



Uncovering the Underground Metropolis: Assessing the Bacterial Composition of Tree Beds in Tribeca

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Abstract

New York City houses over 600,000 trees in sidewalk tree beds. Tree beds can improve air quality, reduce stormwater runoff, and help to lower temperatures with their shade. Our study assessed the biodiversity of tree beds and intended to see if human interference has affected Tribeca's soil microbiome. We hypothesize that human interference lowers biodiversity. 26 total soil samples were collected from 13 different locations, the DNA was extracted with a DNEASY Powersoil Kit, performed PCR with 16S rRNA primers, and samples were sent to Genewiz for Sanger sequencing. DNA was only successfully extracted from three samples. The sequences were input into DNA Subway and we found that the closest hits were: *Paenibacillus sp.*, *Bacillus Halotolera*, and an uncultured proteobacterium. The presence of salt-tolerant bacteria indicates that human activity, specifically the usage of ice melts, may influence the soil biodiversity.

Introduction

- Tree beds improve the air quality, reduce storm water runoff, and lower air temperatures.
- They also support the organisms that inhabit the area with resources like food, water, and space to live and reproduce.
- Our project focused on Tribeca, located in lower Manhattan.
- This neighborhood has a lot of human traffic due to its many famous art galleries and luxury residences,
- Our study aimed to assess how humans have affected the soil biodiversity of the region
- We hypothesize that human interference has increased soil biodiversity.

Materials & Methods

- Soil samples collected from tree bed locations that were easily accessible near Stuyvesant High School on February 20th, 2022
- Soil augers used to collect 1 to 2 inches of soil, stored in 50mL conical centrifuge tubes.
- We collected 2x samples from 13 different tree beds for a total of 26 samples.
- Samples stored in ice and then transferred to a freezer for storage
- DNA extractions were performed using the Qiagen DNEASY Powersoil Kit.
- Soil samples were purified, lysed, and the DNA extracted over 4 hours.
- DNA amplification using PCR with standard 16s rRNA primers
- Gel electrophoresis
- The PCR product was then sent to get purified and Sanger sequenced Sanger at Genewiz
- Sequence analysis using the BLASTN database with NCBI on DNA Subway

References

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Results

Table 1: Table of species matches from BLASTN

Sample	Species	Details	BLASTN Accession#
2	<i>Paenibacillus sp.</i>	Paenibacillus sp. EK-10 16S ribosomal RNA gene, partial sequence	EU910230.1
1	Proteobacterium?	Uncultured proteobacterium partial 16S rRNA gene, clone TWC 14	HE774687.1
19	<i>Bacillus halotolerans</i>	Bacillus halotolerans strain JZ7 16S ribosomal RNA gene, partial sequence	MH512910.1

Table 1 summarizes the three bacterial species that were present in the collected DNA samples.

Figure 1: PHYLIP ML with uncultured proteobacterium as outgroup

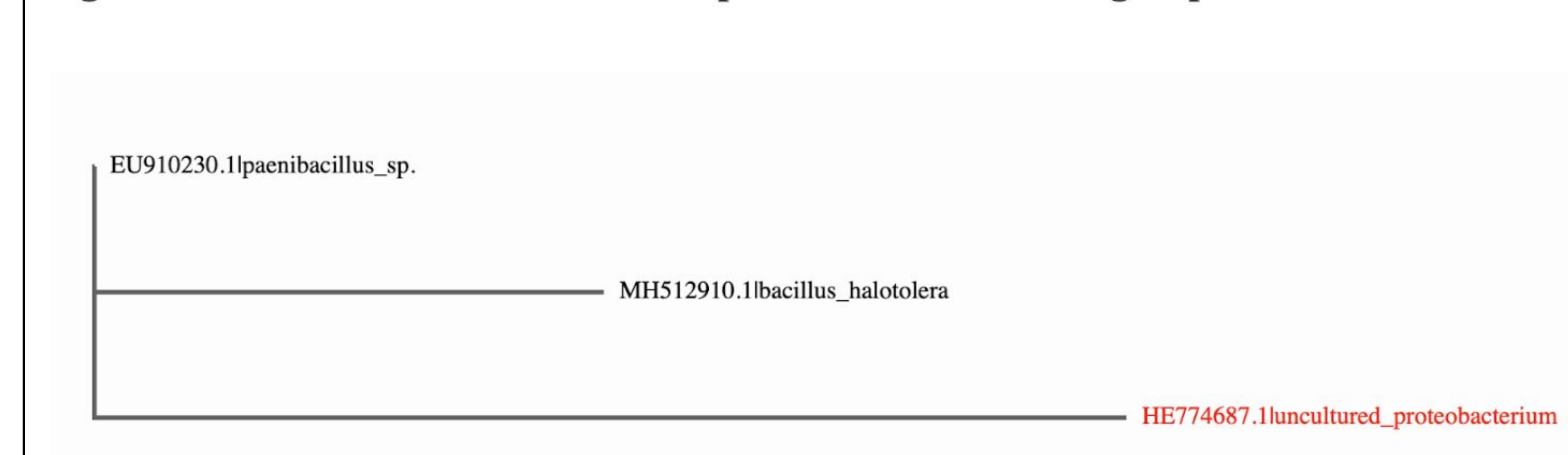


Figure 1 is a PHYLIP ML phylogeny constructed in DNA Subway showing the relatedness of the species present. The Uncultured proteobacterium was the outgroup, the least similar sequence from the other two.

Discussion

- Does the presence of the uncultured proteobacterium hint at potential parallels between the soil conditions found within those hot springs and in NYC?
- Were the sequences used to identify the uncultured bacterium conserved among various bacterial species? Or were the sequences of poor quality and thus matched?
- What are the origins of the uncultured proteobacterium?
- How well do these results reflect the general environmental impacts of anthropogenic activity?

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