Microbial Methanol Sink of a Grass and a Flower Host Species From a Temperate Grassland

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Research

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Abstract

Background: Managed grasslands are global sources of atmospheric methanol, which is one of the most abundant volatile organic compounds (VOCs) in the atmosphere and promotes oxidative capacity for tropospheric and stratospheric ozone depletion. The phyllosphere is a favoured habitat of plant-colonizing methanol-utilizing bacteria. These bacteria also occur in the rhizosphere, but their relevance for methanol consumption and ecosystem fluxes is unclear. The estimated global methanol emission rate is considerably higher than those escaped into the atmosphere. Thus, methanol utilizers in the plant microbiota might be key for the mitigation of methanol emission through consumption. However, information about grassland plant microbiota members, their biodiversity and metabolic traits, and thus key actors in the global methanol budget is largely lacking.

Results: We investigated the methanol utilization and consumption potentials of two common plant species (Festuca arundinacea and Taraxacum officinale) in a temperate and fertilized grassland. The selected grassland exhibited net methanol emission. The detection of 13C derived from 13C-methanol in 16S rRNA of the plant microbiota by stable isotope probing (SIP) revealed distinct methanol utilizer communities in the phyllosphere, roots and rhizosphere but not between plant host species. The phyllosphere was colonized by members of Gamma- and Betaproteobacteria. In the rhizosphere, 13C-labelled Bacteria were affiliated with Deltaproteobacteria, Gemmatimonadates, and Verrucomicrobiae. Less-abundant 13C-labelled Bacteria were affiliated with well-known methylotrophs of Alpha-, Gamma-, and Betaproteobacteria. Additional metagenome analyses of both plants were consistent with the SIP results and revealed Bacteria with methanol dehydrogenases (e.g., MxaF1 and XoxF1-5) of known but also unusual genera (i.e., Methylomirabilis, Methylooceanibacter, Gemmatimonas, Verminephrobacter). 14C-methanol tracing of alive plant material revealed divergent methanol oxidation rates in both plant species but similarly high rates in the rhizosphere and phyllosphere.

Conclusions: The rhizosphere has been shown to be an overlooked hotspot for methanol consumption in grasslands. We also identified unusual methanol utilizers in the phyllosphere and rhizosphere. We did not observe a plant host-specific methanol utilizer community. Our results suggest a model for methanol turnover in which both the sources (plants) and sinks (microbiota) of a volatile are separated but in the same ecological unit.

Full Text

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Table

Due to technical limitations, table 2 is only available as a download in the Supplemental Files section.

