

Microbiome sequencing provides insight into microbially-mediated lead transformations in urban gradient soils

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Lead (Pb) poisoning is a global health problem that causes physical and neurological impairments in millions of people. Urban ecosystems accumulate Pb in the soil through wastewater, industrial materials, and runoff. Many plants take up Pb and store it in their tissues, making urban green spaces potential hotspots for human and animal Pb exposure. Rhizosphere microbes like *Bacillus* and *Pseudomonas* have been reported to transform Pb species and influence Pb availability for plant uptake through processes like biosorption, chelation, and biomethylation [1]. Understanding the role of soil microbes in Pb speciation, bioavailability, and concentration could help decrease illnesses from Pb exposure, however, microbial genes that promote Pb transformation are not well understood. Through targeted gene and shotgun metagenome sequencing, we aim to examine microbial communities that are well-adapted to elevated Pb environments and seek functional genes associated with soil Pb transformation. Here, we extracted microbial DNA from the rhizosphere soil of six plant genera and bulk soil at urban and suburban sites in Minneapolis, MN. Using a portable X-ray fluorescence spectrometer (pXRF) to measure Pb concentration we found significantly higher Pb content in urban soil samples (avg=106.4 ppm) compared to suburban samples (avg=16.6 ppm). Using *16S* rRNA gene amplicon sequencing targeting the V4 region, we sequenced 42 samples to determine relative abundance and taxonomy. While all samples were dominated by similar classes (top classes: Alphaproteobacteria, Vicinamibacteria, and Thermoleophilia), there were distinct communities between the urban and suburban samples with notably more Nitrososphaeria in the urban samples, suggesting that organisms from the Nitrososphaeria class may be adapted to higher pollution environments. Alpha-diversity was high in all samples, but suburban samples were more diverse. We will use shotgun metagenome sequencing to analyze microbes living in the urban site for genes similar to those in known metal detoxification pathways, such as the gene clusters that encode methyltransferases for As and Hg detoxification [2,3], as these may indicate genes essential for Pb transformation and detoxification.

1. Barra Caracciolo & Terenzi (2021), *Microorganisms* 9, 1462.
2. Chen et al. (2013), *Applied and Environmental*