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# **Above- and belowground linkages in *Sphagnum*-peatland: climate warming affects plant-microbial interactions**

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## Abstract

Peatlands contain approximately one-third of all soil organic carbon (SOC). Warming can alter above- and belowground linkages that regulate soil organic carbon dynamics and C-balance in peatlands. Here we examine the multi-year impact of *in-situ* experimental warming on the microbial food web, vegetation, and their feedbacks with soil chemistry. We provide evidence of both positive and negative impacts of warming on specific microbial functional groups, leading to destabilisation of the microbial food web. We found that warming involved a strong reduction (70%) of the biomass of top-predators (testate amoebae). Such a loss caused a shortening of microbial food chains, which in turn stimulated microbial activity, leading to slight increases in levels of nutrients and labile C in water. We further show that warming altered the regulatory role of *Sphagnum*-polyphenols on microbial community structure with a potential inhibition of top-predators. In addition, we found that abundance of *Sphagnum* decreased, whereas that of vascular plant increased with warming. Using structural equation modelling, we show that changes in the microbial food-web affected the relationships between plants, soil water chemistry and microbial communities. These results suggest that warming will destabilize C and nutrient recycling of peatlands via changes in above- and belowground linkages, and therefore, the microbial food web associated with mosses will feedback positively to global warming by destabilizing the carbon cycle. In addition, our findings add another crucial new contributor to the list of mechanisms by which mosses, as ecosystem engineers, tightly regulate peatland functioning.

## Introduction

Ongoing global warming is causing ecological communities to rapidly change, resulting in modifications to their interactions, and to ecosystem functioning and services. Climate warming phenomena can directly affect aboveground communities, by changing plant community composition, carbon allocation patterns, or the quality of plant-derived organic matter, which indirectly affect soil biota (Wardle *et al.*, 2004; Veteli *et al.*, 2007; De Dyn *et al.*, 2008; Wardle *et al.*, 2012). The microbial subsystem in turn supports a wide range of key ecosystem processes by breaking down plant material, and therefore determines the nature and the extent of plant community and functioning (Wardle *et al.*, 2004; Bardgett *et al.*, 2008; Singh *et al.*, 2010). Aboveground-belowground linkages and feedbacks may respond strongly to climate change yet such integrated effects remain poorly quantified (Singh *et al.*, 2010; Eiseinhauer *et al.*, 2012). Understanding warming-induced changes on plants and soil organisms is highly relevant to the growing interest that these components have in driving terrestrial ecosystem processes, both above- and belowground (Wardle & Bardgett, 2002; Bardgett & Wardle, 2010).

Peatlands dominated by *Sphagnum* mosses store more C than any other terrestrial ecosystem owing to imbalance between litter inputs and C outputs from soil respiration (Davidson & Janssens 2006; Dise 2009). Complex linkages between above- and belowground communities regulate this C-sequestration, which may decrease or even reverse in response to warming, leading to a positive feedback to global warming (Bardgett *et al.*, 2008; Dorrepaal *et al.*, 2009; Fenner & Freeman 2011). However, despite recent interest in linkages between above- and belowground communities as powerful mutual drivers of ecosystem processes (Wardle, 2006; Ward *et al.*, 2007; Kardol & Wardle, 2010; Wardle *et al.*, 2012), only a limited number of field experiments considering response to ecosystem change have been conducted in peatlands (Fenner *et al.*, 2007; Kim *et al.*, 2012; Weddon *et al.*, 2012).

Knowledge of how climate warming impacts on the mechanisms behind above- and belowground linkages in peatlands is currently insufficient. Indeed, changes in linkages at one level of organization (e.g. species characteristics and interactions, community composition or carbon storage) can affect above- and belowground biota, and their linkages, at other levels of organization, thus destabilizing peatland functioning.

Monitoring study had shown how peat mosses (*Sphagnum fuscum*) stabilised vegetation composition in response to climate warming by encroaching on vascular plant space (Keuper et al. 2011), underlying the key role of *Sphagnum* in peatlands. By efficiently accumulating nutrients, *Sphagnum* mosses act as ecosystem engineers, creating unfavourable conditions to vascular plant life (van Breemen, 1995; Turetsky, 2003; Gunnarsson, 2005). These mosses are also tightly linked to microbial communities through a variety of both direct and indirect mechanisms that ultimately exert control on peatland ecosystem C dynamics (Lindo & Gonzalez, 2010). Microbial communities living in *Sphagnum* mosses constitute a crucial detrital network for nutrient and C cycling, where protozoans (and especially testate amoebae) play a central role (Gilbert *et al.*, 1998; Mitchell *et al.*, 2003; Lindo & Gonzalez, 2010). *Sphagnum* also produces organochemical compounds such as polyphenols, which are known to have a strong inhibitory effect on microbial breakdown of organic matter, therefore favouring peat accumulation (Verhoeven & Toth, 1995). For instance, a reduction in polyphenol content may stimulate bacterial and microbial enzymatic activity (Fenner & Freeman, 2011; Jassey *et al.*, 2011a). However, despite the global significance of microbial communities in SOC dynamics of peatlands, their sensitivity to climate change has so far received little attention (Jassey *et al.*, 2011b; Kim *et al.*, 2012; Tsyganov *et al.*, 2012; Weddon *et al.*, 2012) and considerable gaps remain in our understanding of the impacts of warming on aboveground-belowground relationships in peatlands following changes in microbial components. Long-term global warming is expected to considerably alter peat-

forming areas, potentially involving substantial C loss due to modifications in microbial processes linked to *Sphagnum* mosses (Dorrepaal *et al.*, 2009; Delarue *et al.*, 2011; Fenner & Freeman, 2011; Jassey *et al.*, 2011a,b). Understanding key mechanisms behind the changing *Sphagnum* – microbial – vascular plant interactions in responses to climate change, is obviously needed to better understand ongoing processes and to predict more accurately future changes in the functioning of peatlands.

In this paper, we focus on the ways in which warming affects above- and belowground subsystems as key components of C fluxes in *Sphagnum*-peatlands. Specifically, we analyse the effect of climate warming on key above- and belowground components in a *Sphagnum* peatland in the Jura Mountains (France) to explore whether changes in peatland properties will be brought by plant communities, microbial communities, or by interactions between the two. Our aims were to (1) quantify over the course of two years how the soil microbial food web (biomass of bacteria, fungi, protozoans, and metazoans), plants communities (species composition and diversity), *Sphagnum*-polyphenols and soil water chemistry composition changed in response to warming, and (2) to clarify whether climate warming destabilized peatland functioning by changing plant-soil-microbial interactions, including polyphenol phytochemical interactions. Linkages amongst these variables were investigated using a path-relation network and structural equation models (SEM) to gain a mechanistic understanding of how warming effects materialized on above- and belowground linkages.

