



**Microbial carbon and nitrogen in abandoned peatlands after peat extraction: patterns of response to regeneration age and plant community at a European scale**

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1 **Microbial carbon and nitrogen in abandoned peatlands after peat**  
2 **extraction: patterns of response to regeneration age and plant**  
3 **community at a European scale**

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## 26 **Summary**

- 27 **1.** Microbial variables are increasingly used to study effects of disturbance on  
28 ecosystem functioning or success of recovery processes.
- 29 **2.** The aim of this work was to assess microbial biomass carbon (C) and nitrogen  
30 (N) and microbial activity as indicators of cut-over peatland regeneration at a  
31 European scale. We hypothesised i) microbial C-N pools and aerobic and  
32 anaerobic basal respiration would increase with regeneration age; ii) plant  
33 community structure would act as a driving force on microbial variables.
- 34 **3.** Fifteen regeneration stages of different ages and plant recolonization over a  
35 chronosequence of 50 years, were investigated. Microbial biomass C and N,  
36 basal aerobic and anaerobic respiration, metabolic microbial quotient (MMQ)  
37 and soluble organic carbon mineralization rate (C-MR) were measured in  
38 surface and deep peat.
- 39 **4.** Microbial biomass dynamics vs regeneration age in the surface peat fitted to a  
40 logistic function, while the microbial C:N ratio was best described by a  
41 gamma function. Other variables were fitted to exponential functions, except  
42 aerobic basal respiration which linearly increased over the chronosequence.
- 43 **5.** Plant species richness positively correlated with microbial biomass C,  
44 anaerobic basal respiration and C-MR in the surface peat. Botanical  
45 composition impacted microbial variables in relation to frequencies of moss  
46 and/or ericaceous shrubs. The moss:vascular plant cover ratio positively  
47 correlated with microbial biomass C and C-MR under anaerobiosis while  
48 MMQ significantly decreased with increasing ericaceous:vascular plant cover  
49 ratio, both under aerobiosis and anaerobiosis.

50 **6. *Synthesis and applications.*** Results clearly showed i) patterns of response to  
51 age of abandonment after peat extraction and ii) a plant-community mediated  
52 control on peat microbial pools, suggesting changes in ecosystem dynamics  
53 over the succession. The described dynamics of microbial variables over the  
54 succession were fitted to relatively simple models that could serve as  
55 references in the study of peatland regeneration. We concluded that microbial  
56 biomass and basal respiration are among the most efficient variables which  
57 could be used as a set of ecological indicators of regeneration dynamics. This  
58 should be carried out together with an analysis of the plant community  
59 structure, which is easily described by indices integrating the frequencies of  
60 key-stone taxa.

61

62 *Key-words:* microbial succession, ecosystem dynamics, ecological indicator, basal  
63 respiration, microbial metabolic quotient, carbon mineralization rate, aerobiosis vs  
64 anaerobiosis, RECIPE

65

## 65 Introduction

66 Microbial biomass is an important pool in the soil and the interest of estimating it  
67 in peat is related to its function in recycling elements, especially in oligotrophic  
68 *Sphagnum* mires in which the decomposition processes are slowed down by  
69 acidity, hydromorphy (leading to anaerobiosis) and poor-nutrient inputs (Clymo  
70 1983). In these ecosystems peat accumulates at an average rate of 0.10-0.15 yr<sup>-1</sup>  
71 which means that 85-90 % of the annual organic matter produced by plants  
72 decayed (Clymo 1984; Francez & Vasander 1995) and the study of the fate of  
73 elements such as N in peat showed mineralization takes place in acrotelm despite  
74 the important retention of nutrients by *Sphagnum* carpet at the mire surface (Li &  
75 Vitt 1997; Francez & Loiseau 1999).

76 Microbial biomass carbon (C) pools in *Sphagnum* fens and bogs, when  
77 estimated with the fumigation-extraction (FE) method range from 0.5 to 14 mg g  
78 dry peat (DP)<sup>-1</sup>, depending on peatland nutrient status, season, depth, or degree of  
79 disturbance (Williams & Silcock 1997; Baum, Leinweber & Schlichting 2003;  
80 Potila & Sarjala 2004; Andersen, Francez & Rochefort 2006). Lower values are  
81 generally registered with the substrate-induced respiration (SIR) method (Brake,  
82 Hoper & Joergensen 1999, Andersen, Francez & Rochefort 2006). Microbial  
83 biomass nitrogen (N) in peat would range from about 200 to 500 µg N g DP<sup>-1</sup>  
84 (Williams & Silcock 1997; Francez, Josselin & Gogo 2000; Baum, Leinweber &  
85 Schlichting 2003).

86 Microbial activity and nutrient cycling in mire ecosystems are controlled by  
87 temperature (Williams & Crawford 1983), oxic/anoxic conditions (Scanlon &  
88 Moore 2000), water table (Blodeau & Moore, 2003) and nutrient status  
89 (Updegraff *et al.* 1995; Chapin *et al.* 2003; Potila & Sarjala 2004), as main factors

90 acting drastically and with synergy when anthropogenic interventions impact mire  
91 dynamics by drainage, peat cutting or fertilization.

92 Peat extraction strongly disturbs the peat microbial pool. Croft, Rochefort and  
93 Beauchamp (2001) demonstrated a negative effect of peat harvesting by vacuum  
94 technique on microbial biomass C while ammonification significantly increased.  
95 However, abandoned peatlands after extraction function as a C source to the  
96 atmosphere because of the lack of vegetation and ongoing CO<sub>2</sub> emissions released  
97 by the microbial activity in peat, though the low nutrient quality of peat decreases  
98 the potential for C mineralization (Waddington, Rotenberg & Warren 2001).

99 Abandoned mined peatlands offer poor conditions for regeneration due to bare  
100 peat surfaces with unfavourable hydrology, wind erosion and high temperature  
101 fluctuations (Campbell, Lavoie & Rochefort 2002; Chapman *et al.* 2003).  
102 Nevertheless, there are many examples throughout Europe and North America  
103 demonstrating that spontaneous recolonization by bog plants is possible (Lavoie *et*  
104 *al.* 2003), when satisfactory microclimatic conditions (Grosvernier, Matthey &  
105 Buttler 1995) and/or substrate quality (Salonen 1994) occur. While vegetal  
106 colonization of bare peat is well documented and monitored (see for instance,  
107 Robert, Rochefort & Garneau 1999; Tuittila *et al.* 2000), little is known about the  
108 microbial communities developing concomitantly. Data on microbial successions  
109 in peatlands are very scarce (Thormann, Currah & Bayley 2003) while patterns of  
110 litter decomposition and gas emissions are rather well-documented (Aerts,  
111 Verhoeven & Whigham 1999; Blodeau 2002; Vasander & Kettunen 2006).  
112 Dickinson & Dooley (1967) emphasized the very limited microbial colonization  
113 of cutover peat, even after 10 years since abandonment while Maire (1983)

114 demonstrated short-term changes in microbial colonization of sterilized eutrophic  
115 peat and interpreted the dynamics as a succession of r and K strategist species.

