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Title: Do testate amoebae communities recover in concordance with vegetation after

restoration of drained peatlands?

Year: 2016

Version:

Please cite the original version:

Daza Secco, E., Haapalehto, T., Haimi, J., Meissner, K., & Tahvanainen, T. (2016). Do testate amoebae communities recover in concordance with vegetation after restoration of drained peatlands?. Mires and Peat, 18, Article 12. https://doi.org/10.19189/MaP.2016.OMB.231

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- 1 DO TESTATE AMOEBAE COMMUNITIES RECOVER IN CONCORDANCE WITH VEGETATION
- 2 AFTER RESTORATION OF DRAINED PEATLANDS?

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11 ABSTRACT

- 12 The environmental importance of peatlands has raised efforts to restore their specific ecosystem functions
- 13 and structure. Monitoring and assessment of peatland ecological state is fundamental in restoration programs.
- 14 However, most studies have focused on the responses of vegetation and, to a lesser extent, on testate
- 15 amoebae (TA). To our knowledge, none have addressed whether these two groups show concordance with
- 16 respect to drained peatland restoration. Here we assessed community concordance between TA and
- vegetation among boreal peatlands of four different landuse management classes (natural, drained, restored
- 18 3–7 and 9–12 years ago). TA and vegetation communities were concordant when comparing all sites studied.
- 19 However, there was no concordance within management classes except for the sites restored 3–7 years ago.
- We found that TA and vegetation communities are not surrogates of each other when measuring restoration
- 21 success and that a holistic understanding of the changes during restoration from an ecosystem perspective
- 22 requires thorough studies of both communities. TA seemed to respond faster to changes caused by
- 23 restoration hence, could be a better early indicator of restoration success than plants. Further, studies of TA
- 24 and plant communities' relationships could provide important insights into understanding the link between
- 25 the recovery of ecosystem structures and functions.
- 26 Key words: Assessment, ecological state, monitoring, indicators of restoration, taxa surrogates.

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INTRODUCTION

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Peatlands of the boreal and subarctic regions cover only 3% of the global land area. Due to the accumulation of organic matter as peat during hundreds to thousands of years, they store ca. 500Gt of C corresponding to one third of the global soil C (Yu 2011, Yu 2012). Like many other ecosystems, peatlands have been heavily exploited. In Finland, more than 50% of the total peatland area has been drained for forestry, 2.6% for agriculture and 0.6% for peat mining (Lappalainen 1996, Vasander et al. 2003). Peatland use is mainly concentrated to central and southern Finland where pristine peatlands now correspond to less than 25% of their original area (Aapala et al. 1996). The increasing threat of environmental degradation has raised awareness of ecological restoration as part of conservation programs (Dobson et al. 1997). The environmental importance of peatlands has led to a growing number of attempts to restore or partially rehabilitate the surface water retention, carbon sink, and specific flora and fauna (Lunn & Burlton 2013). Monitoring and assessment of ecological state is a fundamental part of peatland conservation and restoration programs (Trepel 2007). Studies based on the assessment of the plant community composition after restoration practices have shown promising results (e.g. Haapalehto et al. 2011, Laine et al. 2011, Hedberg et al. 2012, Poulin et al. 2013). However, little is known about changes in the microorganism communities of restored peatlands. Testate amoebae (TA) are a polyphyletic group of shell-building, unicellular protists (Meisterfeld 2002), commonly associated with peatland plants, and especially abundant in Sphagnum mosses (Tolonen 1986). In peatlands, the number of TA can be as high as 16 x 10⁶ individuals per m², making them a significant component of peatland heterotrophic soil community (Sleigh 1989). TA diversity and distribution in bogs is mainly controlled by hydrological variables (e.g. moisture content and water table depth), and in fens by water pH, oxygen concentration, and peat composition (Charman 1997, Bobrov et al. 1999). Depending on taxa and environmental conditions, their generation time ranges from days to weeks, while that of bryophytes and vascular plants is much longer (Schönborn 1986). Under natural conditions, TA communities are stable between seasons (Warner et al. 2007) but when conditions change, they can change within months (Marcisz et al. 2014). Koenig et al. (2015) found that TA provide more accurate information on microenvironmental conditions compared to vegetation, and knowing all the TA taxa is not necessary to obtain valuable ecological information. Thus, TA communities have been proposed as a tool for monitoring and assessment of peatland

conditions, but to date TA have been employed in relatively few studies (e.g. Jauhiainen 2002, Davis & Wilkinson 2004, Raabe & Lamentowicz 2012, Turner & Swindles 2012, Koenig *et al.* 2015).

Well-known taxonomic groups are usually those used as biological indicators in assessment and monitoring of ecosystem health, i.e. the ecosystem's ability to maintain its structure and function when facing external stress (Costanza & Mageau 1999). However, the degree to which certain taxonomic groups actually mirror trends among other groups and can be used as surrogates is still unknown, and studies based on the surrogate-taxa approach have repeatedly been questioned (e.g. Paavola *et al.* 2003, Bilton *et al.* 2006). Most bioassessment studies focus on single taxonomic group responses to environmental factors while few have addressed parallel group responses (i.e. concordance). Community concordance describes the degree of similarity in distributions and abundances of different taxonomic groups across a region and emerges when different communities show similar responses to environmental changes (Infante *et al.* 2009). Studies that have investigated concordance have mostly focused on lakes and fluvial systems (e.g. Heino 2002, Mykrä *et al.* 2008, Infante *et al.* 2009, Jyväsjärvi *et al.* 2014) and very few have examined such patterns for peatland ecosystems (Mitchell *et al.* 2000a, Lamentowicz *et al.* 2010, Hájek *et al.* 2014, Koenig *et al.* 2015, Hunter Jr *et al.* 2016).

