Impact of agricultural practices on soil microbial communities in Belgium

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CONTEXT

The development of new agricultural technologies consuming less energy and chemicals leads to a good understanding of different biological drivers involved in the production process. Bacteria and Fungi are key elements because they are deeply involved in nutrient cycles. In this study, we use massive parallel sequencing to study how two agricultural practices (tillage and residue management) affect the fungal and bacterial communities. Our preliminary study found no difference in the number of species. Therefore we investigated the impact of agricultural practices on species composition.
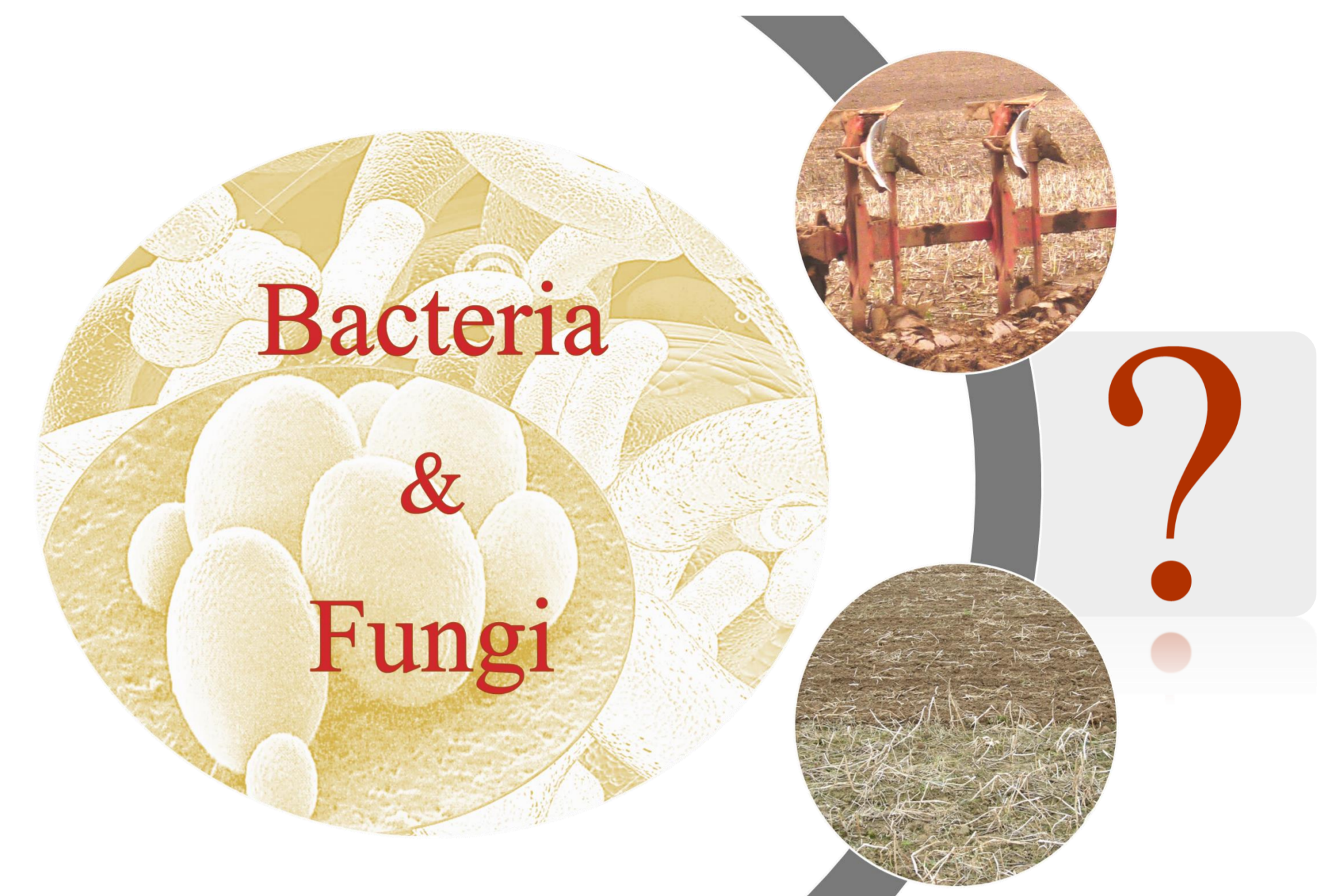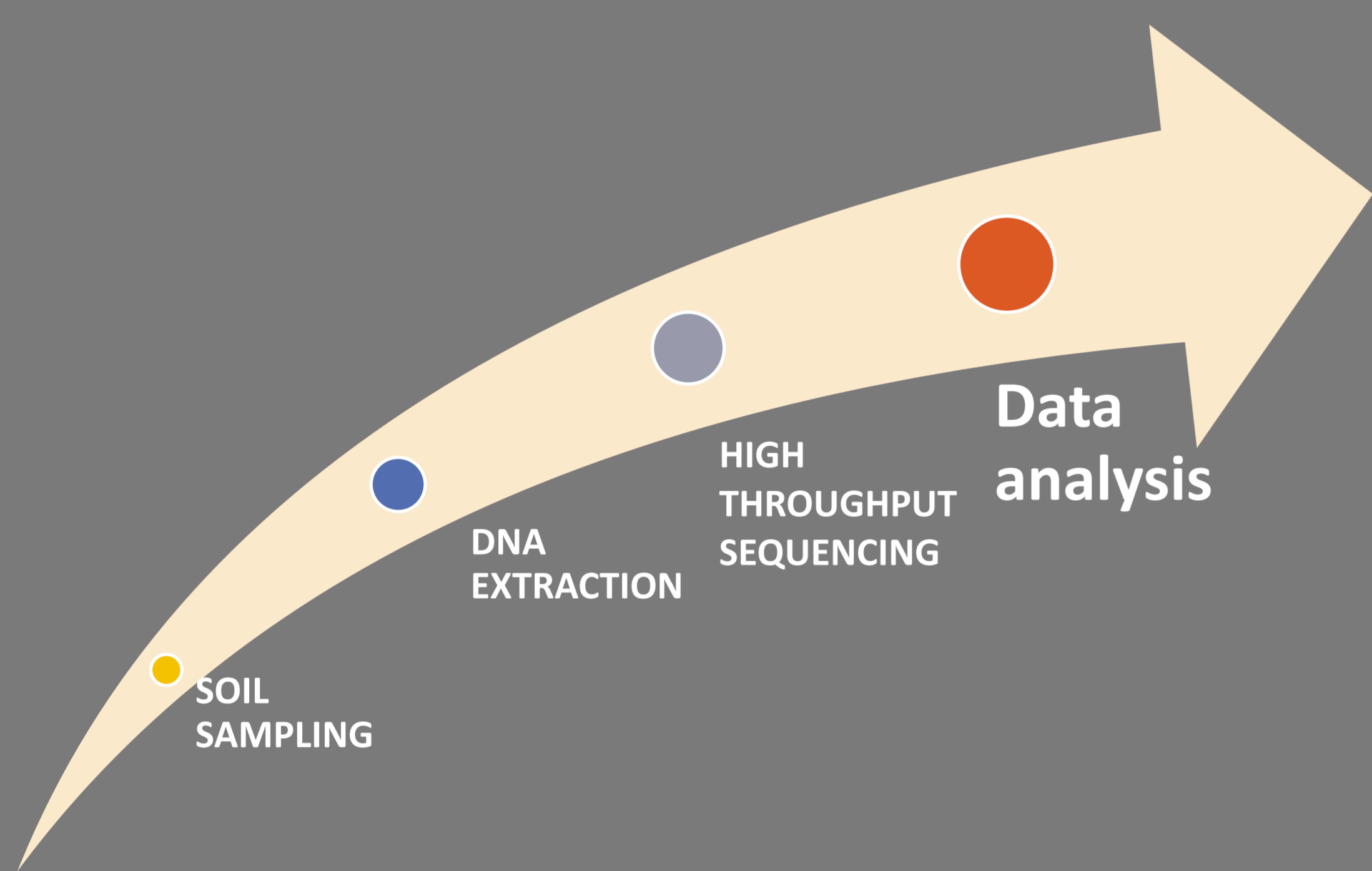
MATERIAL & METHODS

