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Towards fungal descriptors as a new tool for the assessment of the quality of agricultural soils

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INTRODUCTION

Agricultural soils, specifically cropped soils, constitute ecosystems highly disturbed by human activities. The agricultural management of soils has a great impact upon the functional process of soil microbial communities, particularly on **fungal biomass**. This study is a part of a global three years program that **aims to develop and validate an index of soil biological status** in order to assess impacts of pollutants upon soil quality.

OBJECTIVES

Our objective was to estimate how pollutants modify soil biological status in relation to agricultural management. For that purpose, using **field** (considered as non-contaminated references) and undisturbed **microcosm** experiments, we measured the variability of 40 physicochemical and biological quantitative **descriptors**. We focused here on **fungal biomass** and on the **relevance** of its descriptors (**18S rDNA, ergosterol, PLFAs**).

METHODS

I- Fungal biomass determinations

- genetic assay using real time PCR (Polymerase Chain Reaction 18SrDNA)
- chemical assay by extraction and quantification of total ergosterol, free ergosterol and specific PhosphoLipid Fatty Acids (C18:2ω6,9, C16:1ω5)

II- Physicochemical characteristics of soils

- Microbial carbon, cation exchange capacity, carbon content, phosphorus, total nitrogen, pH, bulk density, moisture and particle size distribution data

III- Experimental sites

- Fields located in Normandy with contrasted agricultural practices (meadow or intensive management crop). Samplings have been undertaken in order to observe temporal impact (4 dates: april, june, august, october).
- We developed microcosms fitted with columns of undisturbed soil from the same fields to assess the ecotoxicity of chemical pollutants. All the microcosms were settled in the ground under external conditions.



Meadow and crop fields at Yvetot



Microcosms setup

RESULTS

I - Fungal Biomass descriptors

Average and standard deviations of descriptors

	Meadow	Crop
PLFA C16 ppb	2.31 (±0.45)	0.81 (±0.45)
PLFA C18 ppb	0.34 (±0.1)	0.09 (±0.05)
18S rDNA ppm	6.7 (±0.5)	1.3 (±0.5)
Free ergosterol ppm	3.31 (±0.5)	0.8 (±0.5)
Total ergosterol ppm	6.42 (±0.6)	2.24 (±0.7)

→ The whole data indicates that the fungal content as measured by various descriptors is higher in the meadow than in the crop

II - Intercorrelations

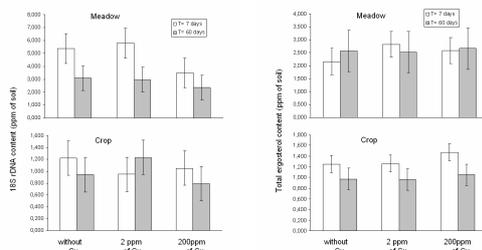
	C18	18S rDNA	Free ergosterol	Total ergosterol
C16	0.758 ^b 0.0000	0.667 ^b 0.0000	0.752 ^b 0.0000	0.807 ^b 0.0000
C18		0.253 ^b 0.0168	0.5421 ^a 0.0000	0.648 ^a 0.0000
18S rDNA			0.736 ^b 0.0000	0.757 ^b 0.0000
Free ergosterol				0.925 ^b 0.0000

Correlation coefficients and p-value.
 (a) Linear correlation (Pearson)
 (b) Rank correlation (Spearman)

Significant intercorrelations have been obtained, indicating that molecular and chemical protocols are relevant to access fungal biomass.

→ Significant intercorrelations have been obtained amongst various descriptors

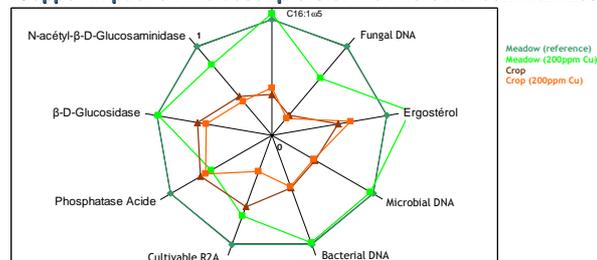
III - Responses of biomass in the presence of copper



Evolution of fungal biomass (18S rDNA and total ergosterol) in the microcosms (without, with 2ppm or 200ppm of copper) for the two agricultural practices.

→ The copper impact is not significant compared to the temporal evolution of fungal community in the microcosm
 → Has the copper induced modification in the structure of communities without having measurable impact on the microbial biomass and the resulting enzymatic activities?

IV - Copper impact on the descriptors of the microbial communities



- All the data have been normalized taking as reference the meadow data.
- We note that, whatever the descriptor chosen, the impact of copper is negligible compared to the impact of the practices

CONCLUSION

We could not highlight an significant impact of copper on fungal communities with this study, but we have nevertheless established a hierarchy of the impacts of anthropic activities on these descriptors: **Practice, Location, Date** and finally, **Copper**.