The potential of ryegrass as cover crop to reduce soil N_2O emissions and increase the population size of denitrifying bacteria

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Background

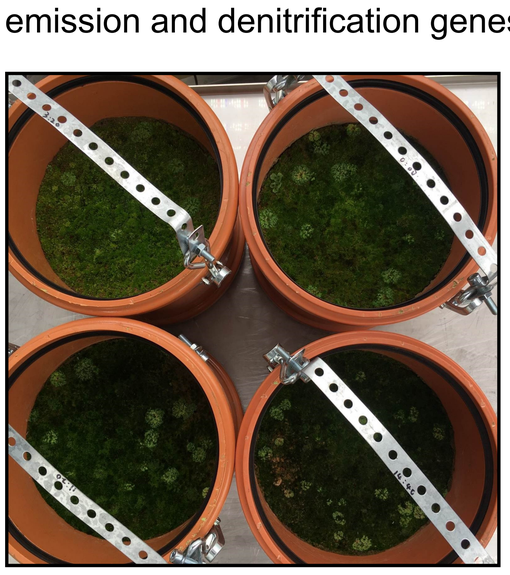
In terrestrial ecosystems, nitrogen (N) fertilization of agricultural soils is the major source of nitrous oxide (N_2O) emissions. Most of previous incubation experiments did not include plants and, therefore, plant-microbe-soil interactions remain mostly unexplored. The presence of plants has multiple effects on the soil and its microbiome. Therefore, it is crucial to understand the influence of plants on the soil denitrifying community.

Methods

Our experiment consisted of two groups, bare soil and soil with grass (*Lolium perenne*), each with 4 different fertilizer levels (0, 5, 10, and 20 g N m^{-2}). The closed-chamber approach was used to measure soil N_2O fluxes. Real-time PCR assays were performed to assess the abundance of genes involved in denitrification.

Objectives

This study aimed to investigate the effect of plant presence on soil N_2O emission and denitrification genes.



Bare soil

Soil with grass

Table 1. Total N uptake and C assimilation from grass shoots and roots throughout the incubation period (56 days).

Fertilizer level (g N m^{-2})	N uptake (g N m^{-2})			C assimilation (g C m^{-2})		
	Shoot	Root	Total	Shoot	Root	Total
0	2.6±0.1**c**	1.5±0.2**ab**	4.1±0.1**d**	58±2**b**	59±3**ab**	117±4**b**
5	4.7±0.2**c**	1.8±0.1**a**	6.5±0.2**c**	98±3**a**	74±1**a**	173±5**a**
10	7.4±0.7**b**	2.0±0.1**a**	9.3±0.5**b**	116±4**a**	75±4**a**	191±1**a**
20	11.8±0.7**a**	2.1±0.1**a**	13.9±0.5**a**	124±8**a**	68±4**a**	192±11**a**

Results

Compared to bare soil, lower soil NO_3^- content in soil with grass was observed.

Cumulative N_2O emissions of soil with grass were lower than in bare soil at 5 and 10 g N m^{-2} fertilization level.

Soil with grass showed greater gene copies of bacterial 16S rRNA, fungal 18S rRNA, *narG, napA, nirK, nirS*, and *nosZ* clade I, whereas *nosZ* clade II was not increased by soil with grass. Fertilization level did not affect gene abundance.

