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Abstract: Peatlands represent globally-important ecosystems and carbon stores. However, large areas of peatland have been drained for agriculture, or peat has been harvested for use as fuel or in horticulture. Increasingly, these landscapes are being restored through ditch blocking and rewetting primarily to improve biodiversity and promote peat accumulation. To date we have little knowledge of how these interventions influence the microbial communities in peatlands. We compared the responses of dominant microbial consumers (testate amoebae) to drainage ditch restoration relative to unblocked ditches in a UK upland blanket peatland (Migneint, North Wales). Two techniques were used for restoration: (i) dammed ditches with re-profiling; and (ii) dammed ditches with pools of open water behind each dam. Testate communities in the inter-ditch areas changed markedly over time and between treatments illustrating the potential of this group of organisms as indicators of blanket peatland restoration status. However, the responses of testate amoebae to peat rewetting associated with restoration were partially obscured by inter-annual variability in weather conditions through the course of the experiment. Although there was considerable variability in the response of testate amoebae communities to peatland drain blocking, there were clearly more pronounced changes in samples from the dammed and reprofiled treatments including an increase in diversity, and the appearance of unambiguous wet-indicator species in relatively high abundances (including Amphitrema stenostoma, Archerella flavum, Arcella discoides type, Difflugia bacillifera and Difflugia bacillarium). This reflects a shift towards overall wetter conditions across the site and the creation of new habitats. However, water-table was not a significant control on testate amoebae in this case, suggesting a poor relationship between water table and surface moisture in this sloping blanket peatland. Our findings highlight the potential of testate amoebae as bioindicators of peatland restoration success; however, there is a need for caution as mechanisms driving change in the microbial communities may be more complex than first assumed. Several factors need to be taken into account when implementing biomonitoring studies in peatlands including: (i) the natural variability of the peatland ecosystem under changing weather conditions; (ii) any disturbance connected with the restoration procedures; and (iii) the timescales over which the ecosystem responds to the management intervention. Our results also suggest an indicator species approach based on population dynamics may be more appropriate for biomonitoring peatland restoration than examining changes at the community level.

Response to Reviewers: Please see separate file.

Evaluating the use of dominant microbial consumers (testate amoebae) as indicators of blanket peatland restoration

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Highlights

- Testate amoebae communities changed after ditch blocking in a blanket peatland.
- Significant drivers of change include type of ditch-blocking treatment and time.
- Pronounced changes in diversity across site relate to creation of new habitats.
- First appearance of key wet indicator taxa is after ditch blocking on the site.
- Water table is not controlling testate amoeba communities in this blanket peatland.

Abstract

Peatlands represent globally-important ecosystems and carbon stores. However, large areas of peatland have been drained for agriculture, or peat has been harvested for use as fuel or in horticulture. Increasingly, these landscapes are being restored through ditch blocking and rewetting primarily to improve biodiversity and promote peat accumulation. To date we have little knowledge of how these interventions influence the microbial communities in peatlands. We compared the responses of dominant microbial consumers (testate amoebae) to drainage ditch restoration relative to unblocked ditches in a UK upland blanket peatland (Migneint, North Wales). Two techniques were used for restoration: (i) dammed ditches with re-profiling; and (ii) dammed ditches with pools of open water behind each dam. Testate communities in the inter-ditch areas changed markedly over time and between treatments illustrating the potential of this group of organisms as indicators of blanket peatland restoration status. However, the responses of testate amoebae to peat rewetting associated with restoration were partially obscured by inter-annual variability in weather conditions through the course of the experiment. Although there was considerable variability in the response of testate amoebae communities to peatland drain blocking, there were clearly more pronounced changes in samples from the dammed and reprofiled treatments including an increase in diversity, and the appearance of unambiguous wet-indicator species in relatively high abundances (including *Amphitrema stenostoma*, *Archerella flavum*, *Arcella discoides* type, *Difflugia bacillifera and Difflugia bacillarium*). This reflects a shift towards overall wetter conditions across the site and the creation of new habitats. However, water-table was not a significant control on testate amoebae in this case, suggesting a poor relationship between water table and surface moisture in this sloping blanket peatland. Our findings highlight the potential of testate amoebae as bioindicators of peatland restoration success; however, there is a need for caution as mechanisms driving change in the microbial communities may be more complex than first assumed. Several factors need to be taken into account when implementing biomonitoring studies in peatlands including: (i) the natural variability of the peatland ecosystem under changing weather conditions; (ii) any disturbance connected with the restoration procedures; and (iii) the timescales over which the ecosystem responds to the management intervention. Our results also suggest an indicator species approach based on population

dynamics may be more appropriate for biomonitoring peatland restoration than examining changes at the community level.

1. Introduction

Peatlands represent globally important habitats and carbon stores which are under threat from human activity and climate change (Holden et al., 2004; Charman et al., 2013; Swindles et al., 2015a). They store approximately one third of global soil carbon, whilst covering only approximately 3% of the land and freshwater surface (Holden, 2005). However, human activity has degraded peatlands through drainage and harvesting of peat in many parts of the world including NW Europe, North America, Russia and SE Asia (e.g. Baldock et al., 1984; Holden et al., 2004; Hooijer et al., 2010, 2012). This has led to recent efforts to re-wet peatlands in order to restore active peat-forming plant communities and promote carbon sequestration (e.g. Ramchunder et al., 2009; Parry et al., 2014).

Blanket peatlands are found in hyperoceanic regions such as those of northern Europe, Alaska, Newfoundland, Tasmania, New Zealand, South America and Eastern Russia (Gallego-Sala and Prentice, 2012; Parry et al., 2014). There has been much research interest in blanket peatlands as it has been suggested they are at risk of progressive erosion and vegetation change as a result of climate change (Gallego-Sala et al., 2010; Li et al., 2015). In the UK, large areas of blanket peatland have become degraded from the effects of atmospheric pollution (Smart et al., 2010), peat extraction (Cruickshank et al., 1995), artificial drainage (Holden et al., 2006), grazing (Ellis and Tallis, 2001), prescribed burning and wildfire (Davies et al., 2008), afforestation (Wellock et al., 2011), and the construction of buildings and access tracks (Holden, 2005). Since the 1940s, many upland blanket peatlands in the UK have been drained through the excavation of ditches which aimed to lower water-table levels and increase land productivity (Holden et al., 2006). The excavation of ditches in blanket peatlands has driven a series of ecosystem-level changes to biodiversity, hydrology, and carbon sequestration, and in some locations has increased the amount of dissolved organic carbon (DOC) flux to water courses at some sites (Holden et al., 2006; Mitchell and McDonald, 1995; Ramchunder et al., 2012; Parry et al., 2014). To reduce the impacts of such management practices, ditch blocking with dams is now a commonplace restoration technique. The blocking of ditches is thought to lead to shallower water tables in peatlands, which can have positive effects on ecological diversity and carbon sequestration (e.g. Beadle et al., 2015). However, the timescales involved for any effects to become apparent after re-wetting are poorly understood, and the effects may be subtle (e.g., within the boundaries of natural variability). As large-scale field experiments are unlikely to exceed two-five years duration due to the availability of financial resources, bioindicators can be used to detect small changes that may not be apparent in hydrological or biogeochemical data (i.e., instrument-based monitoring).

There have been several studies examining the effects of peatland restoration on different groups of organisms including beetles, rotifers, microcrustaceans and macroinvertebrates (Van Duinen et al., 2003, 2006; Watts et al., 2008; Więcek et al., 2013; Beadle et al., 2015). Testate amoebae are a polyphyletic group of amoeboid protists characterised by the presence of a shell (test), and represent an important component of the soil microbial community. Testate amoebae are dominant microbial consumers in peatlands, representing 5–30% of the total microbial biomass, and can have a major influence on the ecological functioning of peatland ecosystems through nutrient cycling (Gilbert et al., 1998; Mitchell et al., 2003; Jassey et al., 2014). They have also been shown to be sensitive hydrological indicators in peatlands (Charman and Warner, 1992; Tolonen et al., 1994; Swindles et al., 2009, 2015b; Turner et al., 2012). The response of testate amoebae to peatland restoration has been investigated previously based on analysis of cores from peat accumulated post-restoration (Buttler et al., 1996; Jauhiainen, 2002; Davis and Wilkinson 2004; Valentine et al., 2013). There have also been some experimental studies examining the response of testate amoebae to hydrological change (e.g Marcisz et al., 2014a,b). However, to date, there have not been any studies on blanket peatlands, and, critically, no time-series investigations of changes in surface testate amoebae before and after management intervention have been carried out relative to control systems. Here we investigate the responses of surface testate amoeba communities to restoration treatments in a UK upland blanket peatland (Migneint, North Wales). We examine changes in community composition, ecology, diversity and use these data to examine their potential as bioindicators of peatland restoration.

