NATURAL ENVIRONMENT RESEARCH COUNCIL

SOIL BIODIVERSITY

The world beneath our feet

Database

The database provides an integrated information resource for the programme's research activities including:

- details of all field site activity at Sourhope with unique IDs for soil samples and experimental set-ups, their site geo-references and sampling dates;
- data and meta-data from the 27 project teams as they become available, each linked directly to its detailed sampling information in the database;
- references to summary reports, publications and other relevant information.

The database has been developed using Oracle by the Centre for Ecology & Hydrology at Lancaster.

Web access to data

You can already freely download core data from the Sourhope site from the programme's website (http://soilbio.nerc.ac.uk/), where you can also find further information about data management procedures and protocols.

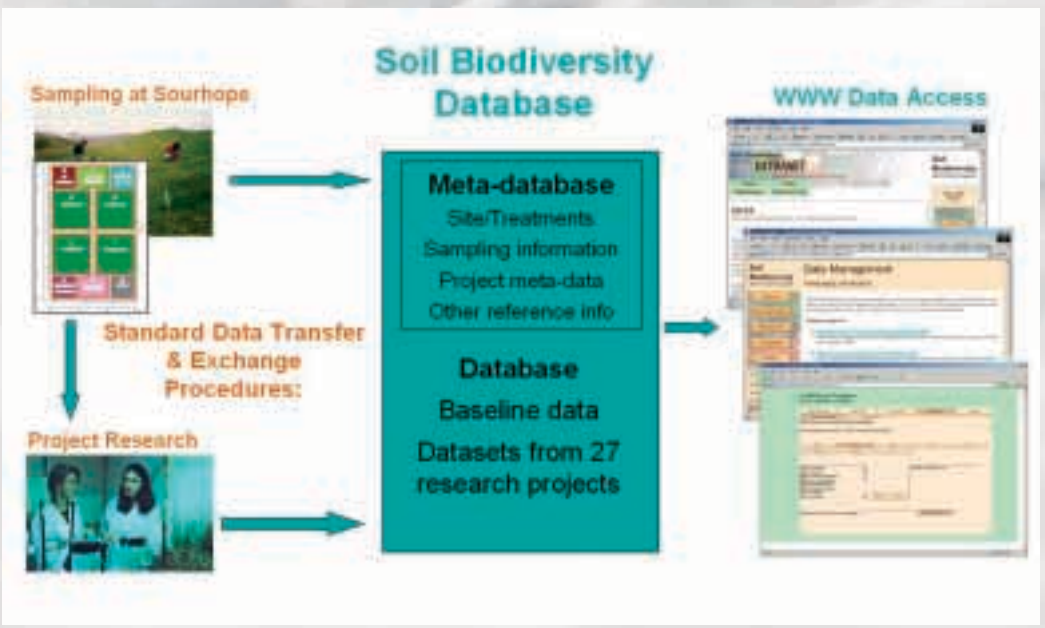
At the end of 2004, you will be able to use a user-friendly web interface to search, explore and download data directly from the Soil Biodiversity database (subject to the data policy's requirements), using keyword and free-text searches based on the knowledge incorporated within the meta-database.

Whilst you'll be able to see the meta-data via the web interface, you will have to register to access the actual data. A security gateway will administer user registration and authentication procedures, and all data accesses will be monitored and reported to the researchers.

According to NERC and Soil Biodiversity data policies, project investigators retain exclusive rights to their data for two years after their project ends. After this, registered users can use the data for academic research.

Further information

For more information on access to the data, database and documentation please visit the website: http://soilbio.nerc.ac.uk/ or contact Lynne Irvine (Soil Biodiversity Data Manager): lirvine@ceh.ac.uk



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The world beneath our feet

Waxcap grasslands at Sourhope

Waxcap fungi (*Hygrocybe spp.*) grow in nutrient-poor semi-natural grasslands. With their large brightly-coloured fruiting bodies they are highly visible members of the soil community. Intensified farming since World War Two has destroyed many waxcap habitats. Several UK species now have *Biodiversity Action Plans*, and we urgently need more information about habitat requirements.

We used a differential Global Positioning Satellite system to produce a very detailed map of fruiting bodies from 11 species of waxcap at Sourhope during 2001-2003. We found waxcaps are severely affected by soil treatments. On plots treated with lime, and with nitrogen and lime, there were 20-fold fewer fruiting bodies. We have found similar responses to nutrient treatments at several other long-term grassland field experiments.

