Influence of Soil Physical Gradients on Spatial Distribution of Bacterial Communities; A Field Scale Study on Soil Inner Space Biology

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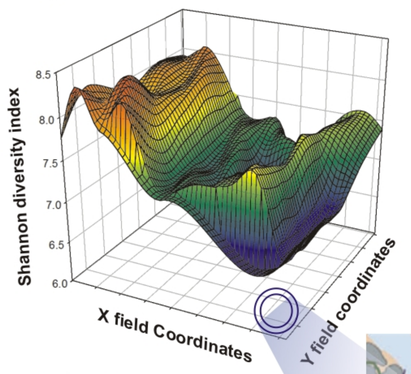
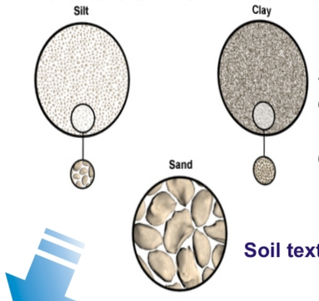
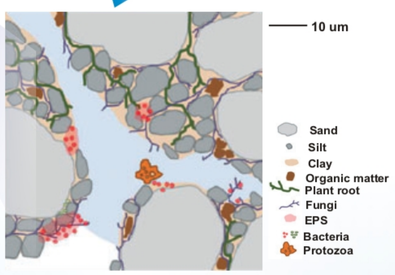
"Spatial distribution of bacterial is not a random process"





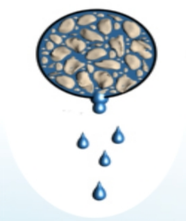
Soil microenvironmental changes cause the variation of the bacterial habitats according to their geographical distances

Soil textural gradient



Vos et al., 2013

Studying microbial community drivers based on soil physical gradients may open a novel platform to study soil ecology

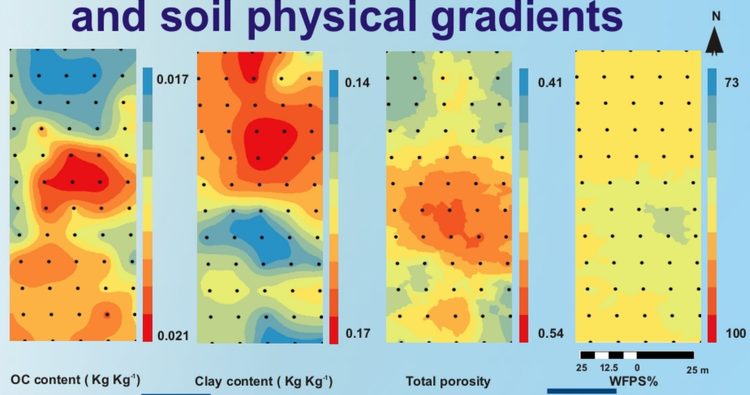


Soil moisture gradient

Soil structural gradient

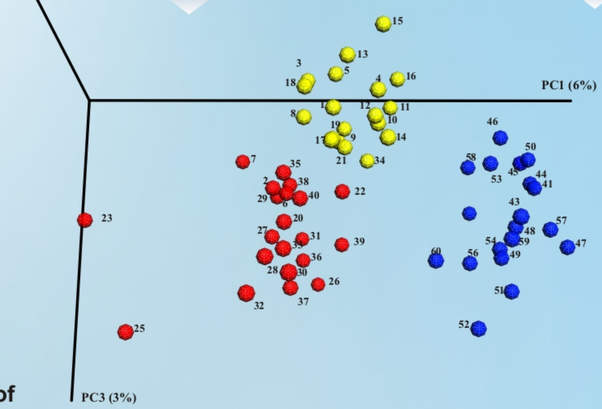
Soil physical gradients which can be seen in agroecosystems could be a major driver to in the variation observed in microenvironments

Evidence of interactions between bacterial communities and soil physical gradients

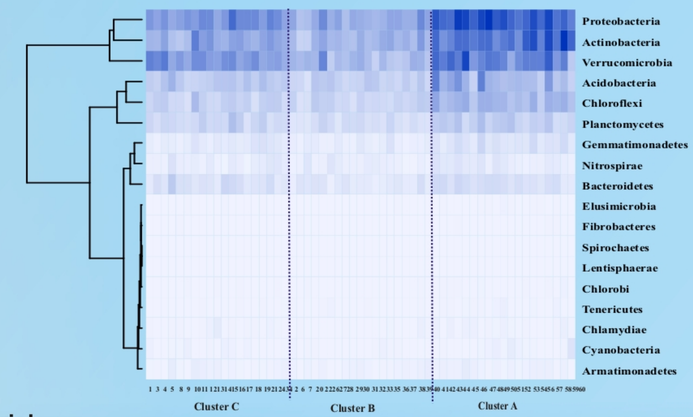


Contour maps of (a) organic carbon (OC) content, (b) clay content, (c) total porosity and (d) water filled pore space (WFPS%) across the experimental field

