

For most of evolutionary history, humans lived in places like this:



Now most of us live in places like this:

BACKGROUND:

By 2050, world population is expected to reach 9.3 billion. All population growth is predicted to occur in urban areas.¹ Cities are complex amalgamations of interdependent systems that are costly and difficult to alter once they are set on a particular trajectory. Urban policy, planning and design decisions that occur now will influence the lives of many generations to come in terms of human wellbeing and environmental sustainability.

Current trends of increasing urban density through *infill development can* result in overall reductions of vegetation within metropolitan areas², although there is abundant evidence that *human well-being in urban areas is linked to* neighborhood greenness^{3,4,5}. Plants are sources of microorganisms in the urban environment⁶ and therefore may contribute to intraurban variation in microbial communities, conceivably playing a role in the maintenance of human health. The mechanisms linking health and green space are not well understood and do not have specific design implications. Better understanding of how vegetation affects microbial communities could lead to healthier urban design and planning. METHODS:

I conducted a pilot study in 2013 to explore the influence of vegetation on urban microbial communities. Air samples were collected from 10 pairs of parks and parking lots in Eugene, Oregon, USA. All sampling was done simultaneously on July 24th, 2013 from 0800 and 1600 using passive settling dishes. Bacterial 16S rRNA genes were sequenced and community structure was analyzed using R.

Urban vegetation was assessed using ArcGIS and aerial photoimagery from the National Agriculture Imagery Program. Buffer zones of 200m, 400m, 800m, 1600m and 3200m were created around each sampling point and the proportion of vegetation cover within each buffer zone was calculated based on normalized difference vegetation index (NDVI), a measure of living green vegetation.





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URBAN MICROBIOME PILOT STUDY: PARKS VS. PARKING LOTS

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IS MICROBIAL COMMUNITY COMPOSITION SIGNIFICANTLY DIFFERENT IN HIGHLY VEGETATED AREAS (PARKS) COMPARED WITH **NON-VEGETATED AREAS (PARKING LOTS)?**

Parks and parking lots cluster separately in a principle coordinates analysis (Morisita-Horn distance metric) The effect is not quite significant ($R^2=0.143$, p=0.056)





WHY ARE TWO OF THE PARKS (AMAZON AND WESTMORELAND) VERY DIFFERENT FROM PARKING LOTS?

wew

0.01

lowes

Both sites had unique contributions from rare taxa Vegetation characteristics specific to the sites (tall unmown grass, dense tree buffer) may have played a role



PRINCIPAL COMPONENTS ANALYSIS OF RARE TAXA (< 0.01%)

A single taxon dominated the entire dataset

- sampling took place July 24th (prime haying season) - wind was primarily coming from the north
- Linn County is known as "the grass seed capital of the world"

Genus	Relative Abund.	Notes
Sphingomonas	32.7186	S. faeni, from livestock barns with hay dust S. aurantiaca, from livestock barns with hay dust





WHY ARE TWO OTHER PARKS (MAURIE JACOBS AND WEST **EUGENE WETLANDS) VERY SIMILAR TO PARKING LOTS?**

Even though they were parks, these two had the





Acetobacteraceae were highly represented in parking lots

22 taxa were significantly more abundant in parking lots, 11 of the 22 were members the Acetobacteraceae family and represented about 2.29% of all sequences.



MOST ABUNDANT "INDICATOR" TAXON FOR PARKING LOTS (0.86% OF SEQUENCES)

Acidobacteriaceae were significantly more common 🗟 in parks

20 taxa were significantly more abundant in parks, 11 g of the 20 were members the Acidobacteriaceae family and represented about 0.88% of all sequences



MOST ABUNDANT "INDICATOR" TAXON FOR PARKS (0.47% OF SEQUENCES)



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