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Integrating soil characteristics, land management and soil microbial communities



Key external stakeholders:

Research community,
Policymakers
Agri-environmental researchers and NGOs

Practical implications for stakeholders:

- Soil microbes play an important role in sustainability and in ecological functioning by providing ecosystem services including, supply of nutrients to plants, water regulation and maintenance of soil structure. Soil pH and soil water regimes play a significant role in the formation of bacterial communities and their functioning.
- Poorly drained soils supported a great abundance of soil microbes but had lower respiration rates. Soils with fluctuating water tables supported microbial communities with a higher proportion of anaerobic species, higher respiration rates and higher N-mineralization potential.

Main results:

This study highlights the importance of soil physicochemical factors in shaping and influencing microbial community structure and nitrogen-cycling gene abundances.

Soil pH was a common driver influencing soil microbial community structure, diversity, nitrification potential and N-cycling gene abundances.

Analysis of soil features revealed that drainage class was an important factor driving microbial abundance (biomass), physiology and community structure. The effect of soil drainage was mainly related to soil bacteria. In this study, poorly drained soils were able to support a higher abundance of soil microbes, but had lower respiration rates (functioning) compared to well drained soils. It was hypothesized that the microbial communities showed an adaptation to soils with fluctuating water status. A shift towards a higher proportional abundance of anaerobic microbial species compared to fast metabolising aerobic microbial species was suggested to have implications on soil mineralization rates. In comparison, drainage class was not significant in shaping N-cycling gene abundances.

Detailed sequencing analysis of bacterial taxonomic abundances across four different soil types and depth profiles revealed soil type specific abundance patterns. These might be related to bacterial taxa being involved in specific soil processes. The study also identified bacterial genera including *Arthrobacter*, *Spartobacter*, *Verrucomicrobia subdivision 3* and *Pseudomonas* to be of similar relative abundance between soil types and might therefore be a stable part of the soil core microbiome.

Opportunity / Benefit:

Overall this project has contributed to knowledge in the broad area of soil microbial ecology and has provided much needed baseline data on soil microbiota and the factors affecting them in Ireland. The study highlights the importance of soil pH and soil water regimes in the formation of bacterial community structure and functioning, including nutrient cycling. Additionally, this study gives the first insight into similarities and differences of bacterial taxa associated with geographically different soil type profiles.

Collaborating Institutions:

University College Dublin, Belfield, Dublin 4

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External collaborators: Dr Evelyn Doyle; University College Dublin
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1. Project background:

Soil microbes play an important role in sustainability and in ecological functioning, by providing ecosystem services, such as the supply of nutrients to plants, water regulation and maintenance of soil structure. The microbial biomass in soil is not only the catalyst of all microbial transformations in soil, but also constitutes a pool of nutrients that has a rapid turnover compared with soil organic matter.

Bacteria and fungi are the major constituents of soil microbial biomass. Soil bacteria play a vital role in the mineralization of organic matter and in improving the availability and efficiency of nutrient utilization. Fungi on the other hand play an important role in the carbon and energy cycles and in the decomposition of organic matter (where they transform the proteins in plant residues into soluble nitrogen which are subsequently available for plants). Fungi also play a positive role in the inorganic nutrient absorption. Biological decomposition by soil organisms is the largest source of nutrients for plants in systems with low input of mineral fertilizers.

Despite the vital role soil microbes play, we only understand a fraction of their involvement in improving plant growth and soil health. Soil type and land-use and management all play extremely important roles in determining the soil community. Furthermore, soil pH and soil substrate and structure are important factors in determining soil microbial activity. Anthropogenic (human) impacts such as changes in nutrient input, climate change and soil management have the potential to directly or indirectly affect soil bacterial and fungal composition, with consequent impacts on soil function, in particular with regard to N mineralization patterns.

An improved understanding of soil microbial communities is imperative due to their role in carbon and nitrogen cycling, ecosystem interactions, ecosystem functioning and global climate change. With increasing pressure on agricultural production and in the context of ever limiting resources, there is a need to optimize soil fertility in a sustainable manner.

