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Bioindication of soil quality based on environmental DNA

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Why a global indicator of soil quality?

- More and more money spent on soil restoration for polluted or degraded sites (>470M€ in 2010).
 - But lack of adapted protocols and indicators to assess the recovery of ecosystems (function, biodiversity)
- Construction of dedicated indicators in link with the ecosystem services for an efficient monitoring of the soil compartment : standardized / reliable / cheap / easily applied



Limits of 'traditional' indicators

- **Physicochemical** (pH, N, C, P...) → Do not allow to assess the level of soil functionality
- **Biological** (Description richness and abundance of specific groups, e.g. annelids, nematods, microarthropods, bacteria, fungi)
 - High temporal and spatial variability according to soil and climatic conditions
 - Morphological identification can be tedious, time-consuming, subjective, and expensive



Why using eDNA metabarcoding?



- A single analysis → diversity of taxa of the target group
- Temporal and spatial standardisation
- Independant of climatic conditions or seasons
- Analysis without « a priori »
- Sampling of soil easy, fast and standardized.



First study on soil eDNA comparing...

Botanical survey

Avenella flexuosa



Poa sp.



Bistorta vivipara



Salix sp.



Taraxacum sp.



Carex sp.



Alchemilla sp.



Anthoxanthum nipponicum



Viola biflora



Festuca sp.



Equisetum sp.



Deschampsia sp.



Rumex sp.



Calamagrostis sp.



eDNA metabarcoding

Yoccoz et al. (2012)

Pilot study on a polluted site

Field work:

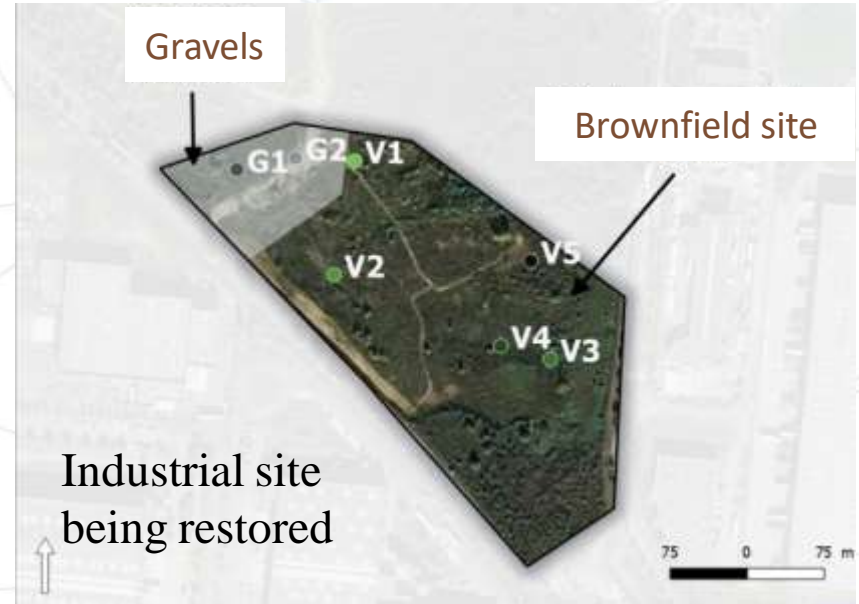
Pollution: hydrocarbons / heavy metals

- Quadrats 1m² - Horizon 0-10cm
- 7 samples (20 pooled subsamples) – 15g
- 2 replicates per sample
- Preserved dry (with silica)



Lab work:

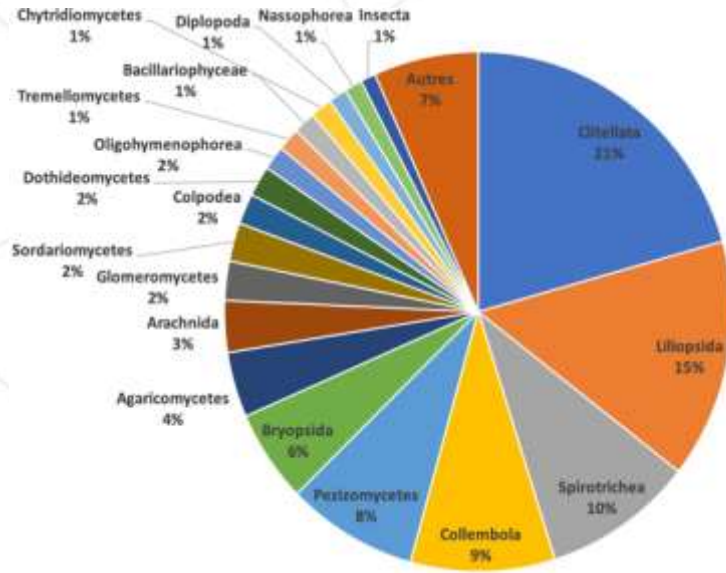
Extraction of extracellular DNA
Amplification using eukaryote primers
4 PCR replicates / sample.
Miseq sequencing run (2*125 bp).