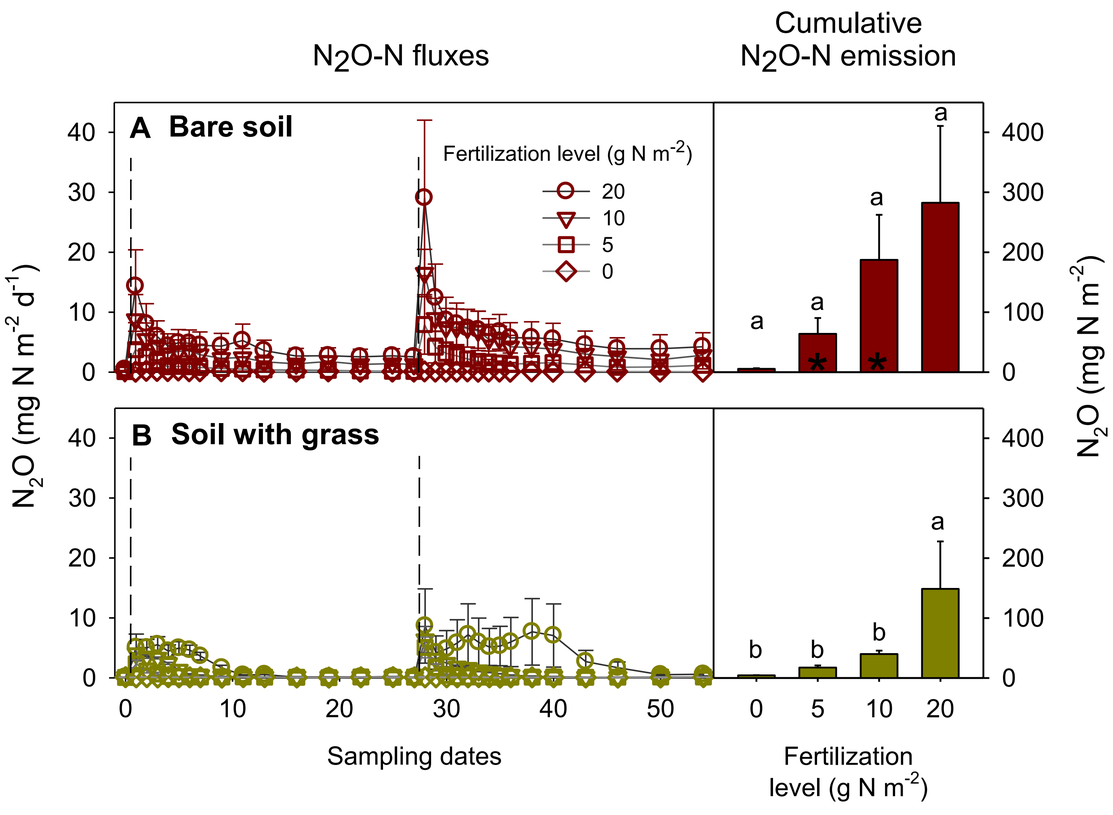


Fig. 1. N_2O emission dynamics and cumulative N_2O emission during the incubation period (56 days) from bare soil (A) and soil with grass (B).

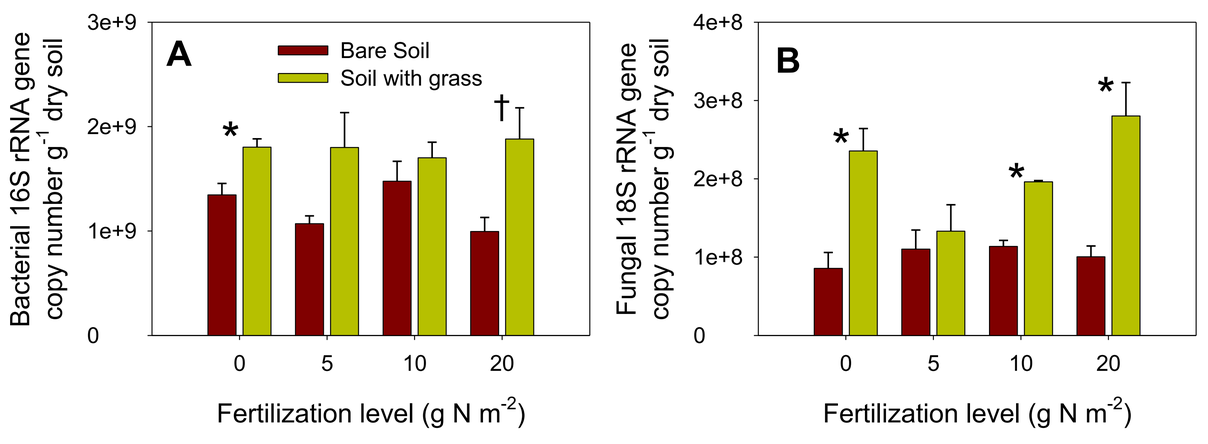


Fig. 2. Bacterial 16s rRNA (A) and fungal 18s rRNA (B) gene copy number per g dry soil in bare soil and soil with grass under different fertilization levels (0, 5, 10 and 20 g N m^{-2}) at the end of the incubation period (days 56) (* $p<0.05$, † $p<0.1$).

