

DOES THE REGENERATION OF CUT-OVER PEATLANDS RESTORE BELOW-GROUND FUNCTIONS AND DIVERSITY?

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RECIPE (Reconciling commercial exploitation of peat with biodiversity in peatland ecosystems) • email: r.artz@macaulay.ac.uk

INTRODUCTION: Abandoned and restored peatlands can sustain re-colonisation by typical peatland vegetation and are able to regain functioning as net carbon sinks. An important part of the carbon balance equation is the level of soil respiration, which is the sum of the metabolic turnover of labile plant-derived carbon and the decomposition of structural plant material (e.g. litter and root turnover). Within the RECIPE project (a three year EU funded initiative) we investigated various measures of the above- and below-ground functions and diversity of the prevailing communities with a view to establish whether succession via natural regeneration processes results in the restoration of the ecosystem functions of peatlands.

METHODS: To investigate the below-ground community responses we analysed a) community level physiological profiles (CLPP) using multiple substrate respiration assays with typical peat labile carbon sources (Figure 1), and the composition of the fungal community (by denaturing gradient gel electrophoresis of fragments of the ribosomal internal transcribed spacer, Figure 2) in peatlands at various stages of restoration within five European sites. Table 1 shows the experimental sites and the plant community structure in each of the successional stages within these gradients of regeneration.

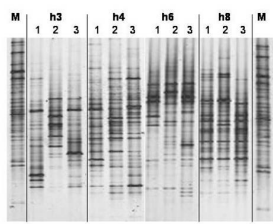


Figure 1: MicroResp™ measures the community level physiological profile of the microbial community as the response to various additions of chemically different types of radiolabelled carbon as respired C14-CD₂ trapped in alkaline.

Figure 2: Example of the effect of depth (h3 = surface, to, h8 = 45 cm) on the fungal community structure in previously cut-over peat.

Peatland	Location elevation	Site code	Dominant vegetation, listed in order of abundance	Plant community age (yr)	Plant cover (%)	Regeneration stage ^a
Chaux d'Abel, Switzerland	47°10' N, 6°57' E, 1040 m	A	<i>Sphagnum fallax</i> , <i>Polytrichum strictum</i> , <i>P. commune</i> , <i>Eriophorum</i> spp.	>29	≥100	E
		B	Same species, intermediate between A and C	>42	≥100	A
		C	<i>S. fallax</i> , <i>P. strictum</i> , <i>E. eriophorum vaginatum</i> , <i>Vaccinium</i> spp.	>21	≥100	A
		D	<i>S. magellanicum</i> , <i>S. fuscum</i> , <i>S. rubellum</i> , <i>Vaccinium</i> spp. (no survey data)	Intact	≥100	I
Le Russey, France	47°18' N, 6°79' E, 867m	A	Bare peat	>4	0	B
		B	<i>S. fallax</i> , <i>E. angustifolium</i> , <i>E. vaginatum</i> (rare)	>22	≥100	E
		C	<i>S. fallax</i> , <i>E. angustifolium</i> , <i>E. vaginatum</i> , <i>Calluna</i> <i>vulgaris</i>	>21	≥100	E
		D	ND (no survey data)	Intact	≥100	I
Middlemair Moss, United Kingdom	57°36' N, 2°9' W, 110m	A	Mostly bare, isolated <i>E. vaginatum</i> , <i>Campylopus</i> <i>imroflexus</i>	<5	5	B
		B	<i>S. cuspidatum</i> , <i>S. auriculatum</i> , <i>E. vaginatum</i>	5-10	≥100	E
		C	<i>E. angustifolium</i> , <i>S. auriculatum</i> , <i>S. cuspidatum</i>	5-10	≥100	E
		D	<i>Sphagnum</i> spp., <i>C. vulgaris</i> , <i>Deschampsia flexuosa</i>	>50	≥100	A
Aitonvea, Finland	62°12' N, 23°18' E, 156 m	A	<i>Eriophorum vaginatum</i>	10	80	E
		B	<i>Eriophorum vaginatum</i>	10	24	E
		C	<i>Carex rostrata</i>	10	42	E
		D	<i>C. rostrata</i> , <i>S. fallax</i>	10	≥100	E
		E	Bare peat, no vegetation	10	0	B
Baupte, France	49°17' N, 1°21' W, 20 m	A	Bare peat, no vegetation	5-10	0	B
		B	<i>E. angustifolium</i> , <i>Hypnaceae</i>	5-10	79	E

^a B = bare, E = early, A = advanced, I = Intact. ^b ND = not determined. ^c Minimum age was determined by tree ring analyses on woody species at CH and FR, and using historical accounts at other sites.

RESULTS: CLPP were strongly dependent on the peat horizon used, suggesting both a microbial biomass effect and adaptation of the microbial communities in these horizons to the prevailing substrate composition. We showed in earlier experiments¹ that a significant proportion of the horizon effect can be explained by a simple proxy measurement of the level of decomposition of the sample using Fourier-transform infrared spectroscopy. Here², we found a significant influence of vascular plant species in RDA, suggesting that the quality and quantity of rhizoexudate are important in determining the catabolic potential of the soil microbial community (Figure 3). Molecular analysis of the composition of the fungal communities showed significant differences between the stages of vegetational succession (Table 2) and further sequence analysis of selected clones from one of the European sites identified a number of fungal functional types involved in the cycling of carbon such as species known to form mycorrhiza with ericoid hosts and fungi involved in the decomposition of plant litter in permanently waterlogged environments³.

