

# Detecting microbial patterns in relation to soil agricultural practices and the plant development stage

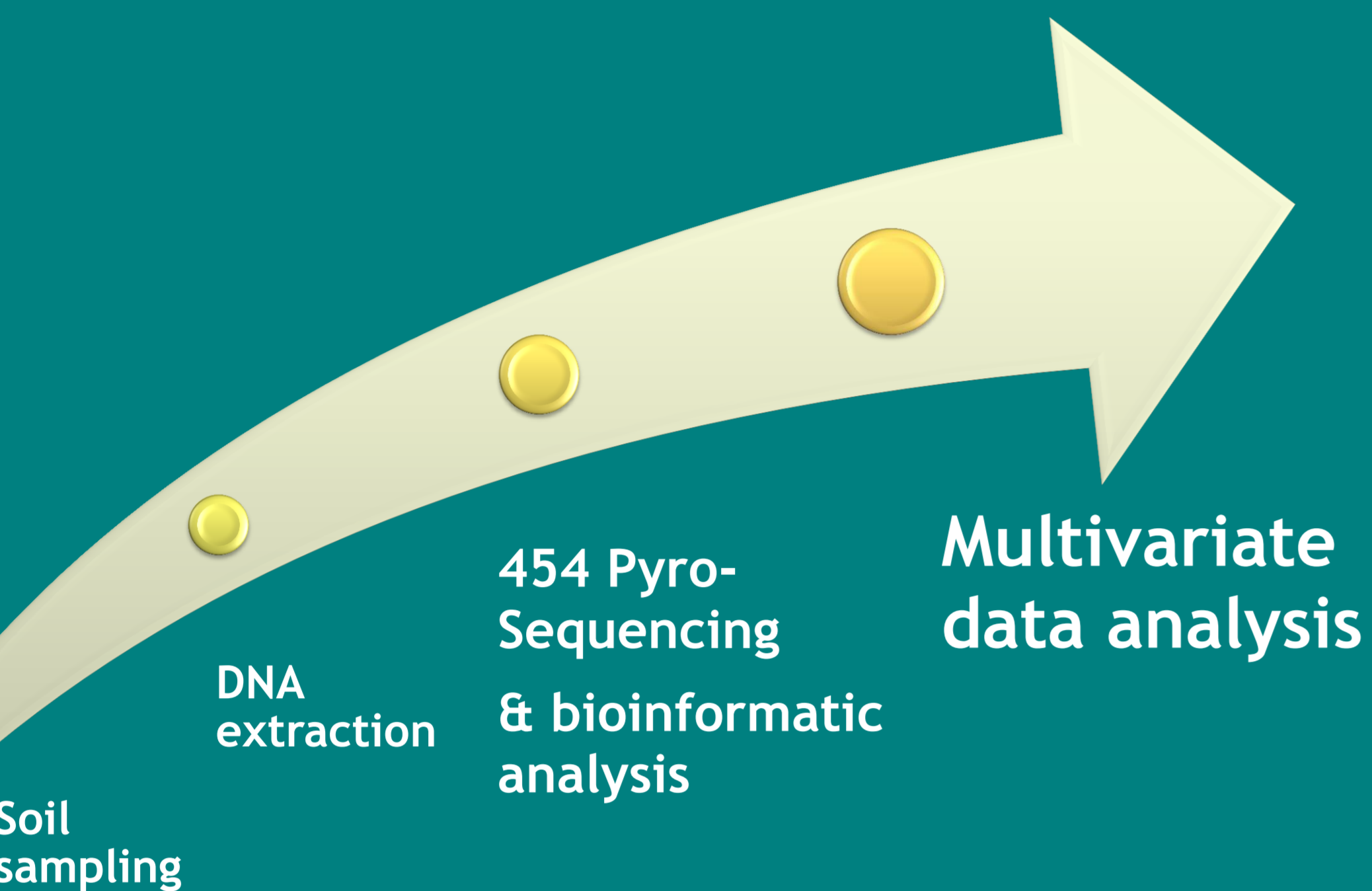
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## CONTEXT

Agricultural practices have a strong impact on soil bacteria and fungi. Furthermore, microbial community composition can change with the stage of plant development. We are interested in exploring these effects in relation to changes induced by agriculture and plant stage in soil conditions. Here, instead of examining this impact at a high taxonomic level such as phylum and/or class, thus missing potentially relevant information from lower levels, we propose an original approach: exploiting the available sequence information at the lowest taxonomic level attainable for each operational taxonomic unit.



**Soil sampling:** Soil samples were collected from an experimental field planted with *Vicia faba*. Part of the field was subjected to conventional tillage (CT) and part of it to reduced tillage (RT). Samples were collected at germination (GS) and flowering (FS) at a depth of 15-20 cm.