## Materials and methods

### *Field site and experimental design*

The experimental site is an undisturbed *Sphagnum*-dominated peatland situated in the Jura Mountains (The Forbonnet peatland, north-eastern France, 46°49'35''N, 6°10'20''E). Above-ground (mosses, vascular plants, polyphenols produced by *Sphagnum*) and belowground (soil water chemistry, microbial communities living in *Sphagnum* carpet) components were measured across a transitional fen-bog area in June 2008, 2009 and 2010 (begin of the warming experiment April 2008). The experimental site has an area of 30m x 30m and the vegetation consists of a mosaic of hummocks and lawns (Jassey et al. 2011a). The moss layer is dominated by *S. fallax* in lawns and by a mixture of *Sphagnum fallax*, *S. magellanicum* and *S. palustris* in hummocks whereas the evergreen dwarf shrubs *Eriophorum vaginatum* and *Andromeda polifolia*, the deciduous dwarf shrubs *Vaccinium oxycoccus* and the graminoids *Calluna vulgaris* and *Carex rostrata* characterize the field layer. We chose 12 sampling plots (six ambient and six warmed plots) across the area placed so as to cover all the possible microforms along the gradient. Six plots were placed in lawns and six plots in hummocks, and in each area three plots were assigned as ambient conditions and three as warmed conditions. We used open-top chambers (OTC) to simulate the regional climate expected for the coming decades (IPCC, 2007; Jassey et al., 2011a). The OTCs significantly increased mean air temperature in spring and summer by up to about 1.3°C, and decreased the water content of *Sphagnum* in summer by up to about 30% (Delarue et al., 2011, Jassey et al., 2011a). The water table depth did not change with warming and was ranged from 13.4 cm to 20.8 cm between 2008 and 2010.

### *Belowground measurements*

We analyzed the entire microbial community using a morpho-type functional group approach rather than focusing on a given group, such as bacteria or fungi. Samples of *S. fallax* were collected for the study of microbial communities from ten permanent markers in each plot and the average altitude (microtopography) was measured. This sampling design allowed for multiple sampling over time and collection of a composite sample from each plot, avoiding any bias due to spatial heterogeneity (Mitchell *et al.*, 2000a). Microbial communities were analysed from surface (0-3 cm) and litter (3-6 cm) layers of *Sphagnum* shoots. Microbial samples were fixed in glutaraldehyde (2%) and extracted following the standard method described in Jassey *et al.* (2011b). We used direct observation by inverted microscopy (x200 and x400 magnification) to determine precisely the abundance and biomass of individual microbial functional groups (fungi, microalgae, ciliates, testate amoebae, rotifers and nematodes). Flow cytometry (FAC-Scalibur flow cytometer, Becton Dickinson) was used for bacterial counts. Fluorescent microbeads (Molecular probes) of diameter 1µm were added to each sample as an internal standard. Bacterial samples were stained with SYBR Green I (1/10,000 final conc.) for 15 min in the dark and run at medium speed (ca 40 µL min<sup>-1</sup>). For each specimen, the average biovolume (µm<sup>3</sup>) was estimated by assuming geometrical shapes using image analysis and converted to biomass using conversion factors (Gilbert *et al.*, 1998). Data were expressed as micrograms of carbon per gram of *Sphagnum* dry mass (µgC.g<sup>-1</sup> DM).

The trophic position of testate amoebae was also estimated by measuring their body size and their shell-aperture size using image analysis. We chose these two specific morphological traits because they are linked to their feeding habit. The species with a low ratio shell aperture size over body size ( $0 < \text{shell-aperture size/body size} < 0.18$ ) were considered as having a low trophic position (i.e. primarily bacterivores and algivores), and species with a high one ( $0.20 < \text{shell-aperture size/body size}$ ) as having a high trophic



position (i.e. primarily predators of other protists and micro-metazoan) in the microbial food web (Yeates & Foissner, 1995; Mitchell *et al.*, 2003; Jassey *et al.*, 2012).

Water chemistry (20 mL) was analysed in each sampling plot at 10 cm depth from piezometers during each sampling campaign. Total dissolved nitrogen (DN) and dissolved organic carbon (DOC) of peatland water were determined with a SHIMADZU SSM-5000A total C and N analyser. Ammonium ( $\text{NH}_4^+$ ), nitrates ( $\text{NO}_3^-$ ) and phosphates ( $\text{PO}_4^{3-}$  and total phosphorus) were analysed colorimetrically using a continuous flow analyser (FLOWSYS, Systea, Roma) after filtering the bog water at 0.45  $\mu\text{m}$ .

#### *Aboveground measurements*

We performed vegetation surveys by the point-intercept method (Buttler, 1992; Keuper *et al.*, 2011). We used a 50x50 cm Plexiglas frame placed above a permanently marked quadrat by means of 4 adjustable poles. A ruler with 20 holes was moved along 20 different positions to obtain 400 measuring points. A metal pin with a 1 mm diameter tip was lowered through each hole in the ruler and each contact of the pin with green living vegetation was recorded by species until the pin reached the moss substrate. Moss and vascular plant abundances were expressed as percentage of mean number of hits (%). Moreover, we measured the average microtopography of the marked vegetation quadrat.

Total water-soluble *Sphagnum*-polyphenols were quantified in living segments of *Sphagnum* shoots (0-6 cm) during each sampling campaign using Folin methods and gallic acid as standard (see Jassey *et al.*, 2011b for details). These samples were collected around the same ten permanent markers used for microbial communities for each plot.

#### *Numerical analyses*

We carried out linear mixed effects models and ANOVAs to test for differences between treatments and years in the following variables: (i) biomass of individual microbial groups; (ii) abundance of individual testate amoeba species; (iii) individual water chemical components; (iv) total abundance of plants (mosses and vascular plants) and abundance of individual moss and vascular plant; and (v) polyphenol content in *Sphagnum*. Linear mixed effects were used to assess the effects of warming (difference of temperature between ambient and warmed plots, delta TC), time and microtopography (fixed effects) on measured of biotic and abiotic variables while accounting for the temporal repeated measurements in each plot on three dates. We fitted all models including plot as a random effect on the intercept, i.e. we corrected for the inflation of the residual degrees of freedom that would occur if we were using repeated measurements as true replicates (Pinheiro and Bates, 2000). Then ANOVAs were applied on the different models to test the fixed effects, and differences among the levels of the fixed effects in the final model were determined using multiple comparison post-hoc analyses (general linear hypothesis test). Finally, we used the *F*-values from the ANOVAs to quantify the impact of warming on the abundance of individual testate amoeba species. Higher *F*-values indicated stronger warming effect on the individual testate amoeba species.