1.1 Hypotheses

We tested the following three hypotheses:

[*H1*] Ditch blocking drives a change in testate amoebae at the community-level owing to the restoration activity.

[*H2*] Key wet-indicator taxa (e.g. wet indicators from the genera *Arcella* and *Archerella*) increase in response to restoration;

[*H3*] An increase in the diversity of testate amoebae is observed following restoration reflecting the greater variety of habitats.

2. Method

2.1 Field site

The study was undertaken in part of the Migneint in North Wales (Figure 1) close to Ffynnon Eidda (52° 58' 06.35" N, 3° 50' 28.67" W). Under the UK National Vegetation Classification (NVC) (Rodwell, 1991), the peatland is a mix of M19 *Calluna vulgaris – Eriophorum vaginatum*, and M18 *Erica tetralix – Sphagnum papillosum* blanket bog. The Migneint has been damaged by drainage, burning, over-grazing and, to a lesser extent, afforestation. Maps compiled by Natural Resource Wales from aerial photography show that most of the area was artificially drained between the 1940s and 1970s. Peat depth across the sampling area ranges from 0.54 – 2.39 m, with a pH (H_2O) of 3.62 – 3.80, bulk density of 0.08 – 0.11 g cm^{-3}, loss on ignition of 98.8 – 99.7 % and a C to N ratio of 30.0 – 36.6 (depending on depth) (Green et al., 2016). Average annual rainfall is 2200–2400 mm yr^{-1}, and average January and July temperatures are 2.2°C and 12.8°C, respectively.

2.2 Treatments

Twelve ditches, which run obliquely (at an angle of *c*. 20°) to the hillslope gradient from east (ditch 1) to west (ditch 12) across the site (Figure 1), were selected for detailed study. The ditches were allocated to one of three treatments, each with four replicates: (i) control (unblocked), (ii) ‘re-profiled' (dammed and re-profiled), and (iii) dammed (dammed with pools of open water behind each dam) (Table 1). The ditches had an average spacing of 16 m (range 11 to 26 m), a mean length of 99 m (range 84 to 107 m) and were on a mean gradient of 4.5° (range 3.9 to 5.1°). Treatments were allocated taking into account measured pre-blocking discharge rate, catchment area, surface features and position on hillslope (i.e. how the blocking might affect inter-grip areas).

2.3 Routine monitoring

Base-line data collection at the site started on the 18th August 2010, after all the field equipment was installed. All equipment was removed on the 2nd February 2011, prior to the damming/re-profiling of eight of the experimental ditches. Re-installation of the equipment was completed by 23rd of February 2011, after which monitoring resumed.

2.4 Measurement of meteorological conditions

A Davis Vantage Pro2 automatic weather station (AWS) monitored air temperature (°C) and rainfall (mm) at 60-minute archive intervals (Figure 2).

2.5 Measurement of water-table depths

As part of a larger study of the greenhouse gas exchanges and hydrology of the site, twenty-four manual dipwells were installed to monitor water-table depth in the inter-ditch zones across the field site (Figure 2). Dipwells were made from 32 mm (outside diameter) × 3.5 mm (wall thickness) × 1000 mm (length) polyvinyl chloride (PVC) pipe, with 8-mm diameter holes drilled at 100 mm intervals along four lines running lengthwise along the pipe. These were located at 2 metres from the ditch to the west ($DW_{x.2W}$) and 2 metres from the ditch to the east ($DW_{x.2E}$) (Green et al., 2016).

2.6 Pore-water chemical composition

Twenty four piezometers for pore-water collection were installed across the site (deployed in pairs). Pore-water electrical conductivity (unfiltered samples) was determined using a Jenway 4320 conductivity meter

(Bibby Scientific Ltd, Staffordshire, UK). Analytical grade standards were analysed at regular intervals to check instrumental drift. pH (unfiltered samples) was analysed by titration using a 0.01N H_2SO_4 solution on Metrohm 888 Titrando (Metrohm UK Ltd, Cheshire, UK) (two buffer standards of pH 4 and 7) (Figure 2).

2.7 Vegetation survey

Four vegetation surveys (October 2010, October 2011, September 2012, September 2013) were undertaken to quantify the abundance (nested frequency) of the plant species in permanent 1 × 1 m quadrats across the site. There were 48 permanent quadrats, 16 associated with each management type, and four associated with each ditch. The quadrats were situated equal distances apart within each inter-ditch area. To determine nested frequency each quadrat divided into 10 × 10 cm squares and presence-absence of each plant species of interest was measured within those squares. We used data from the quadrats nearest the testate amoeba sampling points.

2.8 Sampling of testate amoebae

Testate amoebae sampling dates corresponded to dates of routine site monitoring. The sampling dates were 116 (t_0 - 15/10/2010) and 6 (t_1 - 02/02/2011) days before, and 63 (t_2 - 12/04/2011) and 234 (t_3 - 30/09/2011) days after ditch blocking was carried out (on 08/02/2011). These sampling dates were chosen to fit around the mandatory monitoring and maintenance of the site. A further set of samples were taken 771 days after ditch blocking (20/03/2013) to obtain a sample following assumed stabilisation of the blocked ditches and peat surfaces.

Moss samples of approximately 5 cm^3 were sampled from an undisturbed plot immediately beside each manual dipwell (n = 24) and placed into Ziplock bags. All samples were returned immediately to the laboratory and stored at 4°C prior to further analysis. Testate amoebae were prepared using a modified version of the standard method (Booth, 2010). Sub-samples of the uppermost *Sphagnum* (containing mostly live testate amoebae) were sieved through a 300-µm sieve and no fine-sieving was carried out following Payne (2009). The samples were stored in deionised water. Testate amoebae containing cytoplasm (i.e. those that were recently alive) were counted under transmitted light at ×200–400 and identified using morphology, composition, size and colour to distinguish taxa. At least 150 specimens (mean = 173, min = 150, max = 225) were counted per sample to ensure a statistically significant count was achieved (Patterson and Fishbein, 1989). The taxonomy uses a morphospecies approach in certain circumstances, where a designation that includes other species has been classed as a 'type'. Testate amoebae were identified using illustrated guides (Ogden and Hedley, 1980; Charman et al., 2000).

2.9 Statistical analysis

Statistical analyses were performed using R version 2.15.1 (R Core Team, 2013). Nonmetric Multidimensional Scaling (NMDS) and Redundancy Analysis (RDA) were used to investigate the response of testate amoebae communities using the 'vegan' package (v. 2.0-5) in R (v. 2.15.1). NMDS using the Bray-Curtis dissimilarity index was used to identify the important axes of variation in the data (e.g., Legendre and Legendre, 1998). The analysis 'stress' was recorded in several runs to ensure a robust analysis was achieved. Ordination hulls were used to demarcate treatment category on the NMDS plots. Environmental variables were fitted to the solution post-hoc using the Envfit procedure with 999 permutations. Analysis of Similarity (ANOSIM) and permutational MANOVA (PERMANOVA) were undertaken on the testate amoebae data to determine the significance of treatment and time factors (Bray Curtis dissimilarities, 9999 permutations). Data were transformed by square root prior to ANOSIM and PERMANOVA analysis. A hierarchical cluster analysis using the Bray Curtis dissimilarity index was also carried out to determine the similarity-dissimilarity of the samples.

Gradient lengths were determined using Detrended Correspondence Analysis (DCA) and, as they were found to be non-linear, species data were transformed using the Hellinger distance prior to direct ordination (Legendre and Gallagher, 2001). Redundancy Analysis (RDA) was used to explore the relationships between testate amoebae and environmental variables. A series of partial RDAs was used for variance partitioning, and Monte-Carlo permutation tests (999 permutations) were used to test statistical significance. The Shannon Diversity Index was calculated for each sample to examine the faunal diversity (e.g., Magguran, 1988) in addition to species richness and evenness. Water-table predictions from the testate amoebae data were carried out using the transfer function of Turner et al. (2013). A suite of water-table metrics were calculated and included in the multivariate analyses: (i) water-table depth for each well on the day of sampling for testate amoebae; (ii) averages, maximum and minimum of the two, three, four, and five water-table readings before sampling, and (iii) seasonal averages.

