

### 1. Introduction

Traditionally, soil quality has been assessed through physical, chemical and biological properties without paying enough attention to soil biota and the different associated ecosystem services provided [1]. However, it is highlighted by several authors the need to study soil organisms in order to understand soil ecology as a starting point to implement innovative practical approaches, and therefore sustainable soil managements [2]. For that, the use of molecular methods such as next generation sequencing (NGS) have been shown an optimal tool to assess global microbial diversity in soils [3].

### 2. Materials and methods

The European BiodivERsA “SoilMan” project (Ecosystem services driven by the diversity of soil biota – understanding and management in agriculture) is focused on the study of the relations among soil management (tillage intensity or crop rotations), soil biodiversity, and ecosystem services, at seven different management gradients in agricultural long term observations (LTO’s) trials across Europe, Figure 1.



Figure 1: Location of the LTO’s included in the BiodivERsA “SoilMan” Project.

The samplings were carried out following the same methodology in all the countries during the 2017-2018 field campaigns when wheat was sown in the LTO’s. The soil DNA was extracted and subjected to metabarcoding analysis of 16S and Internal Transcribed Spacer (ITS) ribosomal RNA (rRNA) for bacterial and fungal community analysis, respectively, see Figure 2.

Different alpha diversity metrics, including number of OTUs, Simpsons and Shannon indexes were estimated. A beta diversity estimation based on Jaccard distance matrix and multidimensional scaling ordination plots (PCoA) was used to visualize the existence of community gradients among locations and soil managements. All the statistical data procedure was analyzed using the *vegan* and *phyloseq* R packages [4,5].

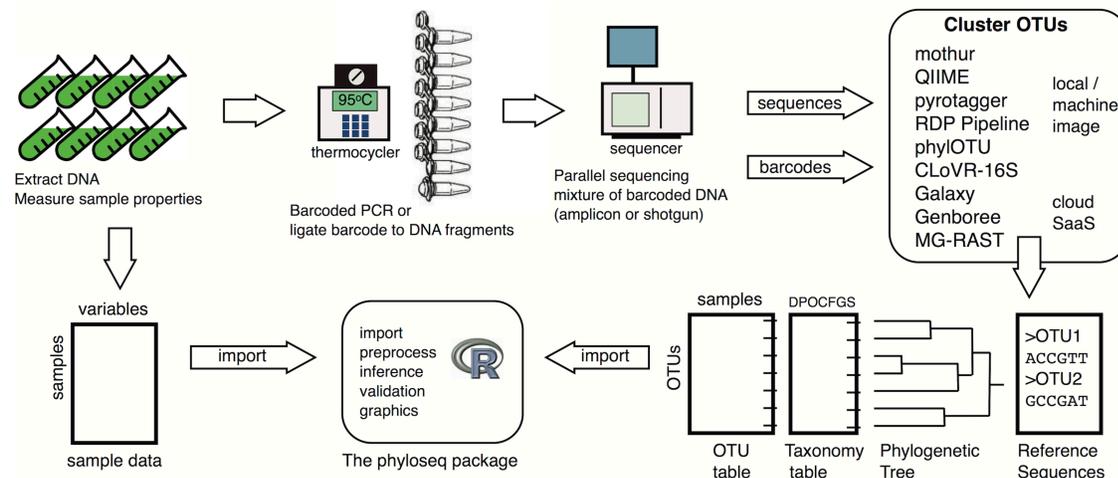


Figure 2: Experimental analysis workflow starting from DNA extraction, NGS analysis of bacterial and fungal amplicon sequences, and bioinformatic data analysis. Reproduced from ? under the terms of the Creative Commons Attribution License.

### 3. Results

The results obtained from different alpha diversity indices show general differences between countries in terms of fungal and bacterial richness in tillage LTOs trials. Although less evident, these differences were also significant when comparing tillage regimes trial or crop rotations within each LTOs. In contrast, crop rotation LTOs trials did not show clear trends in most cases (Data not shown).

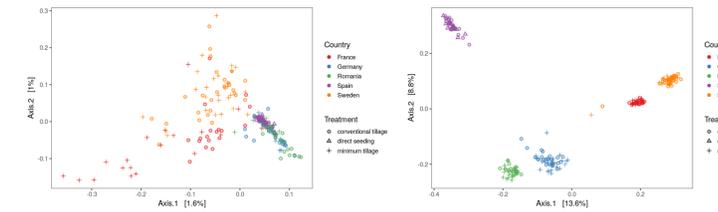


Figure 3: PCoA plots based on Jaccard distance for bacterial (left) and fungal (right) soil communities at the different tillage LTOs trials.

In terms of beta diversity, when analyzing all the tillage LTOs trials jointly, both bacterial (left) and fungal (right) communities showed strong gradients and differences among the different countries but not between the different tillage intensities, being stronger this trend for fungal than for bacterial communities (Figure 3). On the other hand, when each tillage LTO trial was analyzed independently for some countries there was some trend to differentiate microbial communities according to the tillage intensity, especially for fungal communities (Figure 4).

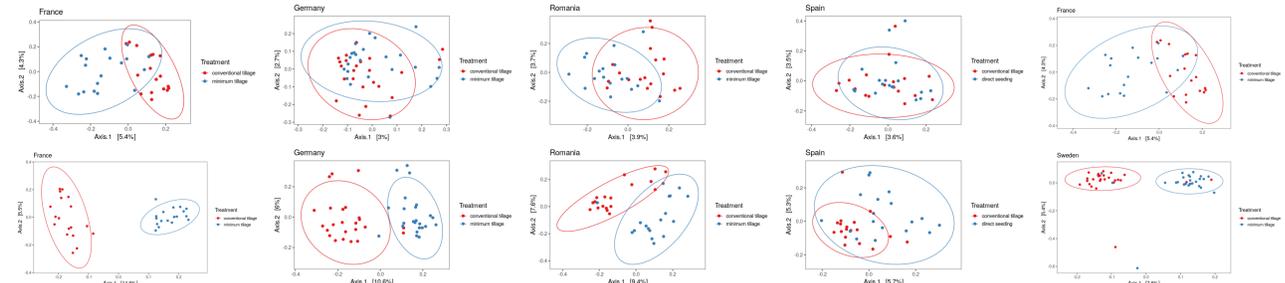


Figure 4: PCoA plots based on Jaccard distance between the tillage managements for bacterial (upper row) and fungal (lower row) soil communities at the different tillage LTOs trials analysed by country.

### 4. Conclusions

1. Results indicate that alpha diversity for both bacteria and fungi clearly differs between countries, while the effects of soil management (both tillage intensity or crop rotation) is less defined among and within countries.
2. Concerning the beta diversity indexes, communities tend to cluster according to the spatial location (country) than due to the soil management regimen (tillage intensity), although some effect of soil management was observed in some countries, especially in the case of fungal communities.
3. Further analysis will identify possible correlations of bacterial and fungal communities with environmental variables and other physical-chemical and biological properties of the soil.

### 5. References

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