We evaluated the warming effect on vegetation and microbial community structure, and water chemistry composition using the principal response curve (PRC) method. PRC was used to focus on the time-dependent treatment effect and applied on the Hellinger-transformed vegetation and microbial assemblages and the standardized water chemistry matrix, including the response of individual plant species, microbial groups or chemical components. PRC analysis is a special case of partial RDA (pRDA) for multivariate responses in repeated observation design. It is based on a pRDA adjusted for overall changes in community structure response over time, as compared to control plots (van den Brink and ter Braak, 1999). In diagrams, the curves represent the time trajectory for the controls as a

horizontal line maintained to 0 (dashed line) and deviation of community structure in warmed plots in course of two years (solid line). This is achieved by taking the control treatment as the reference against which the other treatments are contrasted and by defining “time” as the horizontal axis of the diagram (van den Brink and ter Braak, 1999). With the help of the species weights on the right Y-axis, the PRC can be used to infer about the response of individual species to warming. The species scores on the right Y-axis allow an interpretation at the species level, i.e. values indicate the contribution of individual species/group/component to the deviation of the community structure observed in warmed plots. Individual group with positive scores on right Y-axis are inferred to show a negative effect of warming, whereas groups with negative scores show a positive response to warming. A group near zero scores either show no response or a response unrelated to the pattern shown in PRC. Higher values (positive or negative) on the right Y-axis indicate stronger warming effect on the individual species/group. Permutation tests with 1,000 permutations, stratified by year, were performed for every canonical axis. Additionally, variance partitioning using redundancy analyses (RDA) and adjusted  $R^2$  were applied to compare the respective effect of microtopography, time and warming on each biotic and abiotic matrices. The significance of the each explanatory variables included in RDA were tested using 1,000 permutations.

Above- and belowground data was organized into a path-relation network and subjected to structural equation modelling (SEM) (Grace & Keeley, 2006; Grace *et al.*, 2007, 2010). This enabled us to explore simultaneous influences of several potentially important drivers of peatland functioning that may be affected by warming, and thereby identify their relative importance to obtain a better understanding of peatland response to warming. SEM was based on the overall dataset and predicted causal relationships between variables were based upon prior knowledge, theory and past experience on the role of above- and belowground factors in peatland functioning. The adequacy of the model was determined via

several tests, i.e.  $\chi^2$  tests, goodness fit index (GFI), Akaike value (AIC), root square mean error of approximation (RMSEA) and root mean square residual (RMR) (Grace & Keeley, 2006; Jonsson & Wardle, 2010; Eisenhauer *et al.*, 2012). Adequate model fits are indicated by nonsignificant  $\chi^2$  tests ( $P > 0.05$ ), high GFI ( $0.8 < \text{GFI} < 1$ ), low AIC, low RMSEA ( $< 0.05$ ) and low RMR ( $\text{RMR} < 0.05$ ) (Grace *et al.*, 2010). Models were built and separately tested for ambient and warmed plots based on the biomass of individual microbial groups in surface and litter, abundances of mosses and vascular plants, polyphenol content and a subset of four variables (DOC,  $\text{NH}_4^+$ ,  $\text{NO}_3^-$  and  $\text{PO}_4^{3-}$ ) retained by stepwise selection from the water chemistry matrix. We used RV-coefficients from multiple factor analysis (MFA) to construct our correlation matrices used in SEM (Legendre & Legendre, 1998; Grace *et al.*, 2010). MFA symmetrically linked the six groups of descriptors described above. MFA was selected because it allowed the simultaneous coupling of several groups or subsets of variables defined on the same objects and assess the general structure of the data (Escofier & Pagès, 1994). RV-coefficients (Pearson correlation coefficient) were used to measure the similarities between two data matrices (Robert & Escoufier, 1976; Josse *et al.*, 2008). SEM was performed using Amos 5 (Amos Development Corporation, Crawfordville, FL, USA). For each analysis,  $R^2$  values were obtained for each dependent matrix, showing the amount of the variance explained by the model (Grace & Keely, 2006; Grace *et al.*, 2010; Jonsson & Wardle, 2010).

All statistical analyses were performed with R 2.10.1 using the lme, vegan and FactoMineR packages (Husson *et al.*, 2009; Oksanen *et al.*, 2010; R Development Core Team, 2010).

## Results

## Belowground subsystem

### *Microbial network structure*

The structure of microbial communities clearly responded to warming as showed by PRCs (Fig. 1a, b). Microbial community structure in warmed plots significantly deviated from ambient plots at the surface layers ( $F = 4.6$ ,  $P = 0.02$ ) whereas the same but weaker warming effect was recorded at the litter layers ( $F = 3.1$ ,  $P = 0.05$ ). The response of warmed plots clearly appeared in 2009 in both sampling depth, one year after the beginning of the warming experiment (Fig.1a, b). The respective effects of microtopography, time and temperature increase on the variation of microbial communities living at the surface layers were of 13.7%, 6.6% and 10.5%, respectively (Table 1), while their respective effects at the litter layers were of 0.6%, 24.7% and 14.3%, respectively. Only some microbial groups were affected by microtopography variations (e.g. microalgae and testate amoebae) along *Sphagnum* shoots (Table S1). Furthermore, RDA and variance partitioning revealed that the interaction between microtopography and warming were not significant along *Sphagnum* shoots (Table 1), highlighting a similar warming effect amongst lawns and hummocks.

The detailed examination of the time-dependent warming effect on individual microbial groups revealed a strong negative effect on testate amoebae, especially at the surface layers (Fig. 1a; Table S1). This effect was largely due to a decline of the biomass of the testate amoebae with high trophic level ( $F = 5.6$ ,  $P = 0.002$ ) of 40% and 75%, after one and two warming years respectively. The total biomass of this category of species decreased from 440  $\mu\text{gC g}^{-1}$  DM to 131  $\mu\text{gC g}^{-1}$  DM in warmed conditions over two years (Table S1). Although the decrease of the biomass of testate amoebae with high trophic level was not significant at the litter layers ( $F = 3.9$ ,  $P = 0.063$ ), the trend of their response followed that of testate amoebae in surface layers with a decrease of 28% and 41% of their biomass after one

and two warming years respectively (Table S1). Moreover, we recorded that the warming effect on the abundance of main testate amoeba species was positively correlated to the ratio shell aperture size over body size at the surface layers ( $r = 0.68$ ,  $F = 4.25$ ,  $P < 0.04$ ; Fig.1c). Here again, such trend was non-significant in the litter ( $r = 0.36$ ,  $F = 2.3$ ,  $P = 0.17$ ). We further observed that the microbial network from surface and litter became increasingly enriched in bacteria and depleted in top-predators with warming. The relative biomass of bacteria in the surface layers significantly increased from 31% in ambient plots to 45% in warmed plots, and from 29% to 36% in the litter layers (Fig. 2, Table S1). In parallel, the relative biomass of testate amoebae with high trophic level decreased from 31% in ambient plots to 12% in warmed plots in the surface layers and from 21% to 11% in the litter layers respectively. Consequently, the decrease in testate amoebae with high trophic level explained 10% ( $F = 4.86$ ,  $P = 0.03$ ) and 16% ( $F = 7.91$ ,  $P < 0.01$ ) of the rise of the relative bacterial biomass in warmed plots from surface and litter, respectively.