Aspects driving community concordance include strong species interactions within and between communities (Heino 2002) and co-losses of species in response to environmental stress, including anthropogenic stressors (Mykrä *et al.* 2008, Yates & Bailey 2010). Life histories and reproductive and dispersal capabilities of taxa could influence the extent to which different environmental factors and biotic interactions drive spatial patterns of community composition and subsequently, community concordance (Shurin *et al.* 2009). Being based on species identities instead of only number of species, community concordance provides a wider understanding of similarities between communities than richness measures alone (Pawar *et al.* 2007). Further, when concordance does not occur among taxonomic groups at a specific geographical scale, the use of a single group as an indicator for the state of the ecosystem may not be appropriate (Paavola *et al.* 2006).

Studies examining peatland restoration efforts generally focus on the recovery of vegetation, but whether important microorganisms such as TA are concordant in their responses to restoration and how these responses are linked to general ecosystem functions remains an open question. Because TA are especially common in *Sphagnum* and other mosses, they may potentially be concordant with peatland vegetation. We

therefore assessed concordance of the changes in TA and plant community structures among natural, ditched, and restored boreal peatlands. We specifically aimed i) to analyse changes and concordance between TA and plant communities in response to restoration processes, and ii) to identify which environmental variables drive the changes in these two communities.

METHODS

Study sites

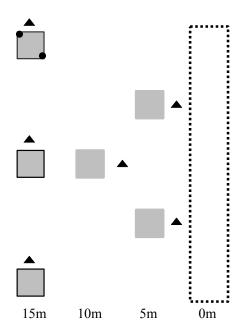
Study sites were located in the south-boreal climatic-phytogeographical zone of Southern Finland between $61^{\circ} 53'-62^{\circ}51'N$ and $22^{\circ}53'-25^{\circ}26'E$. In this region, the larger peatland formations are mainly raised bogs, while small weakly minerotrophic *Sphagnum*-dominated mires are typically found in a mosaic landscape pattern with coniferous forests. Sampling sites are located ca. 150m above sea level with a mean annual temperature of $+4^{\circ}C$ and precipitation ca. 650mm. We selected 19 study sites divided in four land use management classes: i) natural (n=5), ii) drained (n=4), iii) drained and restored 3–7 years before the sampling (n=5), and iv) drained and restored 9–12 years before the sampling (n=5). For brevity, management classes will hereafter be referred to as Natural, Ditched, Res05, and Res10.

Selection of pine fen sites of low minerotrophy was based on field observations and historic aerial photographs ensured that original tree stands of the drained and restored sites were similar. Sites consisting of naturally similar type of vegetation were located in a mosaic of ombro-mesotrophic peatland vegetation, where *Sphagnum* was the main peat-forming plant genus. Based on topographic data and field observations, surface water flow was considered independent for each management class. Peat depth ranged from 95cm to more than 200cm with underlying soil of till or sand.

Sites without altered hydrology by ditches or other direct measures represent the least impacted management class and are subsequently referred to as "Natural". Even though we acknowledge that forestry measures in distant parts of Natural site catchments may have slight impacts on their hydrology (Tahvanainen 2011), such effects were not obvious. Ditched and Restored sites were drained for forestry purposes during the 1960s and 1970s. During the 1980s, peatlands were restored by filling in the ditches and by removing trees in areas where drainage had significantly increased tree growth. More detailed information about the studied peatlands is given in Haapalehto *et al.* (2014).

Field sampling and sample processing

A grid of 20 1m² plots was established at each site (Figure 1). At the Ditched and Restored sites, the plots were situated in five parallel transects, spaced four meters apart and running perpendicular to the ditch. At each transect, there was a plot at 5, 10 and 15 meters distance from the ditch. A 15m x 20m grid of plots was used at the Natural reference sites. Within each of the study sites, the location of the first plot was randomised.



- Sampling plots, Natural sites.
- □ Sampling plots, Ditched, Res05 and Res10 sites.
- Pipe wells for WTD measurement. Two/sampling plot.
- ▲ Pipe well for water samples.
- Ditch (ditched sites), filled ditch (restored sites).