3. Results

In total, fifty one testate amoeba taxa were identified from 31,158 individuals (Figure 3). The most commonly occurring testate amoeba taxa at the site include *Nebela tincta*, *Corythion-Trinema* type, *Euglypha ciliata* type, *Assulina muscorum* and *Cryptodifflugia oviformis*. The taxa with maximum occurrences include *Cryptodifflugia oviformis, Nebela tincta, Corythion-Trinema type, Nebela militaris and Nebela flabellulum* (Figure 3). The Shannon diversity of the communities varies between 0.92 and 2.86 and increases in all treatments after t_2 (Figure 4). Water-table predictions using the transfer function of Turner et al. (2013) suggest the site has become wetter after restoration, with the most pronounced changes occurring in the samples from the dammed treatment (Figures 4 and 5). The application of a testate-amoeba based transfer function highlights changes in relative wetness indicated by the changing testate amoebae communities (Supplementary material 1). However, transfer functions currently have little predictive skill for determining the absolute magnitudes of short-term water-table changes in blanket peatlands, which is not what they were designed to do (also see Swindles et al., 2015).

The following environmental variables were significantly associated with the community dataset (Figure 5): time ($p < 0.0001$), rainfall ($p < 0.001$) and treatment ($p < 0.05$). ANOSIM showed that community composition was significantly different with time (all treatments combined) (R = 0.395, $p = 0.0001$) and treatment (all times combined) (R = 0.119, $p = 0.0001$). Treatment (R = 0.127) and time (R = 0.252) were also significant when only t_{2-4} (after restoration samples) were analysed ($p = 0.0001$ in both cases). There was no significant difference (95% level) between the community compositions at t_0 (t_0: R = 0.109, p = 0.053). However, the difference between the communities under the different treatments changed through time, becoming most significant at t_4 (t_1: R = 0.125, $p = 0.036$; t_2: R = 0.071, $p = 0.142$; t_3: R = 0.117, p = 0.031; t_4: R = 0.162, $p = 0.007$). PERMANOVA corroborated the results of ANOSIM: community composition was significantly different with time (all treatments combined) (F = 10.35, $p = 0.0001$) and treatment (all times combined) (F = 4.923, p = 0.0001). There was no significant difference (95% level) between the community compositions at t_0 (t_0: F = 1.551, p = 0.082). Treatment (F = 3.55) and time (F = 6.04) were also significant when only $t_{2\text{-}4}$ (after restoration samples) were analysed (p = 0.0001 in both cases). However, the difference between the communities under the different treatments changed through time, becoming most significant at t_4 (t_1: F = 2.020, p = 0.021; t_2: F = 1.440, p = 0.126; t_3: F = 1.618, p = 0.029; t_4: F = 2.027, p = 0.007). Treatment*time interaction was non-significant for both ANOSIM and PERMANOVA analyses. Cluster analysis also suggested a clear division before and after restoration in the community characteristics (Supplementary material 2).

Monte Carlo permutation tests highlighted the significance of RDA axis one (p = 0.038) and all canonical axes (p = 0.006) (Supplementary material 3). Axis one explained 43.2% of the species-environment relationship whereas axis two explained 20.8%. A pRDA including all continuous environmental and ordinal variables suggested that the following variables were most important: time (49.3%, $p < 0.001$), temperature (10.5%, $p < 0.001$), treatment (6.2%, $p < 0.05$) and *Sphagnum* abundance (5.5%, $p < 0.05$). A pRDA only including the continuous variables (i.e., not including treatment or time) revealed the following significant environmental variables: rainfall (25.3%, $p < 0.01$), *Sphagnum* abundance (20.1%, $p < 0.01$) and temperature (16.3%, $p < 0.05$). It is noteworthy that none of the water-table depth metrics were deemed significant controls on the testate amoebae communities by either NMDS or RDA.

The response of testate amoebae communities at the site is complex. There is a very clear management effect in some of the dammed and reprofiled samples including the first appearance of key wet indicator taxa in high numbers by t_3 or t_4 (*Amphitrema stenostoma*, *Archerella flavum*, *Arcella discoides* type, *Difflugia bacillifera and Difflugia bacillarium*). This suggests that changes in the testate amoebae communities are at least partially driven by management intervention. However, some of the responses are more muted or ambiguous, or in some cases there is little discernible effect (Figures 5 and 6). Furthermore, key wet indicator taxa also appear in the control samples (albeit in smaller numbers) suggesting that there is interaction between the ditches, or that management has had wider effects across the site. The interaction between ditches may be supported by the observation that no wet indicators appear in ditch 7.2 - a control with the least number of near-by ditches with blocking treatments. Nevertheless, a major increase in wet indicator taxa in some of the reprofiled and dammed treatment plots after management intervention is apparent (Figure 6).

Table 4 illustrates the overall changes in testate amoeba communities between t_0 and t_4 (diversity, richness, evenness and abundance of wet indicator taxa). It is clear that when the data are aggregated, overall changes have been greater in the re-wetted plots compared with the controls. There are also some key differences between treatments; there is a greater increase in diversity, richness and evenness in the re-profiled than the dammed treatments, whereas the abundance of wet indicator taxa is greater in the dammed treatments.

4. Discussion

Our analysis suggests that although there is high variability between sampling points, we can accept all three hypotheses based on multivariate statistical analysis, the appearance of wet indicators, and changes in community diversity:

[*H1*] Ditch blocking drives a change in testate amoebae at the community-level owing to the restoration activity. *Accept*: there are clear changes at the community-level at least partly driven by peatland restoration as illustrated by the NMDS, ANOSIM and PERMANOVA results (see Figure 5, section 3).

[*H2*] Key wet-indicator taxa (e.g. wet indicators from the genera *Arcella* and *Archerella*) increase in response to restoration. *Accept*: wet-indicators appear after restoration including *Amphitrema stenostoma*, *Arcella discoides* type, *Archerella flavum*, *Difflugia bacillifera* and *Difflugia bacillarium* (see Figure 6).

[*H3*] An increase in the diversity of testate amoebae is observed following restoration reflecting the greater variation in habitats. *Accept*: Diversity increases in many of the sample plots after peatland restoration (see Figure 4, Table 4).

Previous studies from other sites in Europe have shown that testate amoebae can be used for monitoring habitat changes after restoration of cutover peatlands (Buttler et al., 1996; Jauhiainen, 2002; Davis and Wilkinson 2004; Valentine et al., 2013). However, these studies have focussed on subfossil testate amoebae in cores taken from peat formed following restoration; which may not be a practical approach for many blanket peatlands owing to slow peat accumulation rates. Instead, we have focussed on generating a time series of changes in testate amoebae communities through sampling of surface vegetation. To our knowledge, this work represents the first study examining the responses of testate amoebae to management in a blanket peatland.

We have shown that there have been distinct changes in testate amoebae communities in response to peatland management efforts; however, the changes have been complex in that some locations show large changes in community composition, whereas some do not. The complexities at the site are probably due to several key factors:

1. The natural variability of the peatland ecosystem under changing weather conditions;
2. Disturbance of the sites connected with the restoration procedures, including trampling and movement of machines. This may also include redistribution of testate amoebae across the site and the creation of new micro-habitats;
3. The site is generally very wet with a high degree of overland flow. The management efforts may have altered the surface hydrology leading to hydrological interaction of some of the ditches from ponding up of ditches and subsequent overland flow. In addition, aquatic testate amoebae from the pools behind the dams may have been transported into the inter-ditch areas during storm events, partly complicating the signal from the inter-ditch areas.
4. A longer timescale may be needed to fully understand how the ecosystem responds to the management intervention.

The appearance of wet-indicator taxa in the control as well as treatment samples may relate to: (i) the general diversification of ecohydrological habitats across the site following management, leading to wider-site colonisation by certain taxa; or (ii) hydrological modification of the site leading to the redistribution of testate amoebae by overland flow. The finding that water-table depth is not a primary driver of change in the testate amoebae communities contrasts with studies from raised bogs (e.g. Swindles et al., 2009; Turner et al., 2013; Swindles et al., 2015c) and probably reflects a poor relationship between surface moisture and water-table in this sloping blanket peatland. This poor relationship may relate to water tables being generally shallow across the site even before blocking and saturated conditions leading to frequent overland flow.

Our study illustrates the importance of having controls before and after management intervention in biomonitoring studies so that the natural variability of the site under changing weather conditions (inter and sub annual) can be taken in account. Our results also suggest an indicator species approach may be more appropriate for biomonitoring the early days of peatland restoration than examining change at the community level. We contend that caution is needed when using biomonitors of peatland restoration including testate amoebae. It could be argued that the actual sample size for any treatment here is n = 4 as the replication within a treatment is arguable pseudo-replication. With this small sample size only the largest differences will be statistically significant. In future, larger experiments (requiring considerable funding) or a larger number of similar-sized experiments can be subjected to further statistical analysis and will hopefully allow firmer conclusions to be drawn.