Figures

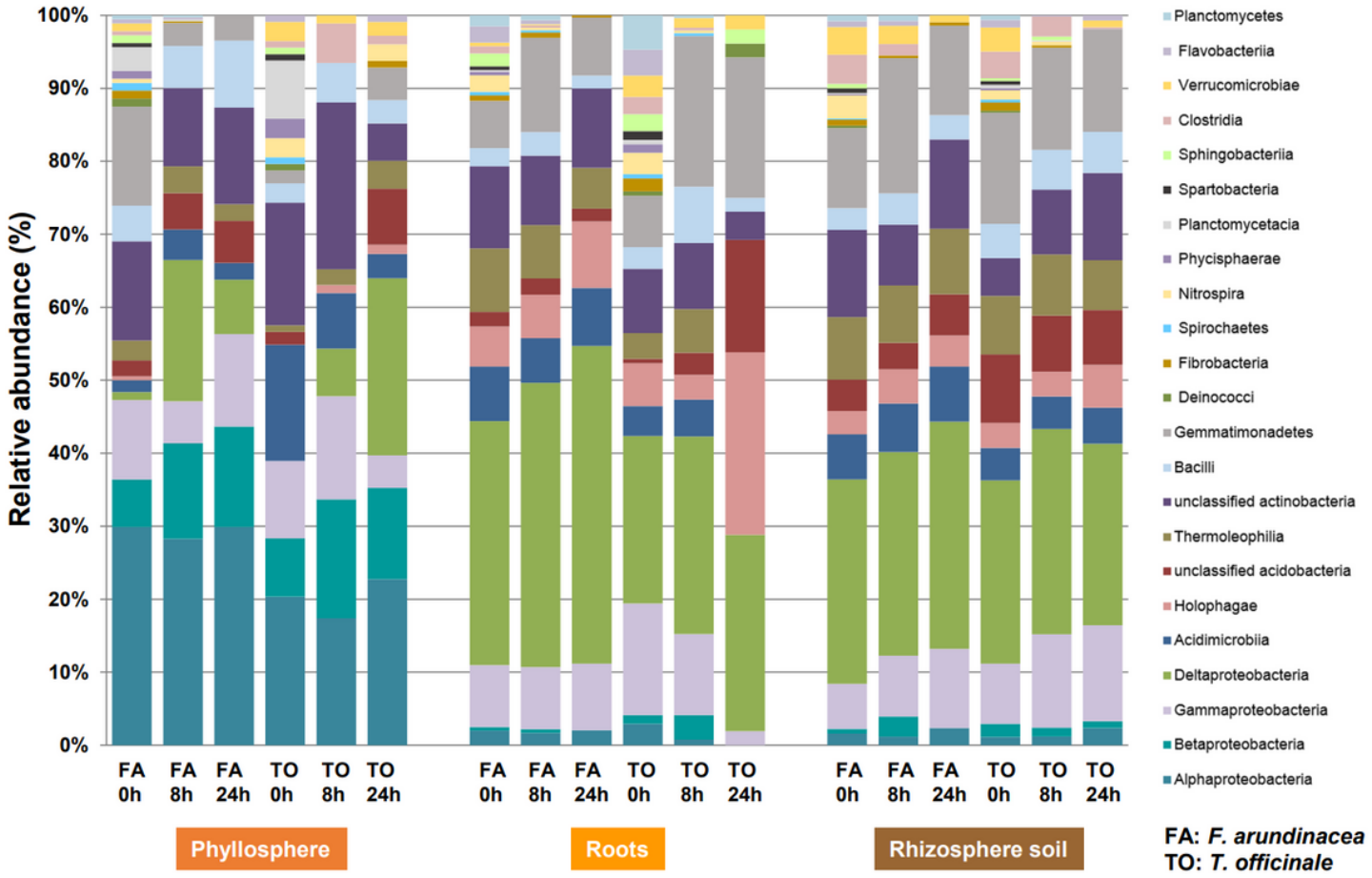

Figure 1

Divergent bacterial 13C-labelled 16S rRNA OTU profiles between the plant compartments. The relative abundance of 13 C-labelled bacterial profiles is shown at the class level for both the plant species (F. arundinacea and T. officinale) between different plant compartments (phyllosphere, roots and rhizosphere soil). Both plants were incubated with 1 mM 13C-CH3OH for 0 hours, 8 hours and 24 hours.