Figure 1. Study sampling design for: testate amoebae, plants and environmental variables. Distances (m) refer to distance of the 1m² plots to the ditches at the Ditched and Restored sites. At Natural sites, a similar arrangement of plots was used. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

For water chemistry analyses at the Natural sites, three 32mm diameter polypropylene pipe wells with 2mm slits spaced at 2–3cm intervals and polypropylene filter gauges were distributed in the central part of the sampling grid. At the Ditched and Restored sites filter gauges were set at a distance of 15m to the ditch and 10m apart (Figure 1). Samples were collected in August 2007. Redox potential (Eh₇), electrical conductivity (EC) and pH were measured between two to five hours after sample collection using a Consort

SP50X meter with SP50X, SK10T and SP10B electrodes, respectively. Samples were then stored in darkness at +4°C before further analysis. Cation concentrations (Al, Ca, Fe, K, Mg, Na) were obtained after filtration with 0.45 µm pore size filters and analysed with a PerkinElmer Optima 4300 DV inductively coupled plasma optical emission spectrometer. Water table depth (WTD) was measured five times (May, June, July, August, and September) in 2008 in selected plots from two permanent polypropylene pipe wells. WTD values were corrected for the natural slope (see Haapalehto *et al.* 2014) and averaged to absolute levels throughout the site. WTD data are usually recorded as negative values, but to facilitate the readability, inverse, positive values are used here throughout the text.

Plants and TA were sampled from the plots located next to the polypropylene pipe wells (three plots at each site). We estimated the relative abundance (percentage of coverage) of each taxon of vascular plants, bryophytes, and some lichens for each sampled plot. Sampling was done during July and August 2007. To obtain TA, approximately 10cm³ of bryophyte mass was extracted (see also Booth *et al.* 2010). Samples were stored in plastic Ziploc bags, frozen, defrosted and oven dried, stored in paper bags and analysed in 2013 using the protocol proposed by Booth *et al.* (2010). To retain TA, each sample was boiled for 10 minutes in distilled water with one tablet of *Lycopodium clavatum* spores (batch 1031) standard preparation from Lund University (Sweden), and sieved it through a 300µm mesh to remove coarse materials and onto a 7µm mesh. Retained TA were centrifuged at 3000 rpm for five minutes and stored in distilled water. A minimum of 150 TA was counted and identified using 40X magnification (Olympus BX41 microscope). As the standing plant community is the result of several years of development, non-living TA were also included in the analysis to integrate the accumulation of tests over the entire time period. TA identification was based on characteristics of the shell following a number of different taxonomic keys (e.g. Charman *et al.* 2000 with modifications by Booth 2008, Meisterfeld 2002, Clark 2003, Mitchell 2003a, Mitchell 2003b, Mazei & Tsyganov 2006).

Data analysis

We calculated species richness, Shannon diversity index, and relative abundances of TA and vegetation communities for each site (using plot averages), and averaged by management classes. For TA communities, density was estimated using the *Lycopodium* counts as an external marker (see Stockmarr 1971 for details) and relative abundances were calculated as a percentage of the total counted. ANOVA and Tukey's (HSD)

post hoc test were performed to assess differences in species richness and Shannon diversity indices between management classes. Due to the unbalanced design, permutational MANOVA (PerMANOVA) was used to test the significance of the differences in structure and composition among the communities in the four management classes. Differences in water chemistry and WTD were analysed using ANOVA or Kruskal-Wallis depending on whether the data met the normality and homoscedasticity assumptions. To summarise variability in the communities, a Non-metric Multidimensional Scaling (NMDS) based on Sørensen's (Bray-Curtis) distance was performed. We used NMDS to examine the degree of concordance of water chemistry variables with community ordinations. WTD was not included in the community ordinations, as these data were not taken at exactly the same time as the biological samples. A two dimensional NMDS solution achieved a moderate stress level for plant communities but not for TA communities; however, for simplicity of comparison we retained the two dimensional TA solution. Concordance between TA and plant communities was tested using the PROTEST analysis (Peres-Neto & Jackson 2001). All calculations were done using R (version 3.0.2) and the vegan package for NMDS and PROTEST analyses (Oksanen *et al.* 2015).

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176 RESULTS

- 177 Community data
- Altogether 44 TA and 45 plant taxa were found in our study. TA taxon richness at Natural sites (\bar{X} = 17.7
- range 14–24, SE= 0.71) was higher than at Ditched, Res05, and Res10 sites (ANOVA $F_{11.31}$ = 15.79, p<
- 180 0.001) whereas no differences were found among Ditched, Res05, and Res10 sites (Table 1; Figure 2a). TA
- Shannon diversity index was generally higher at Natural sites, where the highest value was 2.56, while the
- lowest values were found at Res05 sites (Figure 2c). We observed differences in TA diversity only between
- Natural-Res05 and Natural-Res10 sites (Table 1). The highest cell density was found at Res10 sites (\bar{X} =
- 184 24953 cells/10cm³) and the lowest at Ditched sites (\bar{X} = 6767 cells/10cm³).

- Table 1. Tukey's (HDS) results for TA taxon richness and Shannon diversity. Res05: peatlands restored 3-7
- years ago; Res10: peatlands restored 9-12 years ago.

