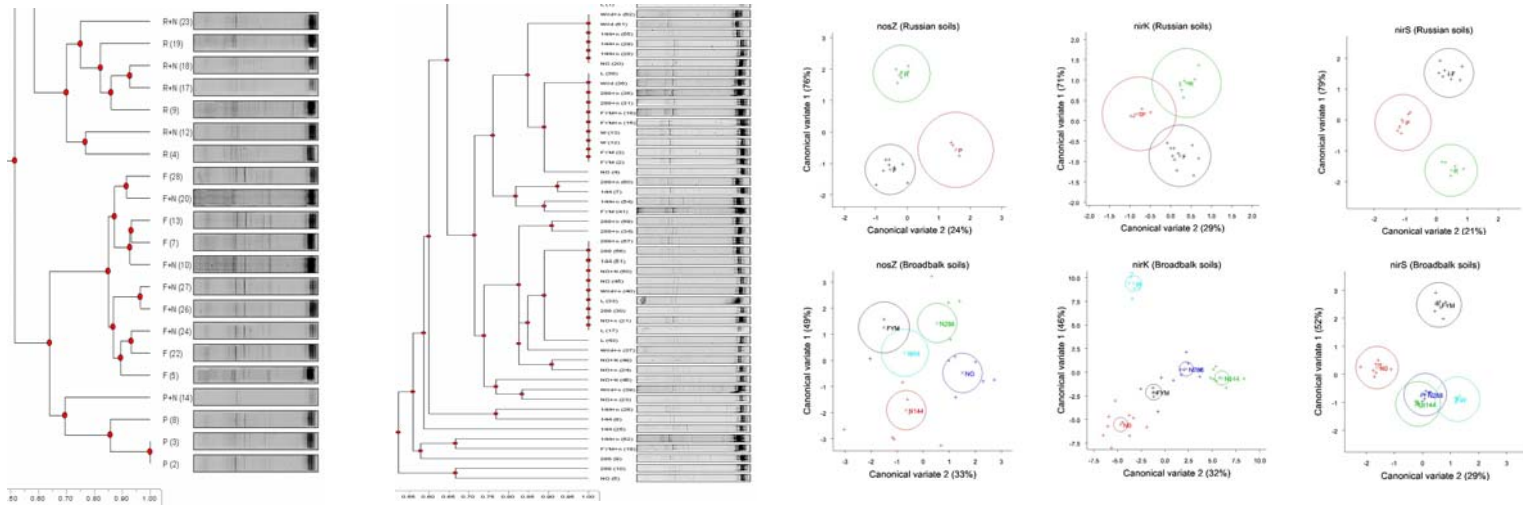


**Introduction:** Different agricultural management systems have direct impacts on soil structure and available nutrients. Do they also affect total microbial and denitrifying bacterial communities? Are differences in soil denitrifying potential due to changes in the denitrifying bacterial population or due to variations in agrophysical properties of the soil?

Denitrifying bacterial populations established on different long-term management systems were compared using PCR-DGGE analysis of genes involved in denitrification, *nirS*, *nirK* and *nosZ*. The long term experimental sites included Broadbalk, the classical field experiment at Rothamsted started in 1843, part of which, Wilderness, has reverted to woodland; the Russian Novgorod forest (>100 years); and Russian agricultural field plots established 10 years ago near St. Petersburg.

**Methods:** Total microbial community DNA was extracted from soil samples when N<sub>2</sub>O fluxes were close to maximum measured in soil cores with (+N) or without the addition of nitrate. PCR products from *nirS* (*nirScd3aF*, *nirSR3cdGC*) *nirK* (*nirKFlaCu*, *nirKR3CuGC*) and *nosZ* (*nosZF*, *nosZ1622RGC*) were run on DGGE gels and profiles compared to determine the effects of long-term treatments on denitrifying bacterial populations. TRFLP analysis was also carried out with PCR products using fluorescently labelled primers *nosZF* and *nosZ1622R*.

## Results:



*nosZ* DGGE profiles for Russian soils

*nosZ* DGGE profiles for Broadbalk soils

Canonical Variate Analysis (CVA) of DGGE banding patterns

**Conclusions:** Predominant denitrifying populations were found for all three functional genes tested and were common to all treatments suggesting that they were not affected by soil management practices. Denitrification rates were shown to be more closely correlated with soil structure than nitrogen inputs (data available but not shown – please ask if interested!).

## Linking Gene Expression of Denitrification Genes with N<sub>2</sub>O and N<sub>2</sub> Emissions

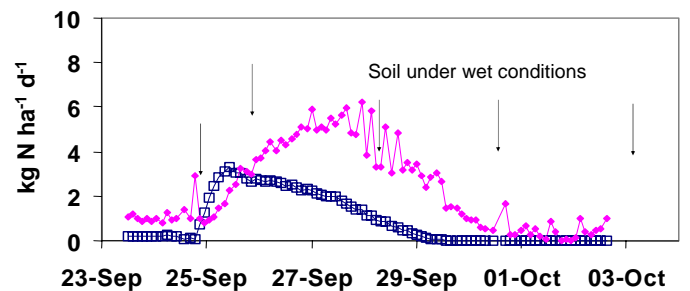
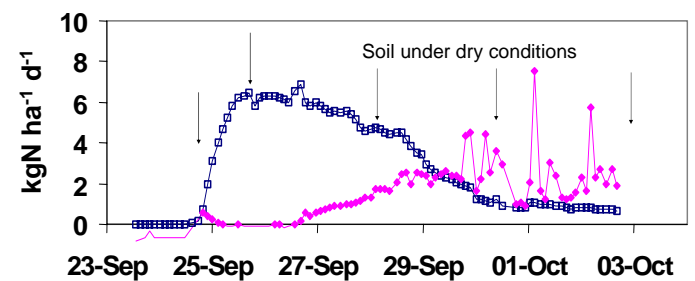
Gilliam, L.M., Cárdenas, L.M., Meijide, A., Clark, I.M., Hirsch P.R., Scholefield, D., and Goulding, K.W.T.

**Introduction:** The aim is to investigate the relationship between N<sub>2</sub>O fluxes and functional gene expression in a automated soil incubation system. Results from a previous experiment carried out with the denitrification incubation system (Denis) showed that N<sub>2</sub>O/N<sub>2</sub> ratios differed depending on the preconditioning of the soil (see adjacent figures of antecedent conditions).

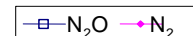
**Method:** Soil samples will be taken and the activity of functional denitrification genes (using RT-qPCR and DGGE profiling) analysed at various time points according to the N<sub>2</sub>O emissions as follows:

1. N<sub>2</sub>O fluxes increase
2. N<sub>2</sub>O fluxes maximum
3. N<sub>2</sub>O fluxes decrease and N<sub>2</sub> starts to increase.
4. High N<sub>2</sub> fluxes
5. O<sub>2</sub> decrease (turning off O<sub>2</sub> supply leads to a spike in N<sub>2</sub>O emissions)

### Denitrification Incubation System (DENIS)



Samples will be taken at these points →



### CONTACT:

Cross-Institute Programme for Sustainable Soil Function (SoilCIP),  
Rothamsted Research, Harpenden,  
Hertfordshire, AL5 2JQ

lucy.gilliam@bbsrc.ac.uk