We also examined the natural abundance levels of stable isotopes of carbon and nitrogen in waxcaps, earth tongues (*Geoglossaceae*) and fairy clubs (*Clavariaceae*). These three groups of fungi, which are unrelated but which are all typical of nutrient-poor grasslands, had significantly elevated levels of ^{15}N and low levels of ^{13}C compared to other decomposer fungi found at Sourhope. This suggests that they feed on similar soil compounds, and that their nutritional behaviour is different to that of other fungi. As such they represent a distinct ecological grouping.

A genetic fingerprinting technique (microsatellite-based ISSR) has allowed us to map the extent of individual fungal colonies, some of which may form extensive 'fairy rings'. We found some that extended over several square metres, making waxcaps possibly the largest soil organism at Sourhope.

Our field studies are continuing with $^{13}CO_2$ and ^{15}N labelling experiments, whilst laboratory experiments are focusing on genetic diversity within/between sites. Our investigations of spore germination suggests that the spores of the rarer waxcap species are more difficult to germinate.

Further information

You can find out more at www.aber.ac.uk/waxcap, or contact Gareth Griffith, gwg@aber.ac.uk

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The world beneath our feet

Earthworms, microbes and soil treatments

Some soil treatments affect earthworms, which in turn affect soil structure, the community of microbes in soil, and hence how organic matter is broken down. In a mesocosm experiment at Sourhope we artificially manipulated the number of earthworms, and investigated the effects of liming. Adding lime explained most of the variation in earthworm abundances. *Lumbricus terrestris* did not survive well in the mesocosm, but *Allolobophora chlorotica* survived well in limed soil, becoming co-dominant with *Dendrodrilus rubidus*. The most abundant species in unlimed soil was *D. rubidus*.

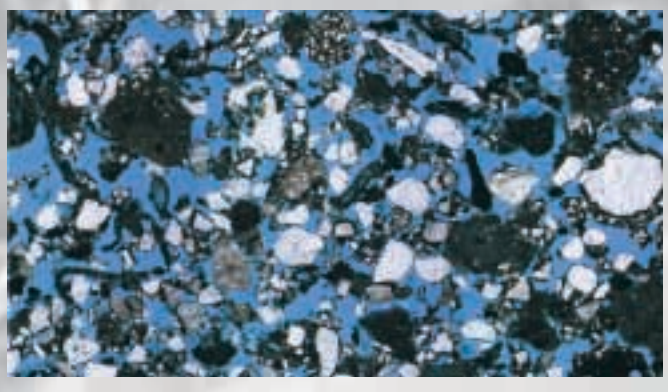
In a laboratory microcosm experiment we investigated how these three worm species affected soil microbial processes. Applying lime changed the community of soil microbes, irrespective of whether earthworms were added. Adding earthworms altered the composition and functional diversity of the microbial community in limed soil, making the community better able to breakdown complex organic compounds. This did not occur when we added worms to unlimed soil.

Thin sections of soil showed that earthworm casts did not significantly change soil structural stability. Earthworms changed the porosity of soil, particularly by increasing the proportion of large pores. These act as channels for air and water to move through soils, and water movement through the limed soils in the mesocosm experiment was significantly increased.

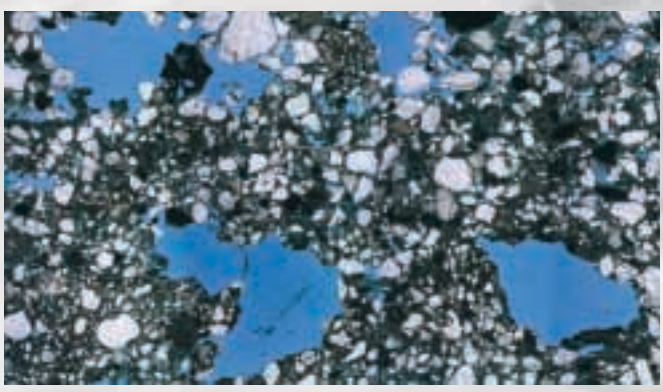
Further information

If you want to find out more, contact David Hopkins, email: d.w.hopkins@stir.ac.uk

Steve Hopkin/Ardea



No worms.