			Ric	hness	Shannon Diversity					
		Difference	lower bound	Upper bound	p	Difference	lower bound	Upper bound	p	
Natural	Res05	5.47	3.00	7.94	< 0.001	0.64	0.23	1.04	0.002	
	Res10	-5.47	-7.94	-3.00	< 0.001	-0.60	-1.00	-0.19	0.003	
	Ditched	4.64	1.96	7.33	< 0.001	0.31	-0.12	0.74	0.205	
Res05	Res10	0.00	-2.47	2.47	1.000	0.04	-0.37	0.44	0.993	
	Ditched	-0.82	-3.51	1.86	0.847	-0.33	-0.76	0.10	0.171	
Res10	Ditched	-0.82	-3.51	1.86	0.847	-0.29	-0.72	0.14	0.253	



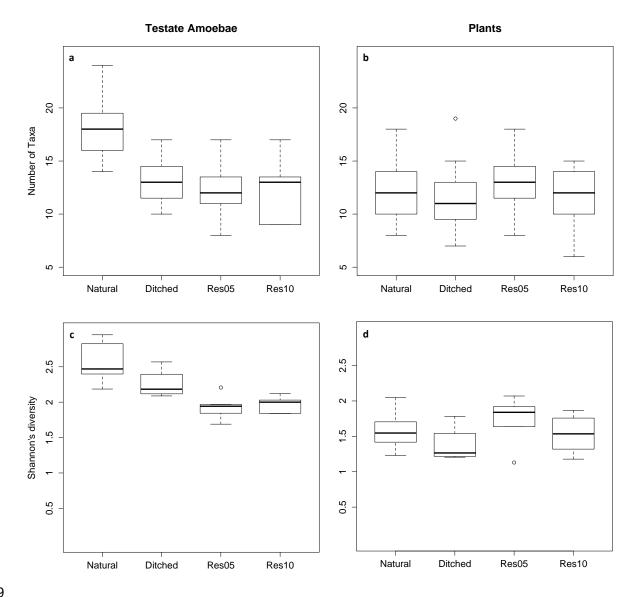


Figure 2. Taxon richness boxplots for testate amoebae (a) and vegetation (b). Shannon's diversity boxplots for testate amoebae (c) and vegetation (d) for each management class. Circles: outliers, upper whisker: maximum value excluding outliers, upper box line: upper quartile, middle line inside box: median, lower box line: lower quartile, lower whisker: minimum value excluding outliers. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

No differences in the mean number of plant taxa were found between management classes (Figure 2b). In general, plant diversity tended to be higher at Res05 sites but, overall, there were no significant differences between classes (F = 0.9, p = 0.46; Table 1; Figure 2d). TA community structure and composition differed between classes except between Res05 and Res10 (Table 2). For vegetation communities, only Natural sites differed from all other classes (Table 2, see also Haapalehto 2014).

Table 2. PerMANOVA pairwise comparisons for TA and plant community structure and composition. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

	_	TA						Plants					
	_	df	SS	MS	Pseudo- F	r²	p	df	SS	MS	Pseudo-F	r²	p
Natural	Res05	1	0.28	0.28	2.74	0.25	0.021	1	0.44	0.44	3.23	0.29	0.042
	Res10	1	0.29	0.29	4.02	0.33	0.016	1	0.15	0.15	1.83	0.19	0.047
	Ditched	1	0.48	0.48	4.90	0.41	0.006	1	0.46	0.46	4.11	0.37	0.016
Res05	Res10	1	0.09	0.09	1.36	0.15	0.259	1	0.33	0.33	2.35	0.23	0.104
	Ditched	1	0.36	0.36	3.90	0.36	0.036	1	0.12	0.12	0.66	0.09	0.499
Res10	Ditched	1	0.59	0.59	10.17	0.59	0.010	1	0.35	0.35	2.98	0.30	0.093

On average, TA communities in Natural, Res05, and Res10 sites were mainly dominated by *Arcella catinus* and *Bullinularia indica*. At Ditched sites, *Trigonopyxis arcula* was the most widely dominant taxon followed by *A. catinus*. More than 50% of the TA species were found over all sites regardless of management class, but some species displayed a more restricted distribution. For example, *Arcella artocrea*, *Centropyxis ecornis*, *Difflugia leidyi*, *Difflugia lithophila*, *Hyalosphenia minuta* and *Pseudodifflugia fascicularis* were present just at Natural sites while *Hyalosphenia elegans* and *Physochila griseola* were absent from Ditched and Res05 sites (Table 3). Vegetation communities were dominated by *Sphagnum angustifolium* at all sites regardless of management class. However, densities were highly variable. *Pleurozium schreberi* was the second most dominant species at Res05 and Ditched sites, while at Res10 and Natural sites *S. magellanicum* and *S. fuscum* were more abundant (see Haapalehto 2014).

Table 3. TA average relative abundances in percentage and standard deviations for each management class.

(*) Taxa found just at natural sites; (**) taxa found at Natural and in sites restored 10 years ago; (***) taxa found at all but Ditched sites; (****) taxa found just at Ditched sites. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

