Microbial and microfaunal variation in soils

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The drive towards so-called sustainable agriculture means a greater reliance on biological processes in soil. The term 'sustainable' is usually not well defined but in relation to agriculture means a move towards lower inputs (of fertilisers and pesticides) and greater in-field diversity of above-ground species. The key to such systems is what happens below-ground, in the soil, as biological processes and populations here drive soil nutrient flows, influence emergent plant communities and affect the outbreak of soil-borne plant diseases.

Understanding how spatio-temporal variations affect N-cycling within an arable context will enable efficient management of sustainable eco-systems. Potential nitrification rate (PNR), defined as the oxidation of ammonium-N to nitrite-N, was studied during the growing season of barley (*Hordeum vulgare* L. c.v *Optic*). PNR showed considerable spatial and temporal variation throughout the sampling period (Fig 1). There was a 500-fold variation in PNR during the season and a variation of up to 2.5 times at any single sampling. We are presently investigating the drivers of this microbially-mediated function with DNA/RNA techniques linked to simultaneous function estimations.

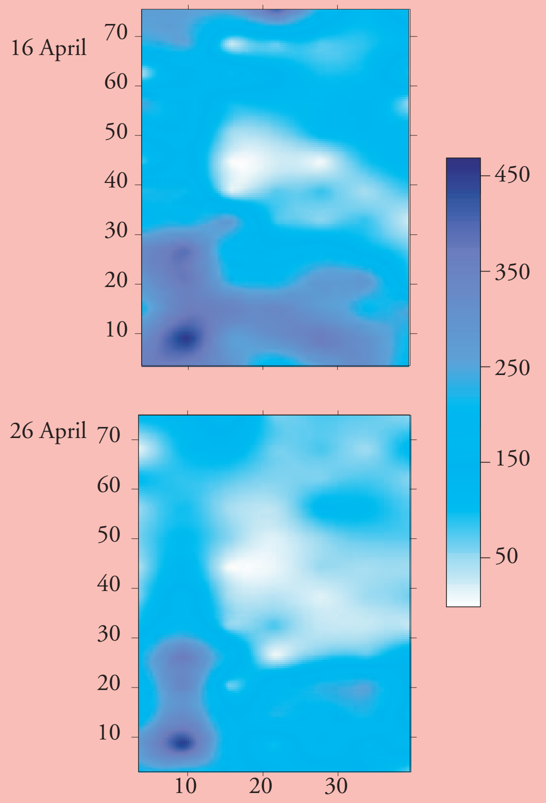

Figure 1 Concentration contours of nitrification activity (0 – 450 µg NO_2-N g^{-1} soil h^{-1}) across a barley field (70 x 30m) on two days in April.

We are also investigating the role of denitrification (the conversion of nitrate to nitrogen oxides, therefore a loss of valuable fertiliser and a source of potent greenhouse gas) in the same arable systems. To understand the biodiversity associated with this process we have applied a high throughput sequencing approach to a key functional gene in bacteria (*Nir*K) that controls denitrification. We have exhausted the common sequence types in three arable fields at SCRI, as shown in the phylogenetic tree (Fig. 2). Nitrification and denitrification are linked microbial processes and we are, for the first time, now able to link biodiversity and activity on a spatio-temporal scale.

Microbial activity in soils is regulated to a large degree by the animals that eat them, which in arable soils are

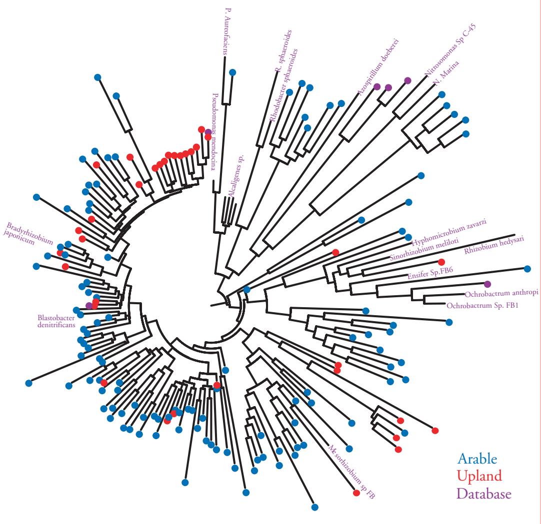

Figure 2 Neighbor joining tree (F84 model with gamma rates) of NirK sequences from arable fields, upland grassland and database sequences. Terminal taxa are representatives of clustering at 0.075 substitutions per base. Blue = Arable types, Red = Upland grassland types from a separately funded project, Purple = Database examples.

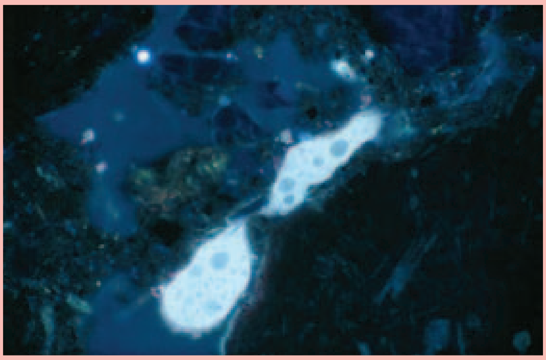

Figure 3 A thin-section through soil showing an amoeba traversing a soil pore.

mainly protozoa (Fig. 3) and nematodes (Fig. 4) and recent work within PSI has confirmed that microbial community structure in soil is significantly affected by both nematodes and protozoa (Fig 5).

Figure 4 Bacterial-feeding nematodes from soil.

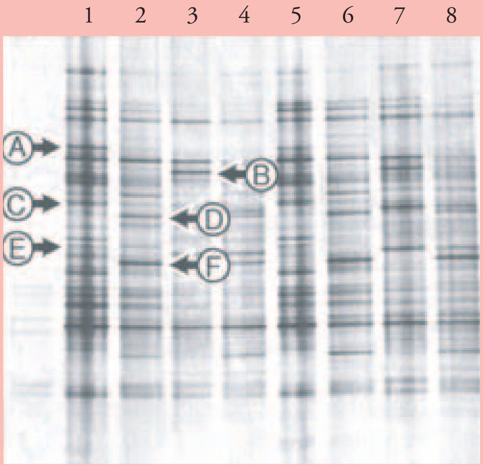

Figure 5 DNA banding patterns of the microbial community as affected by the presence of protozoa and nematodes. Bands A, C and E are absent from treatments with protozoa (lanes 3,4,7,8), B only appears in treatments where protozoa are present (lanes 3,4,7,8), and bands D and F only appear where nematodes are present (lanes 2,4,6,8). Lanes 1 and 5 are treatments with bacteria only.

Whether there is a specific relationship between grazing fauna and bacterial composition will be important in understanding microbial dynamics in the rhizosphere of arable crops.

The aim of the microbial ecology research within the programme is to enhance the sustainability of arable agricultural systems through understanding and manipulating soil biology.