MICROBIAL INDICATORS OF BELOW-GROUND REGENERATION OF CUT-OVER PEATLANDS

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INTRODUCTION

Peatlands cover approximately 20% of the Northern hemisphere and have been estimated to harbour up to 30% of the global reserves of soil carbon. Centuries of peatland drainage and peat extraction for fuel and other uses have resulted in destruction of over 90% of some countries' peatland areas.

Restoration of cut-over peatlands to their function as carbon sinks has obvious implications for the global carbon budget. Naturally restoring peatlands can, under optimal conditions, sustain re-colonization by bog plant species after a short number of years and function once more as carbon sinks. The status of the below-ground recovery of peatland functioning and microbial diversity, however, is largely unknown.

Figure 1: Locations of RECIPE regenerating peatland sites

Table 1. RECIPE peatland site locations and vegetation gradients

Site descriptor	Location	Time (y) since abandonment	Vegetation
SC_A	Middlemuir Moss, UK	< 5	Bare peat
SC_B	Middlemuir Moss, UK	5-10	*Sphagnum fallax*(> 95%)
SC_C	Middlemuir Moss, UK	5-10	*Eriophorum angustifolium* (> 70%), *E. vaginatum* (5-10%), *Sp. fallax* (15-20%)
SC_D	Middlemuir Moss, UK	>50	*Sphagnum* spp. (e.g. *palustre, capillifolium, fallax*; >80%), *Mollinia* spp.; other mosses
FB_A	Baupte peatland, France	5-10	*Bare*
FB_B	Baupte peatland, France	5-10	*Eriophorum vaginatum* (10-20 %)
FR_A	Russey, France	5-10	Bare peat
FR_B	Russey, France	5-10	*S. fallax, E. angustifolium, E. vaginatum* (rare)
FR_C	Russey, France	>50	*S. fallax, E. angustifolium, E. vaginatum, Calluna vulgaris*
CH_A	La Chaux d'Abel, Switzerland	5-10	*S. fallax (discontinuous), Polytrichum strictum, P. commune, E. vaginatum, Potentilla erecta*
CH_B	La Chaux d'Abel, Switzerland	Intermediate	Intermediate
CH_C	La Chaux d'Abel, Switzerland	>40	*S. fallax (continuous), P. strictum, P. commune, E. vaginatum, Vaccinium spp.*
FI_A	Aitoneva, Finland	10	*Eriophorum vaginatum*, wet
FI_B	Aitoneva, Finland	10	*Eriophorum vaginatum*, dry
FI_C	Aitoneva, Finland	10	*Carex rostrata*, wet
FI_D	Aitoneva, Finland	10	*Sphagnum fallax* (+others), wet
FI_E	Aitoneva, Finland	10	Bare peat

APPROACH & HYPOTHESIS

We investigated both the diversity of fungal communities (as primary degraders of plant litter) and the functional diversity of peat microbial communities at five European cut-over peatland sites (Figure 1) with gradients of natural regeneration (Table 1). The investigation focused on whether, as has been proposed recently[1], the microbial community structure in restored peatlands is slower to recover than the vegetation.

METHODS

Fungal diversity was assessed by PCR amplification of a fungal rDNA ITS fragment[2] and subsequent analysis by denaturing gradient gel electrophoresis (DGGE). DGGE gels were analysed by binary bandmatching using GelCompar II software following silverstaining, scanning and digitisation. Gel-to-gel variability was assessed using a marker ITS fragment obtained from an organic soil. Functional diversity, also commonly referred to as the community level physiological profile (CLPP), was assessed using a variation of the MicroResp™ procedure[3]. Samples (300 mg) were weighed into individual wells of 96-well deepwell plates and amended with 15 different 14-C labelled carbon sources prior to 48 h incubation at 25°C. Detected 14-CO_2 was converted to % mineralised CO_2. CLPP and DGGE data were analysed by multivariate statistics. Canonical variate analysis (CVA) was applied using grouping according to country, horizon and vegetation type. Peat humification was assessed by Fourier Transform Infra-Red spectroscopy und used to differentiate horizons.

RESULTS & DISCUSSION

Fungal populations as assessed by DGGE of fungal ITS fragments changed visibly through peat horizons (Figure 2). CVA showed that differences in peat fungal populations were mostly discriminated by grouping according to country of origin (Figure 3A). Reasonable discrimination was also found between horizon depths (Figure 3B) with the undisturbed catotelm samples being most distinct.