		Treatments							
	Taxa	Natural		Ditched		Res05		Res10	
		X	SD	X	SD	X	SD	X	SD
*	Arcella artocrea	0.78	1.56	0	0	0	0	0	0
*	Centropyxsis ecornis	0.09	0.33	0	0	0	0	0	0
*	Difflugia leidyi	0.05	0.17	0	0	0	0	0	0
*	Difflugia lithophila	0.04	0.17	0	0	0	0	0	0
*	Trydrosphenia minuta	0.53	0.85	0	0	0	0	0	0
*	i seudodijjiugia jaseieutaris	0.04	0.16	0	0	0	0	0	0
**	Hyalosphenia elegans	3.60	3.93	0	0	0	0	0.22	0.48
**	Physochila griseola	0.67	1.03	0	0	0	0	0.09	0.35
***	Heleopera petricola	2.56	3.76	0	0	0.34	0.63	0.12	0.34
****	Arcella vulgaris	0	0	0.11	0.37	0	0	0	0
****	Euglypha compressa	0	0	0.11	0.37	0	0	0	0
****	Hyalosphenia subflava	0	0	0.12	0.41	0	0	0	0
****	Phryganella acropodia	0	0	0.06	0.19	0	0	0	0
****	Trigonopyxis minuta	0	0	1.14	3.79	0	0	0	0
****		0	0	0.34	0.81	0	0	0	0
	Archerella flavum	6.02	6.27	0.06	0.19	0	0	0.53	1.71
	Arcella catinus	20.96	20.17	14.05	16.46	37.44	17.27	44.95	30.18
	Arcella discoides	0.13	0.49	0.41	1.03	0.48	1.17	0.16	0.63
	Argynnia vitrea	0.18	0.52	0	0	0.04	0.16	0	0
	Assulina muscorum	4.86	4.54	4.92	2.85	3.62	2.62	3.03	3.18
	Assulina seminulum	0.56	0.89	0.29	0.62	0.09	0.24	0.04	0.17
	Bullinularia indica	8.43	5.41	13.08	10.94	16.81	19.60	10.21	11.62
	Centropyxis aculeata	1.18	2.90	2.29	4.92	0.29	1.11	1.93	4.17
	Centropyxis cassis	0.05	0.17	6.61	6.38	2.02	5.41	0.24	0.65
	Centropyxis platystoma	0	0	0	0	0.04	0.17	0	0
	Corythion spp.	1.95	2.93	3.47	3.71	4.23	3.67	3.93	5.70
	Cyclopyxis arcelloides	0.48	0.66	6.01	5.82	0	0	0.35	0.66
	Difflugia globulosa	0.04	0.16	2.33	5.04	0	0	0.13	0.51
	Difflugia lucida	0.11	0.30	0.06	0.20	0.04	0.17	0	0
	Euglypha rotunda	3.55	4.16	0.97	1.61	0.83	1.04	3.00	3.39
	Euglypha strigosa	3.79	3.30	1.23	1.60	3.01	2.86	2.36	2.31
	Euglypha tuberculata	1.23	2.07	3.97	6.65	3.65	3.29	2.07	4.09
	Heleopera rosea	1.23	1.81	0.18	0.31	0.45	1.23	0.95	1.36
	Heleopera sphagni	5.86	9.24	0.28	0.74	0.68	1.24	0.22	0.48
	Heleopera sylvatica	3.02	4.12	0.18	0.43	0.68	1.28	0.47	0.56
	Hyalosphenia papilio	7.99	8.01	0.29	0.61	4.43	9.75	8.97	10.84
	Nebela bohemica	0	0	0	0	0.04	0.15	0.71	2.06
	Nebela flabellulum	0	0	0	0	0.04	0.16	0.71	0
	Nebela militaris	4.21	3.74	2.03	3.49	3.15	3.99	1.07	1.11
	Nebela parvula	1.12	1.86	0.17	0.57	0.22	0.86	0.27	0.55
	Nebela tincta	5.34	3.42	5.75	6.01	5.15	4.61	4.65	3.41
	Pseudodifflugia fulva	0.04	0.17	0.43	1.43	0	0	0	0
	Trigonopyxis arcula	5.13	5.80	26.61	15.36	7.24	5.86	3.22	3.63
	Trinema lineare	4.17	6.44	2.43	3.23	4.99	4.59	6.10	7.17

Community-environment relationships and community concordance

Water chemistry did not vary significantly between sites (Table 4). However, in some cases (mainly for Al and Mg) chemical concentrations were below the detection limits and were recorded as 0. In general, the highest mean values for studied elements were recorded at Ditched sites except for Fe (Figure 3). WTD varied between the management classes (Table 4) and between months, with the lowest depths recorded at the Ditched sites (Figure 4).

Table 4. ANOVA (*) and Kruskal-Wallis (**) for water chemistry variables. Calculations are based on average values for each site over all management classes.

	df	x²/F	р
*Al	3	2.47	0.481
*Fe	3	2.97	0.397
*Mg	3	4.72	0.194
*Ca	3	7.30	0.063
*K	3	5.14	0.162
**Na	3	2.75	0.079
**EC	3	0.27	0.843
**pH	3	0.89	0.470
**Eh ₇	3	2.06	0.148
**WTD	3	4.16	0.025

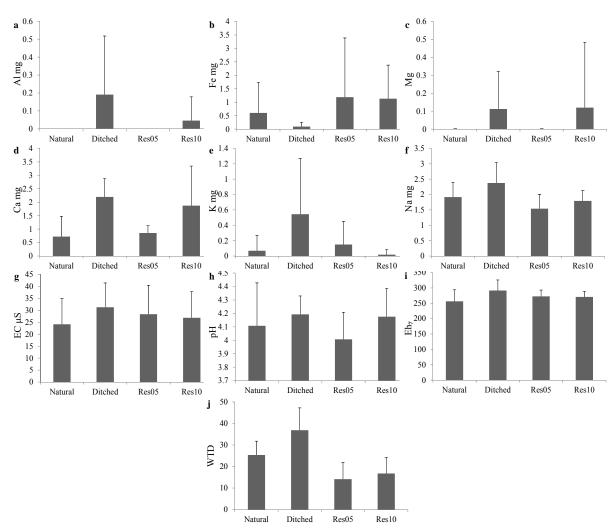


Figure 3. Average values and standard deviations of the environmental parameters measured for each land use management class. (a) aluminum, (b) iron, (c) magnesium, (d) calcium, (f) potassium, (g) conductivity,