Our findings that peatland restoration drives significant changes in testate amoebae populations have parallels from several previous studies that have documented responses amongst other aquatic biological groups (Beadle et al., 2015). For example, Goodyer (2014) reported that desmid diversity recovered from a situation of low richness in drained peatlands to become more similar to nearby intact peatlands, although the timescales of 12 years were longer than we observed for the testate amoebae in this study. Similarly, aquatic macroinvertebrates have been shown to exhibit sensitivity to peatland restoration, with Van Duinen et al. (2003) highlighting how the invertebrate fauna of bogs with remnants of peat cuttings was different (higher richness, and wider compositional variation) from re-wetted peats. Re-wetted peatlands hosted fauna that were more characteristic of undamaged raised bogs, and there were clear successional changes over time in the rewetted peatland invertebrate communities, similar to our findings for testate amoebae. These different studies show that peatland restoration elicits clear responses amongst a range of biological groups, yet the processes by which these groups interact to determine the nature of ecological outcomes still needs to be understood before any particular group can be proposed as definitive indicators of restoration success. For example, we need to understand the nature of species interactions between the testate amoebae and their predators such as Chironomidae (Mieczan et al., 1995), which are often the dominant group of macroinvertebrates in peatland pools (Beadle et al., 2015). This would allow us to understand the relative roles of biotic (i.e., role in food webs) vs. abiotic (i.e., hydrological) drivers of testate communities when trying to interpret their response to restoration.

Testate amoebae are highly abundant and represent a major group of predators in the microbial food web of peatlands (Gilbert et al. 1998; Ogden and Hedley 1980; Jassey et al., 2012). They can exert important effects on the ecological functioning of peatlands in their role as dominant microbial consumers (Jassey et al., 2014). New research suggests that mixotrophic testate amoebae play an important role in modulating peatland C cycle responses (fixation of C) to climate warming (Jassey et al., 2015). Future work should consider the effects of changes in testate amoebae driven by peatland restoration, and how this affects the functioning of the wider microbial ecosystem and carbon cycling.

Conclusions

We examined the responses of dominant microbial consumers (testate amoebae) to restoration treatments in a UK blanket peatland. We found that both time and treatment had a statistically-significant effect on community composition; however, the testate amoebae communities across the entire site have responded to changing weather conditions over the test period which partially obscures the effect of management. Despite considerable variability in the response of testate amoebae communities to management intervention, there were clearly more pronounced changes in several of the samples from dammed and re-profiled treatments including an increase in diversity, and the appearance of unambiguous wet-indicator species in relatively high abundances (including *Amphitrema stenostoma*, *Archerella flavum*, *Arcella discoides* type, *Difflugia bacillifera and Difflugia bacillarium*). This reflects a shift towards wetter conditions adjacent to the managed ditches as well as greater variation in habitats across the study site. Our findings illustrate the potential of testate amoebae as bioindicators for the effects of peatland restoration. However, there is a need for caution when using bioindicators (e.g. testate amoebae) for monitoring peatland restoration efforts as ecosystem responses may be more complex than first assumed.

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Figure captions

Figure 1. Map of study site in the Migneint, North Wales. The location of each ditch is illustrated. The dipwells are located to the east (E) or west (W) of the ditch. Grey = Control; Red = Re-profiled; Blue = Dammed.

Figure 2. Monitored environmental variables over the course of the experiment. Average pH and conductivity are shown for each treatment type.

Figure 3a. Percentage testate amoebae data (Controls).

Figure 3b. Percentage testate amoebae data (Re-profiled).

Figure 3c. Percentage testate amoebae data (Dammed).

Figure 4. Boxplot of transfer function predicted water-table depth and Shannon Diversity Index (determined from the testate amoeba communities).

Figure 5. NMDS analysis of the testate amoeba communities. The analysis is shown for each time of sampling. Ordination hulls show the different treatments: Black = Control; Red = Re-profiled; Blue = Dammed. Taxa and environmental vectors (fitted using 'Envfit') are illustrated in the top left panel. See Table 3 for sample codes.

Figure 6. Percentage abundance of unambiguous wet indicator taxa before and after management intervention. The x axis denotes the ditch number and sampling time (0-4: where 0-1 are before and 2-4 are after management).

Table 1. Information on the *Sphagnum* moss species sampled from each ditch.

Table 2. Mean actual and predicted water table, and SDI for the three treatments (control, dammed and re-profiled) (n = 120). Parentheses show standard deviation. A negative water table indicates that the water table level is above the ground surface (i.e., ponding), whilst positive indicates below the ground surface.

Table 3. Ordination sample codes (for interpretation of Figure 5).

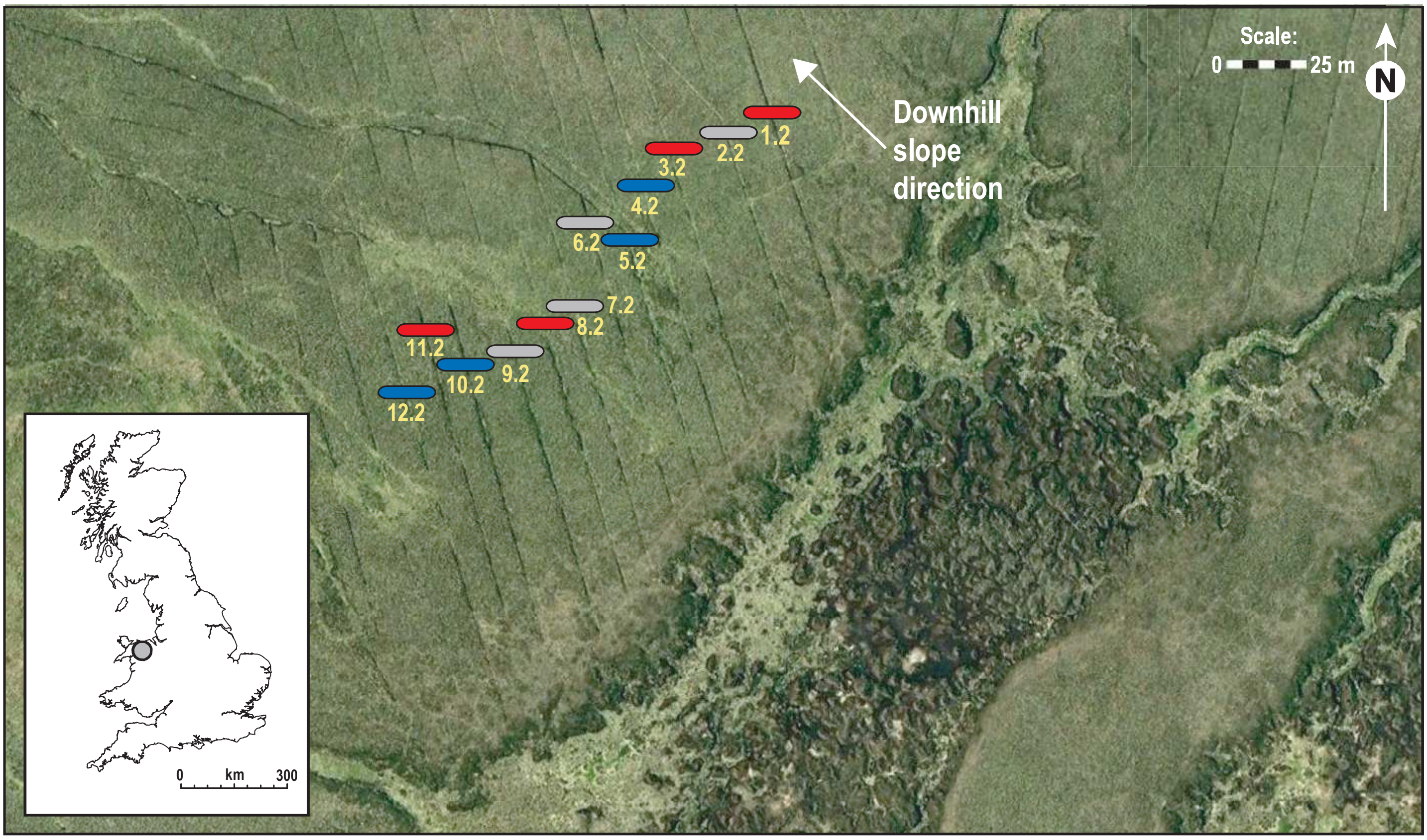
Table 4. Wet indicator taxa and changes in diversity metrics for each sample grouped by treatment.

