



Metagenome analysis of a soil and marine environment

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INTRODUCTION

The Institute of Agricultural and Fisheries Research (ILVO) has established a general Genomics platform, joining forces in the genomics research of the four ILVO Units. One part of the project focuses on the study of microbial communities of four different environments: soil, seawater, rumen (cows) and the intestine (pigs). This poster presents the research of two of these environmental niches: the rhizosphere of the plant (a soil environment) and (micro)plastics (a marine environment).

Soil environment – Rhizosphere

The rhizosphere of the plant is defined as the narrow zone around the roots and can contain more than 10^{11} microbial species per gram of soil. The effect of different soil treatments on the rhizosphere microbiome of lettuce and strawberry, and the influence on plant health are investigated. Initially, biochar, the solid coproduct of biomass pyrolysis (a technique used for biofuel production), is used as a soil additive.



Approach

The microbial rhizosphere of lettuce and strawberry

Amplicon sequencing
16S rDNA (V3-V4 region)

Composition and dynamics
of the microbial community

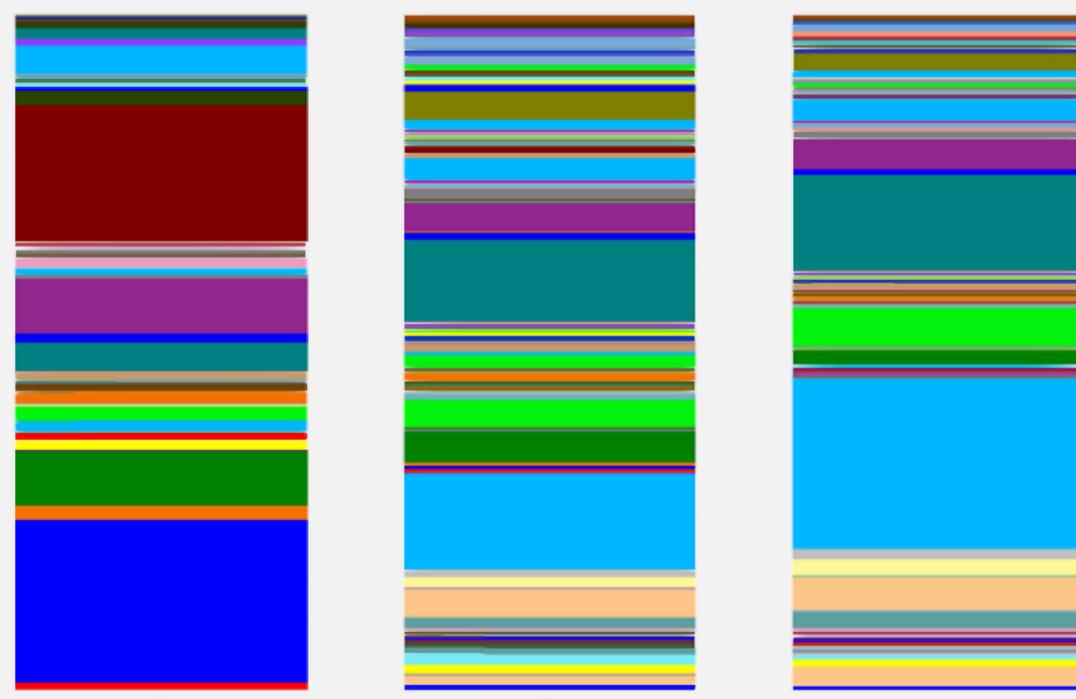
Metatranscriptomics

Analysis of the genes
expressed in the microbial
community

Preliminary Results

Initially, the 16S rDNA V3 region was sequenced of three lettuce rhizosphere samples: potting soil (a), field soil (b) and field soil with 1% biochar (c) (HiSeq 2500, 91bp paired end sequencing).

As expected, the bacterial taxa of potting soil and field soil showed a major difference. Potting soil was dominated by Acidobacteria, whereas field soil contained especially Actinobacteria. In both soil types, Proteobacteria were dominantly present.