116 The role of living vegetation on soil processes has received more and more  
117 attention in mires and wetlands and the importance of interactions between plants  
118 and microbes have now been recognized in peat soils. Root activities regulate  
119 microbial metabolic pathway such as Fe(III) reduction (Neubauer *et al.* 2005) or  
120 microbial activity by transfers of C-molecules such as acetate into the rhizosphere,  
121 controlling partly methanogenesis and methanotrophy (Watson *et al.* 1997; Ström  
122 *et al.* 2003). The influence of botanical composition on microbial variables had  
123 also been recognized. For instance, Chapman, Campbell & Puri (2003) noted a  
124 decreasing C biomass with tree extension while Fisk, Ruether & Yavitt (2003)  
125 registered a higher microbial activity in shrub-*Sphagnum* dominated communities  
126 compared with sedge-dominated sites.

127 Microbial variables have also been recognized as practical indicators of  
128 peatland ecosystem functioning change, being more sensitive than physico-  
129 chemical properties (Chapman, Campbell & Puri 2003) and integrative of  
130 restoration processes, even if a shift between vegetal and microbial recovery  
131 processes persists some years following revegetation management (Andersen,  
132 Francez & Rochefort 2006).

133 However, little information is available on the recovery of biomass and  
134 activity during microbial succession of abandoned surface peat. The aims of this  
135 work were:

136 i) to evaluate the microbial biomass C and N and activity of the microbial  
137 communities of abandoned peatlands with different ages after peat cutting in  
138 Europe and to reveal patterns of response to regeneration age. This would allow

139 us to characterize ecosystem dynamics and transformations over secondary  
140 succession, from bare peat (low microbial biomass and activity) to later stages of  
141 recolonization by vegetation (higher biomass and activity) over a 50 year  
142 chronosequence;

143 ii) to demonstrate the plant-community mediated control on peat regeneration and  
144 associated microbial communities by assessing relations between microbial and  
145 vegetation variables (species richness, dominance index and plant cover ratios).

146 iii) to examine the suitability of microbial variables as potential tools in the  
147 assessment of peatland regeneration trends.

148

## 149 **Material and methods**

### 150 SITE DESCRIPTION

151 Five regenerating peatlands with different stages of plant recolonization were  
152 selected across Europe (Table 1). They were all derived from past peat extraction  
153 of initial raised-bogs and belong to the peatland grid system of the European  
154 programme RECIPE (Reconciling Commercial Exploitation of Peat with  
155 Biodiversity in Peatland Ecosystems).

156

### 157 EXPERIMENTAL DEVICE

158 We studied a series of 15 regeneration stages (= sites) that ranged in age from 3 to  
159 50 years following peat extraction (Table 2). The different sites were selected by  
160 taking into account the age of abandonment and plant composition in relation to  
161 peat-forming key-stone species i.e. *Sphagnum*, *Eriophorum angustifolium* and *E.*  
162 *vaginatum* which were abundant in every peatland, except in Baupte (FB). Sites



163 were more or less covered by vegetation and, in addition to the bare peat situation,  
164 we distinguished 8 plant communities (Table 2).

165 A common protocol of peat sampling was performed using the same kind of  
166 peat corer (Buttler, Grosvernier & Matthey 1998). A sample dispatching protocol  
167 to partners was established by separating aliquots of collected peat slices in order  
168 to carry out the different analysis. The work programme consisted of a set of  
169 microbial and chemical analyses, performed on the same peat cores extracted  
170 from the range of sites, at four depths: 0-5 cm and 5-10 cm (referred as surface  
171 peat) , 22.5-27.5 cm and 42.5-47.5 cm (called deep peat).

172 In each case, 3 plots per site were used as replicates and cores extracted from  
173 each site between October and December 2003.

174

## 175 MICROBIAL BIOMASS AND ACTIVITY

### 176 *C and N pools in the biomass*

177 Microbial biomass C and N were estimated on all peat samples with the  
178 fumigation-extraction method using a peat-modified protocol (Williams & Silcock  
179 1997; Andersen, Francez & Rochefort 2006).

180 Total soluble organic carbon and soluble organic nitrogen were extracted  
181 using 0.5M K<sub>2</sub>SO<sub>4</sub>. C content in the extract was determined using a 1010 TOC  
182 Analyser (OI Analytical). N was oxidized with potassium persulphate (Williams  
183 *et al.* 1995) and measured colorimetrically as NO<sub>2</sub><sup>-</sup> after reduction of NO<sub>3</sub><sup>-</sup> on a  
184 copper-cadmium column with a Bran+Luebbe analytical chain.

185

### 186 *Basal respiration in aerobiosis and anaerobiosis*

187 Basal respiration corresponding to CO<sub>2</sub> production in the dark at 20°C was  
188 measured during a 7 day experiment, carried out both under aerobic and anaerobic  
189 (under N<sub>2</sub> atmosphere) conditions. Twenty-five grams of fresh peat were  
190 incubated over 7 days in hermetically-sealed jars. Gas aliquots were collected  
191 after 1, 2, 3, 4 and 7 day incubation time, and analysed for CO<sub>2</sub> using a portable  
192 gas chromatograph (Chrompack micro GC-CP 2002) fitted with a TCD detector  
193 and a Poraplot Q column. The hourly rate of respiration was calculated as the  
194 mean of linear CO<sub>2</sub>-C production between 2 and 4 days.

195

#### 196 *Microbial ratios*

197 We calculated the microbial metabolic quotient (MMQ) or specific respiration  
198 (Insam & Haselwandter 1989; He *et al* 2003) as the ratio of basal respiration (μg  
199 C g DP<sup>-1</sup> h<sup>-1</sup>) divided by the microbial biomass C (μg C g DP<sup>-1</sup>) (Anderson 1994).

200 The soluble C-mineralization rate (C-MR) is equal to the daily ratio (d<sup>-1</sup>) of  
201 basal respiration divided by the stock of soluble organic C in the peat.