Supplementary material 1. Monitored water tables compared with transfer function-predicted water tables.

Supplementary material 2. Cluster analysis of testate amoebae communities (Q-mode)

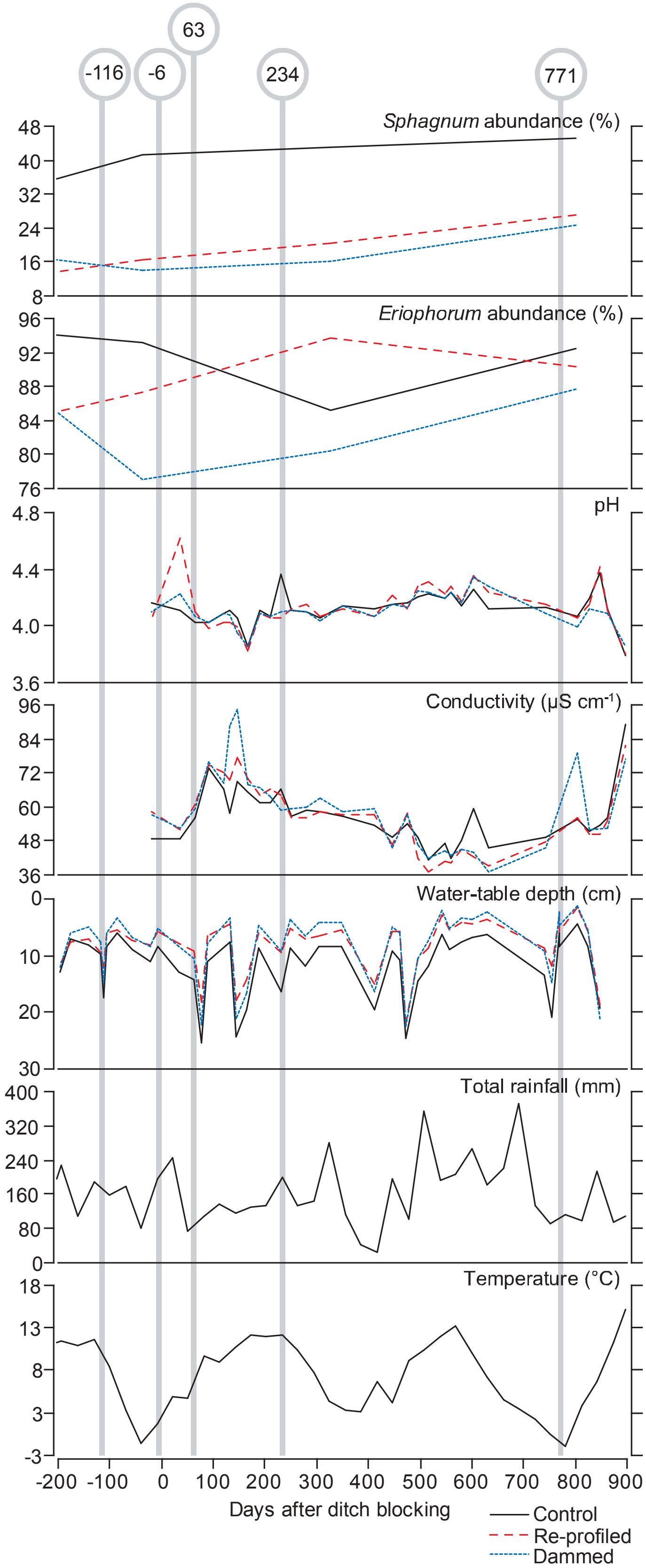
Supplementary material 3. Redundancy analysis of testate amoebae communities.

Figure 1



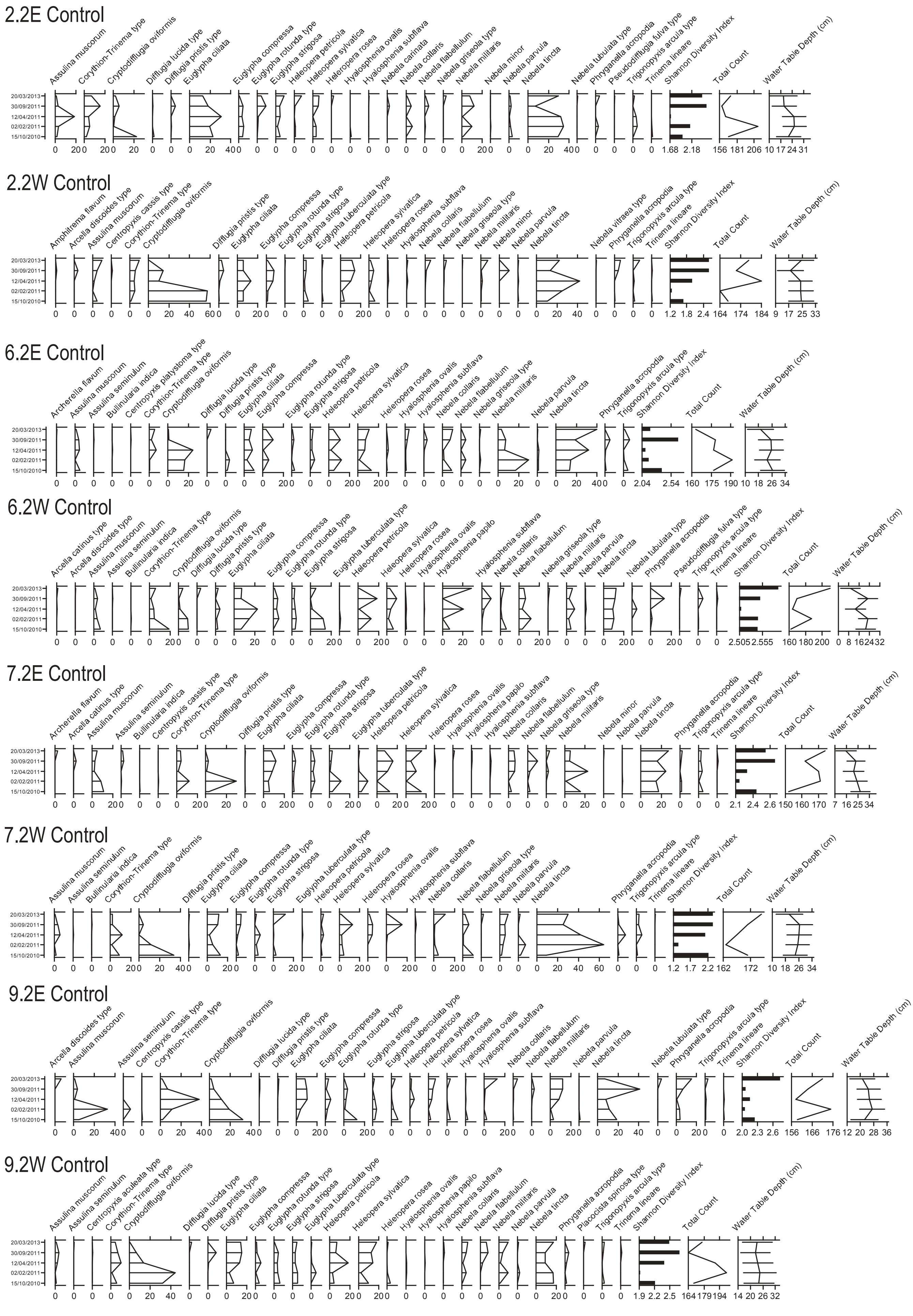
Scale:
0
25 m
N
Downhill slope direction
1.2
2.2
3.2
4.2
6.2
5.2
7.2
8.2
11.2
9.2
10.2
12.2
0
km
300

Figure 2



-116
-6
63
234
771
Sphagnum abundance (%)
48
40
32
24
16
8
Eriophorum abundance (%)
96
92
88
84
80
76
pH
4.8
4.4
4.0
3.6
Conductivity (μS cm⁻¹)
96
84
72
60
48
36
Water-table depth (cm)
0
10
20
30
Total rainfall (mm)
400
320
240
160
80
0
Temperature (°C)
18
13
8
3
-3
-200 -100 0 100 200 300 400 500 600 700 800 900
Days after ditch blocking
Control
Re-profiled
Dammed

Figure 3a



2.2E Control
2.2W Control
6.2E Control
6.2W Control
7.2E Control
7.2W Control
9.2E Control
9.2W Control
Shannon Diversity Index
Total Count
Water Table Depth (cm)