(h) pH, (i) redox potential, (j) water table depth. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

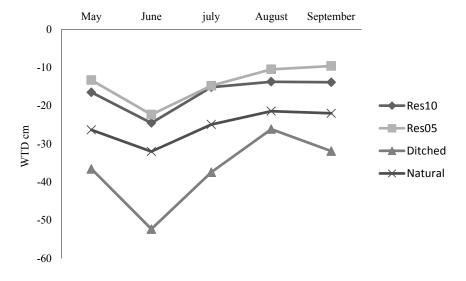


Figure 4. Monthly water table depth variation in 2007. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

A two-dimensional solution NMDS ordination of the TA communities produced the lowest stress at= 0.207. Ca and K were significantly correlated with TA community variability (p= 0.02 and p= 0.01, respectively; Figure 5a). The ordination of the plant community resulted in a two-dimensional solution (final stress= 0.168) with significant relation to Fe (p<0.01), K (p<0.01) and Na (p= 0.04; Figure 5b).

NMDS plots grouped TA communities by management classes. A separation for the communities between the Ditched and Natural sites was observed on NMDS1. Res05 sites were mainly grouped in the centre of the ordination and overlapped with all other management classes, while Res10 sites were fully separated from Ditched sites, and more closely grouped to Natural sites (Figure 5a). Ordination of plant communities showed higher variations compared to TA and less clear separation along NMDS1; however, group separation was observed for Natural and Ditched sites (upper left and central right in the ordination, respectively). Res05 was mostly grouped closer to Ditched sites overlapping only partly with Res10, whereas Res10 sites clustered closer to Natural sites (Figure 5b).

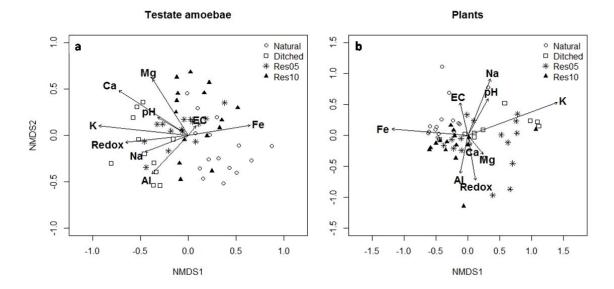


Figure 5. NMDS ordinations of testate amoebae (a) and plant community (a) relationships among management classes. Distance measure: Sørensen (Bray-Curtis). Arrow lengths represent the vector loadings of environmental variables. Res05: peatlands restored 3-7 years ago; Res10: peatlands restored 9-12 years ago.

To look for concordance between plant and TA communities we first ran separate analyses to compare TA to moss species and TA to vascular plant species (results not shown). However as no differences were found, both moss and vascular plants were grouped to form a plant community in all subsequent analyses. We found a significant but weak concordance between TA and plant communities (PROTEST r=0.44, $m^2=0.79$, p=0.001). To assess whether TA and plant communities were concordant within classes, we ran PROTEST separately for each. Results indicated that only communities at Res05 sites were concordant, but even this relation was weak (PROTEST r=0.54, $m^2=0.70$, p=0.01).

DISCUSSION

Natural sites showed higher TA richness with more diverse communities than other management classes. However, we did not find similar results for plant species richness. Res10 sites showed the lowest TA richness and diversity, which could be attributed to the high dominance of *Arcella catinus* at many of the sites, where this species accounted for more than 70% of the community. Spatial limitation is less likely to occur in soils compared to aboveground environments (Wanner & Xylander 2005). Hence, TA might face less competitive pressure as different taxa may simply occupy different ecological niches, whereas plant