- **Questions addressed by the project:**

The aim of this study was to describe variations in microbial biomass, as well as structural and functional microbial properties, across a spectrum of soils and soil depths under managed and unmanaged grasslands in Ireland. The study aimed to:

- identify important drivers of microbial biomass and function,
- examine microbial community structure, related to specific soil categories, and,
- identify eco-physiological preferences of specific bacterial taxa within different soils.

Information gathered in this study will help gain a better understanding of microbial properties and their relation to abiotic factors, soil type and land management. The study will also provide a baseline for future research, resulting in the identification of possible microbial indicators of soil categories which will help with the sustainable management and protection soil as a vital resource in the future

3. The experimental studies:

Two hundred and twenty five sites were sampled over a 2 year period (2012-2013). At each of the 225 selected sites, a profile pit was dug and each horizon sampled separately. Preparation and storage procedures of samples differed depending on methods used

A number of soil categories likely to influence microbial properties were measured and included OM class, drainage class, spodic class (loss of cations from the surface horizon through leaching) and argillicity class (deposition of clay down the soil profile by illuviation).

A number of functional, eco-physiological and molecular methods were used to profile the microbial communities in the soils sampled, to evaluate microbial biomass, eco-physiological properties, microbial community structure and N-cycling gene abundances, these included:

- microbial biomass,
- multiple substrate-induced respiration,
- DNA fingerprinting,
- quantitative PCR and amplicon sequencing was then used.

Multivariate analysis was performed with the SPSS software, with the Pearson method being selected to determine correlations between all measured physicochemical and microbial variables. Multiple regression analyses were performed to select for robust predictor variables of microbial parameters.

Analysis of variance (ANOVA) was used for the statistical evaluation of individual diagnostic class, land-use and soil type effects on all microbial parameters.

Changes in respiration in relation to physicochemical properties, diagnostic classes, land-use and soil type were analysed using the CANOCO 4.5 package.

Redundancy analysis (RDA) was applied to extract and summarise linear relationships between components of response variables which are explained by the set of explanatory variables. Environmental variables were tested for inclusion in the RDA model with forward step-wise selection.

4. Main results:

This study identified pH as the primary driver of microbial community structure, diversity, nitrification potential and N-cycling gene abundances in Irish soils. Bacterial community structure in particular showed changes in relative abundance of specific taxonomic groups between soils of differing pH.

For N cycling gene abundances, pH along with soil texture and soil organic matter, was found to be the main factor driving abundances. pH has also been shown to affect nitrification and denitrification processes rates and would therefore appear to be closely linked to N-cycling.

The study found that soil type (driven by pH and soil texture), contained distinct signature bacterial community structures, regardless of geographical location. Additionally, the relative abundance of some genera was found to be similar across all soil types and depths, suggesting that they are part of the core soil microbiome of grassland soils.

The study found an effect of drainage on bacterial community structure. Poorly drained soils were able to support a higher biomass, but had lower respiration rates compared to well drained soils. The adaptation to fluctuating water saturation stages of the soil was considered to be due to a shift towards a higher proportional abundance of anaerobic and facultative anaerobic microbial species in relation to fast metabolising aerobic microbial species.