Worms.

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The world beneath our feet

Soil protozoan diversity and its role in carbon and nitrogen turnover

Protozoa are a diverse and abundant group of microbial organisms that feed by engulfing other organisms. They live in a wide range of habitats, including soil. In the four major groups (flagellates, naked amoebae, testate amoebae, ciliates), we recorded 365 species at Sourhope – about one third of the world's known soil protozoan species. This ratio is consistent with the developing consensus that microbial species have cosmopolitan distributions.

The abundance of soil protozoa is inversely related to organism size. In the 150 soil samples we collected, the median abundance per gram dry weight ranged from 2000 ciliates (the largest species) to 43,000 flagellates (the smallest species).

Across the size range, species richness varied by a factor of two. Abundance increased by a factor of 20 with decreasing body size.

Soil protozoa live in the water films lining the crevices in soil. Leading off from the relatively few big crevices are progressively smaller crevices. These tend to be self-similar at all spatial scales, so the number of different habitats provided for protozoa is roughly the same in big crevices (housing big protozoa) as in small crevices (housing only small protozoan species). Thus protozoan species richness is similar in big and small crevices.

In microcosm experiments, soil protozoan grazing stimulated the rate of carbon turnover. Stimulation increased with increasing biological diversity in the treatment sequence: bacteria; bacteria + amoebae; bacteria + ciliates; bacteria + amoebae + ciliates. Carbon turnover in the last treatment was up to 50% higher than in the treatment with bacteria alone.

Using soil ciliates and testate amoebae, we tested the hypothesis of ubiquitous dispersal of individual species. Comparing data from 150 Sourhope soil samples and from 1500 soil samples collected worldwide, we found that species that were rare or abundant at Sourhope, were likewise rare or abundant globally. This is consistent with ubiquitous dispersal.

Further information

If you want to find out more contact Bland Finlay, email address bjf@ceh.ac.uk

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The world beneath our feet

Grassland responses to changing communities of soil organisms

Soil organisms perform a range of ecosystem services, from carbon storage to pollutant degradation. They are threatened by human activities, including land-use change and air pollution and their extinction may affect ecosystem functioning. We stress the word may because there is little experimental evidence to draw a satisfactory conclusion. So we designed an experiment to address this.

We created model upland grasslands containing different soil organism diversities, and assessed how this affected ecosystem services. In one set of communities we included only tiny organisms such as bacteria and fungi. In a second set we included tiny and slightly larger fauna (such as mites and springtails). The final set of communities included tiny, medium-sized and large soil organisms (such as earthworms, beetles and centipedes). Our diversity gradient reflected the situation in natural environments, where activities such as agricultural intensification tend to reduce the numbers and types of larger organisms.

Previous studies reported positive effects of these fauna on soil fertility and plant growth; therefore we predicted that the presence of larger fauna would increase grassland yield and carbon storage. Initially, yield was unaffected but over the longer-term we saw marked reductions in the simpler soil communities. However, forage quality was higher when larger fauna were absent because there was more white clover. Carbon storage was suppressed when the large fauna were absent but increased again when the medium-sized fauna were also excluded.

Our work suggests that if environmental change alters soil organism diversity, the services that grassland ecosystems supply will be markedly affected. These impacts were not readily predictable from previous research. If we are to predict the impacts of altered soil community diversity on vital ecosystem services, we need longer-term research using complex model or natural ecosystems.

Further information

If you want to find out more, contact John Newington (j.newington@imperial.ac.uk) or Mark Bradford (mabrad@duke.edu)

NATURAL ENVIRONMENT RESEARCH COUNCIL

SOIL BIODIVERSITY

The world beneath our feet

Soil mesofauna and carbon cycling

Because soils under upland grasslands and peatlands can both store carbon (C) and release the greenhouse gas carbon dioxide (CO_2), we need to understand how and to what extent soil creatures affect this important part of the carbon cycle.Traditionally we have assumed that most soil microbes and animals feed on decaying plant tissues. However, in grasslands, where roots make up over 50% of the plant biomass, live roots shed cells, die, and ooze exudates to produce food for soil organisms. Indeed, matter coming into the soil in this way accounts for a significant percentage of carbon inputs.

