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Disentangling the effects of litter quantity and quality on soil biota structure and functioning: *application to a cultivated soil in Northern France*

M. Sauvadet¹, M. Chauvat², N. Fanin¹, S. Coulibaly², I. Bertrand³

INRA UMR FARE, Reims; University of Rouen; UMR Eco&Sols, Montpellier

Impacts of cultural practices on soil biota

Cultural practices



Alteration

Alteration



Soil organisms

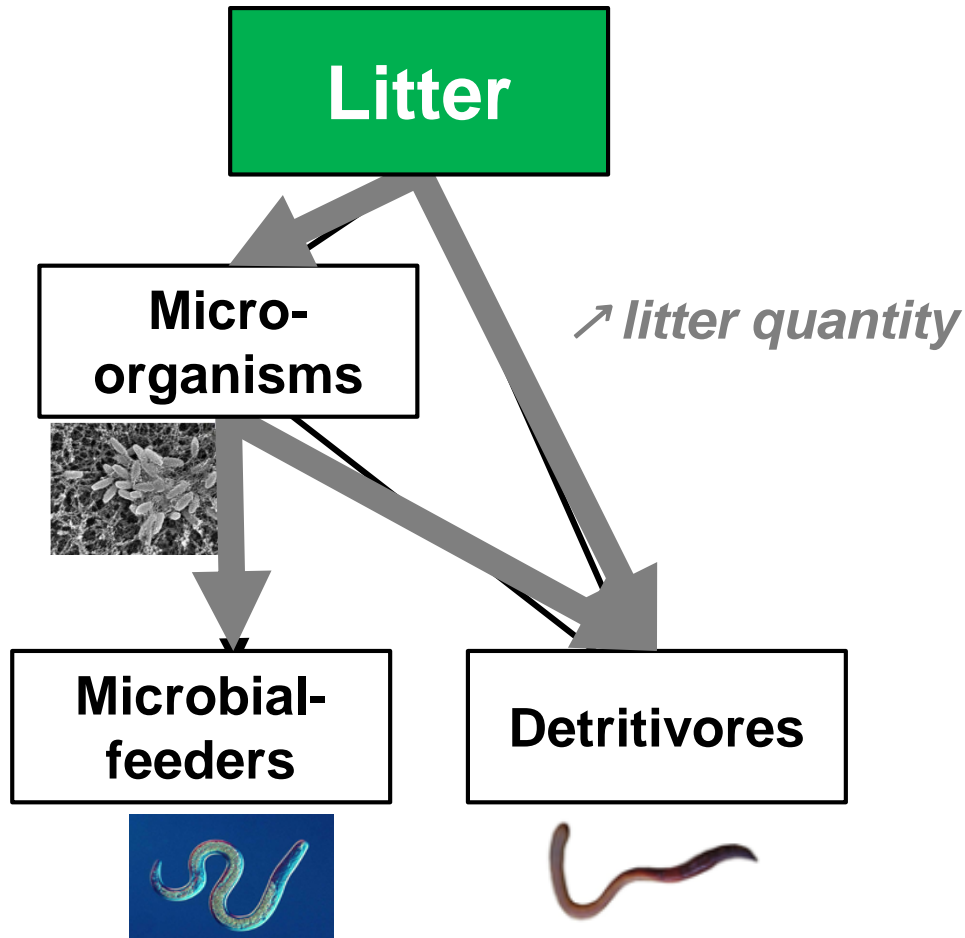
?

Soil functions:

- Respiration versus C storage
- Nutrient recycling ...

Litter quantity effects on soil food web

Crop residues → Main trophic resource for arable soil organisms (Kim & Dale, 2004)



