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The XX International Grassland Congress took place in Ireland and the UK in June-July 2005.

The main congress took place in Dublin from 26 June to 1 July and was followed by post congress satellite workshops in Aberystwyth, Belfast, Cork, Glasgow and Oxford. The meeting was hosted by the Irish Grassland Association and the British Grassland Society.

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Effect of soil chemistry on microbial biodiversity and functionality in grassland and tilled soils

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Introduction Microorganisms are excellent indicators of soil health, because of their rapid response to environmental change. Traditional microbiology is ineffective for the study of soil, as <1% of microorganisms are currently culturable (Torsvik *et al.*, 1996). Nucleic acid based methods, however, allow rapid detection of organisms, or particular genes, directly from soil samples. This work investigated, using polymerase chain reaction (PCR)-based approaches, the relationship between key chemical properties and bacterial biodiversity in grassland and tilled soils, with particular emphasis on the abundance and diversity of ammonium oxidisers.

Materials and methods Thirty grassland soils, and 5 soils under barley (pH from 5.1-7.2), were characterised for a range of key chemical properties: those for one soil (844) were: lime, 10.1 t/ha; P 3.3 mg/l; K 300 mg/l, Mg 109 mg/l; pH 5.1; organic C 4.79%; and total N 0.59%. DNA was extracted with a rapid method developed at NUI, Galway, ensuring a cell lysis efficiency of >80%. Bacterial biomass was calculated based on DNA yield. Denaturing Gradient Gel Electrophoresis (DGGE)-PCR was carried out with 16S rRNA gene-specific primers for all bacteria (Muyzer *et al.*, 1993) and *amoA* gene primers for ammonium oxidisers (Holmes *et al.*, 1995). PCR amplicons were run on DGGE gels to generate banding patterns. Un-weighted Pair Group with Arithmetic Mean (UPGMA) analysis of DGGE profiles was carried out with *MEGA 2.1* (Kumar *et al.*, 2001; Figure 1).

Results This study demonstrated that the microbial biomass and biodiversity in grassland and tilled soils can be related to basic soil properties (Figure 1), as could the functional capacity of soils with respect to ammonium-oxidation. This clear relationship between soil type, vegetation type, land use and microbial communities has significant implications for the study and understanding of nutrient cycling and organic matter decomposition.

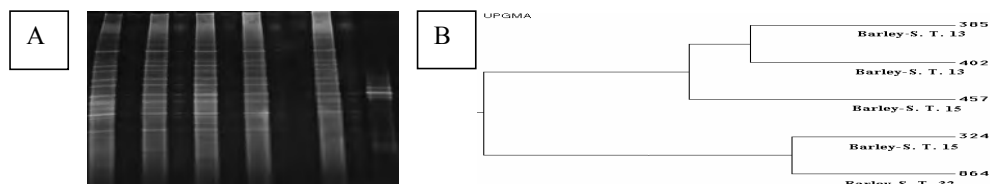


Figure 1 (A) DGGE gel from 5 soil samples under barley. The number and position of bands are indicative of bacterial species within the soil community, common bands are clearly visible. (B) UPGMA analysis of DGGE profiles. The microbial biodiversity of soils could be statistically related to properties such as pH.

Conclusions Microbes play many key roles in soil, but major knowledge gaps exist in our understanding of soil microbiology. Rapid, statistically verifiable, microbial analysis of soils is now feasible for large-scale applications and may be integrated into soil monitoring and research programmes.

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