We examined the role of root carbon inputs for soil creatures, such as earthworms, enchytraeids, nematodes, mites and collembola.

A new 'mobile laboratory' was designed, built and commissioned to 'pulse-label' grassland vegetation with isotopically enriched carbon dioxide ($^{13}CO_2$). We traced carbon journeying from the air, into plants, through their roots, into the soil and through soil creatures back to the atmosphere.

We found that, far from depending on decaying organic matter, soil creatures were rapidly using organic matter containing 'pulse' ^{13}C. We also found that although earthworms made up the majority of the soil animal biomass, other smaller but abundant organisms, such as collembolans and mites, used more of the ^{13}C. Also, liming increased the rate at which $^{13}CO_2$ returned to the atmosphere, because it changed the activity of creatures in the soil around plant roots.

These findings confirm that organisms previously believed to live only on decaying matter readily use carbon from living roots. This means climate and land use changes that affect plants and below ground ecology will play an important part in controlling the release of soil carbon stores in the form of greenhouse gas carbon dioxide.

Further information

If you want to find out more contact Nick Ostle, email address no@ceh.ac.uk

NATURAL ENVIRONMENT RESEARCH COUNCIL

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The world beneath our feet

What is the link between microbial diversity and soil resilience

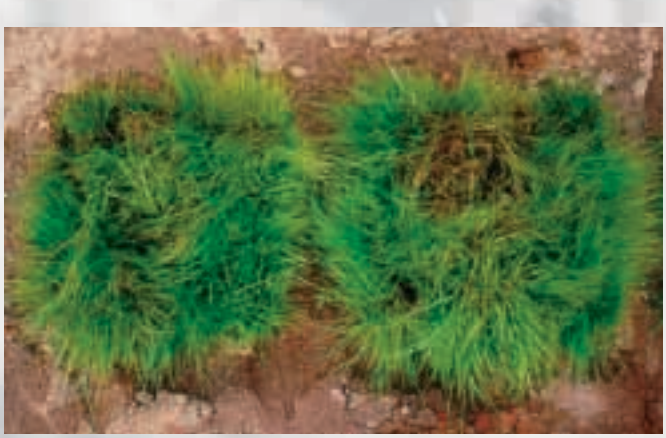
How far is a soil's ability to stand up to stress related to the diversity of the bacteria in the soil? We aimed to find out, by stressing the soil and then measuring changes in both microbial diversity and microbial ability to decompose grass.

We stressed soils in plots at Sourhope and also in the lab, either by heating them briefly to 40°C or adding copper. To find out how well the soil microbes functioned afterwards we measured how quickly they could decompose the grass. We also used molecular techniques to see if the stresses had reduced the number of microbe species.

The microbes in all the samples quickly recovered from the heat stress and carried on breaking down grass. However, the microbes showed little recovery from chronic copper poisoning.

We also treated the field plots in various ways: by reseeding, adding sewage, biocide, and nitrogen and lime. Soil from all the treated plots did not recover as well from heating as the soil from untreated plots. The type of treatment played a marked role in the soils' ability to recover. Also, how each soil functioned when first treated was not indicative of how it would recover over time.

Both the heat and the copper stress led to distinct shifts in the structure of the microbial community. These shifts, and by inference from previous studies, reduction in overall microbial diversity, were associated with a reduction in function.



However, we could find no direct link between soil resilience and microbial diversity from this study. This is because soil resilience varies according to what the stress is and how long it goes on for, microbial community structure, soil characteristics and treatment regimes.

Further information

To find out more contact Anne Glover, email address l.a.glover@abdn.ac.uk

NATURAL ENVIRONMENT RESEARCH COUNCIL

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The world beneath our feet

Worms and soil structure

There is a complex relationship between how soil is organised and the animals, particularly worms, living within it. Since ploughing was abandoned at Sourhope in about 1750, fresh and partially decomposed vegetation and organic material rich in carbon have accumulated at the surface, forming a shallow peaty layer lying over a mixture of organic and mineral matter.

Earthworms and enchytraeids (another small common wormlike creature), process around 90% of the organic matter in soils, churning it very effectively. Their casts dominate the upper soil layers. This processed carbon is more easily 'digested' by the rest of the soil ecosystem.

