

Tetracycline determines N₂O fluxes through changes of microbial assemblages in a plant-soil system

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It is largely unknown how tetracycline results in changes to bacterial community composition and structure as well as in functional guilds involved in N-cycling when plants are present. In the current study, we examined the impact of tetracycline on N₂O emissions, the abundance of bacterial guilds involved in N cycling in bare and planted with *Origanum officinalis* soil microcosms, and the bacterial composition in both bulk and root samples.

Overall, tetracycline had no effect on the abundance of the total bacterial community estimated as 16S rRNA copy numbers in the bulk soil. Tetracycline significantly affected the assembly of bacterial communities both in bulk and root samples. In bulk soil, differential abundance analysis showed that tetracycline caused preferential selection of specific taxa assigned in Firmicutes few days after its application. In bare soil, N₂O fluxes were changing over time, which was associated with tetracycline concentration. Overall, low dose (0.1 mg/kg) application of tetracycline stimulated N₂O emissions and led to an increase in the abundance of *nirS* and *nosZI* bacterial communities.

On the contrary, in the plant-soil microcosms, we observed a substantial reduction in N₂O daily emissions in soils treated with tetracycline, highlighting the importance of plant presence on N₂O fluxes. The presence of antibiotic had no effect on the abundance of AOA or AOB. Redundancy analysis showed that the reduction of N₂O fluxes was associated with a soil community harbouring *nosZII* genes while, the increase of daily N₂O fluxes were mainly associated to the presence of NH₄⁺.