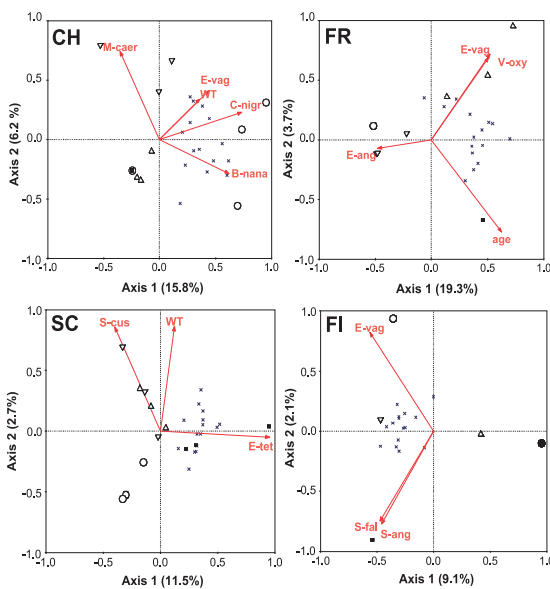


Figure 3: Ordination plot of the effects of alternative explanatory variables in RDA on CLPP data from each individual peatlands at the 'site' level. Effects of environmental variables which contribute significantly to explaining CLPP variance are shown as projected arrows. Sites shown are as described in Table 1 for each peatland, respectively, and are depicted as follows in the graphs: Site A (open circles), Site B (downward open triangles), Site C (upward open triangles), Site D (filled squares) and Site E (FI only, filled circles). Loadings of substrates are shown as crosses. N.B. Missing values in the environmental dataset lead to averaging of the CLPP data for such data (e.g. vegetation at FI reported as averages only, see Table 1; hence only one corresponding CLPP point).

Peatland	Stratum tested	Variance explained (%) ^a
CH	Site	13.5 ***
	Vegetation similarity ^b	15.6 ***
	Core	7.1 ***
	Horizon depth	14.3 ***
	Total variance explained	34.9
FR	Site	19.3 ***
	Vegetation similarity ^b	22.7 ***
	Core	6.5 ***
	Horizon depth	5.0 NS
	Total variance explained	25.8
SC	Site	12.6 ***
	Vegetation similarity ^b	14.1 ***
	Core	4.8 NS
	Horizon depth	6.0 NS
	Total variance explained	12.6
FI	Site	25.0 ***
	Vegetation similarity ^b	25.0 ***
	Core	4.6 **
	Horizon depth	6.9 *
	Total variance explained	36.5
FB	Site	10.5 ***
	Vegetation similarity ^b	19.3 ***
	Core	11.2 NS
	Horizon depth	12.5 NS
	Total variance explained	10.5

^a Estimated using MonteCarlo permutation testing (999 permutations) in RDA within blocks defined by the co-variables: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$ and NS not significant. ^b The first 4 principal component scores, which always explained >75% of variance, were used as factors in RDA.

Table 2: Variance decomposition of the effects of 'site', 'core' and 'horizon depth' and alternative 'site' factors on the fungal community structure by (ITS DGGE) at the smaller spatial scale of individual peatlands.

DISCUSSION & CONCLUSION:

All analyses of below-ground biological diversity and function showed an encouraging return to the composition observed in intact systems, or at least significant shifts towards the characteristics of sites in advanced stages of regeneration (Figure 4). This suggests that the below-ground functioning and microbial diversity of regenerating peatlands is also being restored, and is an encouraging sign that ecosystem function, in the sense of carbon sequestration, may recover with the revegetation of cut-over peatlands.

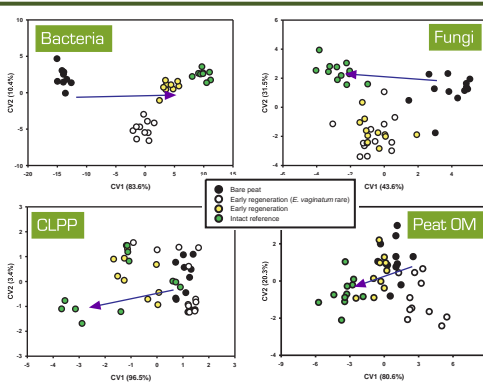


Figure 4: Example of the successional trajectories of various measures of below-ground regeneration in the Le Russey peatland (FR) as assessed using discriminant analysis following variance-reducing PCA/PCA. Peat organic matter (OM) composition was measured by FTIR spectroscopy.

References: 1. Artz, R.R.E., Chapman, S.J. and Campbell, C.D. (2006) Substrate utilisation profiles of microbial communities in peat: are depth-dependent and correlate with whole soil FTIR profiles. *Soil Biology and Biochemistry*, 38, 2958-2962. 2. Artz, R.R.E., Chapman, S.J., Siegenthaler, A., Bortoluzzi, E., Yli-Petäys, M. and Frances, A.-J. (Submitted) Functional microbial diversity in European remediated cut-over peatlands is directed by labile carbon. 3. Artz, R.R.E., Anderson, I.C., Chapman, S.J., Hign, A., Schloter, M., Potts, J. and Campbell, C.D. (2007) Changes in fungal community composition in response to vegetational succession during the natural regeneration of cut-over peatlands. *Microbial Ecology* (in press).