Soil micro-food web structure and functions exhibit contrasting dynamics according to litter quality

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Soil micro-food web structure and functions exhibit contrasting dynamics according to litter quality

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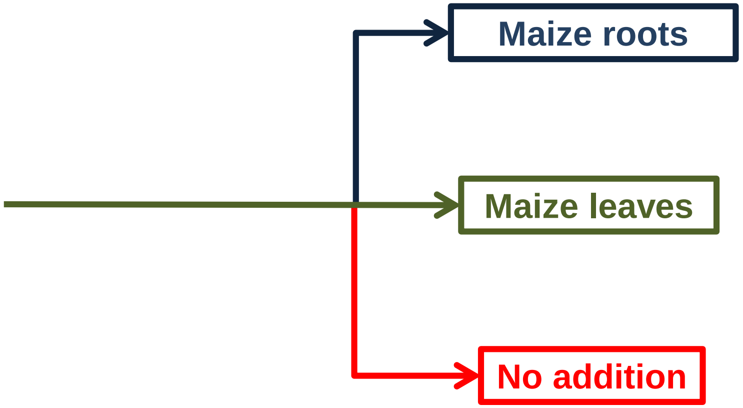
Which effects of litter quality on soil microfood-web structure and functions?

Study approach

Soil sampling
in the Estrees-Mons
SOERE



Incorporation of litter
in the 0-5 cm layer

Maize roots

Maize leaves

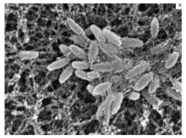
No addition

Incubation at 15°C
in microcosms

4 replicates by litter and date

Variables followed: at 0, 15, 35 and 91 days after incubation

Soil micro-food web structure *(genus level)*



Bacteria & fungi *(pyrosequencing)*