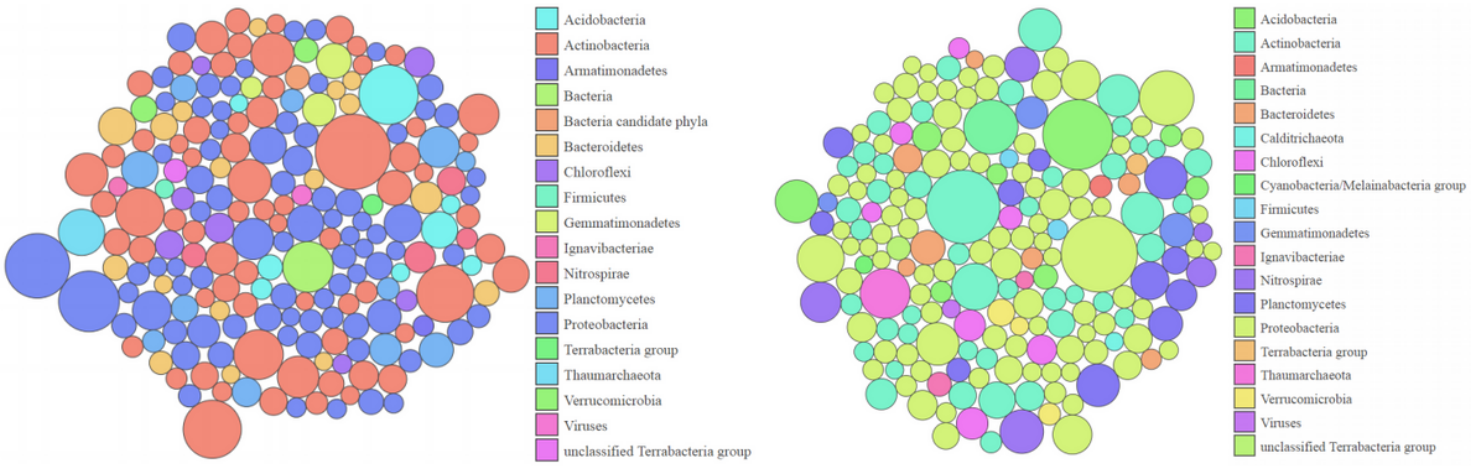

Figure 2

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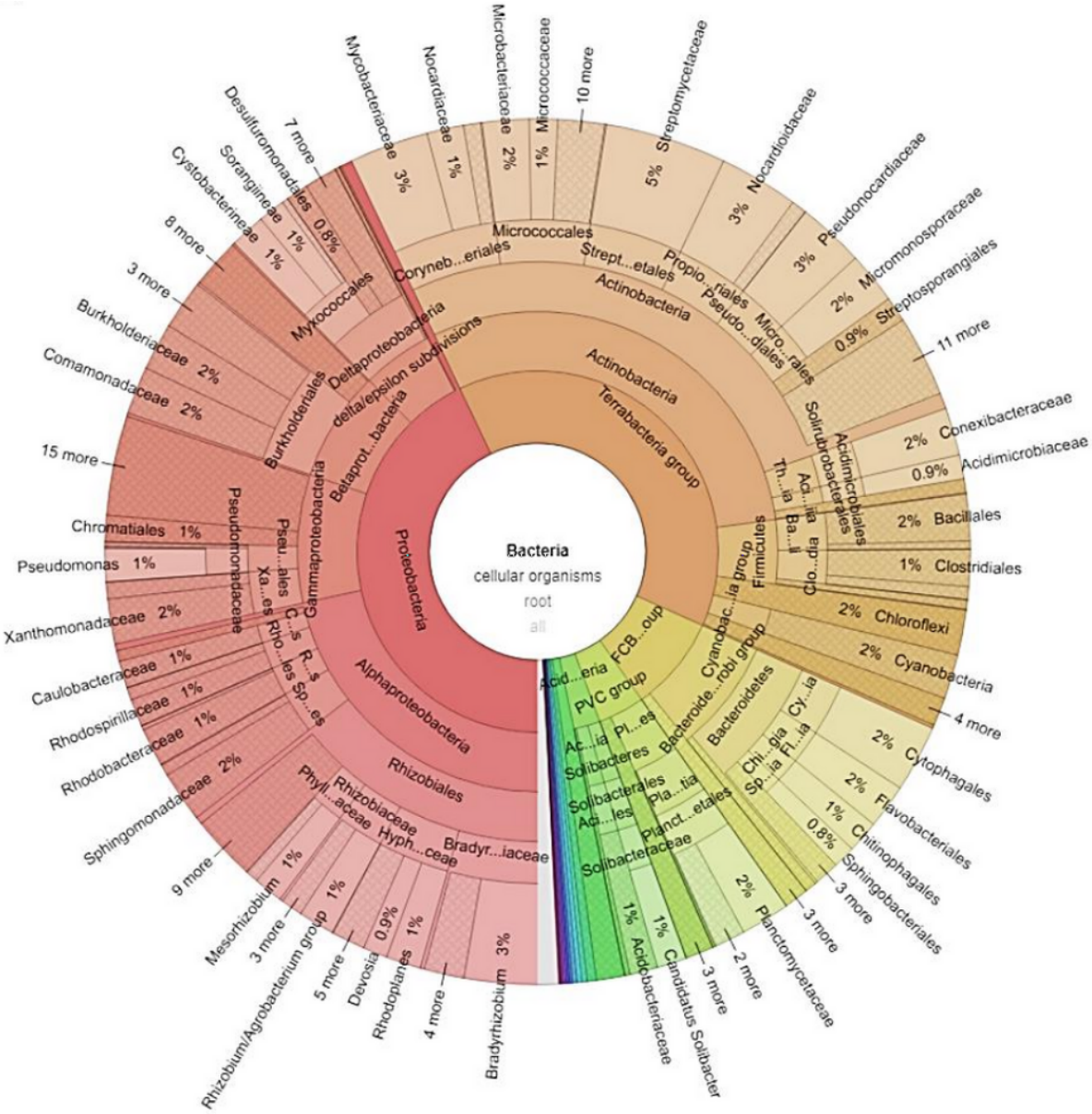