202

#### 203 *Units*

204 In order to compare our data to the literature and as the results expressed in  
205 concentration (μg g DP<sup>-1</sup>) were highly correlated to those expressed as stocks in  
206 peat (g L<sup>-1</sup>), we only present the results expressed in concentration units (μg g  
207 DP<sup>-1</sup>).

208

## 209 PLANT COMMUNITY CHARACTERIZATION

### 210 *Botanical composition*

211 Plant species richness and vegetation composition were recorded at the beginning  
212 of the experiment in July 2003 from 1×1 m quadrats in which plant cover (%) was  
213 estimated.

214

#### 215 *Vegetation indices*

216 Plant dominance was calculated using the Berger-Parker index (d) as follow:

$$217 \quad d = N_{max} : N \quad \text{eqn 1}$$

218 where  $N_{max}$  is the percentage cover of the most abundant species and  $N$  the sum  
219 of covers (%) of all species (Magurran 1988).

220 In order to characterize the plant communities in the different states of the  
221 chronosequence, two other ratios were calculated, a moss (m) and a shrub (e)  
222 index :

$$223 \quad m = \Sigma M : N \quad \text{eqn 2}$$

224 where  $\Sigma M$  is the percentage cover of the moss species and  $N$  as in eqn 1.

$$225 \quad e = \Sigma E : N \quad \text{eqn 3}$$

226 where  $\Sigma E$  is the percentage cover of Ericacea and  $N$  as in eqn 1.

227 These calculations were justified by the importance of these 2 groups of plants  
228 in peatland dynamics: *Sphagnum* species are found all over the mire succession,  
229 from open water to fen and bog, and *Polytrichum* species recolonize many  
230 disturbed surface peatlands (after peat extraction or fire) while the Ericacea  
231 (*Vaccinium*, *Calluna*, *Erica*) colonize *Sphagnum* lawns and hummocks (natural  
232 dynamics leading to raised-bogs) and, sometimes, bare peat surfaces.

233 In addition, we estimated the percentage of bare peat surface which was also  
234 used to separate sites. Then, we firstly distinguished plant communities with bare  
235 peat and secondly considered plants of second and third rank in abundance (%)

236 cover) in communities without bare peat. The codes of vegetation integrate these  
 237 2 points, for example SpBp means *Sphagnum* (Sp) dominant in a site with still  
 238 significant un-colonized bare peat (Bp) while SpEvVa means a first rank  
 239 dominance for *Sphagnum*, a 2<sup>nd</sup> one for *Eriophorum vaginatum* and a 3<sup>rd</sup> one for  
 240 *Vaccinium* (Table 3).

241

## 242 STATISTICAL AND REGRESSION ANALYSIS

243 Due to non-homogeneity of variances following transformations, non-parametric  
 244 Kruskal-Wallis analyses were performed to detect significant differences between  
 245 depths, regeneration ages and plant communities. Post-hoc pairwise comparisons  
 246 were used to identify differences when H value of the Kruskal-Wallis test was  
 247 significant at  $\alpha=0.05$ . The Mann-Whitney (Wilcoxon) W-test was used to  
 248 evaluate significant differences between aerobic and anaerobic conditions.  
 249 Spearman rank correlation coefficients were calculated to estimate the strength of  
 250 association between peat properties, vegetation indices, and microbial variables.  
 251 Statistical analyses were performed with STATGRAPHICS PLUS 2.1 software  
 252 (Manugistics Inc. 1995). Significance of the analyses was accepted at  $\alpha=0.05$ .

253 Depending on the microbial variable responses, time change data were fitted  
 254 to linear (aerobic basal respiration) or non linear regressions. Thus, we used the  
 255 following equations:

256 - exponential regressions expressed as:

$$257 \quad y = a e^{-bAge} \quad \text{eqn 4}$$

258 or

$$259 \quad y = a (1 - e^{-bAge}) + c \quad \text{eqn 5}$$

260 - gamma function:

261  $y = aAge^b e^{cAge^d} + f$  eqn 6

262 or logistic function :

263  $y = a / (1 + (a-b/b) \exp^{-cAge})$  eqn 7.

264 where y is the microbial variable, x is the time since abandonment (Age), a–f are  
265 fitted constants.

266 Non-linear regression analysis and fitting procedures were carried out with  
267 SYSTAT 10 (SPSS Inc 2000).

268

## 269 **Results**

### 270 MICROBIAL BIOMASS C AND N

271 Microbial biomass showed significant differences by all the considered factors i.e.  
272 depth, regeneration age and vegetation (Table 3).

273 Microbial biomass decreased with depth. In the surface peat layers (0-10 cm),  
274 microbial C and N biomass increased significantly from early to late-successional  
275 stages of regeneration and dynamics over time were best described by a logistic  
276 function. We registered a first phase (0-10 years) with no change, a second one of  
277 strong increasing (10-42 years) and a third one of stabilization. In the deep peat,  
278 despite time changes and higher microbial biomass at the intermediate stages, no  
279 satisfactory fit was obtained.

280 Microbial biomass in the surface peat layers also showed patterns of C and N  
281 pools with vegetation (Tables 3 & 4, Fig. 1). Lowest values were registered under  
282 plant communities characterized by incomplete cover of peat surface, whatever  
283 the dominant plant, and highest ones were observed as bare peat decreased and  
284 vegetation developed. Microbial C pool showed a significant positive correlation

285 with plant specific richness and increased significantly with increasing the moss  
286 index  $m$  (Table 4).

287 In the upper part of the peat, changes of microbial C:N ratio over time were  
288 significant and fitted to a gamma function (Fig. 1). The same trend was observed  
289 in deeper peat, values ranging from  $7.1 \pm 6.8$  to  $25.6 \pm 6.8$ .

290 Microbial biomass C and N negatively correlated with organic C:N ratio and S  
291 in the peat but we did not register any correlation between organic N and the  
292 microbial N pool (Table 4).

293

#### 294 BASAL RESPIRATION

295 Basal respiration showed significant differences by all the considered factors,  
296 except aerobic respiration by depth (Table 3). Basal respiration was significantly  
297 higher under aerobiosis compared to anaerobiosis, pooling sites and depths  
298 ( $W=7685$ ,  $P<0.001$ ,  $n=164$ ).

299 Basal respiration showed significant changes over time after abandonment,  
300 considering the mean peat profile but the best data fittings were described in the  
301 surface peat layers (0-10 cm) by exponential (aerobiosis) or linear regression  
302 models (anaerobiosis) (Fig. 2).