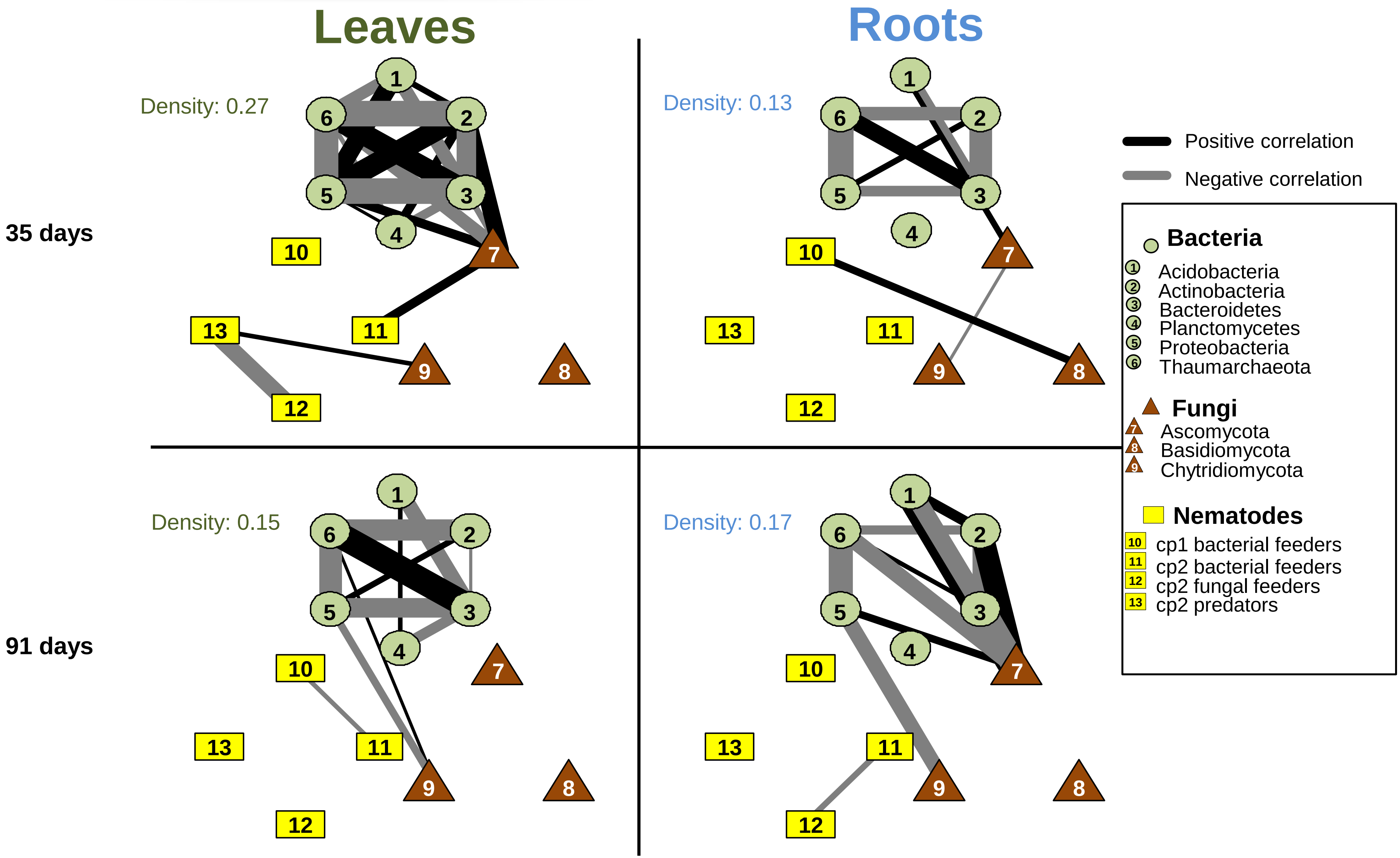
Nematodes *(Baermann extraction)*

Decomposition functions

Litter C mineralization *(NaOH traps)*

Enzymes activities
(C hydrolytic & oxidative)

Litter quality effects on micro-food web interactions



Leaves

Roots

35 days

Density: 0.27

Density: 0.13

91 days

Density: 0.15

Density: 0.17

Positive correlation

Negative correlation

Bacteria

① Acidobacteria
② Actinobacteria
③ Bacteroidetes
④ Planctomycetes
⑤ Proteobacteria
⑥ Thaumarchaeota

Fungi

7 Ascomycota
8 Basidiomycota
9 Chytridiomycota

Nematodes

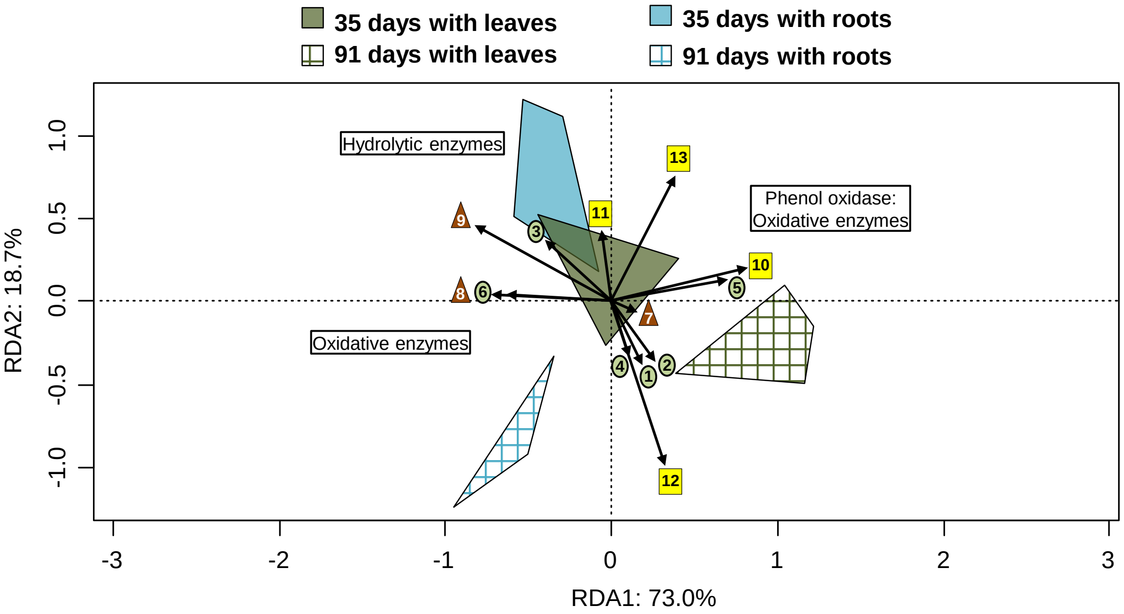
10 cp1 bacterial feeders
11 cp2 bacterial feeders
12 cp2 fungal feeders
13 cp2 predators

Main conclusions

- Significant effects of litter quality on micro-food web structure and functions, but dependent of the stage of decomposition

