



Soil microbial community composition changes according to the tillage practice and plant development stage

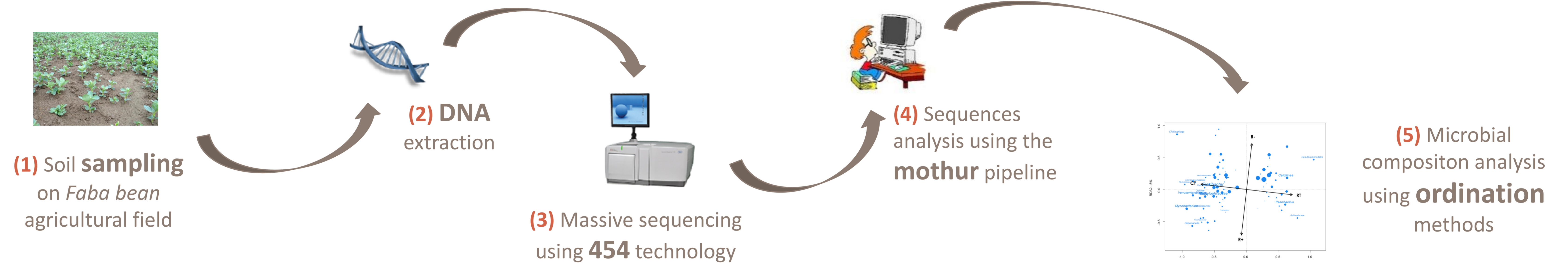
F. Degruene^{1,2}, M. Dufrêne³, B. Taminiau⁴, S. Barbieux^{1,5}, M-P. Hiel^{1,6}, G. Daube⁴, C. Nezer⁷, M. Vandenberg²

¹AgricultureIsLife, ²Unité de Microbiologie et Génétique, ³Unité de Phytotechnie des Régions Tempérées et Ferme expérimentale, ⁴Unité Biodiversité et Paysage, and ⁵Unité Système Sol-Eau (Gembloux Agro-Bio tech, ULg, Belgium), ⁶Unité de Microbiologie des Aliments, Faculté de médecine vétérinaire (ULg, Belgium), ⁷Quality Partner s.a. (Herstal, Belgium)

1 CONTEXT

Agricultural practices have a strong impact on **soil bacterial and fungal community composition**. 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** (conventional and reduced tillage) and **plant stage** (germination and flowering) 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 method**: exploiting the available sequence information at the lowest taxonomic level attainable for each operational taxonomic unit.