Experimental plot: designed with 4 agricultural practices – conventional tillage (CT), reduced tillage (RT), with (R+) or without (R-) residues incorporation – with 4 repetitions in a *Faba bean* crop after sowing. Soil samples were collected at a depth of 15-20cm, and 10 ecological parameters were measured[1] from samples.

Sequencing: 400pb from 16S and 28S rRNA were sequenced with GS junior 454, Roche©. Data were analysed with mothur pipeline. Silva database was used to align sequences and clustering was performed to obtain OTUs (Operational Taxonomic Unit).

Data analysis: Multivariate analysis (RDA) was used to identify (1) the impact of agricultural practices on Bacteria and Fungi communities with ecological parameters as passive variables and (2) the variance partition of the best agricultural practice driver and the two best ecological parameters.

[1] TOC (total organic carbon), pHKcl, Na, Ca, P, Mg, K, NO3, humidity coefficient, and texture

RESULTS

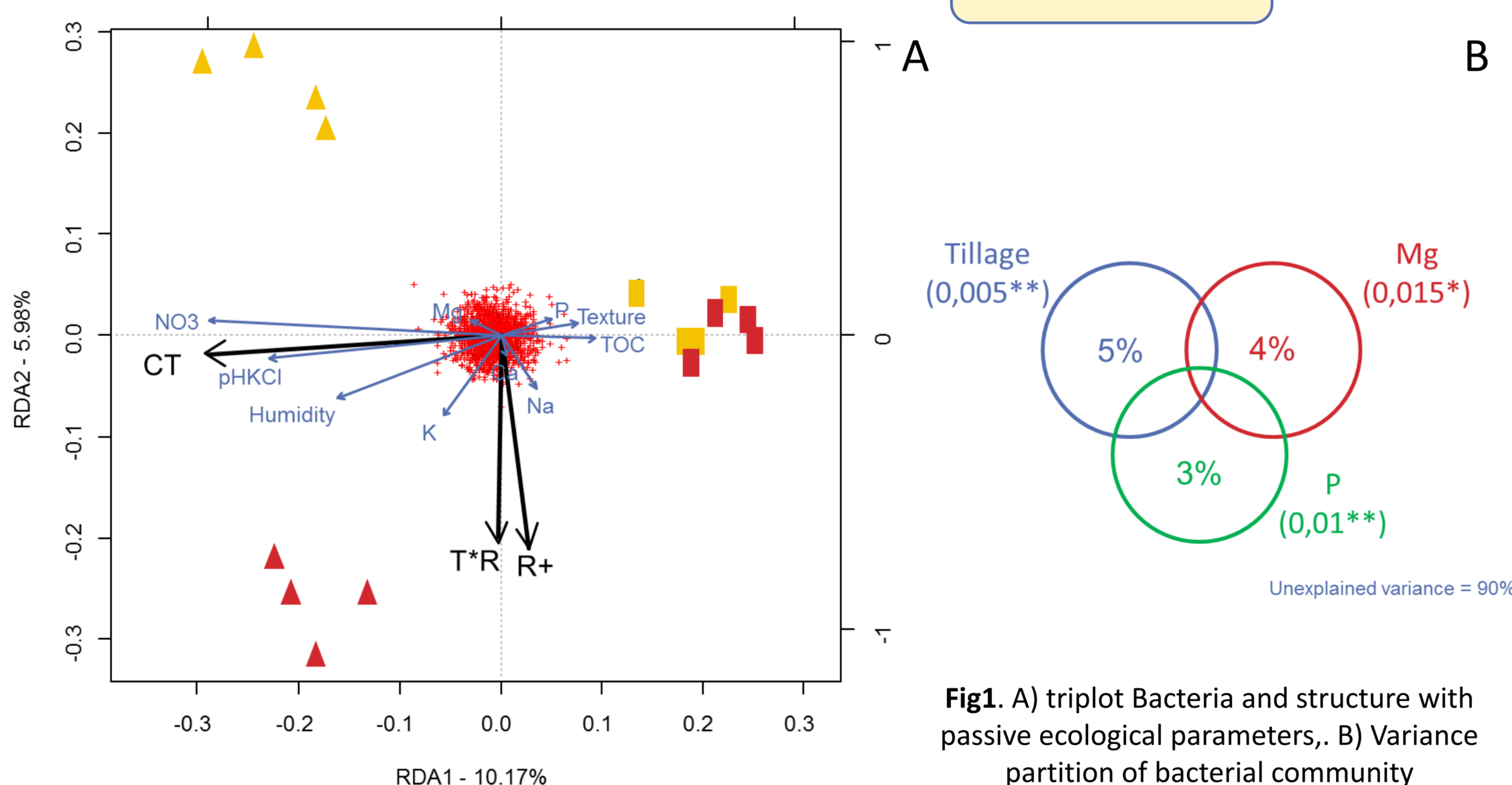### Bacteria

CT R-   🔺 (yellow triangle)   RT R-   🟨 (yellow square)
CT R+   🔺 (red triangle)   RT R+   🟥 (red square)