Δ quantity:
crop residues exportation / restitution



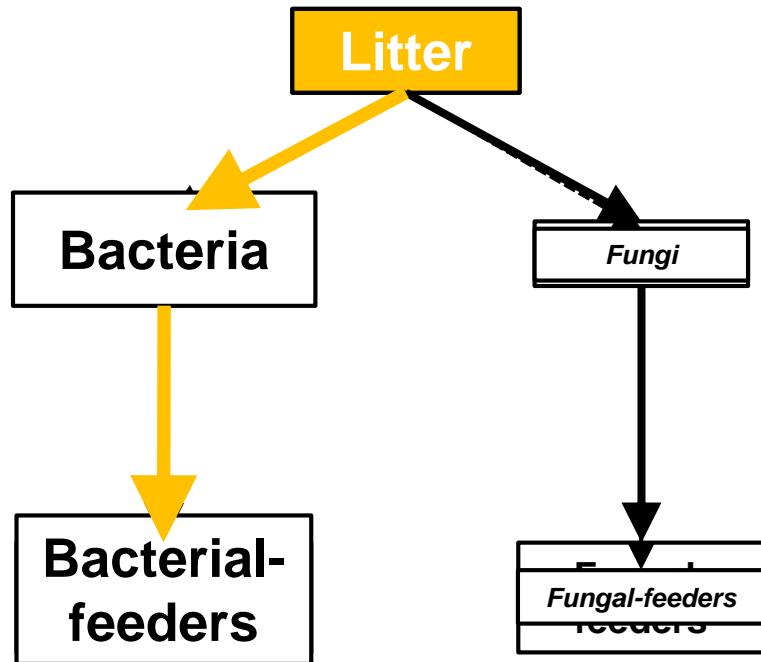
↗ Microbial biomass
(Spedding et al., 2004; Govaerts et al., 2007)

→ Few information at the higher trophic levels

Is litter quantity increasing the biomass of soil fauna?

Litter quality effects on soil food web

Crop residues → Main trophic resource for arable soil organisms (Kim & Dale, 2004)



↗ *litter quality*

Δ quality:
choice of the crop in the rotation
(Sauvadet et al., 2016)



→ Few information on fauna in cultivated soil

Is litter quality increasing the bacterial energy channels?

How can litter quantity and quality affect soil food web composition and functions in cultivated soils?

Litter incorporation (0-15 cm) into 8 m² plots (4 blocks)



- Without litter
 - 5 t.ha⁻¹ Pea
 - 10 t.ha⁻¹ Pea
 - 10 t.ha⁻¹ Barley
- Labile – high quality litter
- Quantity effect
- Quality effect
- Recalcitrant – low quality litter

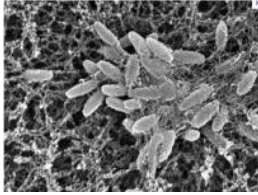
→ Results presentation after 7 months

Material and methods

Food web composition ($\text{mg C} \cdot \text{m}^{-2}$)

Bulk soil 0 – 10 cm

Total microorganisms & fungi



Microbial biomass C & Ergosterol

Soil corers 5 cm \varnothing – 10 cm depth

Nematodes



Baermann extraction

Collembola



Berlese-Tullgrenn extraction

Mites



Hand sorting (soil cubes 25 cm x 25 cm x 25 cm)

Earthworms



Macroarthropods



Food web functions

Incorporated litterbags (8cm depth)

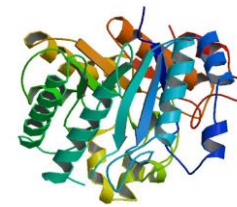
Litter mass loss



Bulk soil 0 – 10 cm

Soil N mineral content

Enzymatic activities (Bell et al., 2013)