#### *Water chemistry composition*

PRC analysis showed that water chemistry composition was not affected by warming ( $F = 2.1$ ,  $P = 0.11$ ). Time mainly explained the variance in water chemistry composition with 17% of the total variation. However, variance partitioning revealed a significant interaction between time and temperature increase on water chemistry composition with 21.9% of the variance (Table 1). Warming slightly affected water chemistry composition over the course of the two years. Elevated temperatures modified the annual dynamic of some chemical components such as  $\text{PO}_4^{3-}$ , DOC, and  $\text{NO}_3^-$  (Table 2), even if these variations remained very low. Most importantly, we found in warmed plots that nitrates ( $r = -0.64$ ,  $F = 8.4$ ,  $P < 0.01$ ) and DOC ( $r = -0.66$ ,  $F = 3.8$ ,  $P = 0.05$ ) were negatively correlated to the decrease of the biomass of the testate amoebae with high trophic levels, whereas no such relationships were

found in ambient plots (Fig. 3a, b, c). In the same way, no such relationships were found with the biomass of the testate amoebae with low trophic levels, both in ambient and warmed plots.

## Aboveground subsystem

### *Mosses and vascular plants abundances*

Plant community structure was stable across years and did not respond to warming over the course of the two years, as showed by the PRC ( $F = 0.61$ ,  $P = 0.96$ ). Our results revealed that microtopography highly affected the composition of vegetation communities across the vegetation patterns ( $F = 12.8$ ,  $P = 0.001$ ; Table 1). The detailed examination of the warming effect on vegetation in lawns and hummocks showed that the total abundance of vascular plants significantly increased with warming in both microtypes ( $F = 5.1$ ,  $P = 0.032$ , ANOVA) and that of mosses decreased in lawns ( $F = 7.15$ ,  $P = 0.019$ , ANOVA). Total vascular plant abundance increased from 29% of mean number of hits to 31% in lawns and from 37% of mean number of hits to 41% in patterns of hummocks and hollows (Fig. 4a). Such increase was due to a rise in the abundance of the evergreen low shrub *Andromeda polifolia* ( $F = 8.37$ ,  $P < 0.01$ ; Fig. 4c). The abundance of other evergreen vascular plants (*Eriophorum vaginatum*, *Vaccinium oxycoccus*), graminoids (*Carex limosa*, *C. rostrata*, *C. pauciflora*) and forbs (*Drosera rotundifolia*) did not respond to climate warming. Total moss abundance decreased in lawns from 55% to 45% after two warming years (Fig. 4b), especially *Sphagnum fallax* which significantly decreased from 49.0% to 42.9% ( $F = 4.1$ ,  $P = 0.03$ ; Fig. 4d). Other moss species such as *S. magellanicum* and *S. palustris* did not respond to warming.

*Sphagnum-polyphenols*. Total water-soluble polyphenol content was comprised between 0.5 mg.g<sup>-1</sup> DM and 2.5 mg.g<sup>-1</sup> DM (Table 2). Phenolic content was not affected by warming over the course of the two warming years, but a significant negative link between phenolics and air

temperatures was found. Furthermore, we found a negative relationship between water-soluble polyphenol and the biomass of testate amoebae with high trophic levels in warmed plots ( $r = -0.6$ ,  $F = 9.9$ ,  $P < 0.01$ ) whereas the same relationship in ambient plots was not significant ( $r = -0.2$ ,  $F = 1.7$ ,  $P = 0.21$ ) (Fig. 5). Moreover, variance partitioning revealed that water-soluble polyphenols and temperature increase explained 13% ( $F = 6.2$ ,  $P = 0.018$ ) and 19% ( $F = 8.9$ ,  $P = 0.005$ ) of the decrease of the biomass of testate amoebae with high trophic levels at the surface layers, respectively. Here again, such relationship was not found with testate amoebae with low trophic levels, as well as in the litter layers.

#### *Effect of warming on above- and belowground linkages*

The use of a path-relation network showed that warming affected above- and belowground interactions (Fig. 6). The final models adequately fitted the data under ambient ( $\chi^2_7 = 6.51$ ,  $P = 0.51$ ; AIC = 34.19; GFI = 0.88; RMSEA < 0.001; RMR = 0.14) and warmed conditions ( $\chi^2_7 = 1.00$ ,  $P = 0.99$ ; AIC = 29.03; GFI = 0.98; RMSEA < 0.001; RMR = 0.034). Under ambient conditions, the model showed that microbial community structure in surface layers had significant links to microbial community structure in litter ( $P < 0.01$ ), and that *Sphagnum*-polyphenols were negatively linked to microbial community structure in surface and litter ( $P = 0.09$ ) (Fig. 6a). Significant associations were further found between microbial communities living in litter and water chemistry composition ( $P < 0.01$ ; Fig. 6a). The model also showed a strong negative association between moss community and vascular plant community ( $P < 0.01$ ). The ambient model explained a low proportion of the variance in mosses (8%) and microbial community structure at the surface (2%), whereas it explained 17.5%, 25.5% and 46.4% of microbial community structure in litter, water chemistry, and vascular plant community, respectively (Fig. 6a).



In warmed plots, treatment effect on testate amoebae with high trophic level significantly increased the link of microbial communities living in surface with moss community structure ( $P < 0.01$ ; Fig. 6b). The link between *Sphagnum*-polyphenols and microbial communities also increased and shifted from a negative association in ambient plots to a positive association in warmed plots, especially on microorganisms living in surface layers. This analysis also revealed a decrease of the negative association between mosses on vascular plants community structure in warmed conditions. Moreover, the model showed that the relationships between water chemistry and microbial communities increased with warming, especially in litter layers ( $P < 0.01$ ). The SEM model on warmed plots explained a larger proportion of the variance in moss community structure (19.4%), water chemistry (49.7%), microorganisms in surface (13%) and litter (27.3%) layers, whereas that of vascular plants diminished (19.5%) (Fig. 6b).

