

# B.19. Soil microorganisms under changing environment. Changes in soil microbial functional diversity across European field crop farms are mostly driven by environmental variables

Eva Lloret<sup>1</sup>, Irene Ollio<sup>1</sup>, Raúl Zornoza<sup>1</sup>, Lieven Waeyenberge<sup>2</sup>, Kristian Koefoed Brandt<sup>3</sup>, Krista<sup>4</sup> Peltoniemi, Stefan Schrader<sup>5</sup>, Merrit Shanskiy<sup>6</sup>, Merit Sutri<sup>6</sup>, Jozsef Dezsö<sup>7</sup>, Nicola Grujic<sup>8</sup>, Barbara Simon<sup>9</sup>, David Fernández Calviño<sup>10</sup>

<sup>1</sup>Polytechnic University of Cartagena, Cartagena, Spain; <sup>2</sup>Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Mellebeke, Belgium; <sup>3</sup>University of Copenhagen, Frederiksberg, Denmark; <sup>4</sup>Natural Resources Institute Finland (Luke), Helsinki, Finland; <sup>5</sup>Thünen Institute of Biodiversity, Braunschweig, Germany; <sup>6</sup>Estonian University of Life Sciences, Tartu, Estonia; <sup>7</sup>University of Pécs, Pécs, Hungary; <sup>8</sup>University of Belgrade, Belgrade-Zemun, Serbia; <sup>9</sup>Hungarian University of Agriculture and Life Sciences, Gödöllő, Hungary; <sup>10</sup>University of Vigo, Ourense, Spain



## Introduction

- The present study is part of the project SoilDiverAgro (H2020 program, GA 817819). This project aims to promote soil biodiversity in European agroecosystems with the goal of promoting their stability and resilience by enhancing crop performance and reducing external inputs.
- To achieve this objective, an initial status on soil biodiversity in cropping systems was needed. This assessment was performed by the analysis of several biological indicators such as bacteria, fungi, nematodes, earthworms, etc. throughout Europe.
- Microorganisms are the major drivers of biogeochemical cycles such as the carbon and nitrogen cycle due to their abundance and high metabolic diversity<sup>1</sup>. Nutrient cycling in agroecosystems is essential to maintain plant growth and development. Here, we measured the abundance of key functional groups of microorganisms involved in the nitrogen and carbon cycles to determine their status across European field crops and link them to soil physicochemical properties and environmental variables.

## Materials & Methods

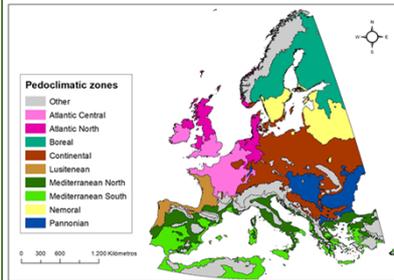


Figure 1. European pedoclimatic regions included in the SoildiverAgro project.

- Soil samples were taken from 188 agricultural wheat fields under both conventional and organic farming systems across nine European pedoclimatic regions (Figure. 1).
- The microbial genetic diversity was evaluated by quantitative PCR using genes involved in the following processes: nitrification (*amoA*), denitrification (*narG* and *nirK*), carbon fixation (*cbbL*), and carbon degradation (GH7).
- Briefly, soil DNA was extracted, purified and quantified. For the construction of qPCR standards, DNA extracted from soil samples served as the template of PCR reactions. The purified PCR product was ligated into the pGEM@-T Easy Vector Systems kit, and the resulting ligation products were used to transform into *Escherichia coli* JM109 competent cells (Promega).
- A myriad of soil properties were also analyzed for each of the farms and climatic conditions were also recorded.

## Results

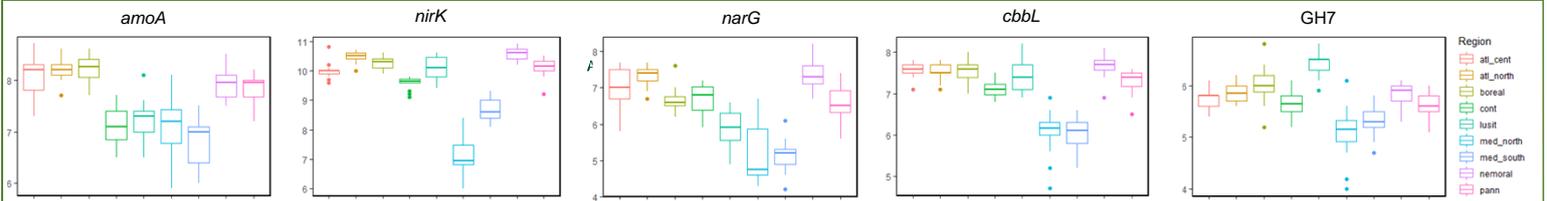


Figure 2. *amoA*, *nirK*, *narG*, *cbbL*, and GH7 gene abundance (log copies g<sup>-1</sup> dry soil) by region. atl\_cent: Atlantic central; atl\_north: Atlantic north; boreal: Boreal; cont: Continental; lusit: Lusitanian; med\_north: Mediterranean north; med\_south: Mediterranean south; Nemoral: Nemoral; pann: Pannonian. ANOVA's significance was p<0.0001 for all the genes.