Figure 3b

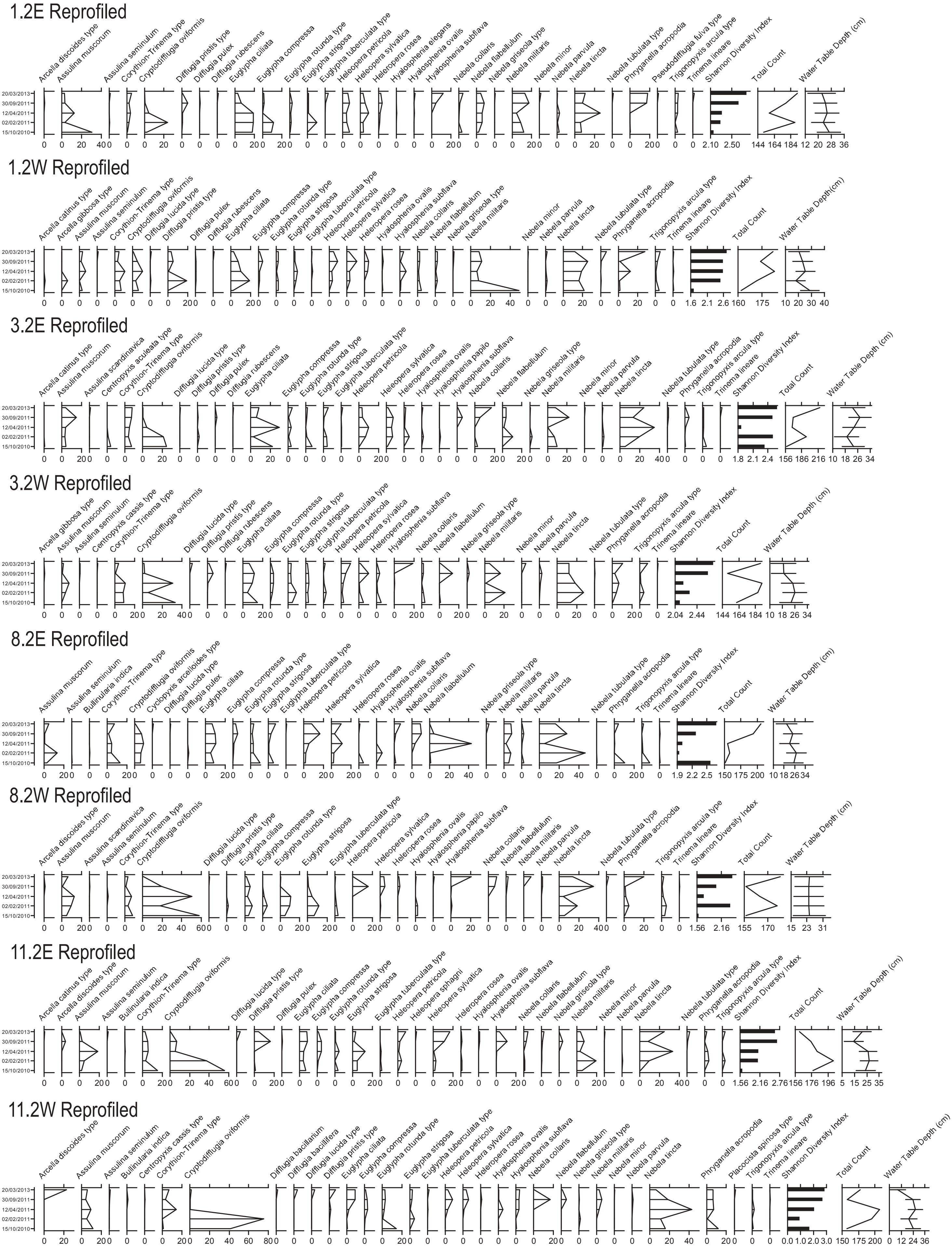

1.2E Reprofiled
Arcella discoides type
Assulina muscorum
Assulina seminulum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia pristis type
Difflugia pulex
Difflugia rubescens
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia elegans
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Pseudodifflugia fulva type
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
20/03/2013
30/09/2011
12/04/2011
02/02/2011
15/10/2010
1.2W Reprofiled
Arcella catinus type
Arcella gibbosa type
Assulina muscorum
Assulina seminulum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Difflugia rubescens
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth(cm)
3.2E Reprofiled
Arcella catinus type
Assulina muscorum
Assulina scandinavica
Centropyxis aculeata type
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Difflugia rubescens
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilo
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
3.2W Reprofiled
Arcella gibbosa type
Assulina muscorum
Assulina seminulum
Centropyxis cassis type
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia rubescens
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
8.2E Reprofiled
Assulina muscorum
Assulina seminulum
Bullinularia indica
Corythion-Trinema type
Cryptodifflugia oviformis
Cyclopyxis arcelloides type
Difflugia lucida type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
8.2W Reprofiled
Arcella discoides type
Assulina muscorum
Assulina scandinavica
Assulina seminulum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilo
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela militaris
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
11.2E Reprofiled
Arcella catinus type
Arcella discoides type
Assulina muscorum
Assulina seminulum
Bullinularia indica
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sphagni
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Trigonopyxis arcula type
Shannon Diversity Index
Total Count
Water Table Depth (cm)
11.2W Reprofiled
Arcella discoides type
Assulina muscorum
Assulina seminulum
Bullinularia indica
Centropyxis cassis type
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia bacillarium
Difflugia bacillifera
Difflugia lucida type
Difflugia pristis type
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Phryganella acropodia
Placocista spinosa type
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)