Fig1. A) triplot Bacteria and structure with passive ecological parameters,. B) Variance partition of bacterial community
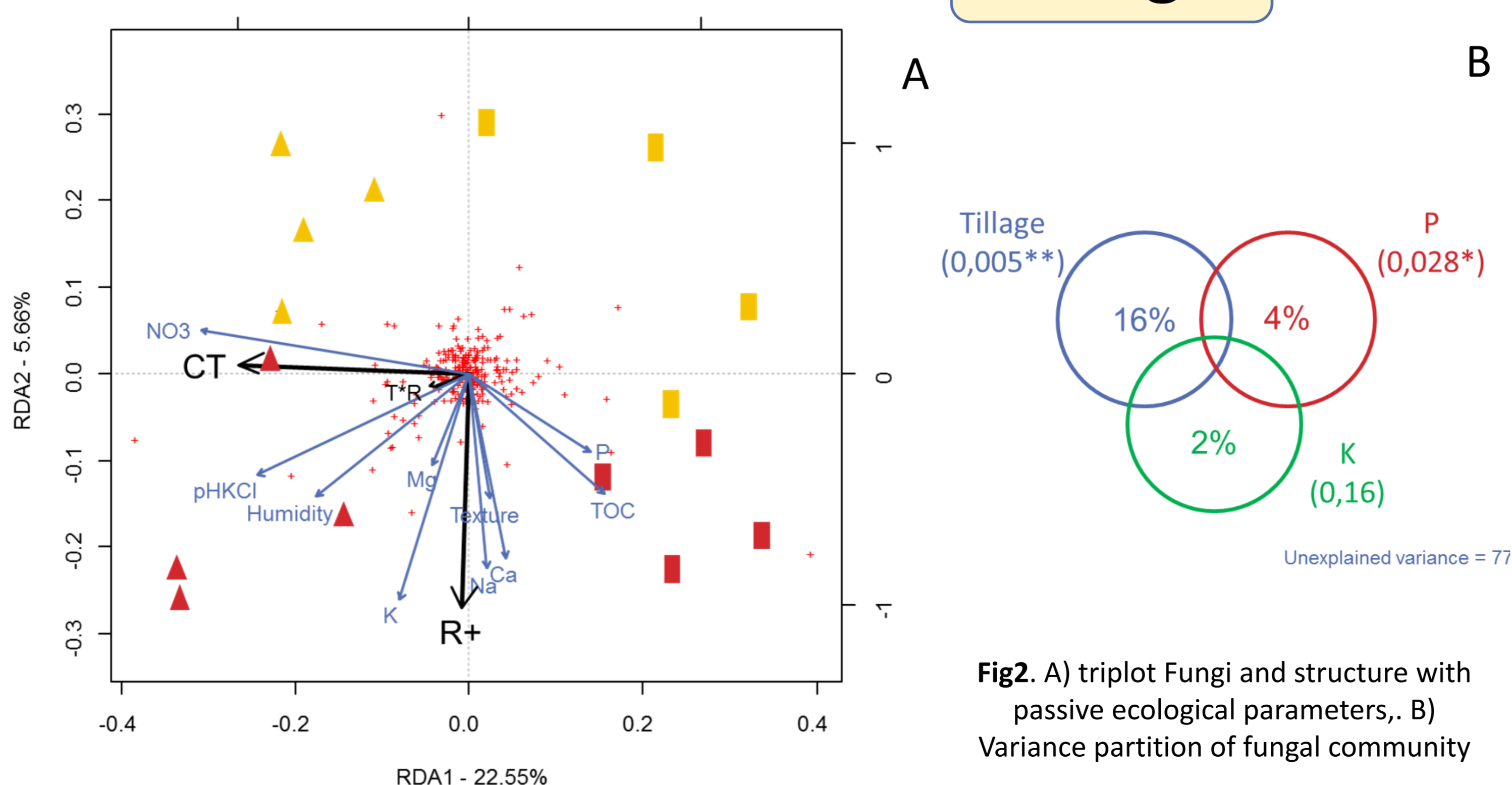
Fungi

Fig2. A) triplot Fungi and structure with passive ecological parameters,. B) Variance partition of fungal community

Bacteria (2511 OTUs): Tillage, Magnesium and Phosphorus are together the best drivers to explain **28%** of the community variance (p_{value}= 0,005).

Fungi (265 OTUs): Tillage, Phosphorus and Potassium are together the best drivers to explain **38%** of the community variance (p_{value}= 0,005).

For both microorganism groups, **Fig. A** shows the partial correlations of agricultural practices with all ecological parameters. NO3, pHKCl and Humidity are positively correlated with CT. And **Fig. B** shows the variance partition between the three drivers for each group.

Moreover, an effect of Residue could be expected in CT (**Fig 1 A**)

CONCLUSION & PERSPECTIVES

Fungi and Bacteria communities are impacted by Tillage practices. But, independently of Tillage, Phosphorus and Magnesium explained also Bacteria community structure while it is Phosphorus and Potassium for the Fungi community structure. Currently we would like to identify indicator species from CT and RT situation. However, the majority of sequenced species are still unidentified and it will be difficult to identify the ecological processes in which they are involved. In the near future, a comparison with data from the same experiment but at the flowering stage will be performed.

COLLABORATIONS

This project is a part of multidisciplinary projects from **AgricultureIsLIfe** plateform (Gembloux Agro-Bio Tech, Ulg, Belgium), focusing on 'Use of residues in agricultural systems' with the close collaboration with other PhD students.