## Discussion

Our results from a field manipulation experiment in a *Sphagnum* peatland show that warming affects total vascular plant and moss abundances as well as the structure and functioning of soil microbial communities so resulting in a modification of linkages between above- and belowground subsystems.

Warming effect on microbial communities resulted to rapid trophic alteration in the microbial food web. The impact of warming on microbial structure decreased with depth; the response of microbial communities was highly significant in the surface layers, similar but weaker in the litter layers. Such result is in line with previous observations of a weak warming effect on *Sphagnum*-polyphenol, enzymatic activities and water-extractable organic matter at this depth (Delarue *et al.*, 2011; Jassey *et al.*, 2011a; Jassey *et al.*, 2012b). Warmed communities disproportionately lost top-predators and omnivores, and became increasingly dominated by decomposers and autotrophs (Fig. 2), showing that the stability of the microbial food web was affected by warming (Petchey *et al.*, 1999; Dossena *et al.*, 2012; Heckmann *et al.*, 2012). More specifically, warming impacted testate amoebae with a large body size and shell aperture size, key organisms of the structure and functioning of microbial network due to their position at the top of the food web (Mitchell *et al.*, 2003; Wilkinson & Mitchell, 2010; Jassey *et al.*, 2012a). This decrease was linked and coincided with an increase in the relative biomass of bacteria, both in the surface and litter layers. Such changes in the relative distribution of microbial group among trophically defined levels potentially lead to differences in ecosystem functioning beyond those expected from ambient conditions (Petchey *et al.*, 1999, 2008; Dossena *et al.*, 2012). Although it was not explore here, warming has been recognized to alter the structure of bacterial communities by favouring bacterial communities over methanogens, which may result changes in balance between CO<sub>2</sub> and CH<sub>4</sub> fluxes from peatlands (Kim *et al.*, 2012). Furthermore, the strong impact of climate warming

on testate amoebae is of particular interest because they link mosses and microbial heterotrophic producers (i.e. fungi and bacteria) via the microbial loop. This loop describes a trophic pathway in microbial food web where dead organic matter is returned to higher trophic levels via its incorporation into bacterial biomass coupled with the microbial food chains (e.g. bacteria → ciliate → testate amoebae; Gilbert *et al.*, 1998). This recycles C and nutrients from dead organic matter to plant communities (Ledeganck *et al.*, 2003; Mitchell *et al.*, 2003). The decline of testate amoebae with high trophic levels probably caused a shortening of microbial food chains that would greatly affect the microbial food web stability and structure, which further could destabilize ecosystem processes they control (Petchey *et al.*, 1999; Mitchell *et al.*, 2003; Wilkinson & Mitchell, 2010; Heckmann *et al.*, 2012). Indeed, testate amoebae with large shell aperture consume a wide range of prey such as small testate amoebae, ciliates, rotifers and small nematodes, typically bacterivores and algivores species (Wilkinson & Mitchell, 2010; Jasey *et al.*, 2012a). Such decrease could accelerate the turnover of microbial biomass due to the diminution of their top-down control (predation), speeding up decomposition and nutrient recycling via the microbial loop in long-term (Petchey *et al.*, 1999; Mitchell *et al.*, 2003; Dossena *et al.*, 2012). Thus these changes in microbial community structure and stability suggest that climate warming will impact belowground subsystem functioning (Allison & Martiny, 2008).

Interestingly, in other *Sphagnum*-dominated peatlands, summer warming accelerates nitrogen cycling due to changes in belowground subsystem (Weddon *et al.*, 2012). In our study, the largest differences in water chemistry composition were found amongst sampling years. Annual variations in evapotranspiration and oxido-reduction processes associated with the water table position probably explained these variations (Proctor, 1994; Andersen *et al.*, 2010). However, our results highlighted that water chemistry composition responded to warming in interaction with annual variations by slightly increasing nutrient (as  $\text{NO}_3^-$ ) and C-

exports (as DOC) levels in the soil solution after two years. Reasons of such slight effect may be explained by the fact that microorganisms living in surface layers are exposed to the chemistry of capillary water rather than water deeper in the peat (i.e. water table) (Lamentowicz *et al.*, 2010). As a consequence of this vertical gradient, the relationships between bryophyte and water deeper in the peat are not optimal (Mitchell *et al.*, 2000b; Hajkova *et al.*, 2004). Warming effects on water chemistry would have been probably higher on water extracted from mosses themselves but this was not analysed here. Nevertheless, increasing amount of DOC and  $\text{NO}_3^-$  in warmed plots, even varying annually, may be interpreted as an indication of a slight destabilization of the belowground functioning of peatland (Evans *et al.*, 2005; Carrera *et al.*, 2009; Weddon *et al.*, 2012). Moreover, the actual amount of C and nutrient fluxes from the microbial loop is dependent of the length of food chains in microbial food webs (Pomeroy, 2006). Thus, the negative correlations between  $\text{NO}_3^-$  /DOC and the biomass of testate amoebae with high trophic levels suggest that the trophic alteration of the microbial structure due to potential shortening of food chains affected these biogeochemical fluxes.

We clearly showed that warming affected belowground subsystem, however, these phenomena are often indirectly linked to changes in aboveground communities (Wardle *et al.*, 2004). A growing number of studies have showed how changes in plant communities affect soil communities (Wardle *et al.*, 1999; Kardol & Wardle, 2010) and how the soil biota in turn affects the plant community, leading to feedbacks between the plant and soil subsystems (De Dyn *et al.*, 2003; Kardol *et al.*, 2006; Wardle *et al.*, 2012). The increase of vascular plants and the decrease of *Sphagnum* in response to warming probably modified the quantity and/or quality of plant-derived organic matter, which in turn affected microbial communities (Delarue *et al.*, 2011). Although it was not explored here, we cannot exclude an increase of root exudates from vascular plants associated to their increase in response to warming, which