Figure 3c

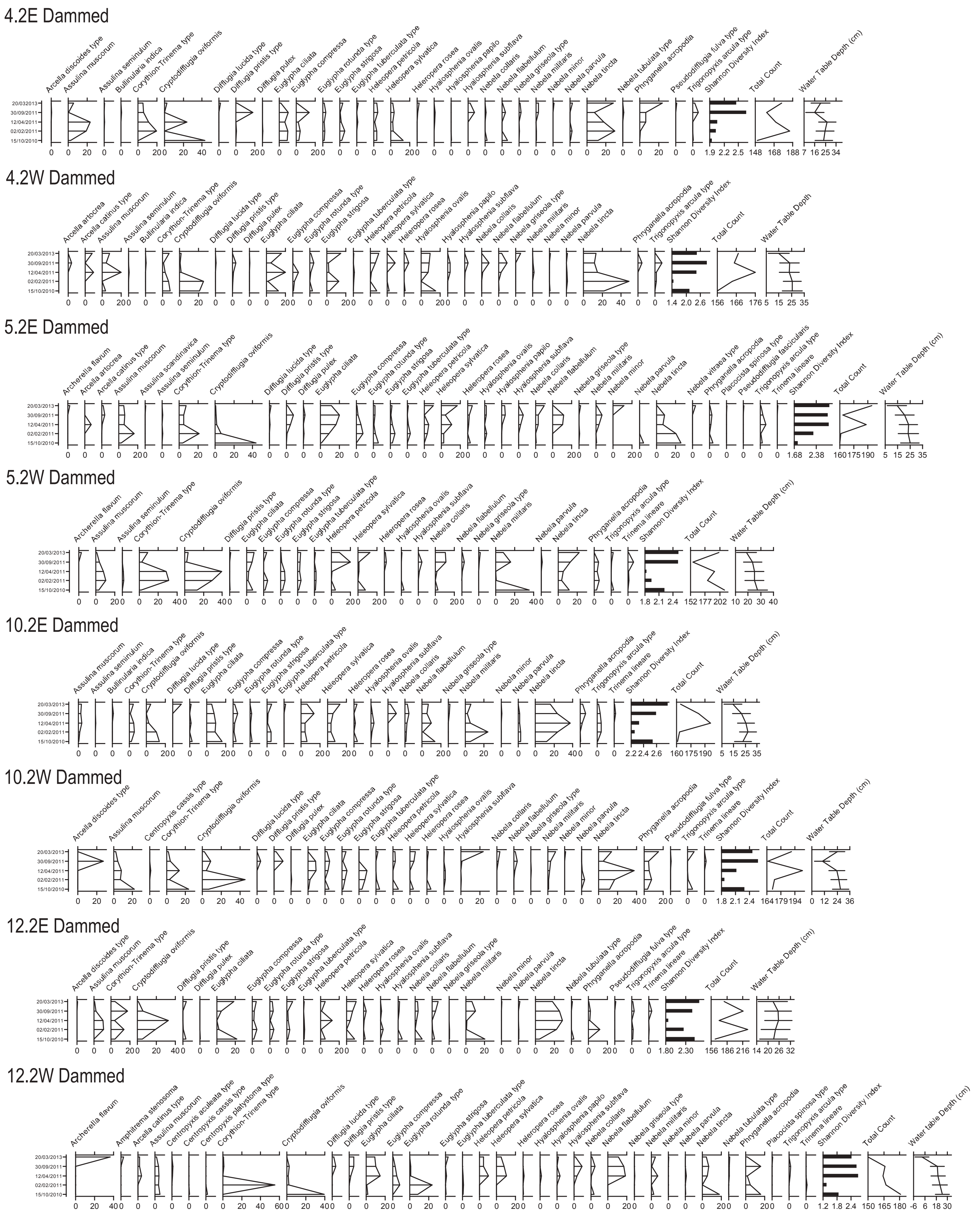
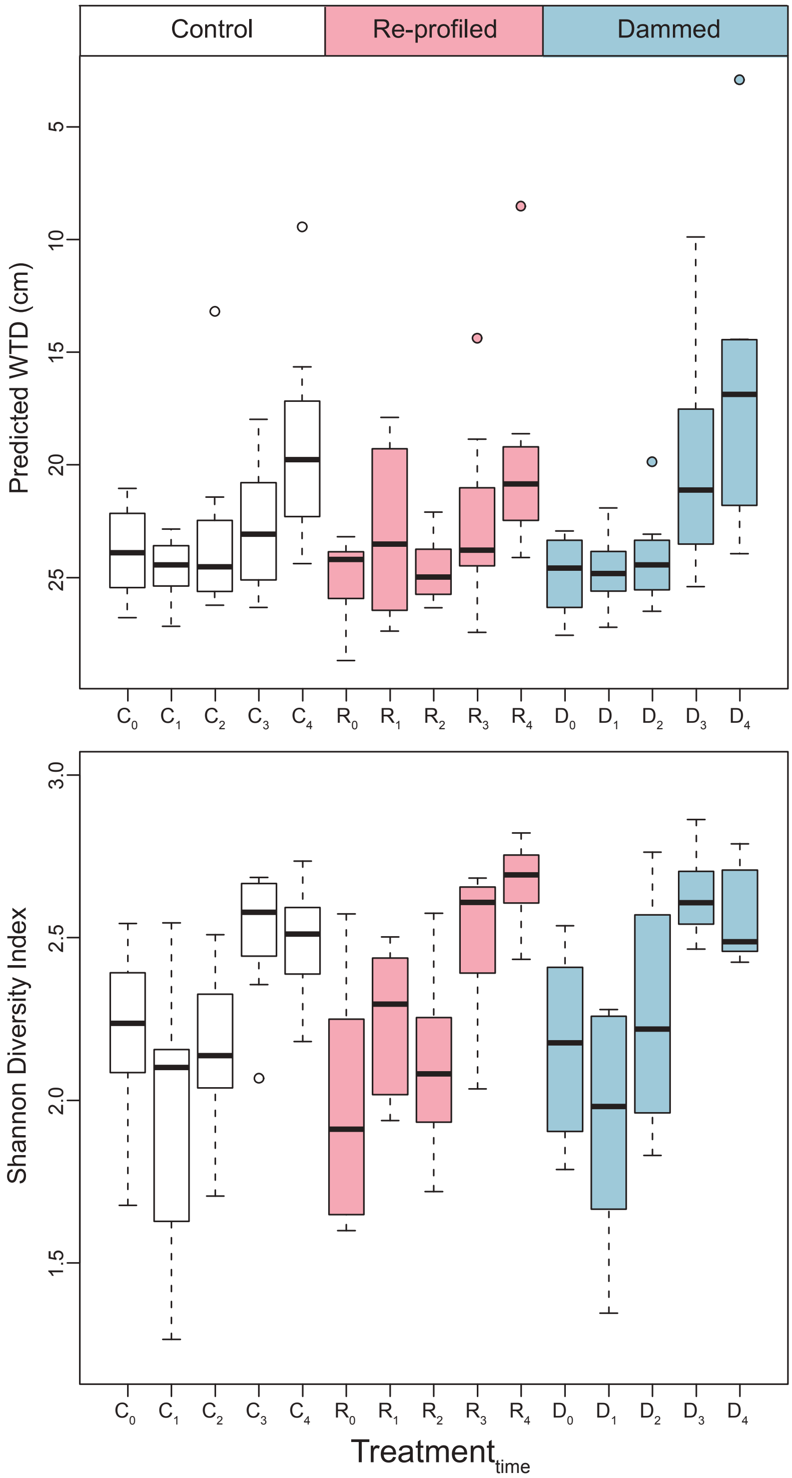

4.2E Dammed
Arcella discoides type
Assulina muscorum
Assulina seminulum
Bullinularia indica
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilio
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Pseudodifflugia fulva type
Trigonopyxis arcula type
Shannon Diversity Index
Total Count
Water Table Depth (cm)
20/032013
30/09/2011
12/04/2011
02/02/2011
15/10/2010
4.2W Dammed
Arcella artocrea
Arcella catinus type
Assulina muscorum
Assulina seminulum
Bullinularia indica
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilio
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Phryganella acropodia
Trigonopyxis arcula type
Shannon Diversity Index
Total Count
Water Table Depth
5.2E Dammed
Archerella flavum
Arcella artocrea
Arcella catinus type
Assulina muscorum
Assulina scandinavica
Assulina seminulum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilio
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela vitraea type
Phryganella acropodia
Placocista spinosa type
Pseudodifflugia fascicularis
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
5.2W Dammed
Archerella flavum
Assulina muscorum
Assulina seminulum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia pristis type
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela parvula
Nebela tincta
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
10.2E Dammed
Assulina muscorum
Assulina seminulum
Bullinularia indica
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Phryganella acropodia
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
10.2W Dammed
Arcella discoides type
Assulina muscorum
Centropyxis cassis type
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Phryganella acropodia
Pseudodifflugia fulva type
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
12.2E Dammed
Arcella discoides type
Assulina muscorum
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia pristis type
Difflugia pulex
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Pseudodifflugia fulva type
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water Table Depth (cm)
12.2W Dammed
Archerella flavum
Amphitrema stenosoma
Arcella catinus type
Assulina muscorum
Centropyxis aculeata type
Centropyxis cassis type
Centropyxis platystoma type
Corythion-Trinema type
Cryptodifflugia oviformis
Difflugia lucida type
Difflugia pristis type
Euglypha ciliata
Euglypha compressa
Euglypha rotunda type
Euglypha strigosa
Euglypha tuberculata type
Heleopera petricola
Heleopera sylvatica
Heleopera rosea
Hyalosphenia ovalis
Hyalosphenia papilio
Hyalosphenia subflava
Nebela collaris
Nebela flabellulum
Nebela griseola type
Nebela militaris
Nebela minor
Nebela parvula
Nebela tincta
Nebela tubulata type
Phryganella acropodia
Placocista spinosa type
Trigonopyxis arcula type
Trinema lineare
Shannon Diversity Index
Total Count
Water table Depth (cm)

Figure 4



Control
Re-profiled
Dammed
Predicted WTD (cm)
5
10
15
20
25
C0 C1 C2 C3 C4 R0 R1 R2 R3 R4 D0 D1 D2 D3 D4
Shannon Diversity Index
3.0
2.5
2.0
1.5
C0 C1 C2 C3 C4 R0 R1 R2 R3 R4 D0 D1 D2 D3 D4
Treatment time