Bioinformatic / biostatistics analyses
(OBIttools – ROBitools)

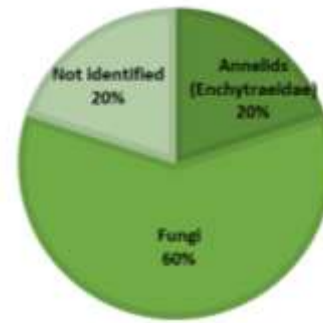


First results: Taxonomic composition

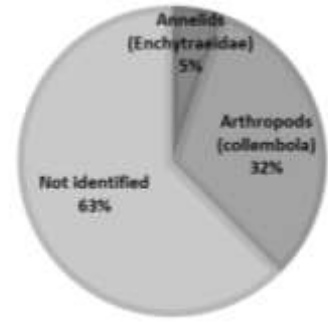


All samples

- Animals: mainly annelids, protozoans, collembols
- Plants: mainly monocotyledons, mosses



Polluted fields



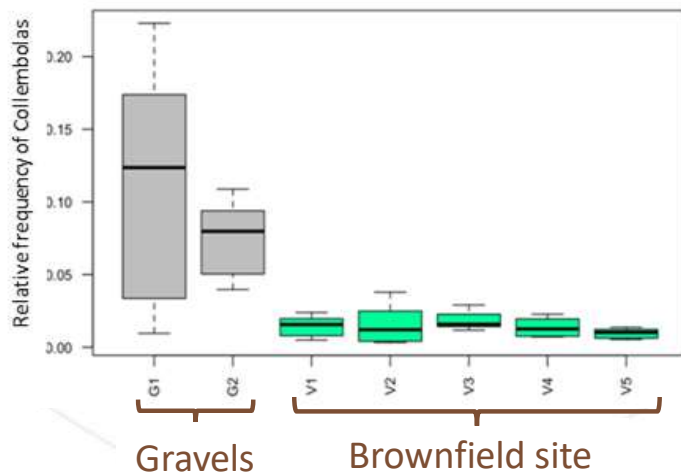
Fields being restored

Identification of different 'composite' bioindicators, depending on habitat type

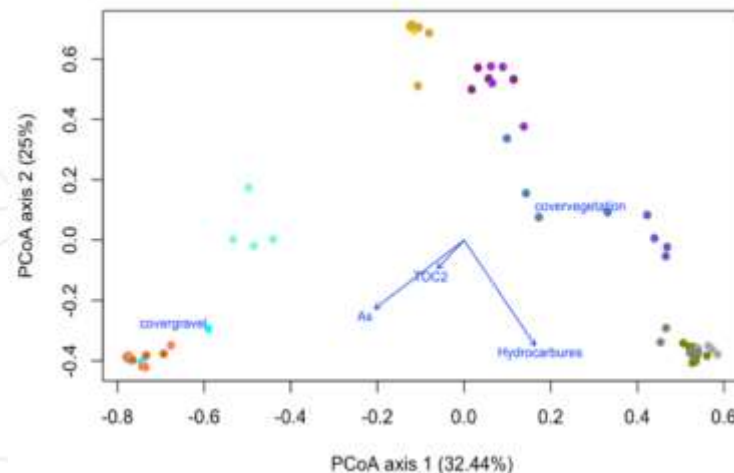
→ can testify of the soil restoration without any a priori knowledge



First results: Focus on collembola



Relative frequency of collembolas between samples.

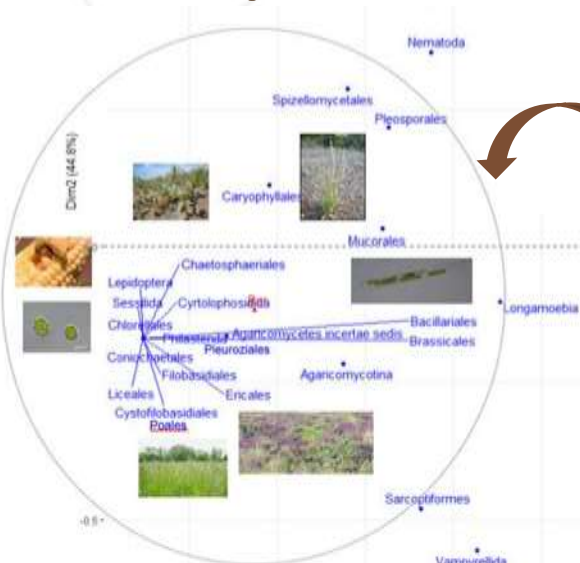


Structure of samples (multivariate analysis)

- This group responds well to environmental variables, i.e. habitats or pollution type
- Pioneer species?



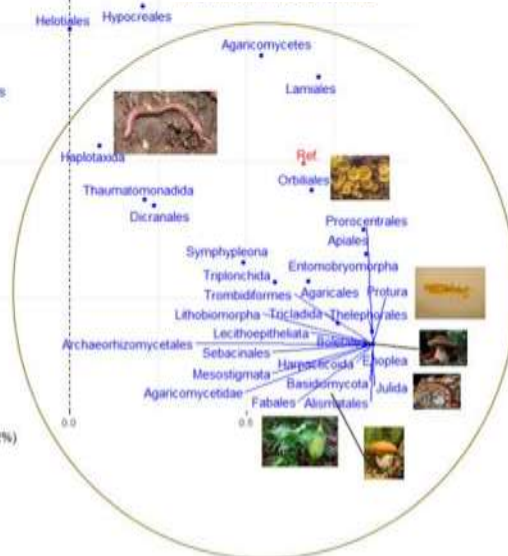
Other study on a rehabilitation site



Open site

Close to corn fields (-> corn moth)
regularly fooded (diatoms, chlorella...)

Forest area



Rehabilitation
after landfill mining

Low anthropic pressure, close
to a river (sometimes flooded)

→ Habitats can be easily
differentiated based on their
composition



Conclusions

- A DNA signature can be established from soil samples
→ With the objective to assess the degree of restoration of soil quality in polluted environments.
- eDNA tool as a global indicator for biological assessment of soils:
 - standardized
 - relatively inexpensive
 - easily applied regardless of climatic conditions.



Perspectives

- R&D project on a pilot site with different levels of pollution.



- Ultimately, a database considering different type of soils will be built at national scale → correlation between DNA signatures and ecosystem functions ('Machine learning' approaches)
- Can also be used in the agriculture sector, to contribute to the assessment of soil biological quality and guide cultural practices.





Thanks for your attention!