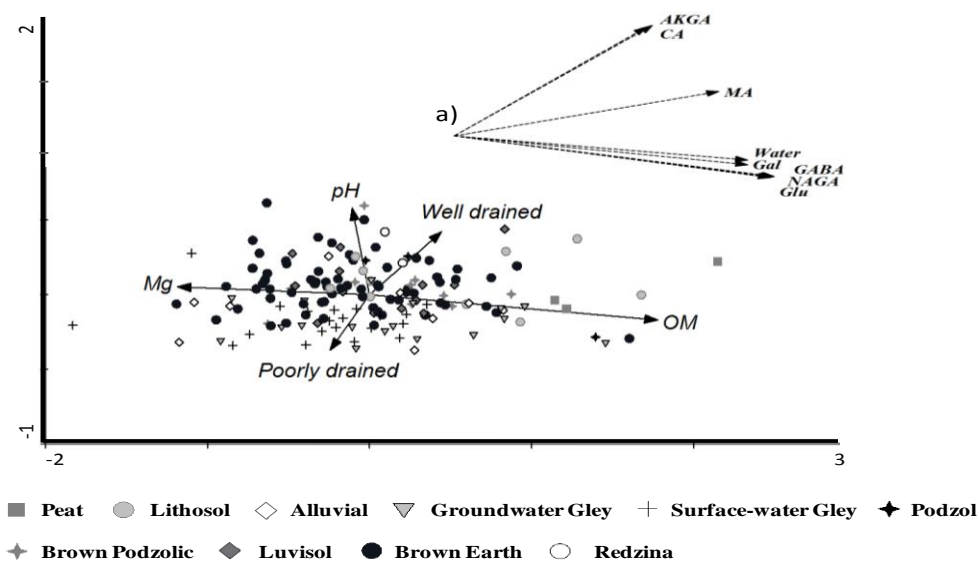


Fig 1. Species composition of Traditional Hay Meadow, Species Rich Grassland and Natura 2000 grassland.

5. Opportunity/Benefit:

Soils have different capacities based on their physicochemical properties, structure, texture and microbial activity. An important consideration for agricultural use for example is that different soils might select for certain microbial community structures, and their function can be related back to soil productivity.

The soil water regime is an important environmental factor driving microbial community structure and C and N dynamics. These findings are of particular relevance for Ireland considering that predictions indicate that we will be subjected to greater occurrences of extreme weather conditions such as intense rainfall, with obvious implications on soil water conditions. However, the trends identified in this study highlight the need for additional research on the impact of transient water saturation in soils and the implications on relevant management strategies. Future long term field studies could investigate detailed community assemblages over longer time periods, as well as assess the implications of community adaptation for plant-microbe interactions to see how different N and C cycling patterns affect plant productivity.

6. Dissemination:

Main publications:

Richter, A. (2016) Integrating soil characteristics, land management and soil microbial communities. PhD Thesis, School of Biology and Environmental Science, University College Dublin.

Richter, A., Creamer, R.E., Doyle, E., Clipson, N., & Ó hUallacháin, D. (2017) Drivers of soil microbial biomass and respiration in agricultural grassland soils, a large scale study in Ireland. *European Journal of Soil Science*, accepted

Conference and popular publications:

Richter, A., Doyle, E., Clipson, N., Creamer, R. & Ó hUallacháin, D. (2015) Integrating soil characteristics, land management and soil microbial communities. *Agricultural Research Forum 2015*, Tullamore, March 2015.

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2014) Integrating soil characteristics, land management and soil microbial communities. *Teagasc Walsh Fellowships Seminar*, Johnstown Castle, December 2014.

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2014) Understanding microbial mediated nitrogen cycling in Irish grassland soils. *First global Soil Biodiversity Conference*, Dijon, December 2014.

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2014) Soil microbial diversity: Does location matter?. *TResearch*, vol 9, pg 22-23.

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2013) Integrating soil characteristics, land management and soil microbial communities. *Microbial interactions in complex ecosystems*, Turin, October, 2013

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2013) Integrating soil characteristics, land management and soil microbial communities. *23rd Irish Environmental Researchers Colloquium*, Galway, January 2013.

Richter, A., Doyle, E., Clipson, N., Creamer, R. and Ó hUallacháin, D. (2013) Integrating soil characteristics, land management and soil microbial communities. In *Ireland's Rural Environment: Research highlights from Johnstown Castle*.

Richter, A., Doyle, E., Clipson, N., Creamer, R., and Ó hUallacháin, D. (2012) Integrating soil characteristics, land management and soil microbial communities. *Society of General Microbial Spring Conference*, Dublin, March 2012

7. Compiled by: Daire Ó hUallacháin, from information provided in PhD thesis by Ms Andrea Richter.