

# Diversity of bacterial communities in a profile of a winter wheat field: known and unknown members

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## Abstract

In soils, bacteria are very abundant and diverse. They are involved in various agro-ecosystem processes such as the nitrogen cycle, organic matter degradation, and soil formation. Yet little is known about the distribution and composition of bacterial communities through the soil profile, particularly in agricultural soils, as most studies have focused only on topsoils or forest and grassland soils. In the present work we have used barcoded pyrosequencing analysis of the V3 region of the 16S rRNA gene to analyse bacterial diversity in a profile (depths: 10 cm, 25 cm, and 45 cm) of a well-characterized field of winter wheat. Taxonomic assignment was carried out with the RDP classifier program with three bootstrap scores: a main run at 0.80, a confirmation run at 0.99, and a run at 0 to gain information on the unknown bacteria. Our results show that biomass and bacterial quantity and diversity decreased greatly with depth. Depth also had an impact, in terms of relative sequence abundance, on 81% of the most represented taxonomic ranks, notably the ranks *Proteobacteria*, *Bacteroidetes*, *Actinobacteridae*, and *Acidobacteria*. Bacterial community composition differed more strongly between the topsoil (10 cm and 25 cm) and subsoil (45 cm) than between levels in the topsoil, mainly because of shifts in the carbon, nitrogen and potassium contents. The subsoil also contained more unknown bacteria, 53.96% on the average, than did the topsoil, with 42.06% at 10 cm and 45.59% at 25 cm. Most of these unknown bacteria seem to belong to *Deltaproteobacteria*, *Actinobacteria*, *Rhizobiales*, and *Acidobacteria*.

**Keywords :** bacterial diversity/16S rRNA gene/agricultural soil/pyrosequencing/depth/RDP classifier