could stimulate decomposers such as bacteria (Delarue *et al.*, 2011). In addition, we revealed significant relationships between *Sphagnum*-polyphenols and microbial communities in warmed plots, suggesting these aboveground factors interact in driving belowground subsystem. *Sphagnum*-polyphenols play a fundamental ecological role in the regulation of soil microbiota and hence of microbial processes by way of chemical interactions (Hättenschwiler & Vitousek, 2000; Inderjit *et al.*, 2011; Jassey *et al.*, 2011a). For the first time, we found that warming greatly impacted polyphenol-microbial community interactions by a shift from a negative to a positive effect in warmed conditions (Fig. 6), and that the amount of *Sphagnum*-polyphenols have a similar influence than warming on key microorganisms such as testate amoebae. The strong negative correlation between polyphenols and testate amoebae with high trophic levels in warmed conditions revealed a potential inhibitory effect of phenols on this category of microorganisms in context of warming (Jassey *et al.*, 2011b). Even if warming did not directly impact the total amount of *Sphagnum*-polyphenols, qualitative changes induced by climate change are quite possible, as previously showed in dwarf shrubs ecosystems (Hansen *et al.*, 2006). Such findings strongly suggest that polyphenols produced by *Sphagnum* play a key role in the regulation of testate amoebae community structure, as well as in the microbial network stability in ways that can positively affect decomposition (Jassey *et al.*, 2011b; Inderjit *et al.*, 2011). Indeed, by their inhibitory effect on top-predators, polyphenols may indirectly enhance C and nutrient mineralization. Bacterial growth and microbial OM breakdown could be stimulated by such inhibition of top-predators, leading to an increase of nutrient levels and C release in peatlands, which further would destabilize the productivity of plant communities and peatland carbon stock (Wardle *et al.*, 2004; Fenner & Freeman, 2011; Jassey *et al.*, 2011a).

Reciprocally, we also assume that direct effects of climate warming on the microbial food web modify the linkages between above- and belowground communities. Warming

effect on microbial food webs could greatly influence aboveground productivity and plant community structure through the stimulation of nutrient dynamics, which indirectly influence nutrient uptake of aboveground consumers such as vascular plants (Mitchell *et al.*, 2003; Carlson *et al.*, 2010; Kardol & Wardle, 2010). The rise of temperature involved a decrease of the negative link between mosses and vascular plants, highlighting a reduction of *Sphagnum* mosses repression on vascular plant life (Fig. 6), as shown in response to other perturbations such as fertilization and drainage (Berendse *et al.*, 2001; Lang *et al.*, 2009). Even if vegetation composition did not change overall with warming, we recorded significant changes in total vegetation cover in course of two years of warming with a decrease of *Sphagnum* in lawns and an increase of vascular plants in lawns and hummocks. The observed slight increases of nutrient and C levels in soil solution are likely to alter the competition between mosses and vascular plants (Berendse *et al.*, 2001; Keuper *et al.*, 2011). *Sphagnum* mosses are known to be efficient at absorbing nitrogen, preventing deep-rooted vascular plants growing in a dense *Sphagnum* carpet (van Breemen, 1995; Turetsky, 2003; Gunnarsson, 2005), but excessive tissue nitrogen accumulation due to warming effect on the microbial food web should exacerbate the decline of *Sphagnum* and the increase of vascular plants (Breeuwer *et al.*, 2008, 2009; Limpens & Berendse, 2003). Such a warming-induced increase of vascular plant cover would further contribute to diminishing carbon sequestration in *Sphagnum*-peatlands due to a plant litter more easily degradable (Verhoeven & Toth, 1995).

We conclude that climate warming greatly destabilises peatland functioning by changing the interactions between plant and microbial communities. These results imply that warming changes peatlands directly by modifying the structure of microbial communities with the loss of top-predators and the increase of bacteria and indirectly by changing ecosystem functions via modifications of plant-soil-microbial interactions through the increase of nutrients cycling and the positive and/or negative effect of *Sphagnum*-polyphenol

on the microbial food web. Our observations support the hypothesis that microbial food web associated to mosses positively contribute to global warming by controlling ecosystem feedbacks (Lindo & Gonzalez, 2010; Singh *et al.*, 2010; Jasse *et al.*, 2011b). Consequently the moss-microbiota system exerts a strong control over the structure and dynamics of peatland ecosystems. Furthermore, these key findings add another crucial new contributor to the list of mechanisms by which mosses, as ecosystem engineers, tightly regulate biogeochemical cycling and climate feedback in peatlands (van Breemen, 1995; Cornelissen *et al.*, 2007; Gornall *et al.*, 2007).

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**Table**

**Table 1:** Summary of RDA on microbial, plant and water chemistry data sets and environmental factors: fraction of variance explained and significance of individual variables taken alone or in interaction. <sup>a</sup> Percentage of variance explained (adjusted R<sup>2</sup>).

	Microbial communities (top)		Microbial communities (inter)		Plant communities		Water chemistry composition	
	% <sup>a</sup>	F-value <sup>P-value</sup>	% <sup>a</sup>	F-value <sup>P-value</sup>	% <sup>a</sup>	F-value <sup>P-value</sup>	% <sup>a</sup>	F-value <sup>P-value</sup>
Microtopography (Alt)	13.7	8.6 <sup>P=0.001</sup>	0.6	1.2 <sup>P=0.35</sup>	26.0	12.8 <sup>P=0.001</sup>	3.6	3.04 <sup>P=0.036</sup>
Time	6.6	3.7 <sup>P=0.007</sup>	24.7	8.7 <sup>P=0.001</sup>	0.6	1.2 <sup>P=0.30</sup>	19.8	8.35 <sup>P=0.001</sup>
delta T°C	10.5	6.1 <sup>P=0.001</sup>	14.3	7.9 <sup>P=0.001</sup>	2.0	0.3 <sup>P=0.89</sup>	1.7	2.3 <sup>P=0.096</sup>
delta T°C * Year	16.5	2.1 <sup>P=0.06</sup>	33.8	4.1 <sup>P=0.002</sup>	5.4	0.6 <sup>P=0.63</sup>	21.9	2.95 <sup>P=0.035</sup>
delta T°C * Alt	22.5	0.44 <sup>P=0.83</sup>	12.6	0.71 <sup>P=0.63</sup>	24.5	1.1 <sup>P=0.30</sup>	4.2	0.45 <sup>P=0.82</sup>

**Table 2:** Mean ( $\pm$  SE) of water chemical variables measured in a *Sphagnum*-dominated peatland subjected to experimental warming (WAR) or ambient conditions (AMB) in 2008, 2009 and 2010. Significant warming effects are shown in bold (ANOVA tests). W = warming effect.