2 METHOD

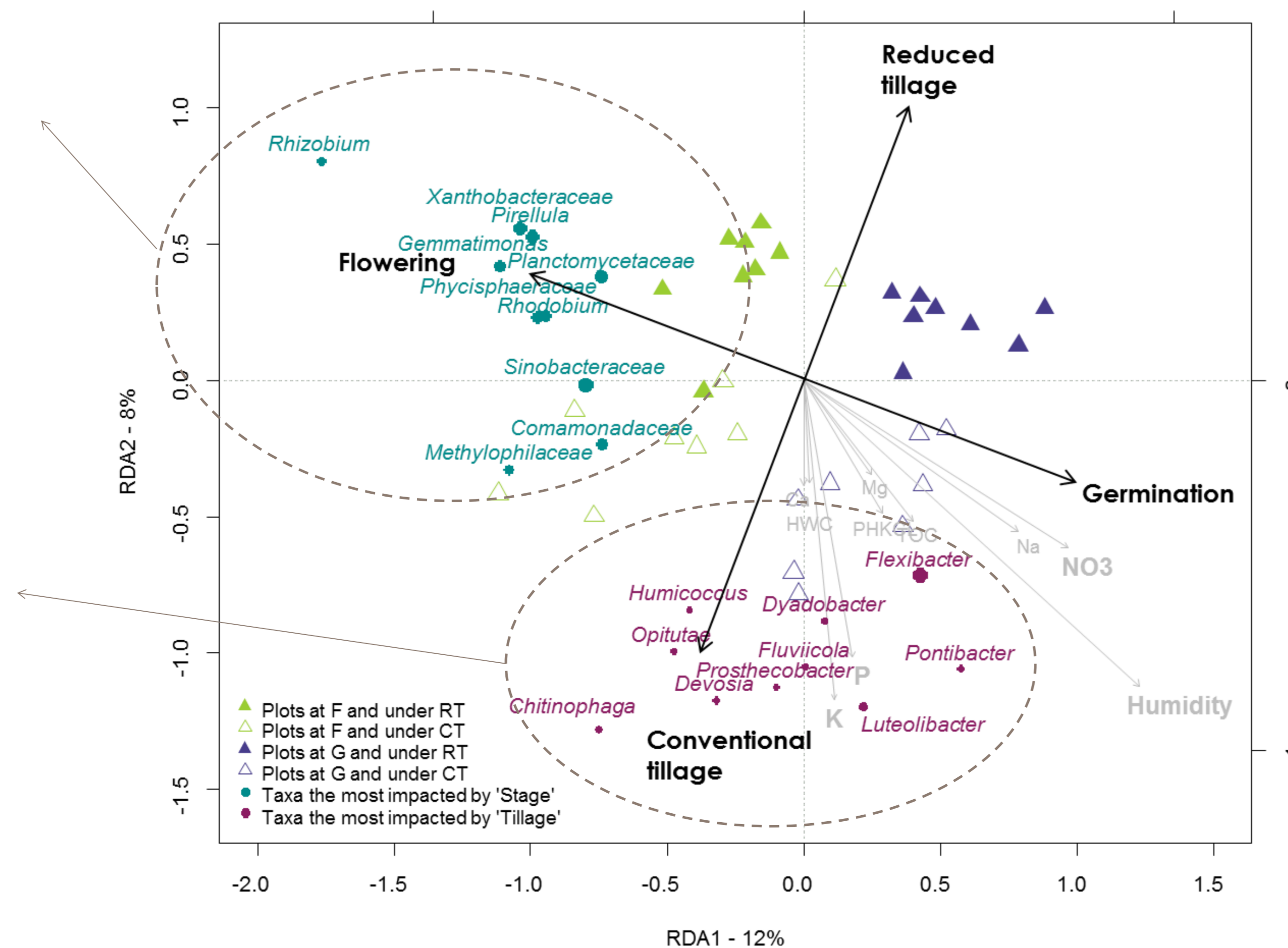


3 RESULTS

BACTERIA

Their abundance are higher at **flowering** stage.

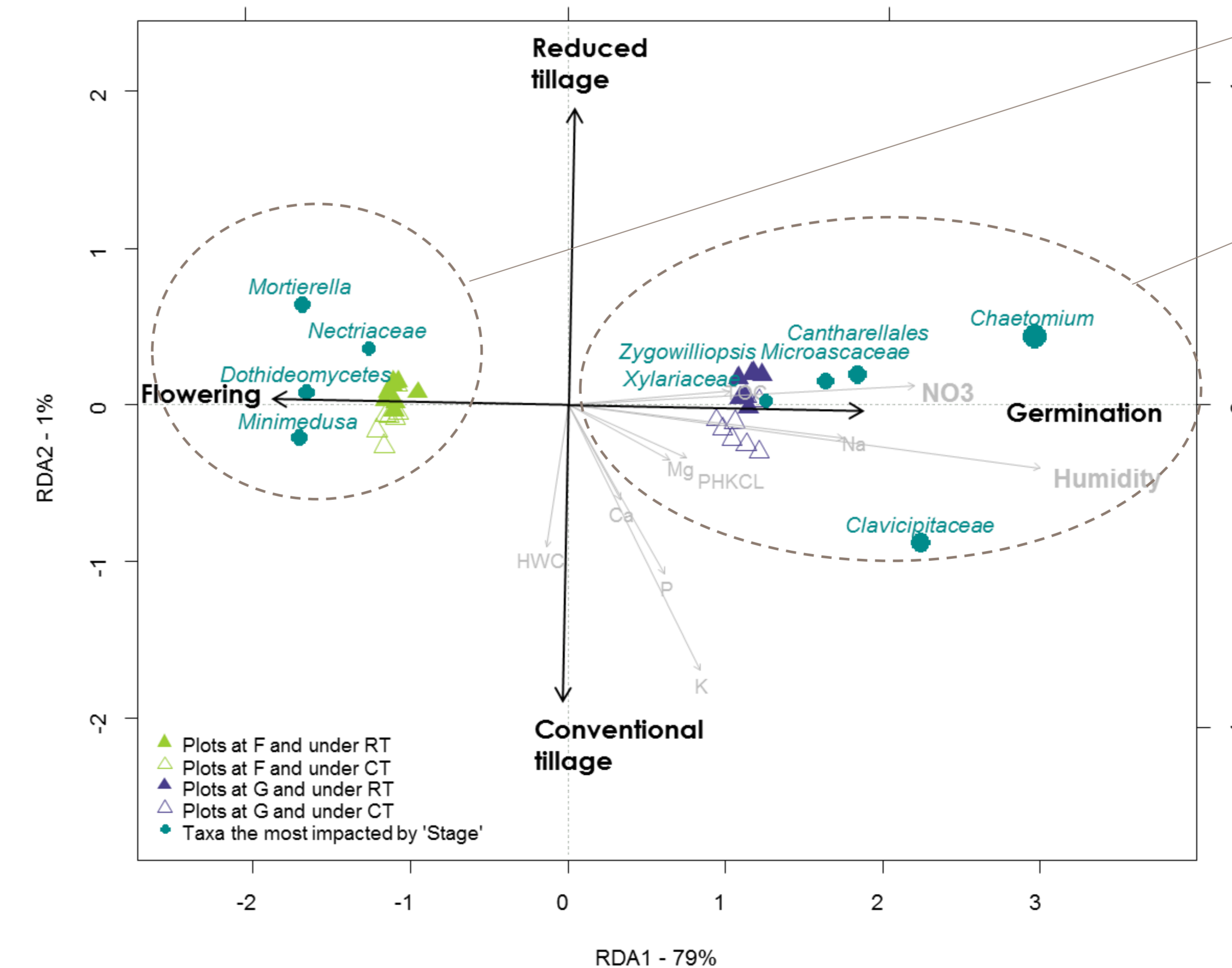
Their abundance are higher under **conventional tillage**.



FUNGI

Their abundance are higher at **flowering** stage.

Their abundance are higher at **germination** stage.



There was **no effect** of tillage practice on fungal communities over plant stage development, **P** and **K** could explained the variation due to the *soil tillage*, **NO3** and **humidity** could explained the variation due to the *plant stage*.