303 In the surface peat, most of plant communities with *Sphagnum* did not show  
304 any significant difference between aerobiosis and anaerobiosis. In sites with bare  
305 peat or incomplete plant cover, aerobic respiration was significantly higher than  
306 anaerobic respiration (Table 5 and Fig. 2). Only basal respiration under  
307 anaerobiosis correlated with plant species richness and bare peat surface (Table  
308 5). No relation with other vegetation indices was detected. In deep peat (data not

309 shown), microbial aerobic respiration was significantly higher than anaerobic  
310 respiration, whatever the site and plant cover, except SpCaDe.

311 Basal respiration was negatively correlated with peat organic sulphur content  
312 but did not show any link to peat C:N ratio or N content (Table 4).

313 Aerobic:anaerobic respiration ratio did not show difference between depths  
314 (Table 3). It was significantly higher 10 years after abandonment of extraction  
315 (data not shown). It also fluctuated significantly with plant community (Table 3).  
316 Highest mean values on the peat profile were registered under EvBp ( $3.14 \pm 0.16$ )  
317 and CaBp ( $2.99 \pm 0.19$ ) while the lowest one was measured in one of the oldest  
318 sites with *Sphagnum spp* associated to *Calluna vulgaris* and Poacea (SpCaDe,  
319  $0.96 \pm 0.19$ ).

320

#### 321 MICROBIAL METABOLIC QUOTIENT (MMQ)

322 MMQ was significantly higher under aerobic conditions ( $W= 10968$ ,  $P<0.001$ ,  
323  $n=148$ ) and we registered significant effects of depth, regeneration age and plant  
324 community, both under aerobic and anaerobic conditions (Table 3). MMQ  
325 responses to regeneration age in surface peat layers were fitted to exponential  
326 regression models (Fig. 2). MMQ decreased with age both under aerobic and  
327 anaerobic conditions.

328 MMQ in surface peat varied significantly among plant communities and we  
329 observed significant decreasing quotients with increasing proportion of ericaceous  
330 shrubs in the plant community (Table 5 and Fig. 2). MMQ showed higher values  
331 as plants did not cover all the peat surface.

332 MMQ positively correlated with peat C:N ratio and organic S content but  
333 decreased with increasing organic N in the peat (Table 4).

334

335 SOLUBLE ORGANIC CARBON-MINERALIZATION RATE (C-MR)

336 C-MR varied significantly with all the considered factors (Table 3) and was  
337 significantly higher in aerobic conditions, pooling sites and depths (W=9351,  
338  $P<0.001$ ,  $n=160$ ).

339 C-MR changes over time and surface peat results were best described by  
340 exponential regressions while in deep peat, C-MR were low and did not show  
341 clear trends over time (Fig. 2). Higher C-MR rates were observed in late-  
342 successional stages (> 20 years old) with values ranging from  $0.329\pm 0.084$  to  
343  $0.507\pm 0.097$   $d^{-1}$ .

344 C-MR was higher in aerobic conditions in most of the plant communities  
345 (Table 5 and Fig. 2). Increasing plant species richness and mosses positively  
346 influenced C-MR under anaerobic conditions (Table 4). No clear trend in relation  
347 to vegetation was observed in aerobic conditions, except the fact that C-MR was  
348 higher under plant communities mixing *Sphagnum* and *Eriophorum vaginatum*  
349 with (SpEvVa,  $0.577\pm 0.098$   $d^{-1}$ ) or without (SpEv,  $0.507\pm 0.089$   $d^{-1}$ ) *Vaccinium*  
350 *spp.* (Fig. 2). Under anaerobiosis, the mineralization rate increased with plant  
351 species richness (Table 4).

352 C-MR under anaerobiosis also significantly decreased with increasing peat  
353 C:N ratio.

354

## 355 Discussion

356 MICROBIAL DYNAMICS OVER THE REGENERATION  
357 CHRONOSEQUENCE



358 The first aim of our work was to assess responses of microbial variables in  
359 abandoned peatlands after peat cutting over a 50 years' chronosequence at a  
360 European scale. The analysis of microbial dynamics in the surface peat (0-10 cm)  
361 revealed 3 major stages. We distinguished a first phase of ca. ten years, described  
362 by a strong increase of basal respiration but at a constant stock of biomass and a  
363 MMQ decrease as a consequence. During this early stage of succession, C-MR  
364 increased too and the microbial C:N ratio reached its higher values (ca.11). The  
365 bare peat situation can be considered as an initial stage of ecological succession  
366 after a strong physical disturbance (extraction). One of the main characteristics of  
367 the C-N dynamics in regenerating cutover peatlands is the strong change from  
368 bare peat, more or less dried and compacted, to a complete revegetation. During  
369 succession, matter and nutrient dynamics relate to many processes (Gorham,  
370 Vitousek & Reiners 1979). In bare peat areas, microbial biomass represents the  
371 most important nutrient living pool and microbial activity is the main factor acting  
372 to alter and transform the chemical and physical properties in the peat profile but  
373 microbial processes depend on peat chemistry. The correlations between peat  
374 properties and microbial variables (Table 4) emphasized the role of substrate  
375 quality. The low biomass during early stages of succession could be related to i)  
376 the disturbance (exploitation before abandonment) which could limit the  
377 development of microbes partly as a consequence of hyphal network disruption  
378 during the extraction years (Wardle 1995, van der Wal *et al.* 2006); ii) the poor  
379 quality of substrate, bare peat being very humified; iii) conditions of dryness,  
380 despite the fact all sites were initially re-wetted. During this phase, the microbial  
381 C:N ratio increased, implying changes in the microbial community composition  
382 in relation to stress.

383 In a second phase, microbial biomass increased while aerobic basal respiration  
384 and C-MR always increased but at a lower rate, demonstrating a better C-use  
385 efficiency and a higher proportion of C incorporated into the biomass (Insam &  
386 Haselwandter (1989; Ohtonen *et al.* 1999). The increase of most of microbial  
387 variables could indicate that no limiting factors acted as controls of the  
388 development of microbial pools and activity. In this stage, significant plant  
389 colonization of the sites probably favoured the increasing microbial pool,  
390 providing available C-sources (Crow & Wieder 2005).

