Fungal denitrification in arable soil

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The greenhouse gas nitrous oxide (N_2O) is a product of denitrification. In Scotland, 83% of total N_2O emissions are released from arable soils[1]. Bacteria are thought to play a predominant role in denitrification but it has been shown that fungi are also capable of denitrification[2]. Earlier experiments have demonstrated that the pH of soils influences the amount of N_2O emissions.

Material and Methods

Soils were sampled from existing long-term pH plots (ranging from 4.5 to 7.5), under grass or spring barley. The soils were treated with cyclohexamide (CY) to suppress fungi, or with streptomycin (S) and chloramphenicol (CH) to suppress growth of bacteria. Potential denitrification was measured. Community structures of eubacteria and fungi in each soil were determined using Terminal-Restriction Fragment Length Polymorphism (T-RFLP).

Sampling site at SAC Craibstone Estate

Results

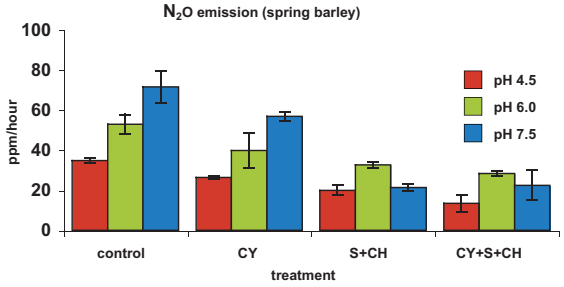


Figure 1: The emission of N_2O in ppm/hour (mean ± standard deviation) from soils under spring barley. Different combinations of CY, S and CH were added to the soils. The emission of N_2O in treated soils was significantly lower ($p<0.001$) than in untreated soils. Untreated soils with pH 4.5 and untreated soils with pH 7.5 showed significant differences in potential denitrification ($p<0.001$).

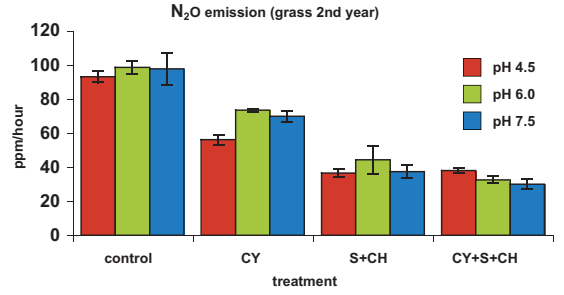


Figure 2: N_2O in ppm/hour (mean ± standard deviation) from soils where grass had been growing for two years. The same combinations of CY, S and CH were added to the soils as for spring barley. The emission of N_2O in treated soils was significantly lower ($p<0.001$) than in untreated soils.

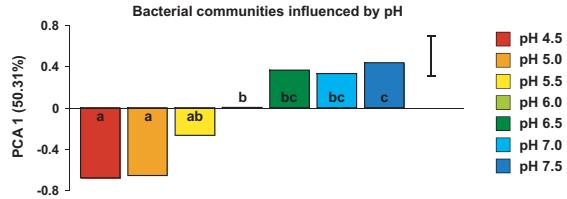


Figure 3: T-RFLP of bacterial communities. First dimension of principal component analysis (PCA) plotted for soils of different pHs. Bar indicates least significant difference (LSD). The bacterial communities changed significantly ($p<0.001$) in soils with low or high pH. The fungal communities were not significantly influenced by pH (data not shown).

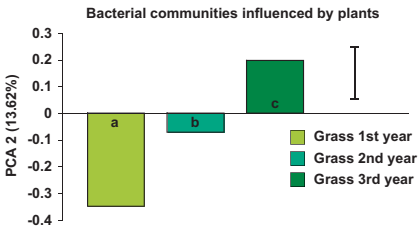
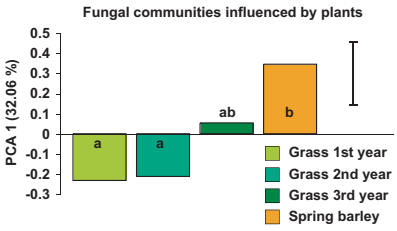


Figure 4: T-RFLP of bacterial communities. Second dimension of principal component analysis (PCA) plotted for soils under grass. Bar indicates LSD. The bacterial communities changed significantly ($p<0.001$) in soils with different grass management.

Figure 5: T-RFLP of fungal communities. First dimension of principal component analysis (PCA) plotted for soils under different plants. Bar indicates LSD. The fungal communities changed significantly ($p<0.003$) in soils with different species of plants.



Conclusions

- There are indications that potential denitrification is lower in acidic soils.
- Bacteria produce potentially higher amounts of N_2O than fungi.
- Fungi seem to contribute a greater proportion of N_2O in soils of low pH.
- Bacterial and fungal communities are differentially affected by pH and plant species in arable soils.

Future work

- Further investigations into the influence of plants and pH on microbial communities.
- Determination of bacterial and fungal biomass.

Reference [1]Changing Our Ways - Scotland's Climate Change Programme (2006)
[2]Shoun, H. and Tanimoto, T. (1991) J Biol Chem 266, 11078-11082

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