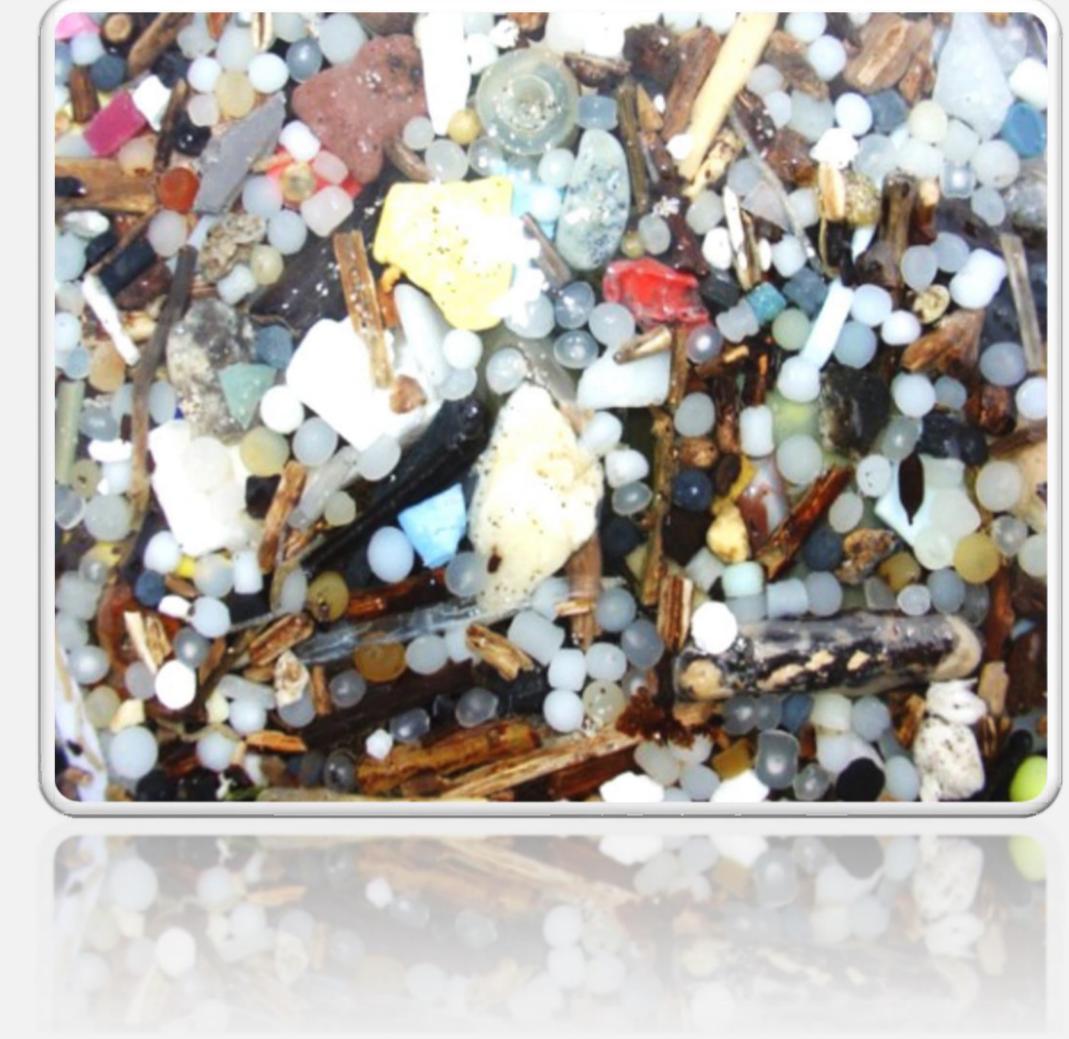
(a) (b) (c)
Bacterial diversity in the different
rhizosphere samples of lettuce. The
taxa are shown on family level.

Future experiments

Amplicon sequencing of the V3-V4 region of the 16S rDNA will be used primarily to investigate the influence of biochar and other soil treatments on the rhizosphere microbiome of lettuce and strawberry. The activity of the rhizosphere microbiome will be studied using metatranscriptomics.

Marine environment – Microplastics

Plastic particles with a diameter less than 5 mm are defined as microplastics. They are produced by the industry or are derived of larger plastics due to the influence of UV light and mechanical/physical factors. These microplastics are colonized by various bacteria. The microbial load of these microplastics is investigated in function of biodegradation.