Soil structural, textural and moisture gradients facilitate different microenvironmental conditions for bacteria at northern, southern and central parts of the field

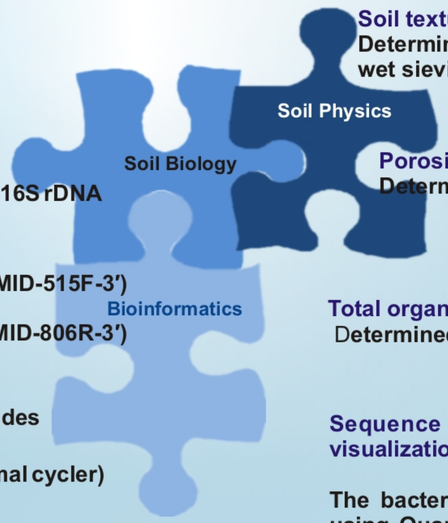


Principal component analysis (PCA) plot for bacterial beta diversity. Cluster A (blue spheres), cluster B (red spheres), cluster C (yellow spheres) respectively represent north, middle and south parts of the field



Heat map that illustrates the species abundance and its clustering. Numbers indicate the sampling locations. Cluster A, B and C corresponds to beta diversity clusters

Cross-disciplinary approach linking soil physics and biology



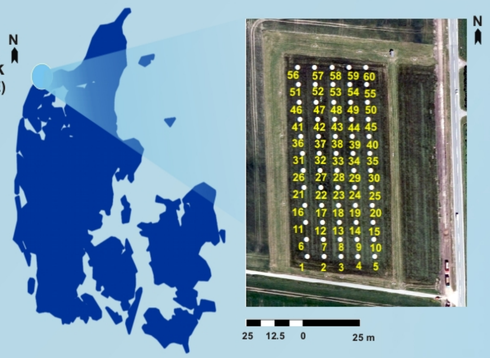
DNA Extraction
PowerSoil DNA Isolation Kit
(Mo Bio Laboratories, Inc.)

PCR Amplification, Purification, and Pyrosequencing
Amplify the V4 domain of bacterial 16S rDNA for 454 pyrosequencing

forward primer
(5′-GTGCCAGCMGCCGCGGTAA-MID-515F-3′)
reverse primer
(5′- GGACTACVSGGGTATCTAAT-MID-806R-3′)

Sample identification,
60 MID primer tags with 10 nucleotides were used on pooled samples
(GeneAmp PCR System 9700 thermal cycler)
(PE Applied Biosystems)

Study site
Silstrup, Denmark
(56° 56' 0" N, 8° 39' 0" E)



Soil texture
Determined 2-mm sieved soil by a combination of wet sieving and hydrometer methods

Porosity and volumetric water content
Determined by oven-drying at 105 °C for 24 h

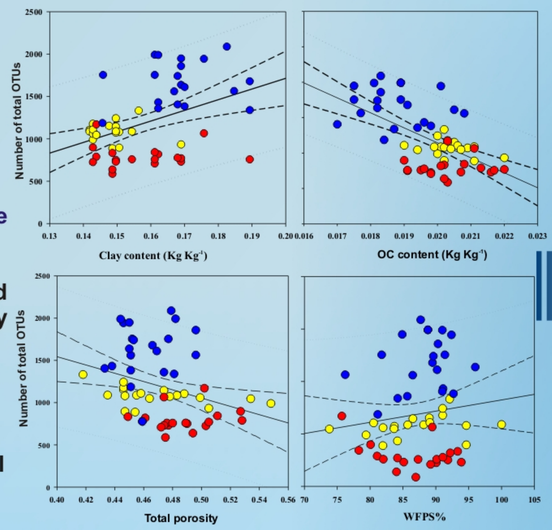
Total organic carbon
Determined with a CNS-1000 (LECO) analyser

Sequence analysis and community structure visualization

The bacteria V4 region sequences were analysed using Quantitative Insights Into Microbial Ecology software package
(QIIME 1.8.0 v, http://qiime.org/)

Statistical Analysis
The beta diversity matrix was illustrated as principal coordinate analysis (PCA) plot (EMPeror,QIIME)

Clustering of main bacterial phyla visualized via heat map plot which developed based on availability and abundance of bacterial species at each sampling location (R Development core team)



Relationship between total OTUs at each sampling location and (a) clay content, (b) organic carbon (OC) content, (C) total porosity and (d) WFPS%. Blue, red and yellow data points respectively indicates northern, middle and southern parts of the field

"physical complexity of the soil matrix created by soil textural and structural gradients controls the microenvironment for soil bacteria"

Soil structural and textural variations in the field highly influenced the bacterial community structure

Field clay content, OC content and porosity were the significant contributors that influenced bacterial community composition

may be due the low variations in the field moisture content did not show any significant influence on bacterial communities

Vos, M., Wolf, A.B., Jennings, S.J., Kowalchuk, G.A., 2013. Micro-scale determinants of bacterial diversity in soil. FEMS Microbiol. Rev. 37, 936-954

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