Carbon substrate utilisation patterns in CLPP were also different in different peat horizons (Figure 4). Analysis by CVA showed that, for CLPP, best separation was also achieved with country of origin as grouping factor (Figure 5A). Better separation than for the fungal populations also occurred using grouping by horizon depth (Figure 5B).

Although fungal and functional diversity in the regenerating peat sites were most affected by country-specific differences, it was possible to visualise shifts according to peat humification or vegetation by different bog plant species. An example for the Finnish sites is shown below (Figure 6). The spread and direction of change of the CLPP pattern can be observed especially in the plant-affected peat layers.

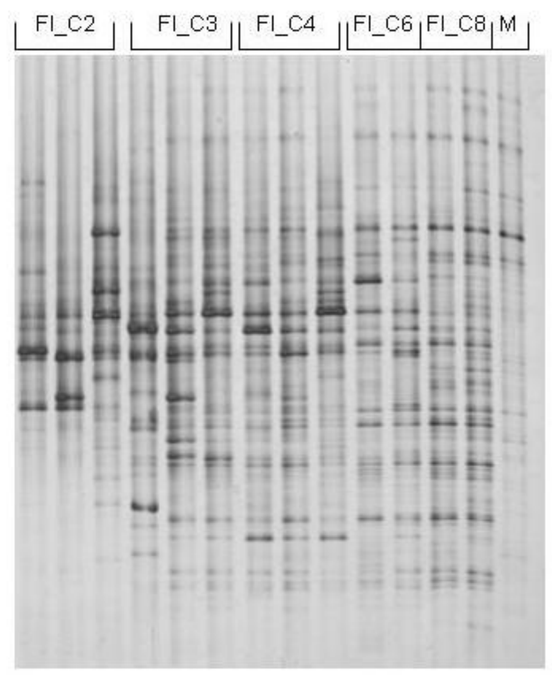

Figure 2: Example of fungal ITS DGGE profiles for Finnish site C. Numbers designate different horizons in order of depth (2 = plant litter; 3 = plant tissue; 4 = decaying plant tissue; 6 = oxidised catotelm peat; 8 = undisturbed catotelm peat). M is a DGGE marker originating from an organic soil.

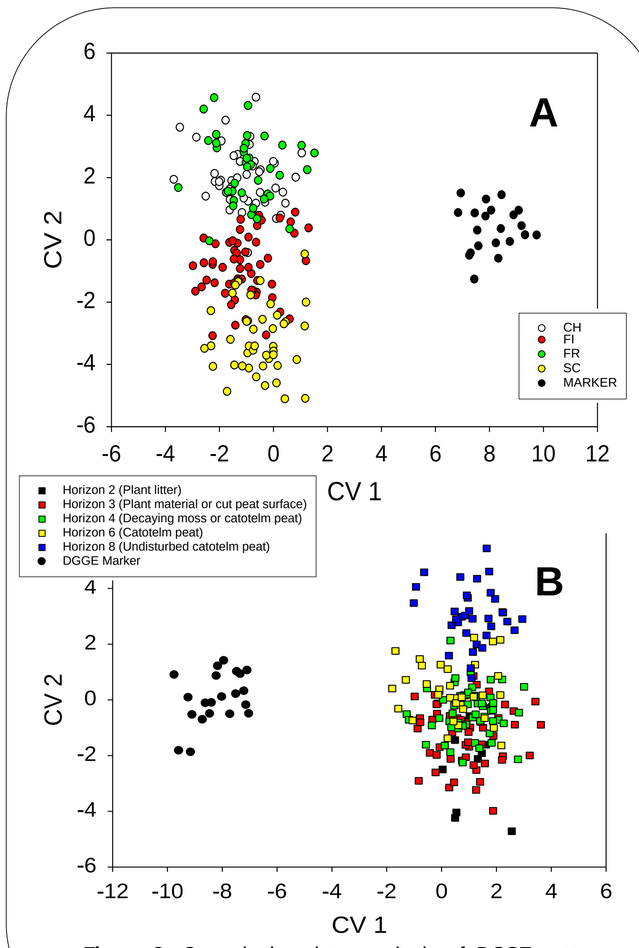

Figure 3: Canonical variate analysis of DGGE pattern differences according to country of origin (Fig. A) or peat horizon (Fig. B)

