CASE STUDY

GREATSOILS

British Beet BBRO Research Organisation

AHDB

Soil Biology and Soil Health Partnership Research Case Study

The role of molecular-based indicators for measuring soil health

Background

Food and fibre crop production require soils to be maintained in a suitable state that provides optimal soil structure, water retention and nutrient availability. The physical, chemical and biological properties of soil interact to deliver these functions. Measuring soil health therefore requires an integrated approach that combines the assessment of the chemical, physical and biological properties of soil. There is a good understanding of the soil chemical and physical constraints to crop and grassland productivity, however, the role of soil biology is less clear.

A key aim of the Soil Biology and Soil Health Partnership is to improve our understanding of soil biology and to explore ways that farmers can measure and manage soil health. The Partnership is investigating the value of DNA markers for estimating the effect of soil- and crop-management practices on the microbiological diversity of soils as well as to study the population dynamics of beneficial versus plant pathogenic fungi and bacteria.

Estimating the effect of long-term organic material additions on soil microbial diversity

To investigate the impact of repeatedly adding different organic materials to soil in a predominantly arable rotation (cereals and potatoes), samples were collected from a long-term trial at Harper Adams University in October 2017. Details of routine measurements of topsoil chemical, physical and biological properties were undertaken (see Research Case Study: ***Testing the effect of organic material additions on soil health).***

For comparison, soil samples were also taken for total DNA analysis. The DNA was extracted and purified using three different methods and then analysed using high-throughput sequencing technology. This compares DNA sequences of marker genes that are unique to all bacteria (16S rRNA) or fungi (ITS rRNA) in a process known as metabarcoding. Using this molecular technique, most soil organisms can be identified at higher taxonomic levels (e.g. phylum, class or order), although fewer can yet be accurately assigned at the levels of family, genus or species. Nevertheless, the numbers of taxonomically distinct individuals can be compared across the different treatments and bioinformatics software can be used to measure biological diversity in each sample.

Table 1. Organic material treatments at the long-term trial at Harper Adams University

Harper Adams (Shropshire)	
Sandy loam (12% cl) arable rotation	
Treatments:	Applications up to autumn 2017
Cattle FYM	23 years
Cattle slurry	23 years
Green compost	13 years
Green/food compost	7 years
Food-based digestate	9 years

Results to date

Between 100,000–200,000 DNA sequences were obtained for both bacterial and fungal groups from each soil sample from the Harper Adams trial. Irrespective of the method used to extract the DNA, similar types of bacteria and fungi were recognised within the soil communities (Figure 1). The extraction method did, however, influence estimates of the relative abundances of these types of bacteria and fungi (Figures 1 and 2). Standardisation of methods will therefore be important when comparing samples collected from different locations and at different times. When results from plots with and without organic amendments were compared, no significant effects of any of the amendments on bacterial or fungal types or abundances were found (Figure 2).