391 In a third phase, from 30-40 years after abandonment, the rates of increasing  
392 biomass slowed down while aerobic basal respiration and C-MR tended to reach a  
393 maximum level, illustrating new processes and changes in the functioning of these  
394 regenerating peatlands. MMQ and microbial C:N ratio decreased through the  
395 second and third stages. These trends could be linked with progressive growth of  
396 roots through peat and revealed the increasing influence of plants in the  
397 functioning of regenerating peatlands, especially on the microbial compartment  
398 and their activity as new competitors for nutrients (Kaye & Hart 1997). Zak *et al.*  
399 (1990) observed a similar trend in an old-field succession. The stabilization in the  
400 model could correspond to the maximum carrying capacity, depending on growth  
401 control factors (N and P content, organic matter, etc.) and secondly, the existence  
402 of threshold values of some key soil properties which need to be exceeded before  
403 development of microbes could occur (Van der Wal *et al.* 2006).

404 Anaerobic basal respiration in the surface peat showed a linear increase over  
405 the chronosequence, suggesting that the full potential of anaerobic activity was  
406 not reached. In the deeper peat, it was more difficult to bring out patterns of  
407 change over time. Re-wetting disturbed peat is the most important factor during

408 the regeneration of peatland but re-humectation of peat at the local scale would be  
409 more difficult and time consuming, in relation to the strong disturbance generated  
410 by extraction. With time, anaerobic conditions would become widespread and  
411 permanent and corresponding potential activity would increase while aerobic  
412 zones stabilize.

413

#### 414 MICROBIAL VARIABLES VS PLANT COMMUNITY STRUCTURE

415 Our second objective focused on possible relationships between microbial  
416 variables and plant community composition and structure, measured by estimation  
417 of species richness and calculation of simple indices, including dominance and  
418 frequency of key-stone taxa such as *Sphagnum* and ericaceous shrubs. While the  
419 dominance index did not give any information, most of microbial variables  
420 correlated with bare peat surface (negatively) and plant species richness  
421 (positively) demonstrating the positive effect of plant development and diversity  
422 on microbial biomass in regenerating peatlands, as already demonstrated,  
423 especially in experimental grassland (Tilman *et al.* 1997; Hooper & Vitousek  
424 1977; Loranger-Merciris *et al.* 2005). Correlations with moss and/or ericaceous  
425 indices are of some interest, in relation to peatlands dynamics. The development  
426 of shrubs (and trees) had already been recognized as a determinant factor of peat  
427 microbial biomass and MMQ changes (Chapman, Williams & Hawkins 2001;  
428 Fisk, Ruether & Yavitt 2003).

429 It was possible to separate the influence of 2 main groups of plant  
430 communities, on the one hand, sites with incomplete cover of vegetation and on  
431 the other hand, more diversified plant communities without bare peat, on both  
432 microbial C and N (Table 4). Despite no direct estimates of plant productivity, our

433 results probably illustrate the positive influence of increasing plant productivity  
434 on microbial compartments (Zak *et al.* 1990 & 2003, Wardle *et al.* 2004). This  
435 positive influence is most likely due to a combination of litter quality and quantity  
436 inputs and root activities as already demonstrated (Aerts, Verhoeven & Whigham  
437 1999; Ström *et al.* 2003; Crow & Wieder 2005). In the first set of plant  
438 communities, the root activity and the input of litter are less important, both in  
439 quality and quantity. It was not possible to register any effect of plant  
440 composition on microbial biomass, i.e. to separate *Carex*, *Eriophorum* or  
441 *Sphagnum* when these plants were the dominant species on sites with incomplete  
442 colonization by plants. Nevertheless, different MMQ suggested differences in this  
443 set of plants. For instance, MMQ under *Sphagnum* was very low, while MMQ  
444 under *Carex* was the highest, suggesting different potentiality of energy sources  
445 for microbes. In the second set more consequent and diversified litter inputs  
446 would support higher microbial C and N biomass. Nevertheless, the EaPoCa site  
447 did not show significant difference of microbial biomass (C and N) with sites of  
448 the first set. This could be due to the contribution of *Polytrichum* species by  
449 which inhibition of microbes by allelopathic processes is recognized (Rozé 1987).

450

#### 451 MICROBIAL VARIABLES AS INDICATORS OF CHANGE IN 452 REGENERATING PEATLANDS

453 The third objective of this work was to assess the ability of microbial variables to  
454 be suitable indicators of peatland regeneration at a European scale. Microbial  
455 variables are increasingly used as ecological indicators of change after disturbance  
456 or stress (He *et al.* 2003) and soil quality (Winding, Hund-Rinke & Rutgers 2005).  
457 There are several definitions of ecological indicators that have been applied in

458 many ways (Niemi & McDonald 2004). He *et al.* (2003) and Winding, Hund-  
459 Rinke & Rutgers (2005) reviewed the relationships between a set of  
460 microbiological variables and their role in the soil and concluded of the interest in  
461 studying several variables together. Here, we would especially focus on the  
462 existence (or not) of thresholds or trends which could be used in relation to  
463 disturbance and resilience as time of recovery (“engineering resilience”,  
464 Gunderson 2000). This aspect implies the existence of sufficient knowledge in  
465 order to assess the results in comparison with reference systems. The variables  
466 used need to keep the same accuracy over time in order to minimize the deviation  
467 in assessment of responses to disturbance and resilience.

468 MMQ was one of the first variables used to study microbial succession and  
469 changes over time (Insam & Haselwandter 1989; Anderson 1994) but its  
470 disadvantages have been discussed (Wardle and Ghani 1995; Ohtonen *et al* 1999).  
471 These authors suggested the MMQ would not be efficient in characterizing  
472 microbial succession after disturbance because this quotient integrates both stress  
473 and disturbance effects. In our chronosequence, MMQ fitted well to an  
474 exponential regression, but high fluctuations were observed in the earlier-stages,  
475 probably for both stress and disturbance effects.

476 In peatlands, a few authors have already used microbial variables as ecological  
477 indicators in the context of land-use changes or to monitor the success of  
478 restoration and wetland creation (Brake, Hoper & Joergensen 1999; Chapman,  
479 Campbell & Puri 2003; Croft, Rochefort & Beauchamp 2001; Andersen, Francez  
480 & Rochefort 2006).