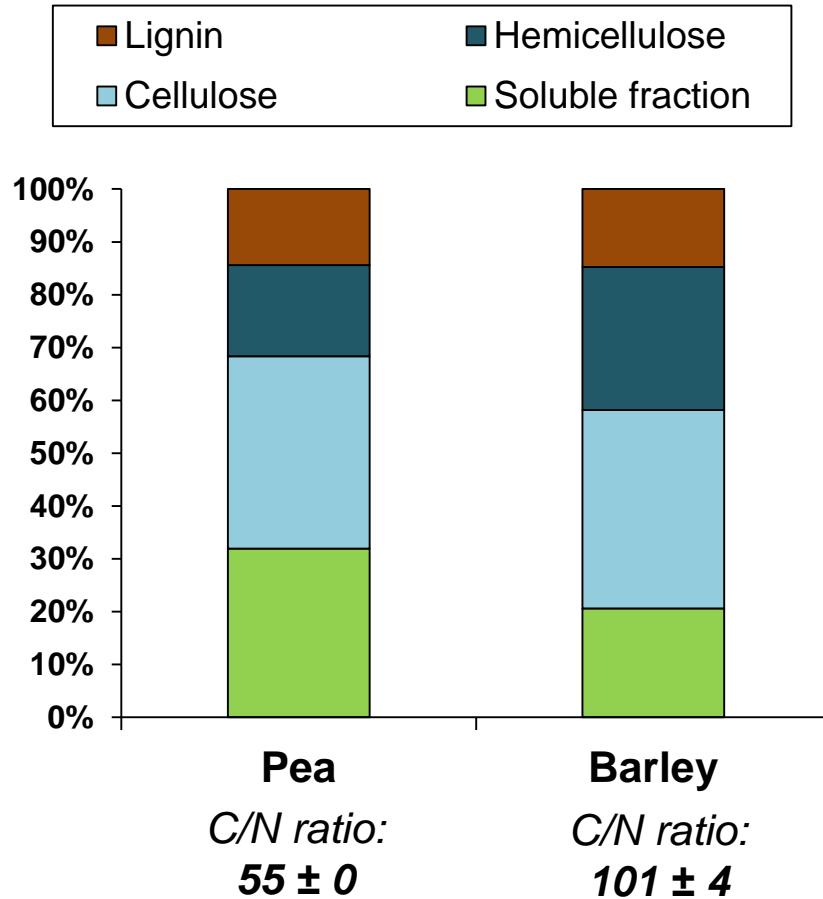


www.rcsb.org

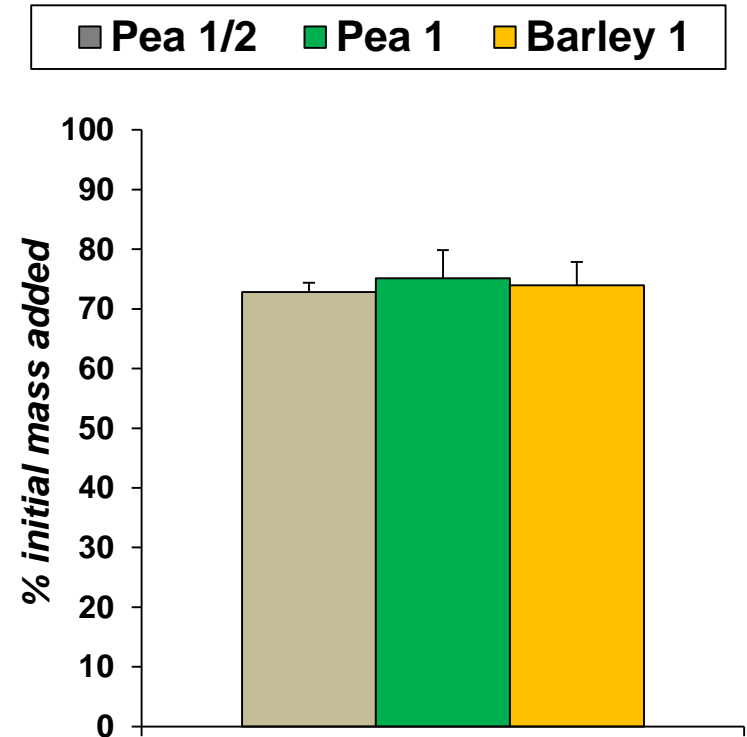
- C hydrolytic enzymes
- N hydrolytic enzymes
- Oxidative enzymes