**Sequencing:** 400-bp fragments of 16S and 28S rRNA were sequenced with GS junior 454, Roche©. The data were analysed with the Mothur pipeline. The Silva database was used to align sequences and clustering was performed to obtain operational taxonomic units (OTUs).

**Data analysis:** Multivariate analysis (RDA) was used to reveal bacterial and fungal patterns in relation to (1) tillage practice: conventional tillage (CT) or reduced tillage (RT) and (2) plant development stage: germination (GS) or flowering (FS).

## RESULTS

### Bacteria

### Fungi

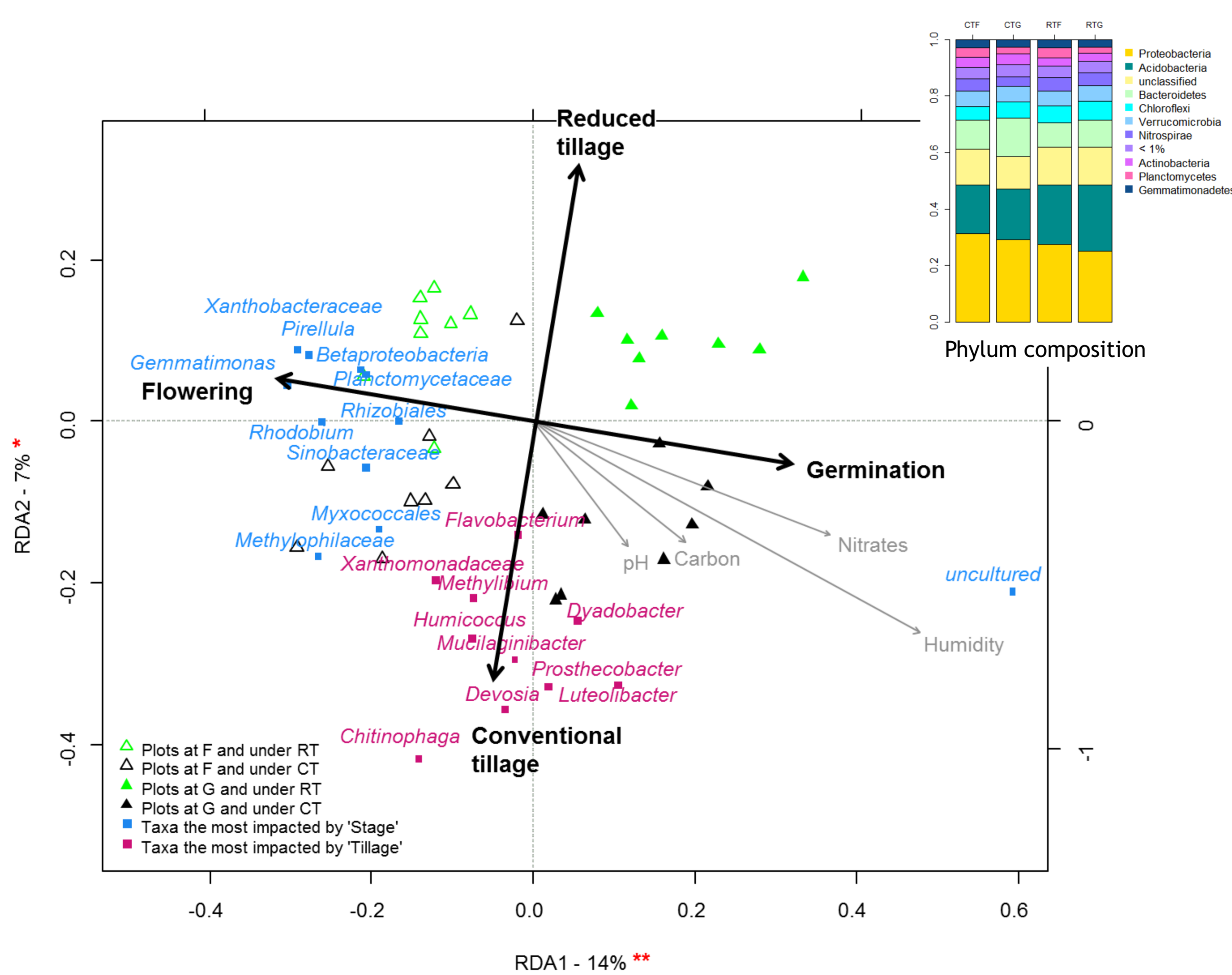


Fig 1. RDA ordination graph showing the bacterial pattern in relation to tillage practice (conventional tillage, CT and reduced tillage, RT) and plant development stage (flowering, FS or germination, GS).