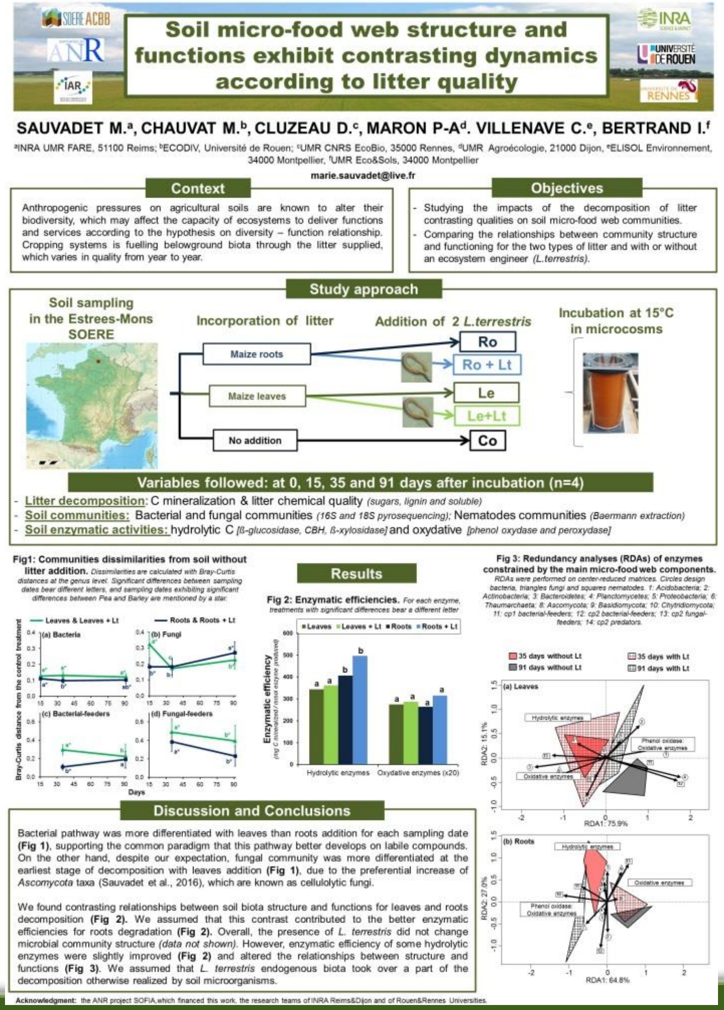
- Biotic interactions varied with litter quality and stage of decomposition, and were higher during the early stage of leaf decomposition

- Contrasting micro food-web structure – functions relationships according the litter degraded



Acknowledgments

Projet SOFIA (Soil Functional diversity as an indicator of sustainable management of Agroecosystems)



Soil micro-food web structure and functions exhibit contrasting dynamics according to litter quality

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Context

Anthropogenic pressures on agricultural soils are known to alter their biodiversity, which may affect the capacity of ecosystems to deliver functions and services according to the hypothesis on diversity – function relationship. Cropping systems is fuelling belowground biota through the litter supplied, which varies in quality from year to year.

Objectives

- Studying the impacts of the decomposition of litter contrasting qualities on soil micro-food web communities.
- Comparing the relationships between community structure and functioning for the two types of litter and with or without an ecosystem engineer *(L.terrestris)*.

Study approach

Variables followed: at 0, 15, 35 and 91 days after incubation (n=4)

- Litter decomposition: C mineralization & litter chemical quality *(sugars, lignin and soluble)*
- Soil communities: Bacterial and fungal communities *(16S and 18S pyrosequencing)*; Nematodes communities *(Baermann extraction)*
- Soil enzymatic activities: hydrolytic C *[ß-glucosidase, CBH, ß-xylosidase]* and oxydative *[phenol oxydase and peroxydase]*

Results

Fig1: Communities dissimilarities from soil without litter addition. *Dissimilarities are calculated with Bray-Curtis distances at the genus level. Significant differences between sampling dates bear different letters, and sampling dates exhibiting significant differences between Pea and Barley are mentioned by a star.*

Fig 2: Enzymatic efficiencies. *For each enzyme, treatments with significant differences bear a different letter*

Fig 3: Redundancy analyses (RDAs) of enzymes constrained by the main micro-food web components. *RDAs were performed on center-reduced matrices. Circles design bacteria, triangles fungi and squares nematodes. 1: Acidobacteria; 2: Actinobacteria; 3: Bacteroidetes; 4: Planctomycetes; 5: Proteobacteria; 6: Thaumarchaeta; 8: Ascomycota; 9: Basidiomycota; 10: Chytridiomycota; 11: cp1 bacterial-feeders; 12: cp2 bacterial-feeders; 13: cp2 fungal-feeders; 14: cp2 predators.*

Discussion and Conclusions

Bacterial pathway was more differentiated with leaves than roots addition for each sampling date **(Fig 1)**, supporting the common paradigm that this pathway better develops on labile compounds. On the other hand, despite our expectation, fungal community was more differentiated at the earliest stage of decomposition with leaves addition **(Fig 1)**, due to the preferential increase of *Ascomycota* taxa (Sauvadet et al., 2016), which are known as cellulolytic fungi.

We found contrasting relationships between soil biota structure and functions for leaves and roots decomposition **(Fig 2)**. We assumed that this contrast contributed to the better enzymatic efficiencies for roots degradation **(Fig 2)**. Overall, the presence of *L. terrestris* did not change microbial community structure *(data not shown)*. However, enzymatic efficiency of some hydrolytic enzymes were slightly improved **(Fig 2)** and altered the relationships between structure and functions **(Fig 3)**. We assumed that *L. terrestris* endogenous biota took over a part of the decomposition otherwise realized by soil microorganisms.

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More informations:

- Sauvadet et al. (2016) Soil Biology&Biochemistry 95: 262-274

Projet SOFIA