The effects of urbanization and agriculture on soil bacterial diversity at the phylum level

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Abstract

The limiting factor involved in past assessments of soil bacterial diversity has been the lack of sampling and analytical methods that can identify the different species with confidence. It is now possible to sequence the bacterial 16S rRNA genes from soil samples to determine the composition of the bacterial community and identify the species present. However, the application of such techniques is limited by the fact that soil samples are heterogeneous in nature and contain a large number of different species. In this study, we have used molecular techniques to determine the diversity of bacterial species in soils from different land use types. The results of this study suggest that there is a significant difference in the diversity of bacterial species in soils from different land use types. Specifically, soils from urbanized areas have a lower diversity of bacterial species than soils from agricultural or natural habitats.

Methods

The analysis of bacterial diversity in soils was performed using the 16S rRNA gene sequences. DNA from soil samples was extracted and amplified using the polymerase chain reaction. The amplified DNA was then sequenced using automated sequencing and the sequences were compared to a database of known bacterial species to identify the species present.

Results

Phylum Abundances. Representatives of 15 phyla were identified from the clone library data. Two phyla displayed abundance patterns across the four land use types (Fig. 1. Proteobacteria was more dominant in open desert soils than urban and desert remnant soils. Most of the land use effect is explained by the abundance of alpha Proteobacteria, while the Betaproteobacteria and Actinobacteria are slightly more prevalent in urban and agricultural soils. Moreover, correspondence analyses revealed that inter-phyla abundance patterns are different between urban, agricultural and desert soils, while desert remnant soils show some similarity to all other land use types (Fig. 2.)

TABLE 2. LIBSHUFF comparisons of specific phyla contained in CAP LTER soil clone libraries

<table>
<thead>
<tr>
<th>Library</th>
<th>Prochlorococcus</th>
<th>Chloroplasts</th>
<th>Cyanobacteria</th>
<th>Actinobacteria</th>
<th>Acidobacteria</th>
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<tr>
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</tbody>
</table>

Discussion

Changes in abundances of bacterial phyla across land use types suggest selective advantages occurring in CAP LTER soils, resulting in unequal allocation of specific populations. These results are consistent with previous studies that have shown that land use has a significant impact on the composition of bacterial communities. The results of this study suggest that urbanization and agriculture can have a significant impact on the diversity of bacterial species in soils.

Conclusions

Significant changes found in Proteobacteria and Firmicutes abundance across land use types. Land use categorization does not predict significant changes in intra-phyla diversity, although there is an overall reduction in bacterial diversity across all land use types. Urbanized soils had a higher proportion of Proteobacteria and Firmicutes, while agricultural soils had a higher proportion of Actinobacteria and Bacteroidetes. Desert remnant soils had a higher proportion of Acidobacteria and Proteobacteria, while the Open desert soils had a higher proportion of Firmicutes and Proteobacteria.

References

1. Rash, B.A. (2018). The effects of urbanization and agriculture on soil bacterial diversity at the phylum level. Louisiana State University, Baton Rouge, LA.

Acknowledgements

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