272 species tend to compete for the same space and nutrients. As Natural sites have not undergone extreme 273 environmental changes compared to the other management classes, their higher taxon richness could be 274 attributed to a longer time for cumulative colonisation without a significant TA taxon replacement. This 275 supports the observations by Wanner & Xylander (2005) who studied TA colonisation and successional 276 processes, and found temporal changes in TA species composition but no or very little species replacement. 277 Restoration efforts to rehabilitate peatlands focus mainly on raising the water table to recreate natural 278 habitat conditions. Substratum moisture is often found to be the main factor controlling TA communities 279 (Tolonen 1986) particularly in Sphagnum dominated peatlands (Booth 2001) with higher densities of TA 280 cells usually found in soils with a high water holding capacity (Fournier et al. 2012). Despite the lack of 281 corresponding moisture data, we assume that restoration measures increased peat moisture due to elevated 282 water table levels. As a consequence, increasing TA cell densities should be expected at restored sites over 283 time. We did observe such patterns, as the highest TA densities were found at Res10 sites and the lowest at 284 Ditched sites. 285 Testate amoebae communities at the wettest sites (Natural, Res10, and Res05) were mostly dominated by 286 A. catinus and B. indica while at Ditched sites, taxon dominance shifted towards T. arcula. However, both A. 287 catinus and B. indica were highly abundant across all sites suggesting that despite these species are 288 considered indicators of dry conditions, they can display a broad moisture tolerance. Some less abundant 289 species, such as A. artocrea, C. ecornis, D. leidyi, D. lithophila, H. minuta, and P. fascicularis, were found 290 exclusively at Natural sites. This suggests that not all species recolonize even within a decade after 291 restoration. Poor re-colonization of some typical plant species after restoration (Haapalehto et al. 2011, 292 Hedberg et al. 2012) highlights the need to avoid degradation of natural habitats, as species that disappear 293 from a site may be very difficult to reinstate without costly and uncertain re-introduction programs (see also 294 Moreno-Mateos et al. 2015). H. elegans and Ph. griseola only occurred at Natural sites and sites restored 10 295 years ago, suggesting that they either have a longer recolonization time, or that disturbed habitats are just not 296 appropriate for those species. Among plant species, S. angustifolium remained dominant across all sites. This 297 species has a wide ecological niche, and is known to survive in drained peatlands. However, S. angustifolium 298 densities increased rapidly following restoration measures (Haapalehto et al. 2011). 299 Ordinations showed significant relationship of TA communities with Ca and K. Strong relationships 300 between Ca and TA communities have been reported before (e.g. Lamentowicz et al. 2010, Hájková et al.

2011, Raabe & Lamentowicz 2012, Jassey *et al.* 2014). These could be due to the importance of Ca for the shell building process of some TA species (Lamentowicz *et al.* 2011). TA relationships with other nutrients have also been observed (e.g. Mitchell *et al.* 2000a, Jauhiainen 2002, Mitchell *et al.* 2004) but their direct effects on TA are not fully understood. Such correlations could arise when water chemistry and nutrient availability indirectly affect TA communities by controlling their prey organisms such as bacteria, fungi, other Protista, and micrometazoa (Mitchell *et al.* 2004).

Plants were strongly related to levels of K and Fe, indicating the vital importance of pore water chemistry. The highest K concentrations were found at Res05 sites, and the lowest in Natural and Res10. As an easily leachable cation, K may be released from dying biomass and rewetted organic material after hydrological restoration. Hence the lower concentrations of K in pore water at Res10 sites might indicate that K is efficiently taken up during the regrowth of *Sphagnum* and other peatland species. Additionally, after ditch filling small ponds, topographically lower areas are formed at restored sites enabling the establishment of anaerobic and reducing conditions that could favour reduction of Fe³⁺ to Fe²⁺ (Haapalehto *et al.* 2014). This reduced form of Fe is readily available for uptake by plants and facilitates plant regrowth.

In NMDS ordination vegetation communities displayed more within-class variation compared to TA. While TA communities differed between Ditched & Res5 (PerMANOVA) plants did not show differences. These results suggest that TA taxa might be better suited than plants as indicators of early restoration success thanks to their rapid response to hydrological variations. This indeed was observed by Warner & Chmielewski (1992) who found changes in TA taxa composition within 2½ years of peatland drainage. Further, also Talbot *et al.* (2010) who studied peat cores of drained peatlands found that TA species indicative of dry conditions reached their highest percentages around the time of drainage, suggesting a very quick response potential of the TA communities to environmental disturbance. Our results highlight the severity of hydrological disturbance by drainage as TA communities still displayed clear differences from those at Natural sites even a decade after restoration. Observed long-term drainage impacts on TA are paralleled by changes in plant communities after drainage (Laine *et al.* 1995, Kareksela *et al.* 2015). From visual inspection of NMDS, vegetation communities 10 years after restoration appeared more similar to Natural sites. Further, Maanavilja *et al.* (2014) suggested that only a large rise in the water table level would induce significant changes in vegetation communities. Indeed, in our study plants were sampled 15m from the ditch where water table changes to drainage and restoration are smallest and where plant community

compositions still largely overlap (Haapalehto *et al.* 2015, Kareksela *et al.* 2015). Finally, Wardle (2002) pointed out that aboveground vegetation communities and soil microorganisms differ in their resistance, resilience, adaptation strategies, and dispersal abilities. These differences might also relate to the observed time lags in responses of TA and plant communities to restoration measures.

When comparing all sites, TA and vegetation communities were concordant although this relationship was weak. When each management class was separately analysed we found no within management class community concordance except for Res05 sites. Some studies on stream community concordance (e.g. Infante *et al.* 2009) have suggested a scale dependency, which could explain the observed patterns. However, the fact that TA and vegetation community concordance was found to be weak, and the apparent lack of within-class community concordance suggest that TA and vegetation community composition are determined in different ways except during early post-restoration. Our results thus suggest that either overall communities i) respond differently to the same set of environmental factors, or ii) are affected by different environmental factors over timespans exceeding 5 years, or iii) have different time scales of succession processes, and/or iv) display low overall interaction. Additionally, Hájek *et al.* (2014) from their comparison of vascular plants, bryophytes, fungi, diatoms, desmids, and TA suggested that body size and life span play a key role when determining concordance between communities.