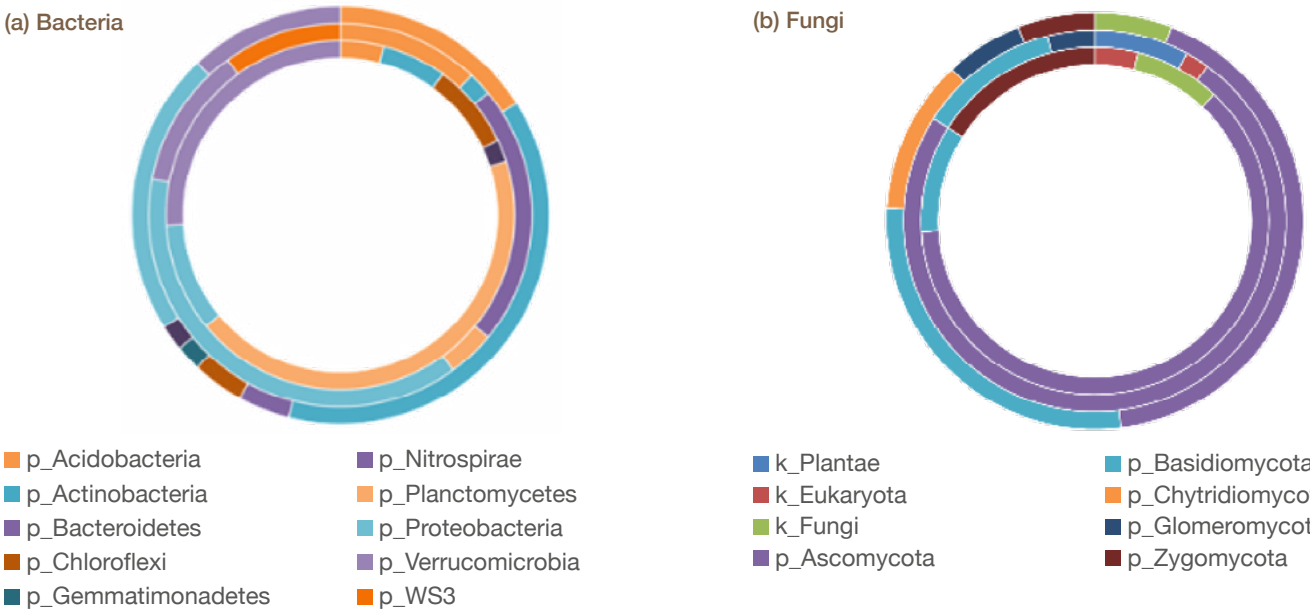
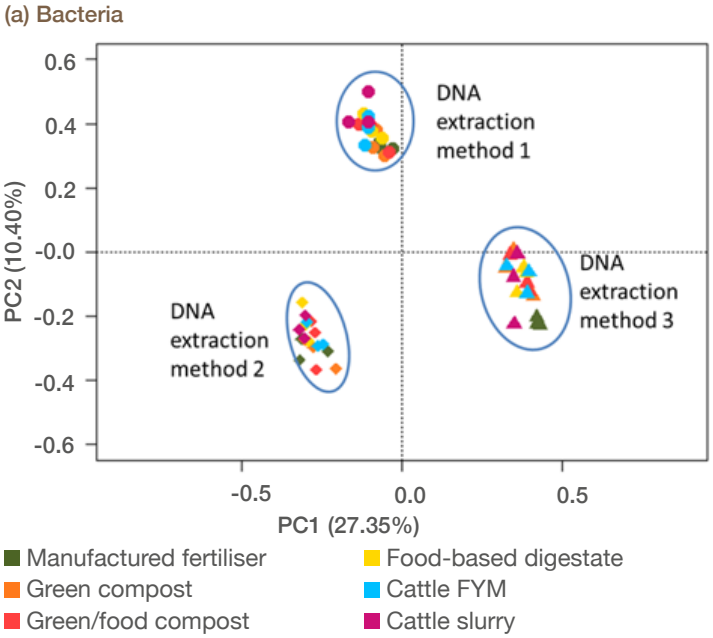


Figure 1. Relative proportions of the most abundant types of bacteria (a) and fungi (b) estimated using three different DNA extraction methods. Estimates obtained using methods 1, 2 and 3 are shown from the inner to outer rings respectively. The coloured bars in each ring represent the proportion of the total community for each type of bacterium or fungus



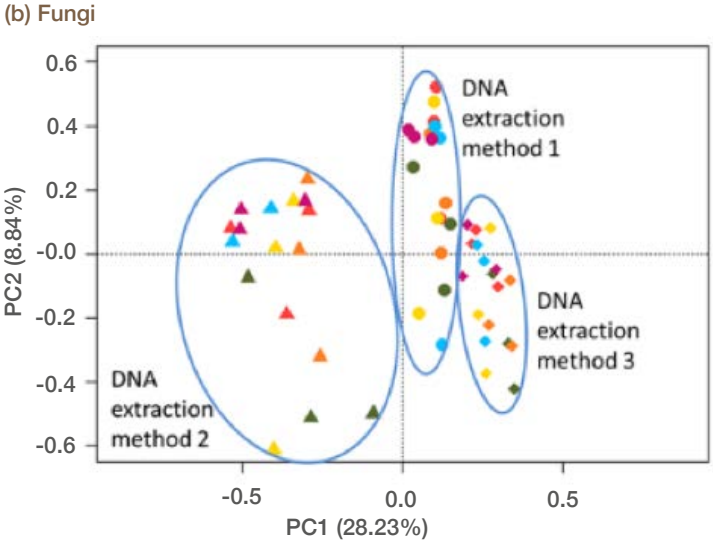


Figure 2. Principal component analysis comparing relative abundances of different bacteria and fungi in soils treated with different organic amendments, estimated by metabarcoding with three different DNA extraction methods

Future work

Sampling will be repeated at this and other long-term trial sites. Standardised DNA analyses will be used to identify specific changes that occur in fungal and bacterial communities as a result of different soil-management practices. Molecular data will be compared against the more traditional physical, chemical and biological measurements of soil health also being collected by the Partnership.

Acknowledgements

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