

No favorable effect of reduced tillage on microbial communities in a silty loam soil (Belgium)

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Microbial Richness



Microbial Community composition



Tillage System



CT/RT

Crop residue fate



R+/R-

Depth



0-5/15-20 cm

Objectives were to (1) determine **richness levels** and (2) changes in microbial **community composition** under different combinations of tillage system (conventional vs. reduced) and crop residue fate (residue removal vs. residues left), at two depths. Indicator taxa, i.e. the taxa most representative of a given set of soil conditions, were also identified (IndVal). The experimental field is located in central **Belgium**, whose **loess-derived soils** are among the most fertile in the world and have long been used for intensive agriculture.

METHOD



(1) Soil sampling (Winter wheat)

(2) DNA extraction

(3) Massive sequencing using 454 technology



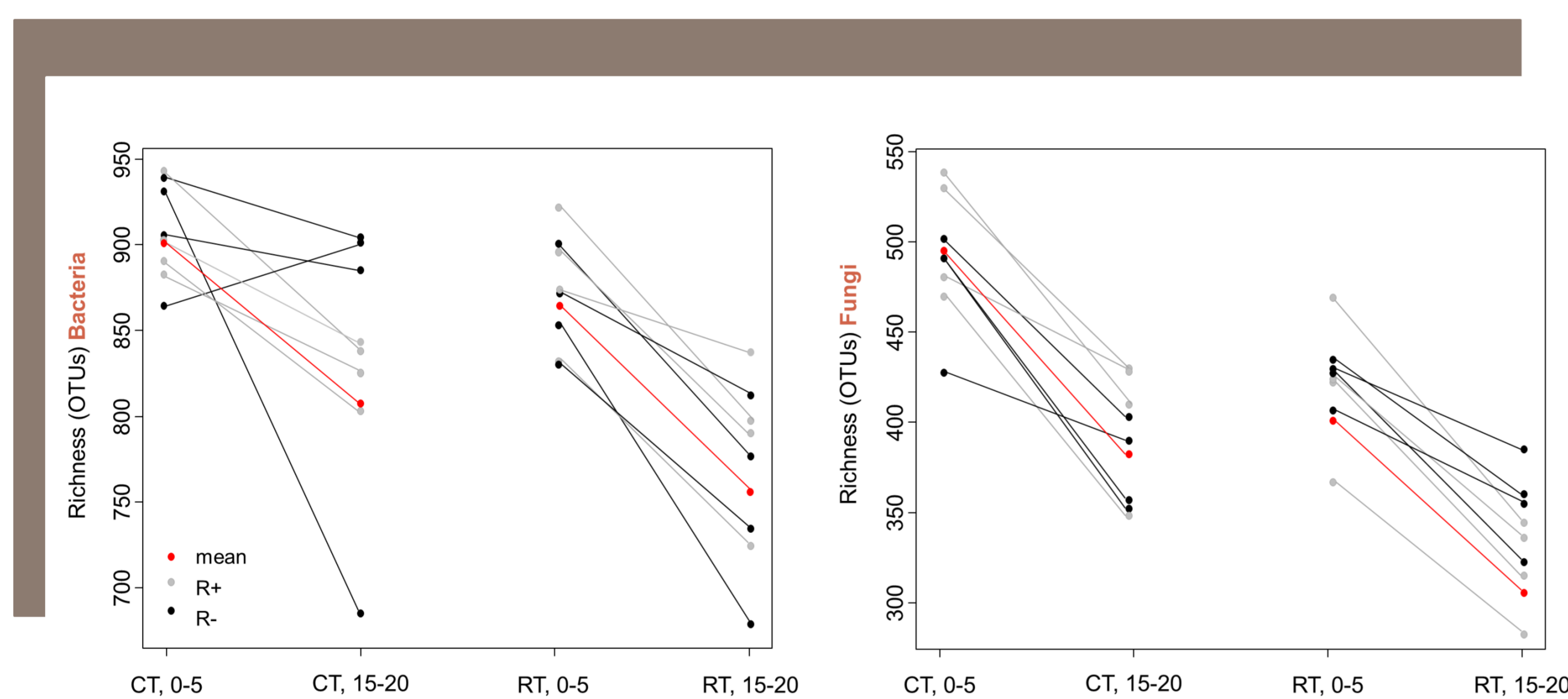
(4) Reads processing using the **mothur** pipeline

(5) Microbial **richness** (OTUs), **community composition** (CAP, Bray-Curtis), and **indicator taxa** (IndVal) analysis

RESULTS

Microbial richness (OTUs)