Approach

The microbial load of microplastics

Amplicon sequencing
16S rDNA (V3-V4 region)

Composition and dynamics
of the microbial community

Whole genome shotgun
sequencing

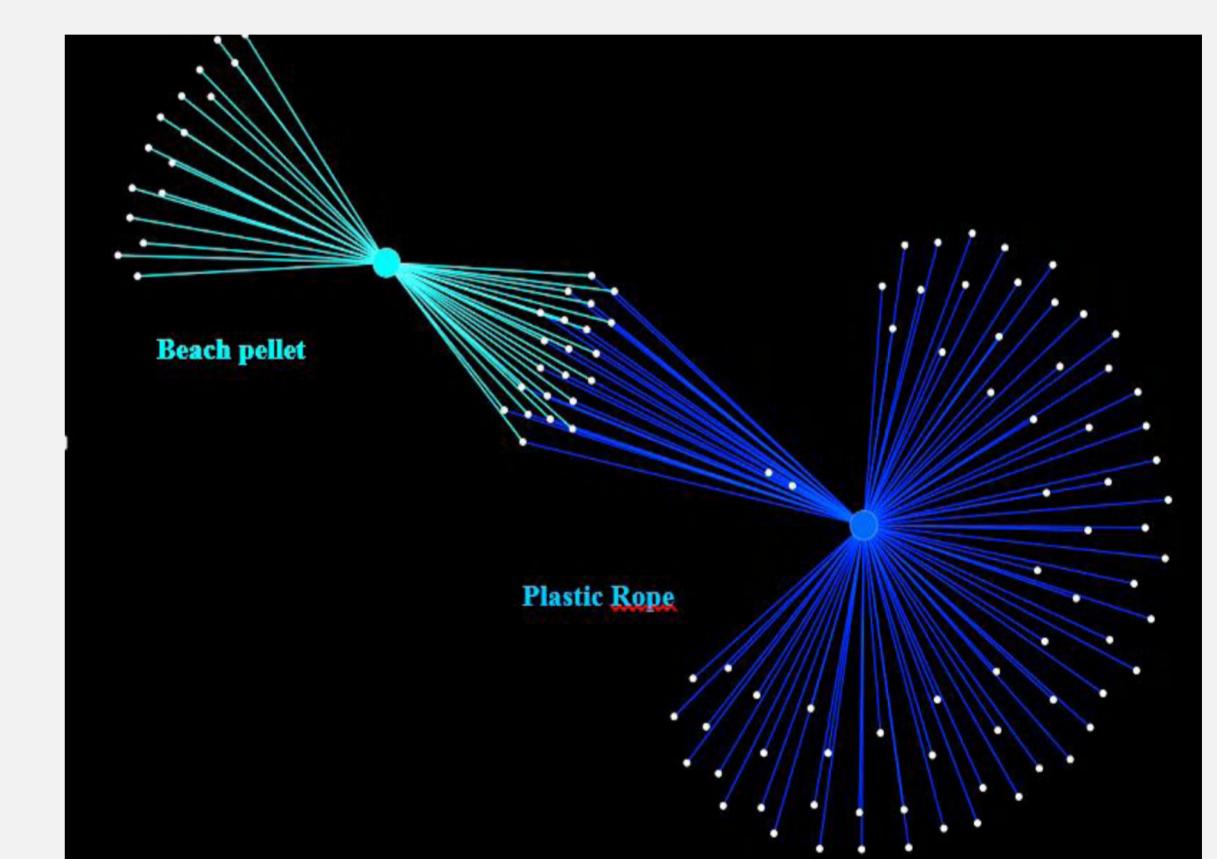
Functional profiling of microbial community
and identification of genes involved in
biodegradation

Preliminary Results

Initially, a pilot study was performed. The 16S rDNA V3 region was sequenced of two samples: a beach pellet and a blue synthetic rope of the marine environment (HiSeq 2500, 91bp paired end sequencing).

The bacterial community of both kind of plastics was different. The beach pellet mainly showed a colonization of *Psychrobacter*, whereas the Pseudoalteromonadaceae dominated the synthetic rope.

These results confirmed previous tests with DGGE analysis, cultivation of the bacteria and cloning.



Cluster of the OTU's present on the
beach pellet and the plastic rope.

Future experiments

The bacterial species present on the microplastics will be identified using V3-V4 16S rDNA amplicon sequencing. To identify plastic degrading bacteria, the functions present in the microbial environment will be studied by using whole genome shotgun sequencing.

CONCLUSION

Metagenomic research of microplastics and the rhizosphere of lettuce gives information about the microbial composition and functions of the species present in their environment. Knowledge about the microbial load on microplastics and the functions these bacteria perform could help in the detection of **marine plastic-degrading bacteria**.

Understanding the influence of biochar on the rhizosphere microbiome and the effect on soil-borne pathogens, could lead to the development of novel ways to restore soil quality and **enhance plant health**.