Litter decomposition

Litter initial qualities

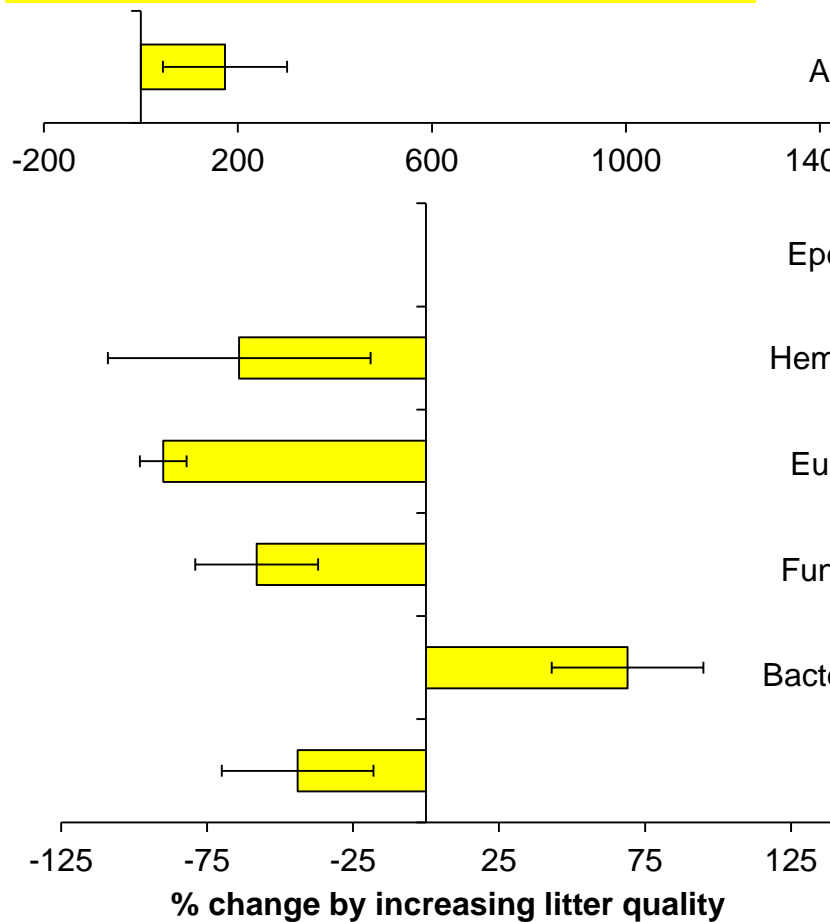


Litter mass loss after 7 months



Quality – quantity effects on soil food web composition

Quality effects: Barley → Pea 10t.ha⁻¹



Quantity effects: Pea 5 t.ha⁻¹ → 10 t.ha⁻¹

Anecic earthworms



Epedaphic collembola

Hemiedaphic collembola



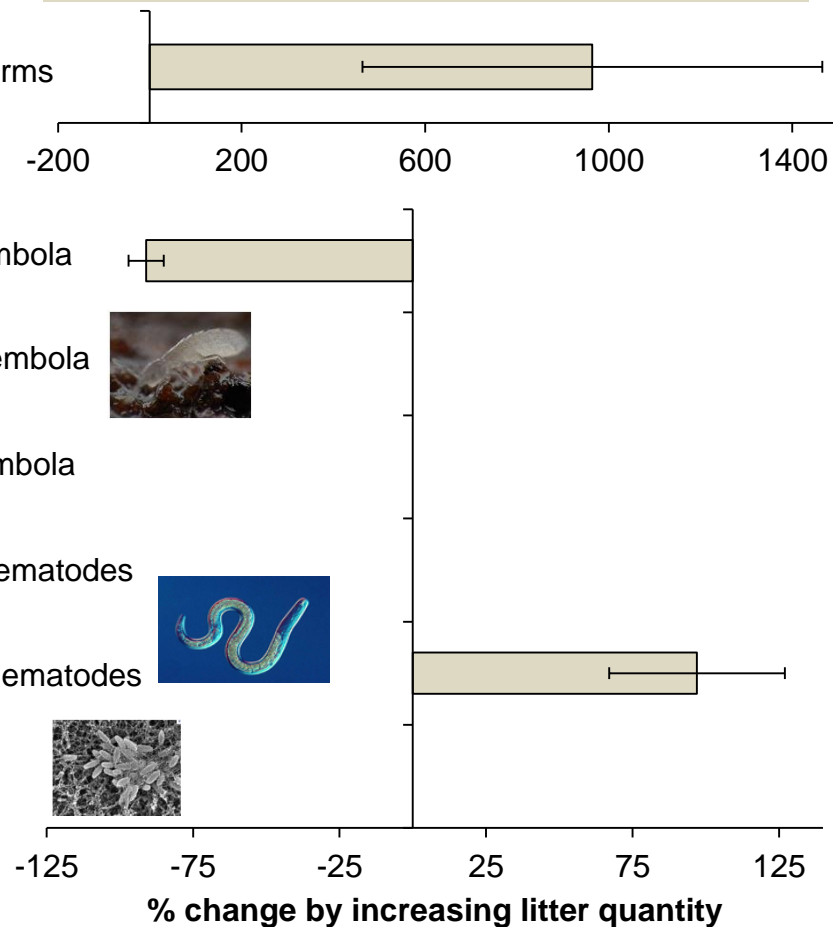
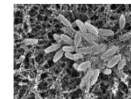
Euedaphic collembola