		2008		2009		2010		<i>F</i> -value <sup><i>P</i>-value</sup>		
		AMB	WAR	AMB	WAR	AMB	WAR	warming	time	microtopography
pH	Mean	3.88	3.41	4.54	4.23	3.96	3.91	1.97 <sup><i>P</i> = 0.17</sup>	0.76 <sup><i>P</i> = 0.39</sup>	4.2 <sup><i>P</i> = 0.07</sup>
	SE	0.03	0.17	0.30	0.26	0.05	0.07			
DOC (mg L <sup>-1</sup> )	Mean	42.0	40.2	40.7	40.5	47.3	<b>48.5</b>	4.2 <sup><i>P</i> = 0.001</sup>	87.2 <sup><i>P</i> = 0.001</sup>	3.2 <sup><i>P</i> = 0.11</sup>
	SE	4.3	0.8	1.1	0.7	1.0	0.8			
DN (mg L <sup>-1</sup> )	Mean	1.00	0.70	0.74	0.63	0.70	0.71	0.88 <sup><i>P</i> = 0.35</sup>	1.8 <sup><i>P</i> = 0.19</sup>	0.2 <sup><i>P</i> = 0.90</sup>
	SE	0.20	0.03	0.11	0.01	0.01	0.02			
PO <sub>4</sub> <sup>3-</sup> (mg L <sup>-1</sup> )	Mean	1.9	2.3	11.5	<b>10.5</b>	10.1	9.7	8.93 <sup><i>P</i> = 0.001</sup>	28.2 <sup><i>P</i> = 0.001</sup>	0.17 <sup><i>P</i> = 0.69</sup>
	SE	0.2	0.7	2.3	0.2	0.3	0.3			
P <sub>tot</sub> (mg L <sup>-1</sup> )	Mean	12.4	13.4	20.3	19.6	11.7	13.5	0.24 <sup><i>P</i> = 0.78</sup>	0.25 <sup><i>P</i> = 0.61</sup>	0.55 <sup><i>P</i> = 0.47</sup>
	SE	0.4	0.8	2.2	2.2	0.5	2.0			
NH <sub>4</sub> <sup>+</sup> (mg L <sup>-1</sup> )	Mean	55.0	50.2	43.4	51.5	43.2	40.2	1.1 <sup><i>P</i> = 0.31</sup>	5.23 <sup><i>P</i> = 0.03</sup>	4.32 <sup><i>P</i> = 0.07</sup>
	SE	6.2	1.7	2.6	2.8	2.2	9.3			
NO <sub>3</sub> <sup>-</sup> (mg L <sup>-1</sup> )	Mean	8.7	7.7	10.3	<b>4.4</b>	25.7	<b>28.0</b>	6.23 <sup><i>P</i> = 0.02</sup>	21.2 <sup><i>P</i> = 0.001</sup>	0.29 <sup><i>P</i> = 0.59</sup>
	SE	2.0	1.5	4.4	2.6	1.6	1.8			
Phenol (mg.g <sup>-1</sup> DM)	Mean	1.20	1.11	1.00	0.95	1.49	2.31	0.03 <sup><i>P</i> = 0.87</sup>	5.49 <sup><i>P</i> = 0.03</sup>	10.4 <sup><i>P</i> = 0.001</sup>
	SE	0.06	0.07	0.09	0.13	0.20	0.22			

## Figures

**Figure 1:** Microbial community response to climate warming in a *Sphagnum*-dominated peatland. Principal response curve diagrams with scores for microbial functional groups living in the surface (a) ( $P = 0.02$ ) and the litter (b) ( $P = 0.05$ ) layers of the *Sphagnum* carpet. (c) Warming effect on testate amoeba species in relation to the size of their shell-aperture over their body size. The warming effect was determined using the  $F$ -value from ANOVA tests. Testate amoebae that contributed to less than 3% of maximum abundance in all samples were removed from the data set to reduce the influence of rare taxa in this analysis. Lines are regression line, *asterisks* indicate significant regression at  $P < 0.05$  level (ANOVA test).

**Figure 2:** Barplot of the relative contribution of microbial groups to the total microbial community (% of total biomass) living at the surface (a) and litter (b) layers in ambient and warmed conditions. *Asterisks* indicate a warming effect (ANOVA tests). TAS = testate amoebae with a low trophic level; TAB = testate amoebae with a high trophic level.

**Figure 3:** (a) Nitrates ( $\text{NO}_3^-$ ) and (b) labile C (DOC) concentrations plotted against the biomass of testate amoebae with high trophic levels in ambient and warmed plots. Lines are regression line, *asterisks* indicate significant regression at  $P < 0.05$  level (ANOVA test).

**Figure 4:** Total abundance of (a) vascular plants and (b) mosses (expressed as % of mean number of hits). Abundance of (c) *Andromeda polifolia* and (d) *Sphagnum fallax* (expressed as % of mean number of hits). *Asterisks* indicate significant differences between treatments ( $P < 0.01$ , ANOVA tests).



**Figure 5:** Total water-soluble polyphenol content ( $\text{mg.g}^{-1}$  DM) plotted against the biomass of testate amoebae with high size of shell aperture over body size ratio. *Asterisks* indicate significant differences between ambient and warmed plots (ANOVA tests).

**Figure 6:** Structural equation models of above- and belowground components in a *Sphagnum*-dominated peatland subjected to (a) ambient conditions or (b) experimental warming. Biomass of individual microbial groups living in surface and litter layers of *Sphagnum* carpet, percentage cover of moss and vascular plant species, polyphenols produced by *Sphagnum*, and water chemistry matrices were used to build the path-relation network. Dashed arrows indicate negative relationships. Numerals near each path indicate the weight of the path relationship; \*  $P < 0.01$ .

## Supplementary information

**Table S1:** Average biomass ( $\pm$  SE) and average relative abundance (%) of microbial groups in a *Sphagnum*-dominated peatland subjected to experimental warming (WAR) or ambient conditions (AMB) in 2008, 2009 and 2010. Significant warming effect appeared in bold (ANOVA tests).