Figure 3

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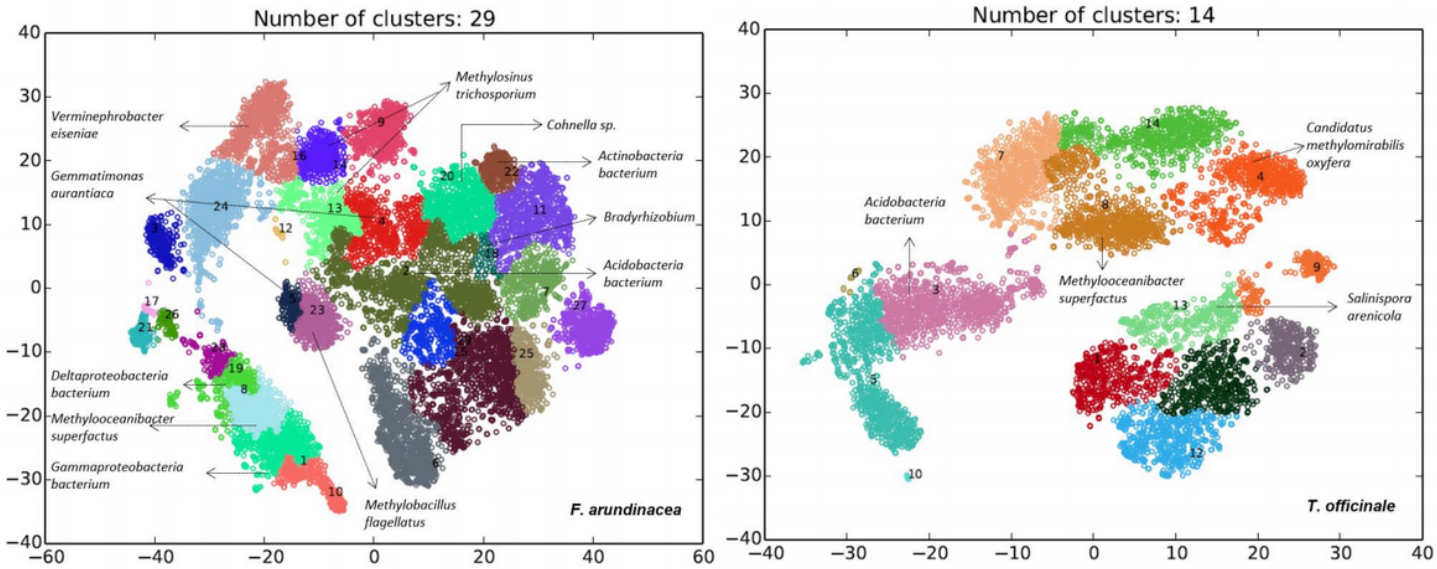