Fungal-feeding nematodes



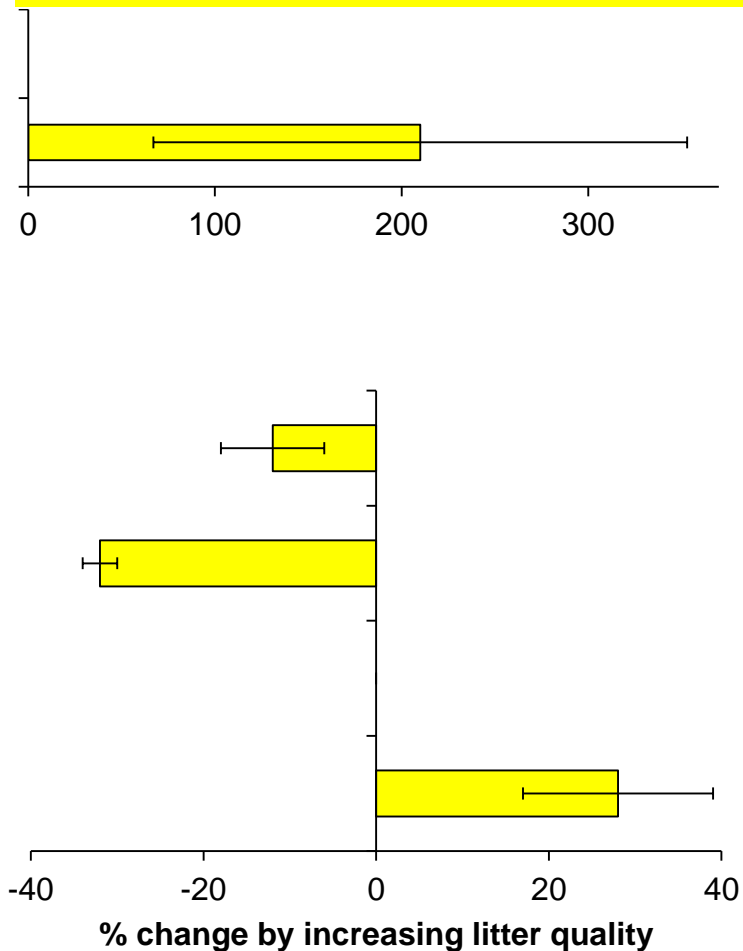
Bacterial-feeding nematodes

Fungi

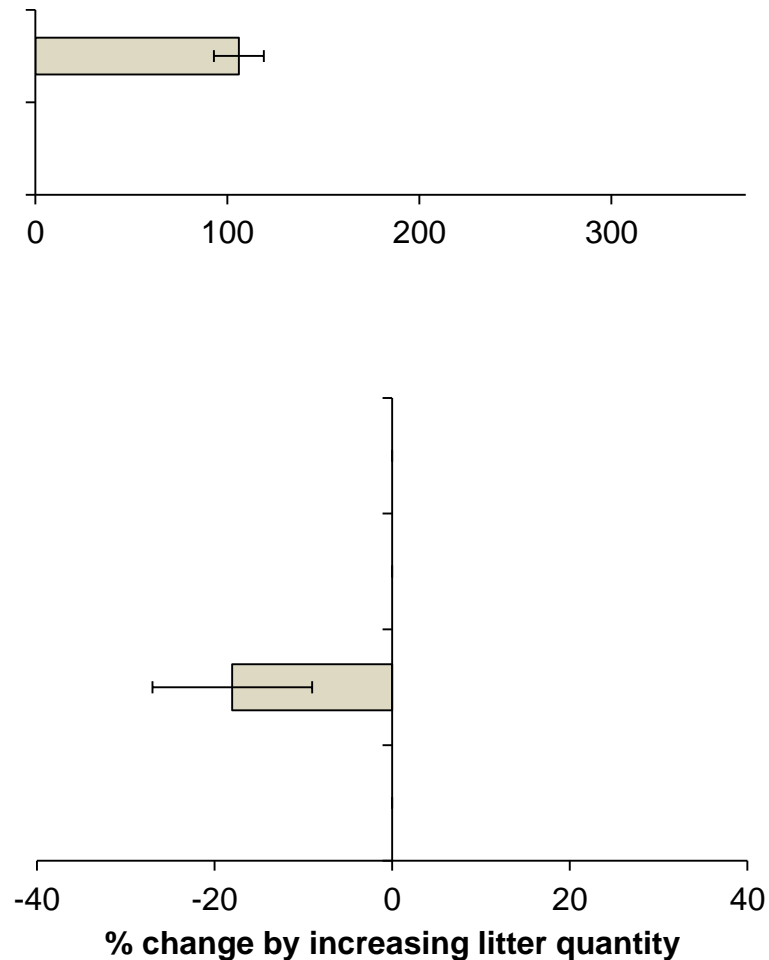


Quality – quantity effects on soil food web functions

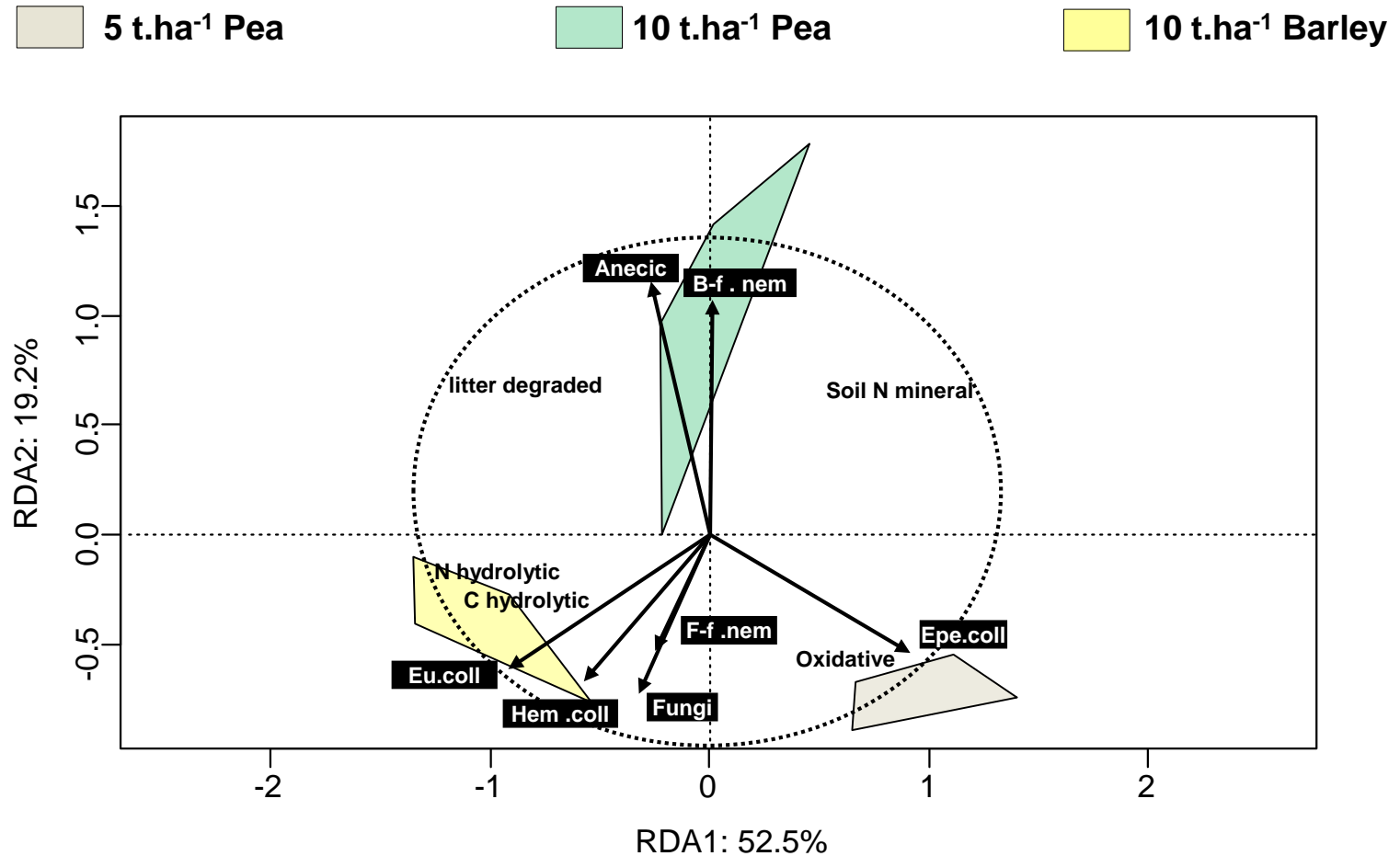
Quality effects: Barley → Pea 10 t.ha⁻¹



Quantity effects: 5 t.ha⁻¹ → 10 t.ha⁻¹



Linking soil food web composition and functions



Conclusions

↗ Litter quality

↘ fungal : bacterial pathway

6 groups impacted
Amplitude change $\approx 85\%$

↘ N enzymatic demand from biota

*Selection of biota with different N
acquisition strategy?*

↗ Litter quantity

↗ detritivores size

3 groups impacted
Amplitude change $\approx 385\%$

↗ amount of litter degraded by
biota

Long term impact on soil C?

Possibility to use litter addition in specific quantity and/or quality to favor one specific ecosystem service or restore one specific functional group?

Acknowledgments

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