Liming caused changes in the stability of soil, partly because it caused more earthworm activity and casts. We used automatic image analysis to distinguish worm casts from other soil features, and confirmed that casts change the soil structure, by making the voids between clumps of particles larger. By adding a fluorescent dye, we also looked at the distribution of bacteria. There were more bacterial in limed than in untreated plots in both the peaty and lowest layers. In the peaty layer the increase is linked to enchytraeid casts. In the organo-mineral layer it is linked to earthworm casts.

When we fed plants with radio-labelled carbon and followed it in the soil, we found the labelled carbon was taken up unevenly, even within plant roots. It did not become concentrated in worm casts.

Stephen Dalton/NHPA

John Mason/Ardea

Further information

If you want to find out more, contact Patricia Bruneau, email address: patricia.bruneau@snh.gov.uk

NATURAL ENVIRONMENT RESEARCH COUNCIL

SOIL BIODIVERSITY

The world beneath our feet

Soil treatments and chitin-degrading microbes

We wanted to investigate how treating soils with lime and sewage sludge affected soil microbe diversities. Rather than investigating the organisms themselves, we looked at their genes, in particular an ecologically important group of enzymes that break down chitin. Chitin is a common nitrogen-containing polymer that is food for some bacteria and fungi, and is abundant in soil.

Chitin is usually broken down by a group of enzymes called 18 glycoside hydrolases. We developed a molecular tool kit to detect bacterial and fungal genes coding for these enzymes, using Polymerase Chain Reaction (PCR) techniques. This was the first ever study of the molecular diversity of chitinase genes within a terrestrial microbial community.

We buried litter bags baited with chitin at Sourhope, and sampled microbes from nearby soil several months later. Our PCR toolkit let us take a snapshot of the molecular diversity of chitinase enzymes present.

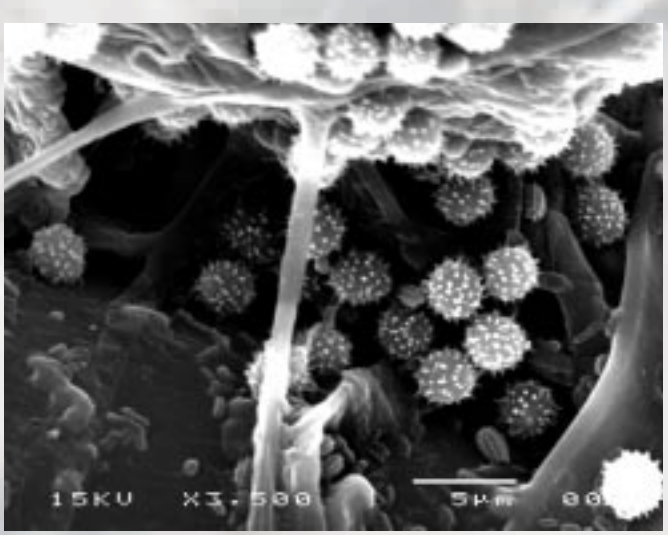
We found over 60 unique clones, ie at least 60 different versions of genes coding for chitinases. Many were similar to genes from a group of bacteria called actinobacteria, and we conclude this group are important in breaking down soil chitin.

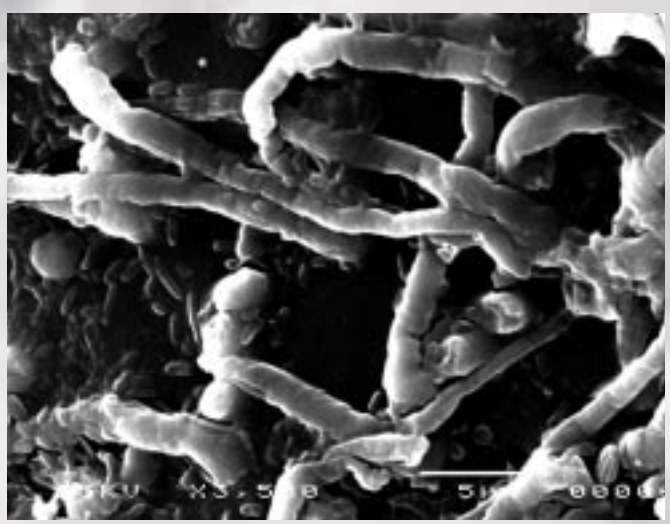
More detailed analysis suggested the bacteria were from the genera *Arthrobacter, Streptomyces* and *Rhodococcus*, *Stenotrophomonas, Cellovibrio* and *Prosthecobacter*. Fungal genes were similar to *Chaetomium* and *Mortierella* fungi.

