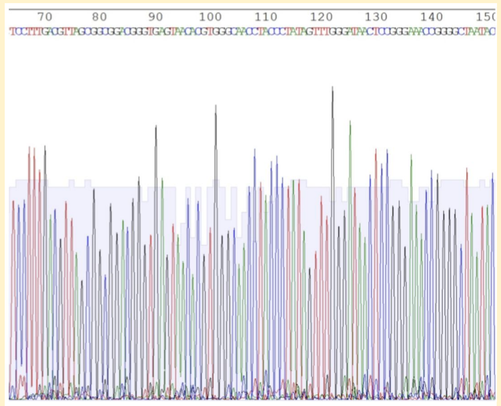

Figure 5: Chromatogram of Sample 3, Isolate 5 (cropped)

Results

- DNA barcoding identified multiple bacterial genera with potential antimicrobial activity
- Identified species included: *Bacillus megaterium, Bacillus cereus, Lysinibacillus cavernae, Pseudomonas putida, Pseudomonas fluorescens,* and *Staphylococcus epidermidis*
- Isolates produced observable zones of inhibition against E. coli
- PCR and gel electrophoresis produced visible 16S rRNA bands
- Phylogenetic analysis showed isolates belonged to distinct bacterial lineages
- **Sample from a highly populated Manhattan location showed more potential antibiotic-producing isolates**
- Limitations: Weak inhibition zones, low DNA concentrations, failed PCR/DNA extraction, and ambiguous BLAST matches

Future Directions

- Investigate whether isolates contain clinically relevant antibiotic-resistance genes
- Compare resistance genes in soil bacteria with those in human pathogens
- Use additional PCR screening and sequencing for resistance analysis
- Increase sample sizes for stronger ecological and statistical conclusions → establish a definitive relationship between human activity and bacterial diversity
- Further study environmental microbial diversity and resistance patterns

Acknowledgments

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