SURFACE		2008		2009		2010		F-values <sup>P-values</sup>		
		AMB	WAR	AMB	WAR	AMB	WAR	year	microtopography	warming
<b>Bacteria</b>	MEAN	552	554	478	524	540	516	0.12 <sup>P=0.71</sup>	0.12 <sup>P=0.72</sup>	0.001 <sup>P=0.97</sup>
	SE	34	88	88	75	113	85			
	%	28	26	25	<b>31</b>	31	<b>45</b>	0.49 <sup>P=0.49</sup>	1.3 <sup>P=0.28</sup>	14.8 <sup>P=0.009</sup>
<b>Fungi</b>	MEAN	92	65	138	244	114	76	0.02 <sup>P=0.91</sup>	26.1 <sup>P=0.005</sup>	0.60 <sup>P=0.45</sup>
	SE	38	36	36	94	30	14			
	%	5	3	14	7	7	7	0.78 <sup>P=0.39</sup>	28.4 <sup>P=0.003</sup>	4.3 <sup>P=0.052</sup>
<b>Microalgae</b>	MEAN	325	476	515	371	264	226	0.49 <sup>P=0.48</sup>	0.27 <sup>P=0.61</sup>	1.5 <sup>P=0.23</sup>
	SE	78	250	250	104	68	45			
	%	17	22	22	15	15	20	0.53 <sup>P=0.47</sup>	1.3 <sup>P=0.3</sup>	0.01 <sup>P=0.92</sup>
<b>Cyanobacteria</b>	MEAN	28	50	36	16	14	7	1.57 <sup>P=0.23</sup>	0.16 <sup>P=0.69</sup>	2.9 <sup>P=0.11</sup>
	SE	15	20	20	6	6	2			
	%	1	2	1	1	1	1	0.71 <sup>P=0.41</sup>	0.19 <sup>P=0.67</sup>	1.73 <sup>P=0.21</sup>
<b>Ciliate</b>	MEAN	19	<b>60</b>	19	20	21	10	0.85 <sup>P=0.36</sup>	0.05 <sup>P=0.82</sup>	6.28 <sup>P=0.02</sup>
	SE	6	3	3	4	7	4			
	%	1	3	1	1	1	1	0.8 <sup>P=0.41</sup>	0.08 <sup>P=0.78</sup>	2.2 <sup>P=0.15</sup>
<b>Rotifers</b>	MEAN	342	386	140	135	112	<b>87</b>	28.8 <sup>P=0.001</sup>	0.34 <sup>P=0.58</sup>	31.5 <sup>P=0.001</sup>
	SE	78	28	28	32	28	29			
	%	18	18	7	8	6	<b>8</b>	21.1 <sup>P=0.002</sup>	0.23 <sup>P=0.24</sup>	12.2 <sup>P=0.002</sup>
<b>Nematodes</b>	MEAN	68	75	90	71	83	55	0.2 <sup>P=0.68</sup>	3.6 <sup>P=0.09</sup>	0.99 <sup>P=0.33</sup>
	SE	19	26	26	27	37	14			

	%	4	3	5	4	5	5	0.36 <sup>P=0.55</sup>	3.3 <sup>P=0.09</sup>	0.36 <sup>P=0.55</sup>
Testate amoebae (small)	MEAN	35	50	42	43	40	28	0.01 <sup>P=0.91</sup>	0.001 <sup>P=0.97</sup>	3.42 <sup>P=0.08</sup>
	SE	8	9	9	9	16	8			
	%	2	2	2	2	2	2	0.09 <sup>P=0.73</sup>	0.66 <sup>P=0.44</sup>	0.09 <sup>P=0.73</sup>
Testate amoebae (large)	MEAN	479	440	474	<b>283</b>	540	<b>131</b>	0.55 <sup>P=0.47</sup>	5.95 <sup>P=0.03</sup>	21.3 <sup>P=0.001</sup>
	SE	114	86	86	42	78	44			
	%	25	20	25	<b>17</b>	31	<b>12</b>	3.9 <sup>P=0.061</sup>	4.36 <sup>P=0.063</sup>	5.2 <sup>P=0.03</sup>
<b>LITTER</b>										
Bacteria	MEAN	778	847	840	857	718	962	0.15 <sup>P=0.71</sup>	5.8 <sup>P=0.04</sup>	1.1 <sup>P=0.32</sup>
	SE	183	133	133	43	156	159			
	%	29	25	23	25	29	<b>36</b>	1.8 <sup>P=0.19</sup>	0.26 <sup>P=0.66</sup>	11.9 <sup>P=0.002</sup>
Fungi	MEAN	283	436	974	1175	514	569	0.29 <sup>P=0.59</sup>	2.72 <sup>P=0.13</sup>	0.95 <sup>P=0.34</sup>
	SE	36	220	220	256	133	213			
	%	11	<b>13</b>	27	<b>34</b>	21	21	3.8 <sup>P=0.06</sup>	0.2 <sup>P=0.66</sup>	5.1 <sup>P=0.03</sup>
Microalgae	MEAN	178	207	266	281	241	361	0.93 <sup>P=0.34</sup>	5.1 <sup>P=0.05</sup>	2.24 <sup>P=0.15</sup>
	SE	51	70	70	82	66	95			
	%	7	6	7	8	10	<b>14</b>	9.2 <sup>P=0.002</sup>	0.2 <sup>P=0.66</sup>	13.3 <sup>P=0.015</sup>
Cyanobacteria	MEAN	35	27	37	154	41	30	0.05 <sup>P=0.83</sup>	0.001 <sup>P=0.97</sup>	0.32 <sup>P=0.58</sup>
	SE	27	10	10	71	26	18			
	%	1	1	1	4	2	1	0.29 <sup>P=0.59</sup>	0.86 <sup>P=0.38</sup>	1.1 <sup>P=0.30</sup>
Ciliate	MEAN	70	<b>180</b>	37	21	16	15	10.6 <sup>P=0.023</sup>	4.5 <sup>P=0.06</sup>	10.6 <sup>P=0.004</sup>
	SE	24	11	11	5	5	7			
	%	3	<b>5</b>	1	1	1	1	12.4 <sup>P=0.002</sup>	0.45 <sup>P=0.64</sup>	7.5 <sup>P=0.01</sup>
Rotifers	MEAN	436	<b>637</b>	222	225	118	<b>83</b>	32.6 <sup>P=0.001</sup>	1.6 <sup>P=0.24</sup>	31.9 <sup>P=0.001</sup>
	SE	53	39	39	60	39	36			
	%	16	<b>19</b>	6	6	5	<b>3</b>	73.1 <sup>P=0.001</sup>	0.65 <sup>P=0.44</sup>	38.7 <sup>P=0.001</sup>
Nematodes	MEAN	162	222	298	136	119	126	0.52 <sup>P=0.47</sup>	0.02 <sup>P=0.89</sup>	2.65 <sup>P=0.12</sup>
	SE	48	88	88	26	32	42			
	%	6	6	8	4	5	5	0.29 <sup>P=0.59</sup>	0.86 <sup>P=0.38</sup>	1.1 <sup>P=0.30</sup>
Testate amoebae (small)	MEAN	180	323	364	192	150	217	0.31 <sup>P=0.58</sup>	0.03 <sup>P=0.86</sup>	0.48 <sup>P=0.49</sup>
	SE	27	99	99	23	34	143			

	%	7	9	10	6	6	8	0.12 <sup>P=0.74</sup>	2.24 <sup>P=0.17</sup>	2.8 <sup>P=0.11</sup>
<b>Testate amoebae (large)</b>	MEAN	543	561	604	438	521	307	0.06 <sup>P=0.93</sup>	4.9 <sup>P=0.051</sup>	3.85 <sup>P=0.063</sup>
	SE	64	179	179	118	232	99			
	%	20	16	17	<b>13</b>	21	<b>11</b>	0.22 <sup>P=0.64</sup>	0.44 <sup>P=0.45</sup>	10.7 <sup>P=0.004</sup>