Treating soils with lime did not affect diversity, but applying sewage reduced diversity. However, chitin was broken down faster, and enzyme activity was increased in soils treated with sewage. So sludging may improve soil fertility by increasing the activity of key bacteria that can metabolise chitin, but at the expense of overall bacterial diversity.

Further information

If you want to know more, contact Liz Wellington, E.M.H.Wellington@warwick.ac.uk





NATURAL ENVIRONMENT RESEARCH COUNCIL

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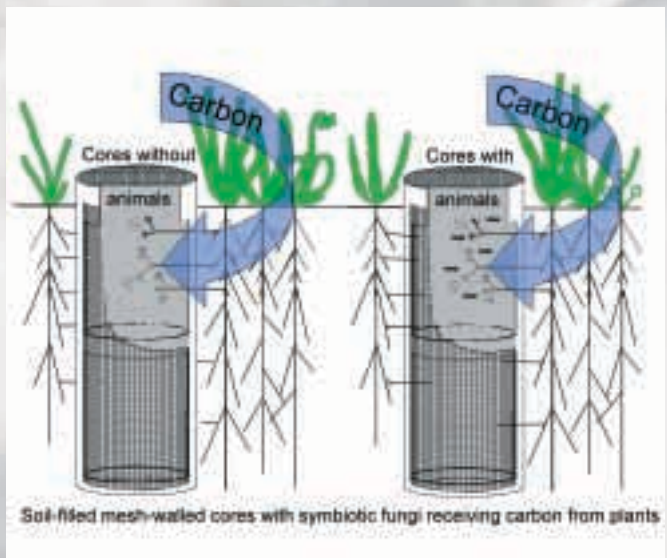
The world beneath our feet

Carbon flows and mycorrhizal fungi

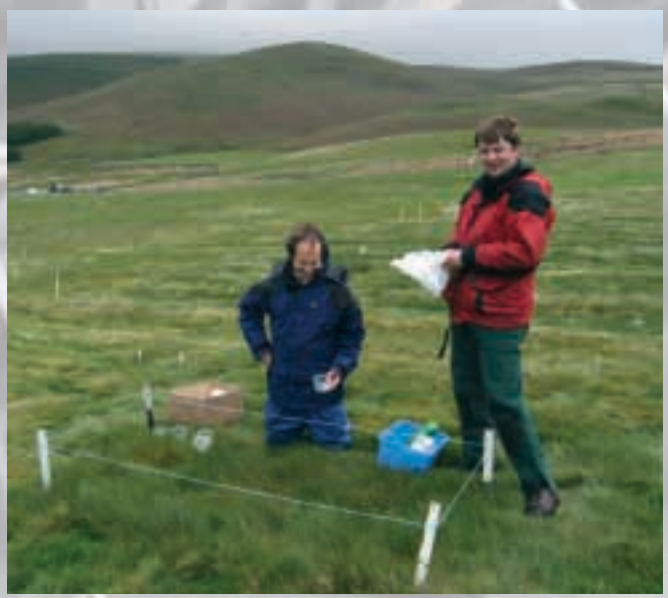
Arbuscular mycorrhizal fungi invade the roots of most grassland plants to form a mutually beneficial relationship. The fungi obtain carbon (sugars) from roots, and in return provide the plants with nutrients absorbed from soil through extensive networks of filaments (mycelia). There are up to 100 kilometres of mycorrhizal mycelium per kilogramme of soil.

We developed ways to measure, for the first time in the field, carbon flowing from plant roots to symbiotic soil fungi. We inserted mesh-walled soil cores into field plots. The mesh allowed the fungi to grow into the core from the surrounding soil, whilst excluding plant roots. By supplying the surrounding plants with heavy carbon (^{13}C) we could trace carbon flowing from plant roots through the mycorrhizal mycelium in the cores. Twisting some of the cores severed their mycorrhizal hyphal links to roots, giving us appropriate controls.