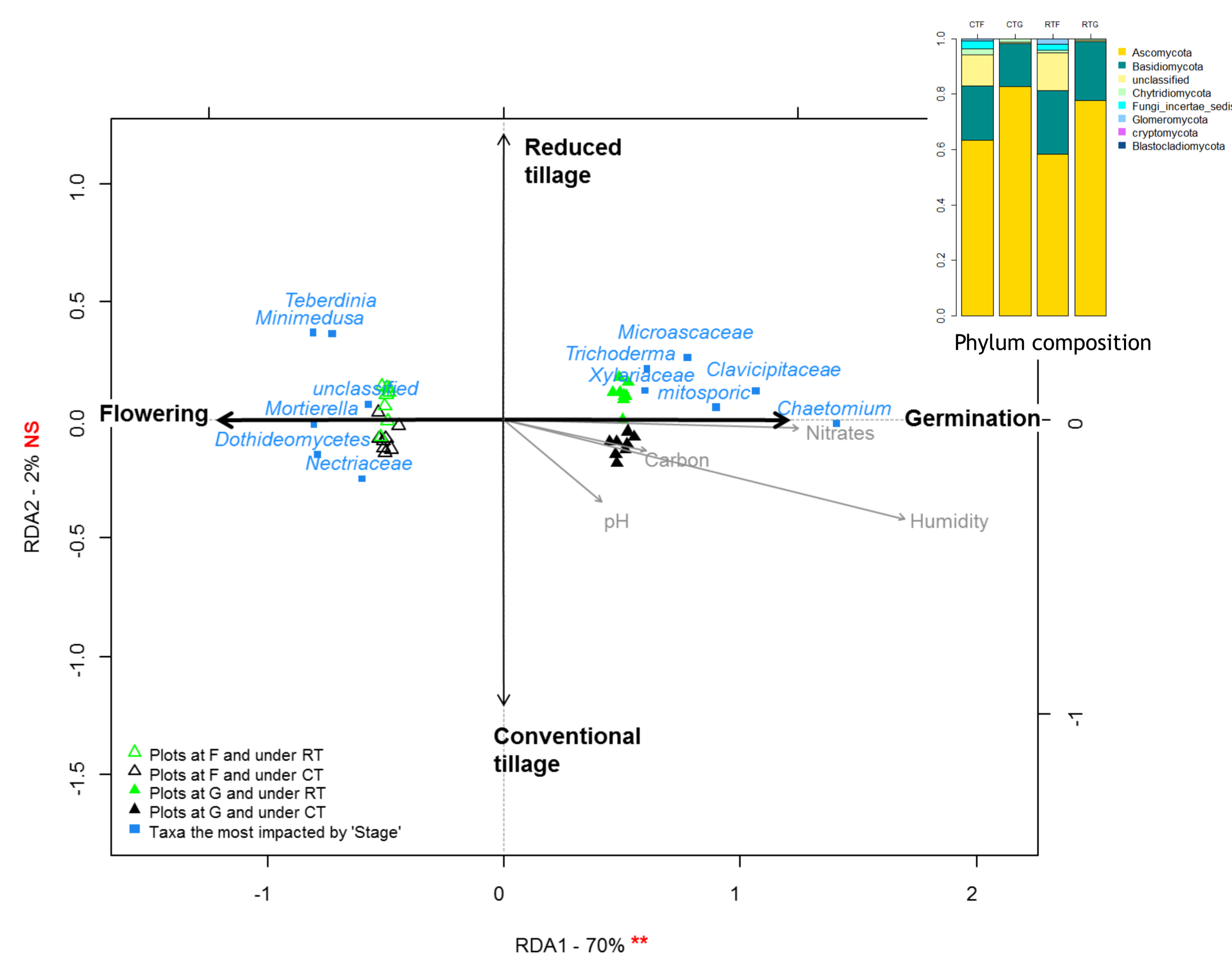


Fig 2. RDA ordination graph showing the fungal pattern in relation to tillage practice (conventional tillage, CT, or reduced tillage, RT) and plant development stage (flowering, FS or germination, GS).

- 14% and 70% of the bacterial (Fig. 1) and fungal (Fig. 2) patterns can be explained by the soil conditions induced by **plant stage**. The bacteria and fungi plotted on the left side of the ordination graph tend to be more abundant at the flowering stage, characterized by low levels of soil nitrates, humidity, carbon, and pH. Those plotted on the right part tend to be more abundant at the germination stage, characterized by high values of these soil parameters (blue).
- 7% of the bacterial pattern can be explained by the soil conditions induced by the **tillage practice** applied (Fig. 1). Bacteria plotted at the bottom tend to be more abundant under conventional tillage (pink). The soil parameters responsible for this pattern have not yet been identified. Fungi were not affected by tillage practice (Fig.2).

## CONCLUSION

Some bacteria are influenced only by the plant stage, which induces changes in soil humidity, pH, nitrates, and carbon. We would thus expect these bacteria to be highly sensitive to these parameters.

Other bacteria are affected only by the tillage practice applied. Further study is needed to identify the soil parameters responsible for this effect.

The plant stage also has a great impact on fungal community composition.