481 Peat microbial pools (mainly C-N estimated with the fumigation-extraction  
482 method), show significant higher values in pristine mires compared to peatlands

483 disturbed by mining (Croft, Rochefort & Beauchamp 2001) or young restored  
484 peatlands (Andersen, Francez & Rochefort 2006). Land-use changes impacted  
485 microbial C that ranged from a few hundred  $\mu\text{g}$  to about  $14 \text{ mg g DP}^{-1}$ , depending  
486 on the water regime (undrained *vs* drained, Baum, Leinweber & Schlichting  
487 2003), nutrient content (pristine *vs* fertilized, Karsisto 1992, Williams & Silcock  
488 1997) or vegetation (Fisk, Ruether & Yavitt 2003). Our models illustrated that  
489 microbial biomass levelled off around 5000 (C) and 1000 (N)  $\mu\text{g gDP}^{-1}$ . This level  
490 would correspond to a significant new equilibrium, following resistance and  
491 resilience processes, as theoretically described by Herrick (2000). As we did not  
492 know what were microbial C stocks before peat cutting in the different peatlands,  
493 we can only consider values of pristine peatlands published in literature as  
494 reference systems. Thus, microbial C biomass in natural raised-bogs would range  
495 from 3 to 6 mg C gDP<sup>-1</sup> in the upper part (0-30 cm) of the peat profile (Karsisto  
496 1992, Croft, Rochefort & Beauchamp 2001; Andersen, Francez & Rochefort  
497 2006). More investigation is needed in order to propose detailed models,  
498 especially around the crucial question of thresholds (Groffman *et al.* 2006).  
499 Whatever it will be, our study illustrated that microbial biomass is of strong  
500 interest to model responses of peatland functioning after peat-cutting. It also  
501 showed that others variables such as basal respiration measured in both aerobic  
502 and anaerobic conditions constituted helpful complementary tools, demonstrating  
503 the validity of considering a set of variables as ecological indicators in the  
504 assessment of responses to changes.

505

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514

For Peer Review

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- 707

707 **Figure Legends**

708

709 **Fig. 1.** Responses of microbial biomass carbon (C) and nitrogen (N) and C:N ratio  
710 vs a) time over the chrono-sequence ( $P < 0.01$ ,  $n = 7$ ; ■=surface, ▲=deep peat) and  
711 b) plant communities (dotted histograms=surface, grey=depth) (detailed  
712 abbreviations, see Table 3). Histograms with different letters are statistically  
713 different ( $P < 0.01$ ).

714

715 **Fig. 2.** Responses of basal respiration, MMQ and C-MR to: a) time after  
716 abandonment (square=surface, triangle=deep peat; black=aerobiosis,  
717 open=anaerobiosis); b) plant community (only surface results shown; histograms  
718 with different letters are statistically different at  $P < 0.05$ ).

719



**Table 1.** Peatland location and general characteristics.

Peatlands (Country code)	Coordinates	Altitude m	10-year average air T °C	Precipitation mm yr <sup>-1</sup>	Water table depth (annual range) cm <sup>#</sup>	Bulk density (g DP L <sup>-1</sup> )*	C:N*†	N (%)*†	S (%)*†
Aitoneva (FIN)	62°12N-23°18E	156	4.2	694	-9.4±14.5(-32/36)	141±30	44±2	1.3±0.4	0.227±0.045
Middlemuir Moss (UK)	57°36N-2°9W	110	8.0	1109	14±14 (-51/-6)	147±87	38±5	1.5±0.2	0.395±0.037
Baupte (FB)	49°17N-1°21E	4	11.4	890	58±7 (-95/-15)	121±32	22±2	2.4±0.2	0.500±0.053
Le Russey (FR)	47°10N-6°47E	867	7.7	1417	11±7 (-26/0)	119±40	29±4	1.9±0.4	0.028±0.047
La Chaux d'Abel (CH)	47°10N-6°57E	1040	6.4	1463	16±7 (-41/-4)	101±53	27±6	2.1±0.6	0.074±0.045

<sup>#</sup> Negative value indicates site with periodic flooding

\* mean ± SD; DP = dry peat

† Total organic element in peat, performed by combustion at 1100°C with a CNS-2000 LECO apparatus (Comont, Laggoun-Défarge & Disnar 2006).

**Table 2.** Description of studied sites and used codes in modelling of microbial variables responses to regeneration age and plant community structure (index mean  $\pm$  SD).

Peatland (Code)	Sites	Age*	Dominant plant species	Vegetation code	Bare peat cover (%)	Richness S	Indices d	m	e
Aitoneva	A	10	<i>E. vaginatum</i> †, <i>Utricularia</i>	EvBp	21	8.0 $\pm$ 2.0	0.42	0.25	0.00
(FIN)	B	10	<i>E. vaginatum</i>	EvBp	81	4.7 $\pm$ 1.5	0.95	0.00	0.00
	C	10	<i>Carex rostrata</i> , <i>Sphagnum</i>	CaBp	47	6.3 $\pm$ 0.6	0.42	0.42	0.00
	D	10	<i>Sphagnum</i> spp	SpBp	10	6.7 $\pm$ 1.5	0.61	2.30	0.00
	E	10	Bare peat	Bp	100	0	-	-	-
Middlemuir	A	3	Bare peat	Bp	95	1	-	-	-
Moss	B	7	<i>Sphagnum</i> spp	SpBp	12	8.3 $\pm$ 0.6	0.29	0.413	0.22
(UK)	C	7	<i>E. angustifolium</i> , <i>Sphagnum</i> spp	EaBp	14	7.7 $\pm$ 2.3	0.57	0.313	0.08
	D	55	<i>Sphagnum</i> spp, <i>C. vulgaris</i> #, <i>D. flexuosa</i> †	SpCaDe	0	11.3 $\pm$ 2.1	0.33	0.487	0.37
Baughte	A	7	Bare peat	Bp	100	0	-	-	-
(FB)	B	7	<i>E. angustifolium</i>	EaBp	22	6.7 $\pm$ 1.1	0.574	0.314	0.00
Le Russey	B	22	<i>E. angustifolium</i> , <i>Polytrichum</i> spp, <i>C. vulgaris</i>	EaPoCa	0	7.5 $\pm$ 2.1	0.478	0.600	0.20
(FR)	C	34	<i>Sphagnum</i> spp, <i>E. vaginatum</i> , <i>V. oxycoccos</i> ‡	SpEvVa	0	9.3 $\pm$ 0.5	0.577	2.025	0.48
Chaux d'Abel	B	42	<i>Sphagnum</i> spp, <i>E. vaginatum</i>	SpEv	0	6.5 $\pm$ 1.3	0.605	1.642	0.00
(CH)	C	55	<i>Sphagnum</i> spp, <i>E. vaginatum</i> , <i>V. spp</i>	SpEvVa	0	5.3 $\pm$ 2.2	0.641	2.946	0.19

\* mean age estimation from local surveys and dendrochronology

† *E. = Eriophorum* ; # *C. = Calluna*, †*D. = Deschampsia*, ‡ *V. = Vaccinium* (nomenclature after Daniels & Eddy 1985; Tutin *et al.* 1985).