Figure 4

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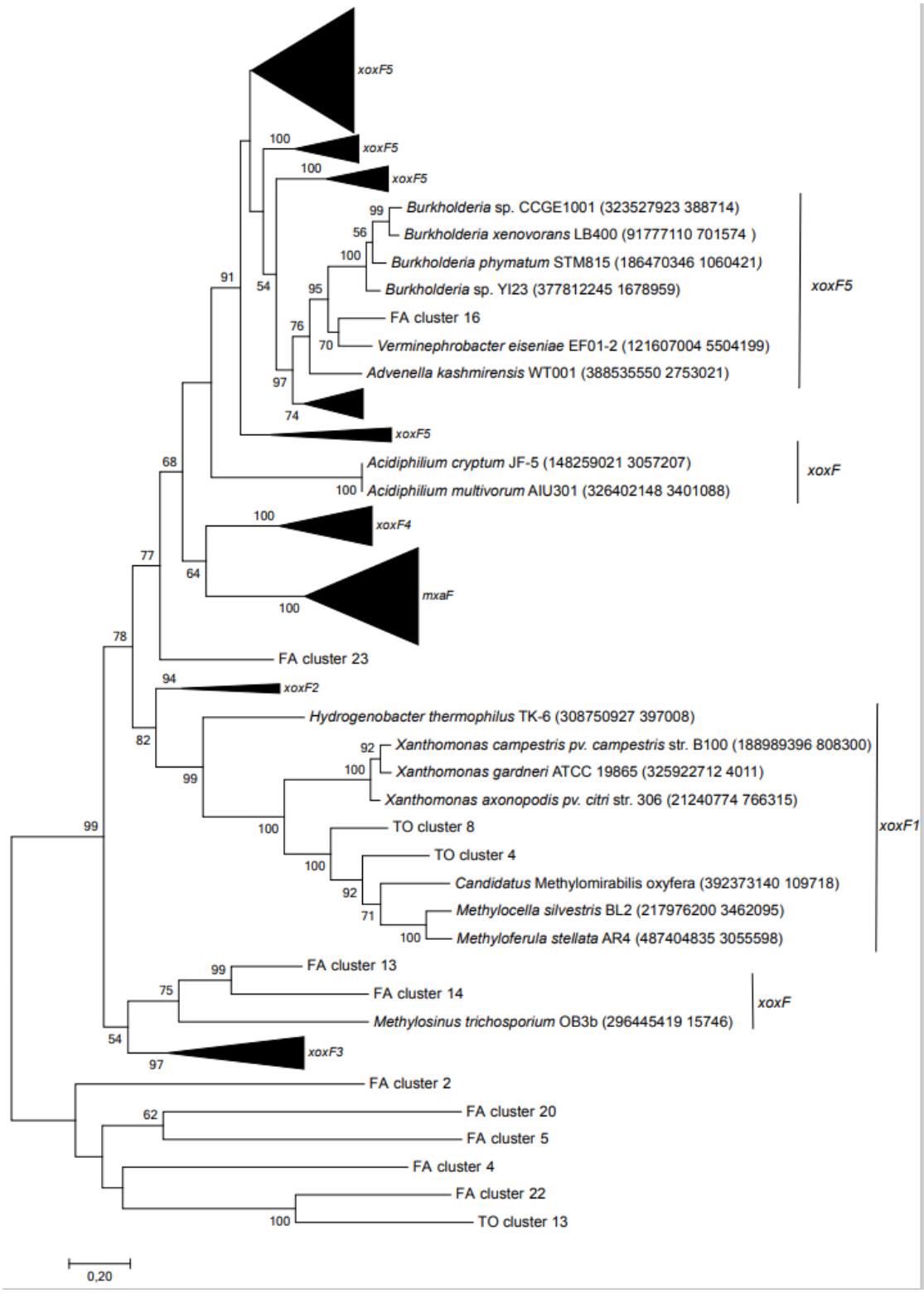