Fig. 1



Indicator taxa (IndVal)

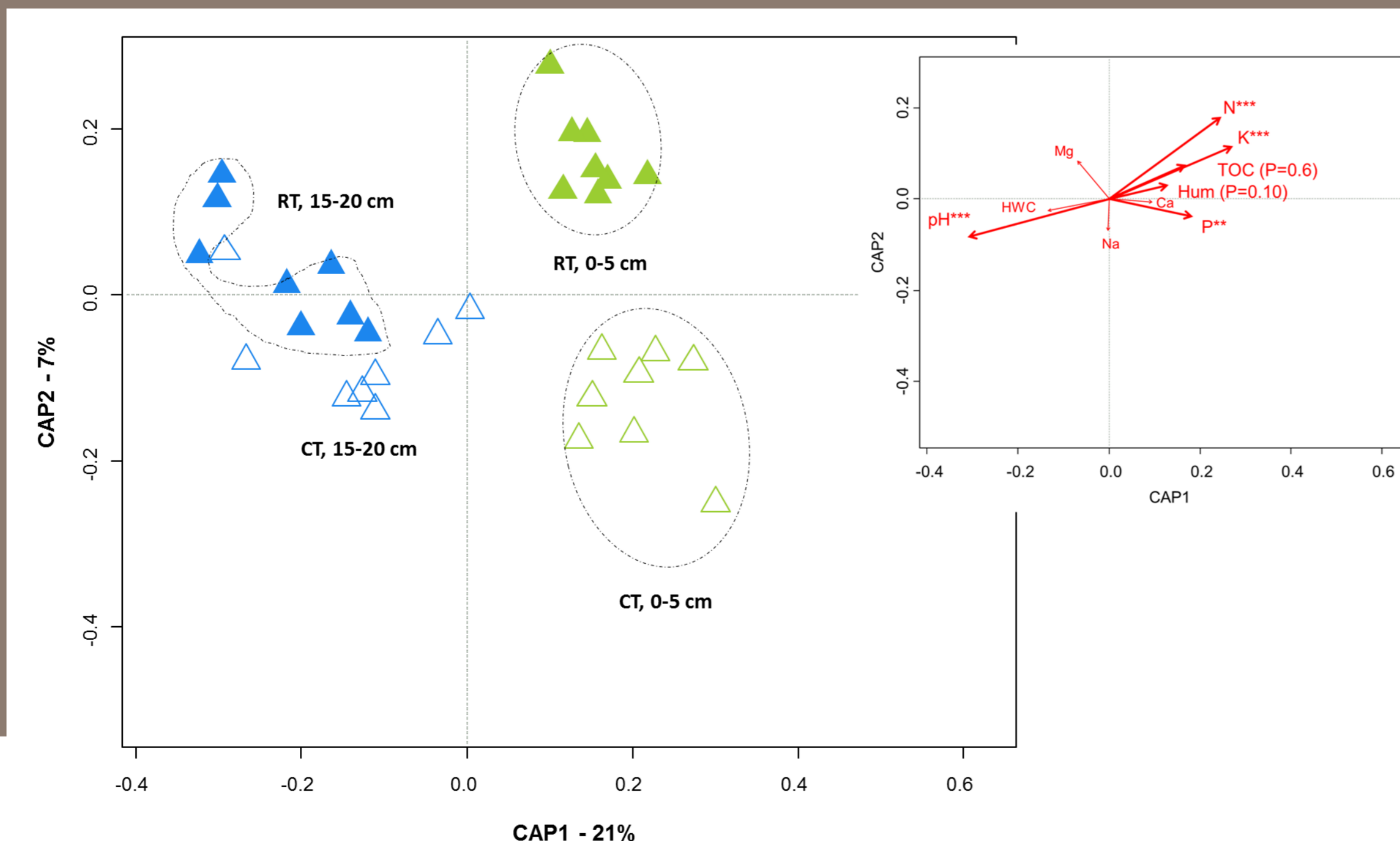
Fig. 4

Number of indicator bacterial taxa		
After 6 years of experiment		
	RT	CT
0-5 cm	3	21
15-20 cm	3	0
Number of indicator fungal taxa		
After 6 years of experiment		
	RT	CT
0-5 cm	2	5
15-20 cm	2	0