**Table 3.** H-statistics and P-values of Kruskal-Wallis test for microbiological variables by depth, age of regeneration and vegetation.

Variables:	Effect:	Depth	Age	Plant
Microbial biomass				
Carbon ( $\mu\text{g C g DP}^{-1}$ )		24.6***	68.2***	71.3***
Nitrogen ( $\mu\text{g N g DP}^{-1}$ )		12.5**	41.3***	45.5***
Microbial C:N		6.0 NSD	6.4 NSD	10.0 NSD
Basal respiration ( $\mu\text{g CO}_2\text{-C g DP}^{-1} \text{ h}^{-1}$ )				
Aerobiosis		7.8 NSD	81.7***	57.2***
Anaerobiosis		15.7**	34.5***	31.5***
Aerobic:anaerobic basal respiration		5.8 NSD	109.0***	72.1***
MMQ ( $\text{d}^{-1}$ ) †				
Aerobic MMQ		21.2***	84.4***	75.9***
Anaerobic MMQ		17.0***	73.8***	77.1***
C-MR ( $\text{d}^{-1}$ ) ‡				
Aerobic C-MR		13.5**	60.1***	43.9***
Anaerobic C-MR		34.7***	26.9***	16.4*

† Microbial Metabolic Quotient, ‡ Soluble organic C Mineralization Rate  
 NSD, no significant difference; \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ .

**Table 4.** Matrix of Spearman rank correlation coefficients between microbial variables vs peat properties (surface + deep peat;  $34 \leq n \leq 57$ ) and vegetation indices over the succession ( $n=7$ , peat surface only).

	C:N	N (%)	S (%)	Bare peat cover (%)	Dominance (d)	Richness (S)	Moss index (m)	Ericaceous index (e)
C-FE microbial biomass	-0.357*	0.253 NSD	-0.605***	-0.847*	0.318 NSD	0.728*	0.700*	0.610 NSD
N-FE microbial biomass	-0.338*	0.257 NSD	-0.446**	-0.712*	0.316 NSD	0.586 NSD	0.333 NSD	0.475 NSD
Aerobic respiration	-0.027 NSD	-0.056 NSD	-0.411***	-0.441 NSD	0.467 NSD	-0.167 NSD	0.483 NSD	-0.051 NSD
Anaerobic respiration	-0.119 NSD	0.016 NSD	-0.374**	-0.746*	-0.183 NSD	0.728*	0.833*	0.458 NSD
MMQ aerobiosis †	0.380**	-0.300**	0.423**	0.797*	-0.001 NSD	-0.879*	-0.667 (*)	-0.797*
MMQ anaerobiosis	0.365**	-0.279*	0.496***	0.848*	-0.133 NSD	-0.946**	-0.583 (*)	-0.763*
C-MR aerobiosis ‡	-0.049 NSD	0.019 NSD	0.197 NSD	-0.288 NSD	0.600 (*)	-0.042 NSD	0.367 NSD	-0.051 NSD
C-MR anaerobiosis	-0.312*	0.261 NSD	-0.159 NSD	-0.932**	-0.367 NSD	0.778*	0.767*	0.661 NSD

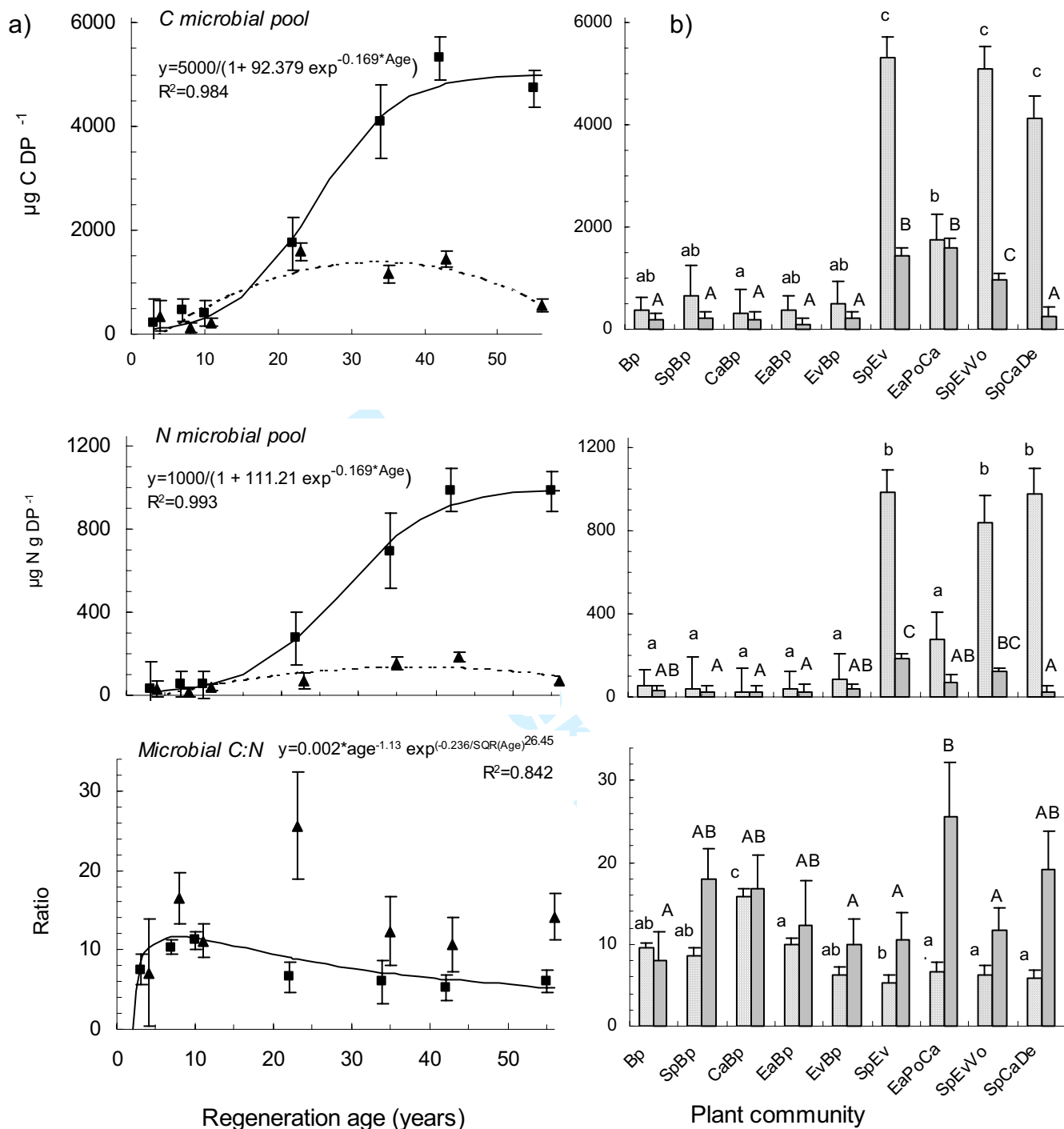
† Microbial Metabolic Quotient, ‡ Soluble organic C Mineralization Rate  
NSD, no significant difference; \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ .