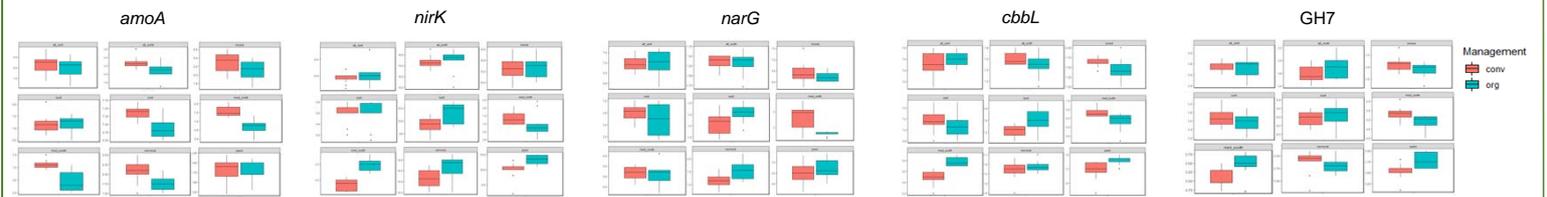


Figure 3. Differences in *amoA*, *nirK*, *narG*, *cbbL*, and GH7 gene abundance (log copies g<sup>-1</sup> dry soil) under different management systems. conv = conventional; org = organic.

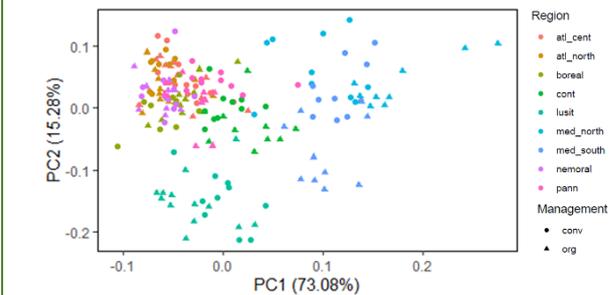


Figure 4. Principal component analysis (PCA) of all the functional genes across the pedoclimatic regions under conventional and organic farming systems.

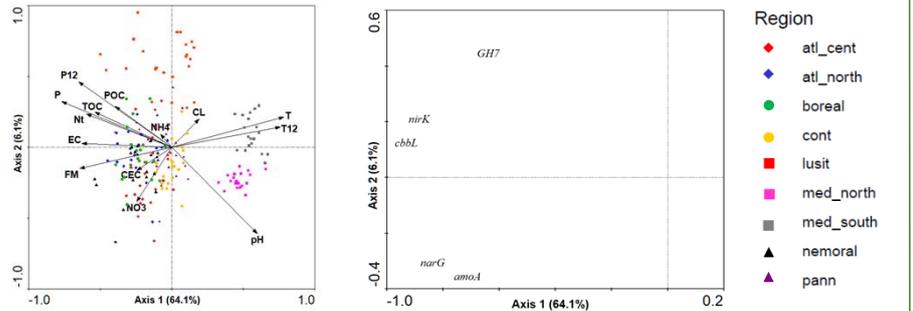


Figure 5. Redundancy analysis (RDA) between gene abundance, soil physicochemical properties, and environmental variables. P: mean annual precipitation (avg. last 30 yrs.); P12: prev. 12 mos.); POC: particulate organic carbon; TOC: total organic carbon; NT: total nitrogen; EC: electrical conductivity; NH<sub>4</sub>: NH<sub>4</sub><sup>+</sup>; FM: field moisture; CEC: cation exchange capacity; NO<sub>3</sub>: NO<sub>3</sub><sup>-</sup>; CL: clay; T: Mean annual temperature (avg. last 30 yrs.); T12: mean T (prev. 12 mos.); pH: pH.

## Conclusions

- Gene abundance strongly differed across pedoclimatic regions, showing the northern regions the highest abundances and the Mediterranean regions the lowest.
- Conventional farming significantly increased the abundance of the *amoA* gene, whereas organic management significantly increased *nirK* gene abundances. The content of *narG*, *cbbL*, and GH7 genes were not significantly altered by the management practice.
- Multivariate analysis showed that *amoA* and *narG* were strongly associated to soil nitrate and moisture, while negatively associated to mean annual temperature. The genes *nirK*, *cbbL*, and GH7 were strongly associated to annual precipitation, followed by soil organic carbon and nitrogen while negatively associated to soil pH.