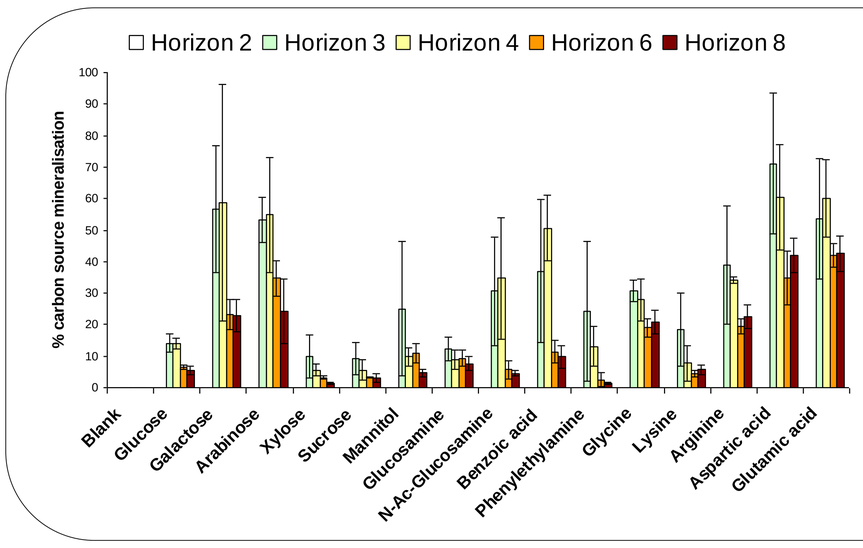

Figure 4: Example of a CLPP profile for Finnish site C. See legend for Figure 2 for explanation of the horizons. There was insufficient material of Horizon 2 for analysis. Error bars represent SD of $n = 3$.

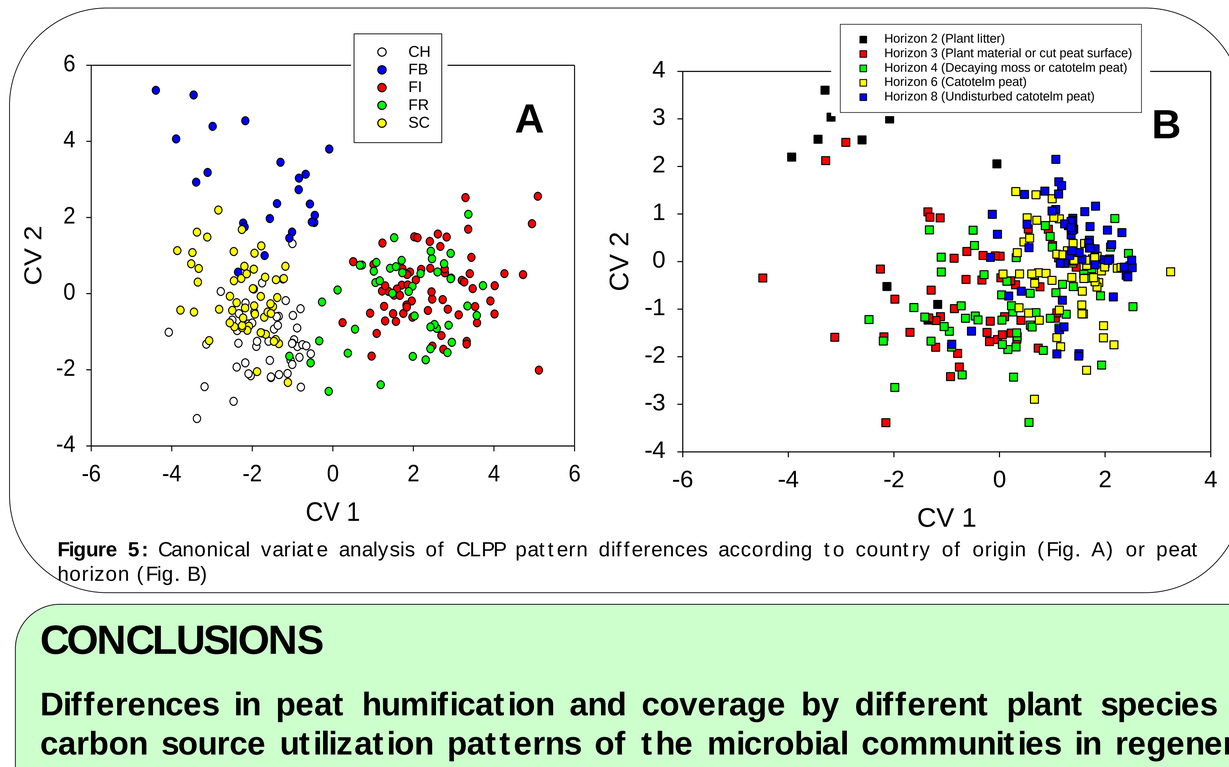

Figure 5: Canonical variate analysis of CLPP pattern differences according to country of origin (Fig. A) or peat horizon (Fig. B)