Figure 5

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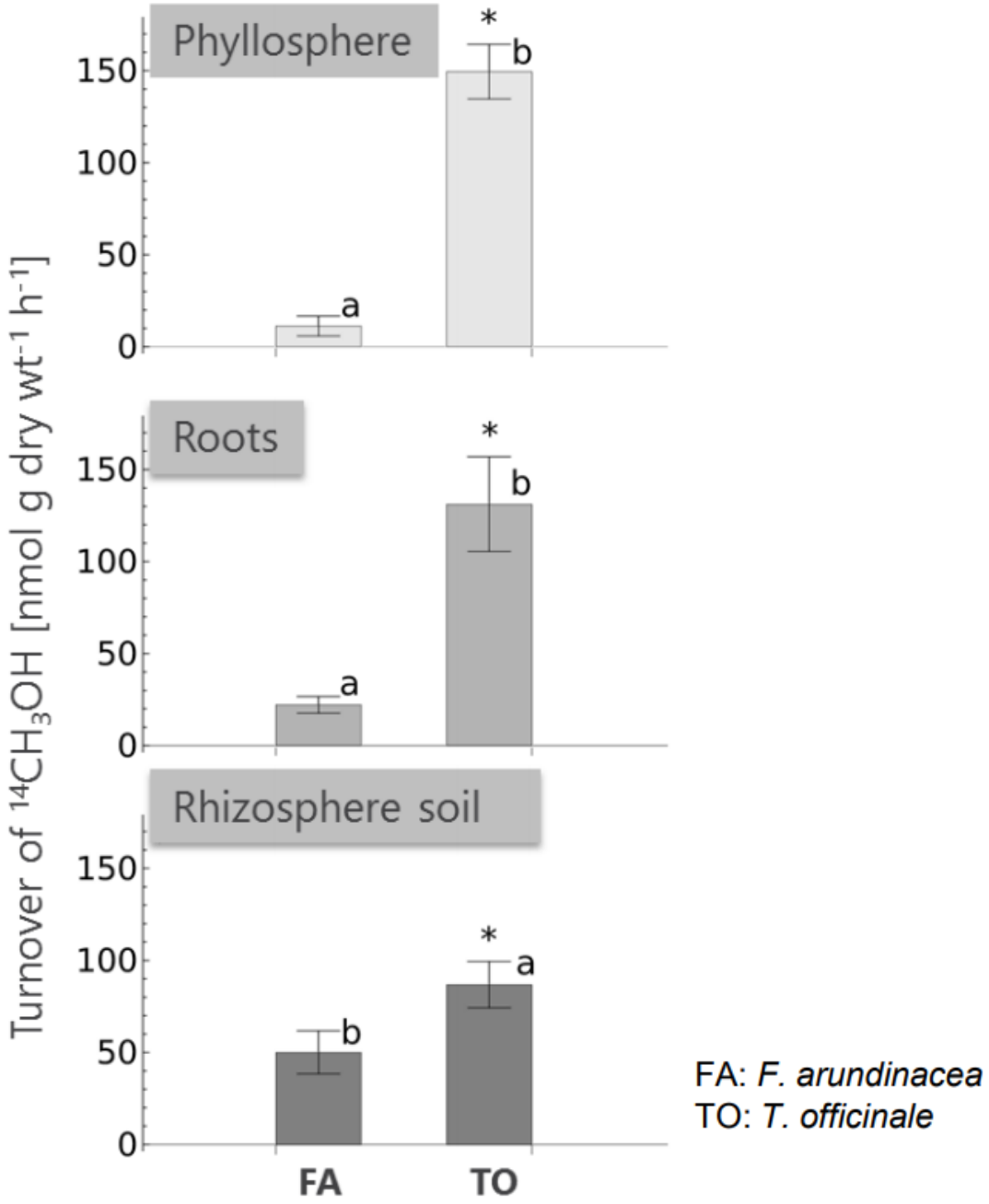

Figure 6

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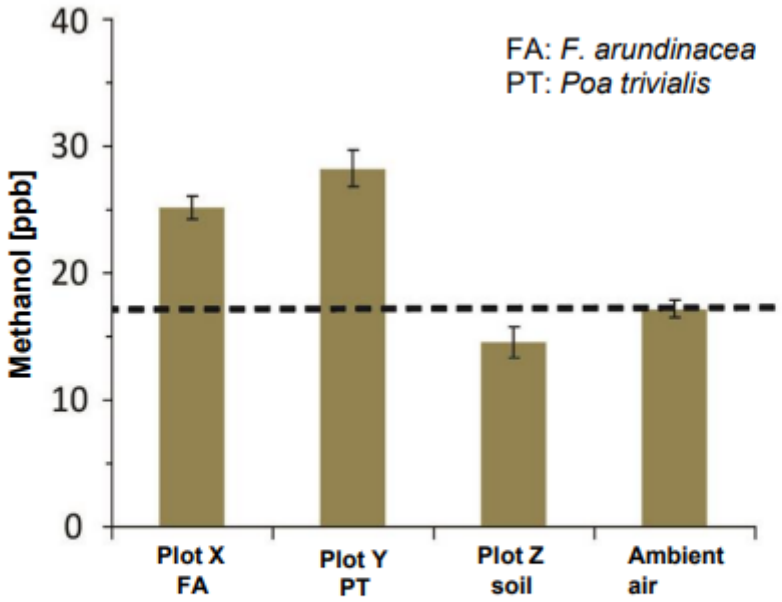

Figure 7

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