In peatland ecosystems, microtopographic transitions can occur at scales of a few centimetres reducing the ability to avoid ecological gradients when sampling. Even though microtopographic transitions at the centimetre scale are specifically important when designing the sampling, even smaller gradients may still exist at the scale of TA (Mitchell *et al.* 2000b). This vertical variation is mainly caused by differences in the chemical composition of ground water and rainwater and is enhanced by *Sphagnum* cation exchange (Mitchell *et al.* 2000a). As moss species and TA are dependent on microsite conditions, they might reflect different conditions than vascular plants, which are rooted at different depths (Mitchell *et al.* 2000a). However in separate analyses to compare TA to moss species and TA to vascular plant species we found no differences in concordance patterns (results not shown). Restoration strategies such as rewetting of drained peatlands aim mainly at restoring the vegetation coverage of sites (e.g. Similä *et al.* 2014). To this end, plant communities are obvious indicators of restoration success. However, our results suggest that restoration effects on other components (e.g. TA communities) in peatlands might not be reflected properly by the use of vegetation-based indicators alone. Gilbert *et al.* (1998) studied the microbial loop in peatlands and revealed

that TA can account for almost half of the microbial community using a wide range of organisms as prey. Through their feeding TA regulate bacterial biomass, contribute to nutrient mineralisation, nutrition of soil animals, and plant growth. Griffiths (1994) found that, in general, Protista and mainly TA can account for 20-40% of N mineralisation as they excrete bacterial N into the soil. As the TA communities of Res05 sites were more similar to the targeted original ecosystem than Ditched ones, restoration by rewetting appears to be efficient in inducing a rapid recovery of an important structural ecosystem component. While the relationship is still poorly understood, previous studies suggest that recovery of some important ecosystem functions like surface peat accumulation precedes the recovery of ecosystem structure (Kareksela et al. 2015). In accordance with that study, our results suggest that the recovery of TA community structure precedes that of plants and in fact may even be a prerequisite for the recovery of higher plants and ecosystem functions. Thus, TA might play a fundamental role in the facilitation of plant succession by providing nutrients and consolidating the assembly process on newly exposed land surfaces (Hodkinson *et al.* 2002). In conclusion, despite some similarities in early responses, TA and vegetation communities cannot be used as surrogates of each other when measuring restoration success. To gain a holistic understanding of the changes in important ecosystem components during restoration from an ecosystem perspective requires the use of both vegetation and TA communities as also suggested by Raabe and Lamentowicz (2012). However, the shorter generation time of TA compared to vegetation enable them to respond faster to environmental changes making them better suited as early indicators of restoration success particularly because postrestoration successional changes in TA communities appear to be targeted towards the re-establishment of the site's original community composition. Our results also suggest that further studies on the relationship between TA and plant communities could provide important insights into understanding the crucial link between the recovery of ecosystem structure and functions. Better assessment of the dynamics and interplay of the post-restoration re-colonisation processes of the two communities in the boreal region will require

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ACKNOWLEDGMENTS

studies spanning longer time scales than were studied here.

Thanks to Dan Charman and Matthew Amesbury for their guidance on testate amoebae taxonomy and data analysis, and to Heikki Hämäläinen for his valuable comments on the community concordance interpretations. Thanks to Santtu Kareksela and Riikka Juutinen who collected the plant community data and

388 to Rose Matilainen who analysed the pore water data at the Department of Chemistry (University of 389 Jyväskylä). Special thanks to Roger Jones for language corrections and his valuable input into this work. 390 Emmanuela Daza Secco thanks the Maj and Tor Nessling foundation for financial support. 391 392 REFERENCES 393 Aapala, K., Heikkilä, R. & Lindholm T. (1996) Protecting the diversity of Finnish mires. In: Vasander, H 394 (ed). Peatlands in Finland, Finnish Peatland Society, Jyväskylä, Finland, 45–57. 395 396 Bilton, D.T., MacAbendroth, L., Bedford, A. & Ramsay, P.M. (2006) How wide to cast the net? Cross-taxon 397 congruence of species richness, community similarity and indicator taxa in ponds. Freshwater Biology, 51, 398 578-590. 399 400 Bobrov, A.A., Charman, D.J. & Warner, B.G. (1999) Ecology of testate amoebae (Protozoa: Rhizopoda) on 401 peatlands in western Russia with special attention to niche separation in closely related taxa. Protist, 150, 402 125-136. 403 404 Bobrov, A.A., Charman, D.J. & Warner, B.G. (2002) Ecology of Testate Amoebae from Oligotrophic 405 Peatlands: Specific Features of Polytypic and Polymorphic Species. *Biology Bulletin*, 29, 605–617. 406 407 Booth, R.K. (2001) Ecology of testate amoebae (Protozoa) in two lake superior coastal wetlands: 408 implications for paleoecology and environmental monitoring. Wetlands, 21, 564–576. 409 410 Booth, R.K. (2008) Testate amoebae as proxies for mean annual water-table depth in Sphagnum-dominated 411 peatlands of North America. Journal of Quaternary Science, 23, 43–57. 412 413 Booth, R.K., Lamentowicz, M. & Charman, D.J. (2010) Preparation and analysis of testate amoebae in 414 peatland palaeoenvironmental studies. *Mires and peat*, 7, 1–7.

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