Microbial community composition

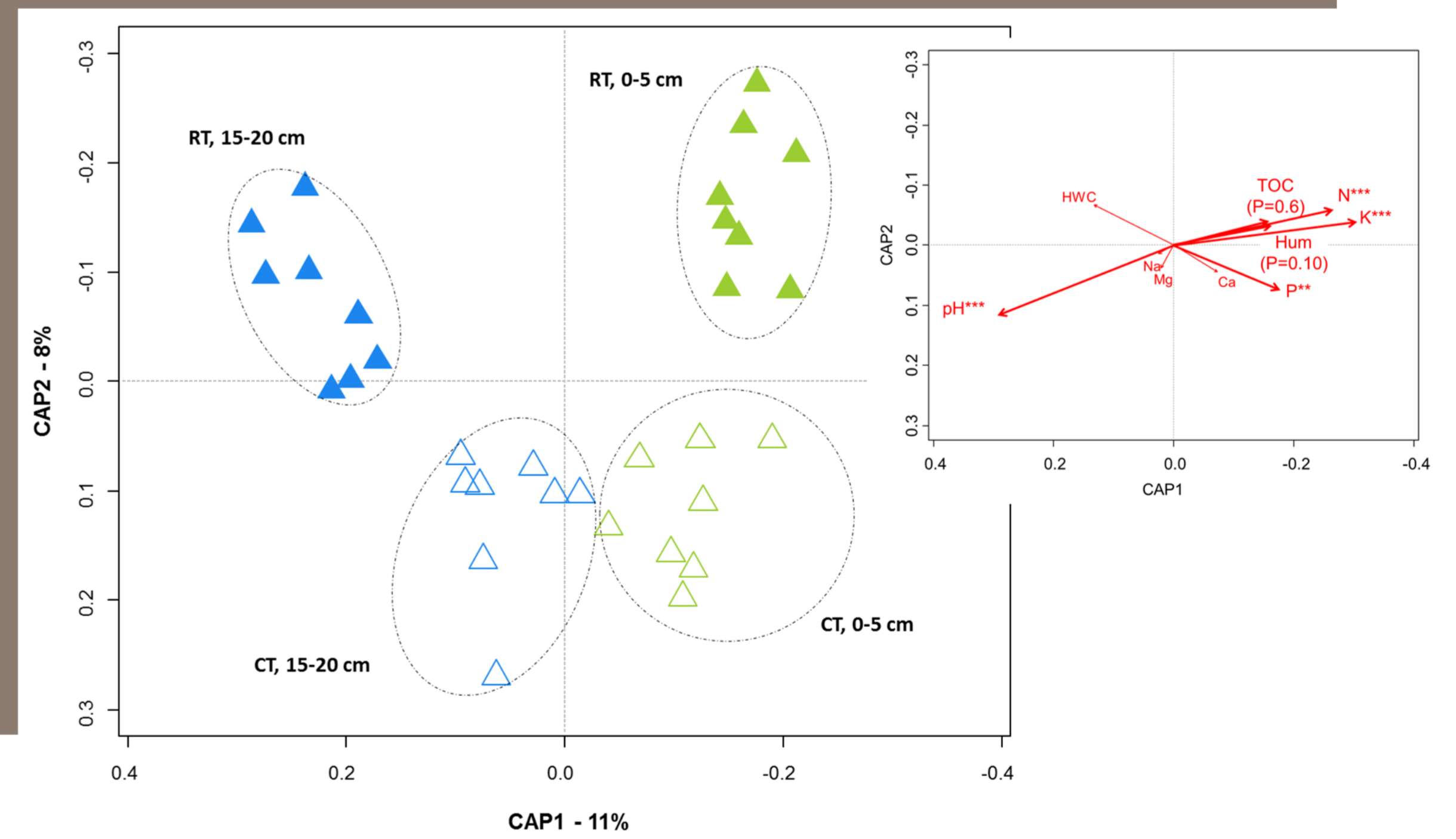
Bacteria

Fig. 2



Fungi

Fig. 3



After 6 years of conversion from Conventional to Reduced Tillage:

- For both bacteria and fungi, the richness appeared higher at 0 to 5 cm than at 15 to 20 cm, and surprisingly, higher under CT than under RT (Fig. 1). Crop residue fate had no influence on microbial richness.
- Depth** emerged as the main factor responsible for variation in microbial diversity, **tillage system** ranked second, and finally, **crop residue fate** had no influence on microbial community composition (Fig. 2 and 3).
- These differences are explained by changes in community composition due to **taxon loss rather than taxon replacement** (Fig. 4). The specific local set of environmental conditions (a loess-derived soil and an oceanic temperate climate) may explain these results. These observations raise the question: **does impoverishment in indicator taxa influence soil processes, and thus crop production?**

CONCLUSION