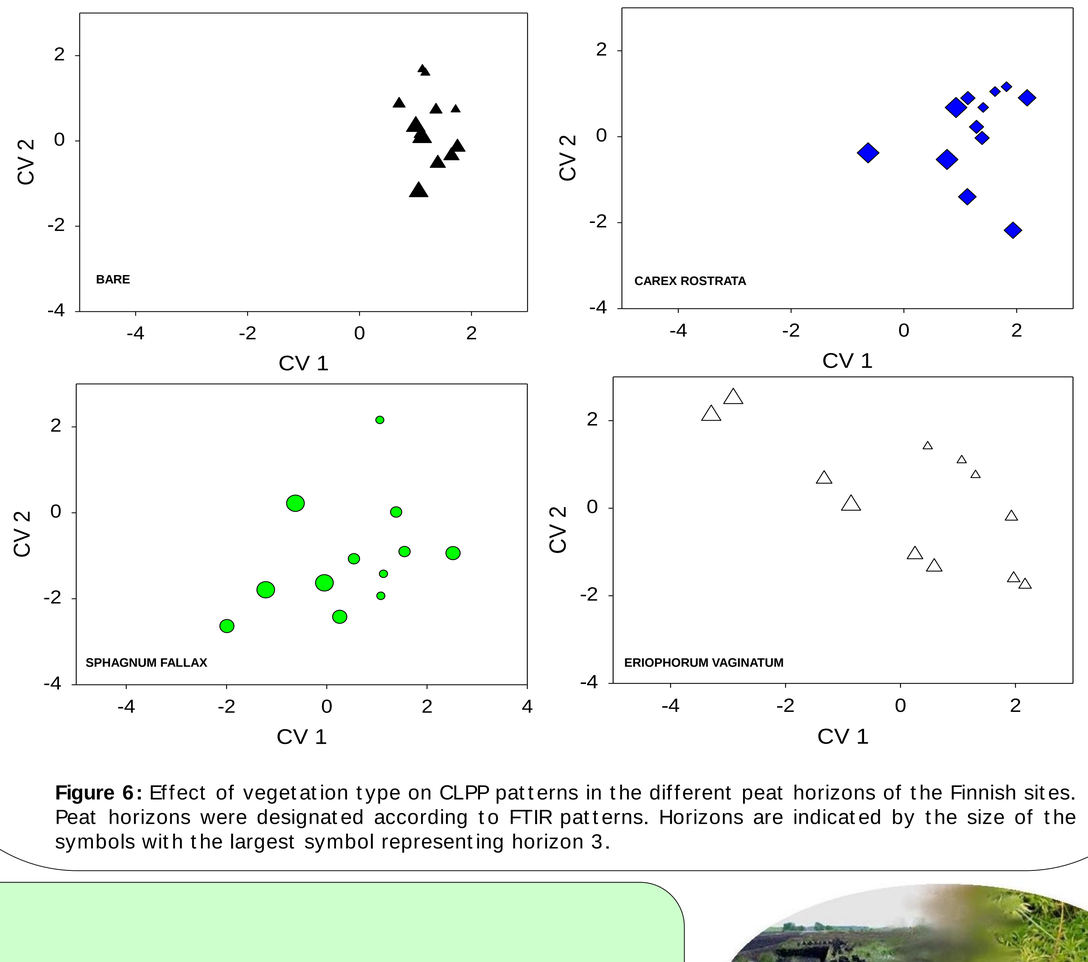

Figure 6: Effect of vegetation type on CLPP patterns in the different peat horizons of the Finnish sites. Peat horizons were designated according to FTIR patterns. Horizons are indicated by the size of the symbols with the largest symbol representing horizon 3.

CONCLUSIONS

Differences in peat humification and coverage by different plant species influence both the fungal communities and the carbon source utilization patterns of the microbial communities in regenerating peatlands although peatland location (i.e. country of origin) determines the underlying patterns. These results do suggest that functional recovery of the microbial community, at least, in regenerating peatlands is slower than plant community recovery.

http:// www.macaulay.ac.uk/ RECIPE

1 Francez *et al.*, European Journal of Soil Science **36:** 161 (2000)
2 Anderson *et al.*, Environmental Microbiology **5:**1121 (2004)
3 Campbell *et al.* Applied and Environmental Microbiology **69**:3593 (2003)

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