Nearly 10% of the total carbon fixed by grassland plants is allocated to the mycorrhizal fungal mycelium outside the roots. This transfer occurs much faster than is usually recognised – most passes to the fungus within 24 hours. Adding lime to grassland increased mycorrhizal colonisation of roots, the amounts of carbon fixed by plants, and amounts allocated to fine roots and mycorrhizal mycelium.



Soil-filled mesh-walled cores with symbiotic fungi receiving carbon from plants



We also used carbon isotope tracers to determine the effects of different numbers and species of springtails (both singly and in mixtures) on the amounts of carbon passing through mycorrhizal mycelium. Many springtails eat fungi, and they are amongst the most abundant of soil animals. Our work showed they reduced carbon flow through mycorrhizal networks by a third.

Models of carbon flowing from grassland plants to soil assume only root exudation and cell death are important. We have confirmed the importance of mycorrhizal fungi, and provided effective new methods for their study.

Further information

You can find out more by contacting Jonathan Leake, J.R.Leake@sheffield.ac.uk and Dave Johnson, D.Johnson@abdn.ac.uk

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The world beneath our feet

A model of soil biodiversity

We have developed a model that simulates tracking carbon through the soil community, allowing scientists to quantify research outputs into a coherent picture of diversity and function.

The model assumes that the biomass of each functional group (roots, prostigmatic mites, earthworms, etc.) is constant, i.e. inputs balance outputs. By enforcing this balance across a food web, and taking account of inefficiencies and extrinsic death rates, the model can calculate the carbon flows between groups. With this information we can then simulate applying a carbon isotope (^{13}C) to the soil and covering plants, tracking changes in ^{13}C concentration as it is transferred from producers to consumers and recyclers.

The model's software is intuitive and user-friendly. The user can manipulate the food web directly, using the mouse to add new groups or links between groups, and to change parameter values. The model's output graphically predicts the changing ^{13}C signal in the various groups over time, and the user can export these values to allow more detailed investigation.

The model allows experimentalists to infer food web structure from their data. For example, if data show a strong peak in ^{13}C signal in enchytraeid worms on day three, but the software predicts a small peak on day 14, then the user can edit the food web (e.g. via a direct link from roots to enchytraeids) until its predictions more closely match the observations. The user can then validate the resulting food web against other experimental data, and possibly use it to help focus future experimental effort.

We are developing and refining the model, for example to take into account the importance of spatial variation and connectivity in soil systems. We are also developing models to help understand how population fluctuations might distort ^{13}C signals.

For a copy of the modelling software please visit the Soil Biodiversity Programme web site, http://soilbio.nerc.ac.uk, for more information, or contact the Programme Manager:

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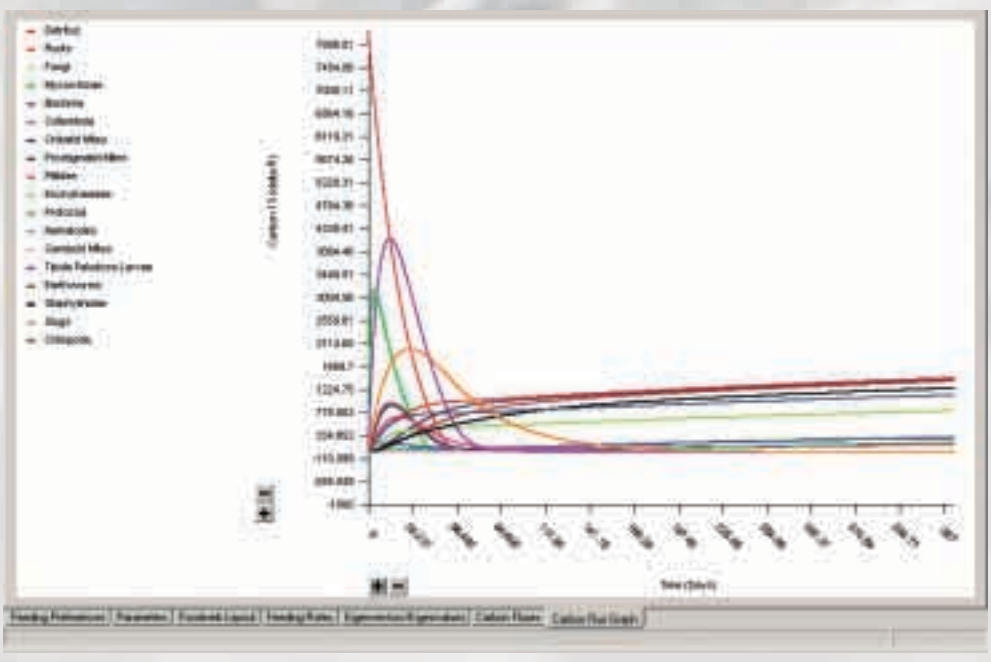