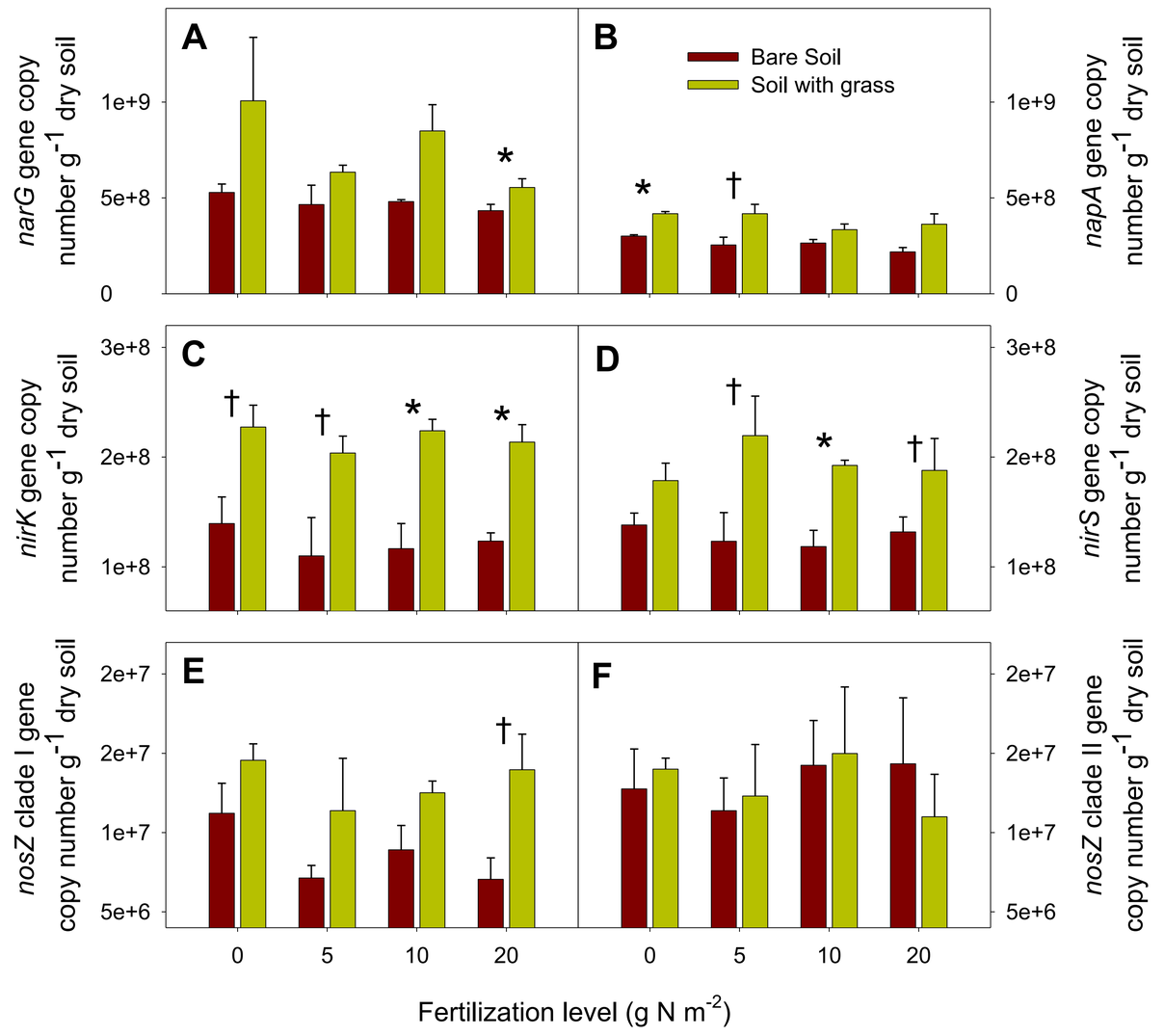


Fig. 3 *narG* (A), *napA* (B), *nirK* (C), *nirS* (D), *nosZ* clade I (E) and *nosZ* clade II (F) gene copy number per g dry soil in bare soil and soil with grass under different fertilization levels (0, 5, 10 and 20 g N m^{-2}) at the end of the incubation period (days 56) (* $p<0.05$, † $p<0.1$).

Conclusion

Our results showed a great influence of the presence of *Lolium perenne* on N_2O emission and denitrifying gene abundance, whereas soil N_2O emission was probably decreased by plant N uptake, and microbial community size was likely increased by root exudates. We suggest that future research should explore how different plants affect denitrifying communities in soil to further uncover the drivers of denitrification. (see full text in DOI: 10.1111/ejss.13047)

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