Million S. & F., Alavoine G., Thiébeau P., Delfosse O., Habrant A., Portelette A., Chiter K., Henneron L., Brunet N., Chauchard B., Villenave C., Recous S., Lashermes G.



Acknowledgments

Poster: session 34



SAUVADET M.^a, CHAUVAT M.^b, CLUZEAU D.^c, MARON P.-A.^d, VILLENAVE C.^e, BERTRAND I.^f

^aINRA UMR FARE, 51100 Reims; ^bECODIV, Université de Rouen; ^cUMR CNRS EcoBio, 35000 Rennes; ^dUMR Agroécologie, 21000 Dijon; ^eELISOL Environnement, 34000 Montpellier; ^fUMR EcoSols, 34000 Montpellier

marie.sauvadet@univ-rouen.fr

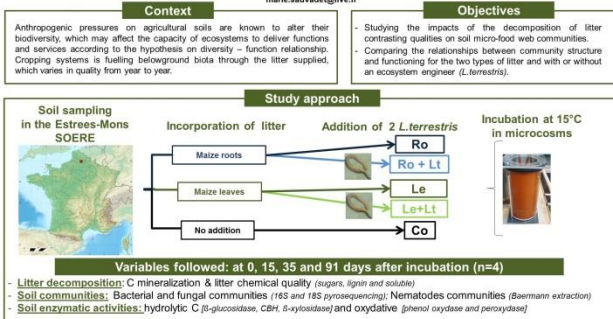


Fig1: Communities dissimilarities from soil without litter addition. Dissimilarities are calculated with Bray-Curtis distances of the species level. Significant differences between sampling dates bear different letters, and sampling dates exhibiting significant differences between Pea and Maize are mentioned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