**Table 5.** W-statistics and P-values of Mann-Whitney Wilcoxon test for aerobiosis vs anaerobiosis microbial variables in surface layers by vegetation. “Bare peat” results are added as a comparison, see Table 2 about vegetation codes.

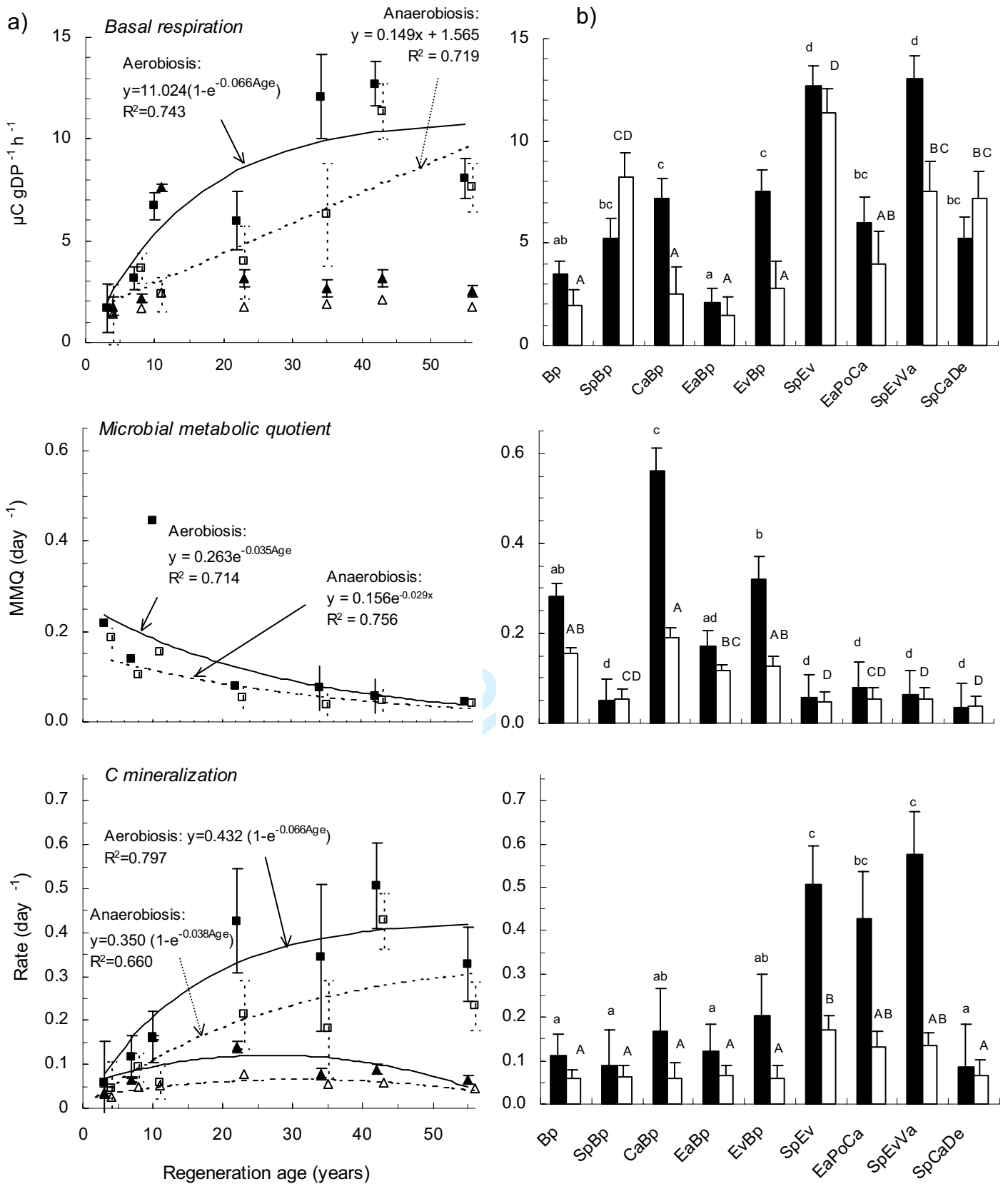
Vegetation	Basal respiration	MMQ	C-MR
<i>SpBp</i>	NSD, P=0.609	NSD, P=0.936	NSD, P=0.999
<i>Carex</i>	A>aN, 0**	A>aN, 0**	A>aN, 0**
<i>EaBp</i>	A>aN, 22**	A>aN, 41*	A>aN, 36*
<i>EvBp</i>	A>aN, 0**	A>aN, 0**	A>aN, 0**
<i>SpEv</i>	NSD, P=0.701	NSD, P=0.753	NSD, P=0.936
<i>EaPoCa</i>	NSD, P=0.470	NSD, P=0.194	NSD, P=0.312
<i>SpEvVa</i>	A>aN, 2*	A>aN, 3*	NSD, P=0.144
<i>SpCaDe</i>	A<aN, 30*	NSD, P=0.531	NSD, P=0.531
Bare peat ( <i>Bp</i> )	A>aN, 80**	A>aN, 74 **	A>aN, 88*

† See Table 2 for codes

NSD, no significant difference; \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ .



**Fig. 1.** Responses of microbial biomass carbon (C) and nitrogen (N) and C:N ratio vs a) time over the chrono-sequence ( $P < 0.01$ ,  $n = 7$ ; ■=surface, ▲=deep peat) and b) plant communities (dotted histograms=surface, grey=depth) (detailed abbreviations, see Table 3). Histograms with different letters are statistically different ( $P < 0.01$ ).



**Fig. 2.** Responses of basal respiration, MMQ and C-MR to: a) time after abandonment (square=surface, triangle=deep peat; black=aerobiosis, open=anaerobiosis); b) plant community (only surface results shown; histograms with different letters are statistically different at  $P < 0.05$ ).