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The world beneath our feet

The Sourhope research site

The Soil Biodiversity Programme chose Sourhope Research Station for its field research. The name Sourhope (pronounced 'Sirrup') is said to mean 'the valley of sour pastures'. The site is in the Scottish Borders, 15 miles south of Kelso at the head of the Bowmont valley. There has been farming at Sourhope since the 14th century. On the western slopes of Cheviot, the land rises from 213m to 605m. Annual rainfall is 1015mm (10 year mean). The research station now comprises two working farms, of 940ha and 179ha respectively. Sourhope is managed by the Macaulay Institute, based in Aberdeen.

Soils

The soils developed from Old Red Sandstone Age andesitic lavas that were picked up and deposited by glaciers. Acid brown forest soils characterise the lower slopes. More acid peaty podzol soils and peaty gleys occur at higher elevations with small areas of deep peat on hill summits. Steep slopes have stony skeletal soils.

The soils at the programme's research site have been intensively studied. Researchers have characterised five soil profiles on the site, and recorded a range of chemical determinands for samples taken across the site, including nitrogen and carbon content, moisture loss and acidity.

Vegetation

Sourhope has rough pastures dominated by *Agrostis* and *Festuca* grasses, associated with bracken of varying intensity. There are also grass heaths dominated by *Molinia* and *Nardus* grasses. The research site is representative of mid-altitude upland grasslands on base-poor, damp, mineral soils. *Agrostis capillaris* is the dominant grass. The most closely matching National Vegetation Classification (NVC) community, which has been assigned to each plot, as well as the site as a whole, is U4d. This classification describes the site as a *Festuca ovina-Agrostis capillaris-Galium saxatile* grassland, *Luzula multiflora-Rhytidiadelphus loreus* subcommunity.

The programme surveyed the vegetation at the research site annually from 1998 until 2003. All soil and vegetation survey data for the site are freely available on the Soil Biodiversity Programme web site http://soilbio.nerc.ac.uk/.

Livestock

A large flock of sheep graze the research station's rough pastures. A herd of beef cattle control the sward height, and a herd of goats are kept for cashmere wool.

Research facilities
Visiting scientists can use the station's offices and laboratories. The laboratories are equipped with ovens and freezers, and computers are linked to the main Macaulay server. Self-catering hostel accommodation is available on site.

The Macaulay Institute is maintaining the Soil Biodiversity Programme's study site until November 2006, three years longer than originally planned. This is to enable scientists to use the facilities there, and build on the programme's work. The advantages of using the site for soil ecology research include:

- The site is fenced to prevent entry by grazers.
- The grass is regularly mown to simulate grazing.
- The treatments (lime, nitrogen, nitrogen + lime, and biocide) are still being applied to the randomised treatment blocks.
- Past research at the site is well-documented, and there are plenty of usable 50 x 50 cm cells.
- Meteorological data, collected by an automatic weather station, are available to anyone using the site.
- The site has been intensively studied in the Programme, and much of the data are freely available to other researchers.
- Work could also be carried out on other parts of the research farm, with the approval of the Macaulay Institute. A large amount of research has been conducted on the farm, particularly into grazing, sustainable management and alternative farm enterprises.
- Sourhope was one of the research sites in the SEERAD-funded Micronet programme on soil microbial ecology.
- This is undoubtedly the best-understood piece of soil in the world, at least in terms of soil biodiversity, and how the soil ecosystem functions.
- Sourhope is also an Environmental Change Network (ECN) long-term environmental monitoring site, and a large amount of data, including physical, chemical and biological measurements, is available for the site. For more information visit www.ecn.ac.uk.

Using Sourhope Research Station
If you would like to conduct research at Sourhope, please contact the following:

For further information about the site:

Gordon Common
Site Manager
Macaulay Institute
Sourhope Research Station
Yetholm
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For further information about the NERC Soil Biodiversity Programme:

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