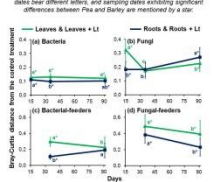


Fig 2: Enzymatic efficiencies. For each enzyme, treatments with significant differences bear a different letter.

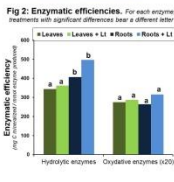
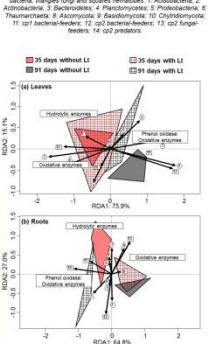


Fig 3: Redundancy analyses (RDAs) of enzymes constrained by the main micro-food web components. RDAs were performed on center-reduced matrices. Cross design: bacteria, fungi and square nematodes; 1: Acidobacteria; 2: Actinobacteria; 3: Basidiomycota; 4: Basidiomycota; 5: Proteobacteria; 6: Thaumarchaeota; 7: Ascomycota; 8: Basidiomycota; 9: Chytridiomycota; 10: Chytridiomycota; 11: q22 bacterial feeders; 12: q22 bacterial feeders; 13: q22 fungal feeders; 14: q22 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 cellulytic 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) Applied Soil Ecology, 107: 261-271
- Sauvadet et al. (2016) Soil Biology&Biochemistry 95: 262-274

Thank you for your attention