Figure 5

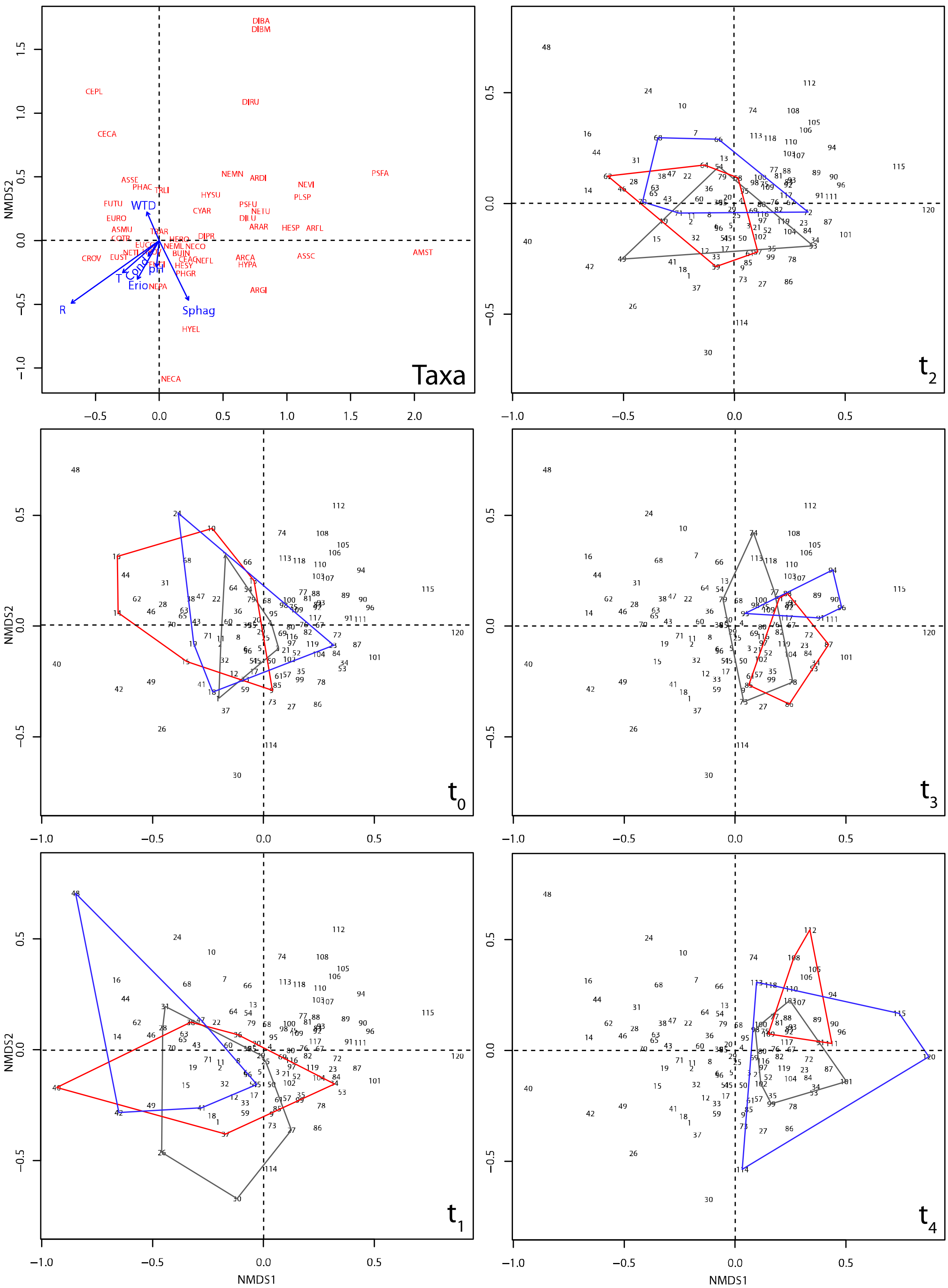

Taxa
NMDS1
NMDS2
DIBA
DIBM
CEPL
DIRU
CECA
PSFA
NEMN
ARDI
NEVI
ASSE
PHAC
TRLI
HYSU
PLSP
FUTU
WTD
PSFU
CYAR
NETU
EURO
DIEU
ARAR
HESP
ARFL
ASMU
DIPR
AMST
ASSC
ARCA
HYPA
CROV
R
T
Cond
pH
Erio
Sphag
ARGI
HYEL
NECA
t0
t1
t2
t3
t4

Figure 6

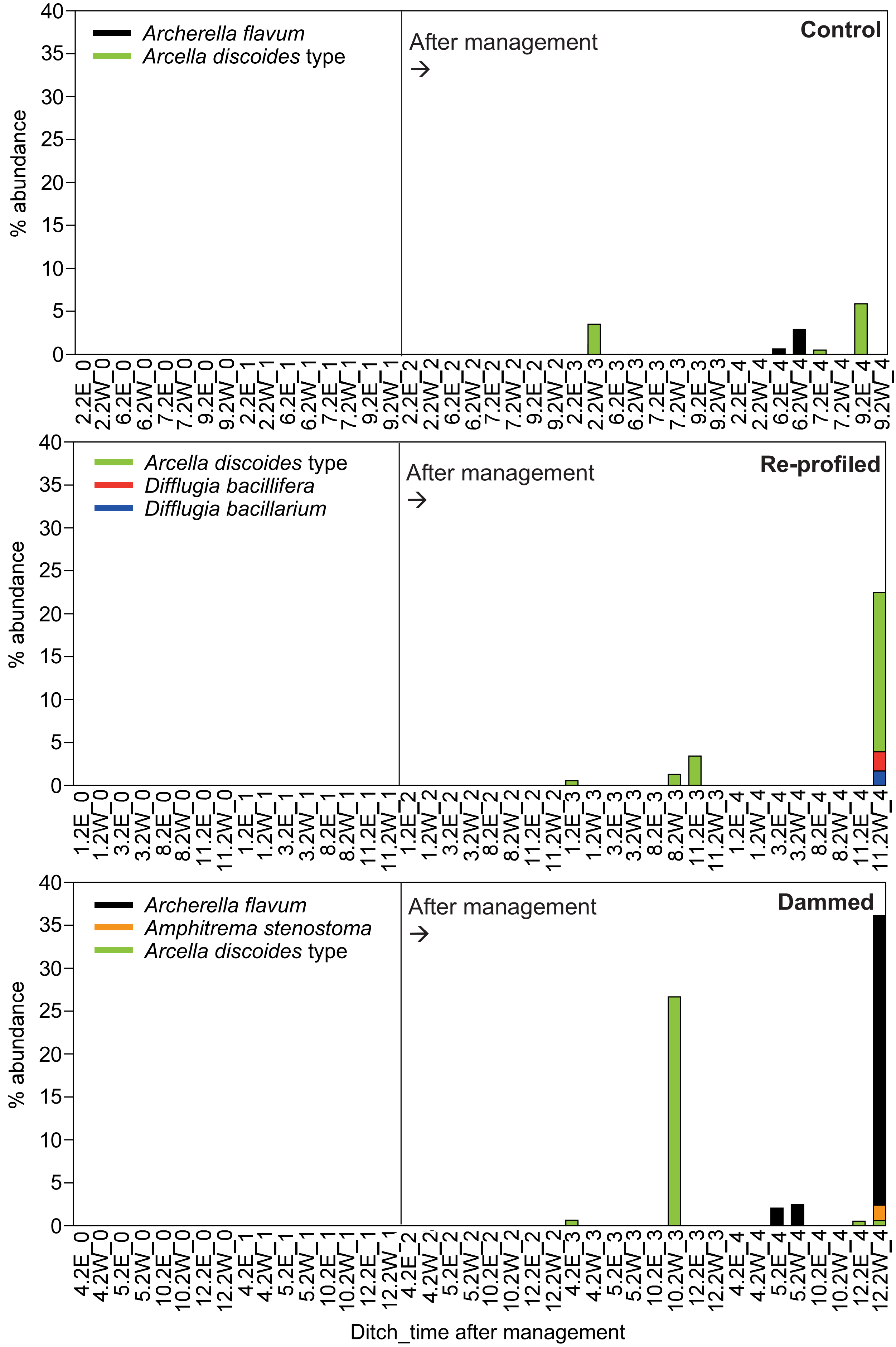

Control
Archerella flavum
Arcella discoides type
After management
Re-profiled
Arcella discoides type
Difflugia bacillifera
Difflugia bacillarium
Dammed
Archerella flavum
Amphitrema stenostoma
Arcella discoides type
% abundance
Ditch_time after management

Table 1

Replicate #	Control	Re-profiled	Dammed
1	**6.2** E - *S. capillifolium* W - *S. capillifolium*	**3.2** E - *S. capillifolium* W - *S. capillifolium*	**12.2** E - *S. capillifolium* W - *S. capillifolium*
2	**2.2** E - *S. capillifolium* W - *S. capillifolium*	**1.2** E - *S. capillifolium* W - *S. papillosum*	**4.2** E - *S. fallax* W - *S. capillifolium*
3	**7.2** E - *S. subnitens* W - *S. capillifolium*	**8.2** E - *S. capillifolium* W - *S. capillifolium*	**5.2** E - *S. capillifolium* W - *S. capillifolium*
4	**9.2** E - *S. capillifolium* W - *S. capillifolium*	**11.2** E - *S. capillifolium* W - *S. capillifolium*	**10.2** E - *S. subnitens* W - *S. capillifolium*

Table 2

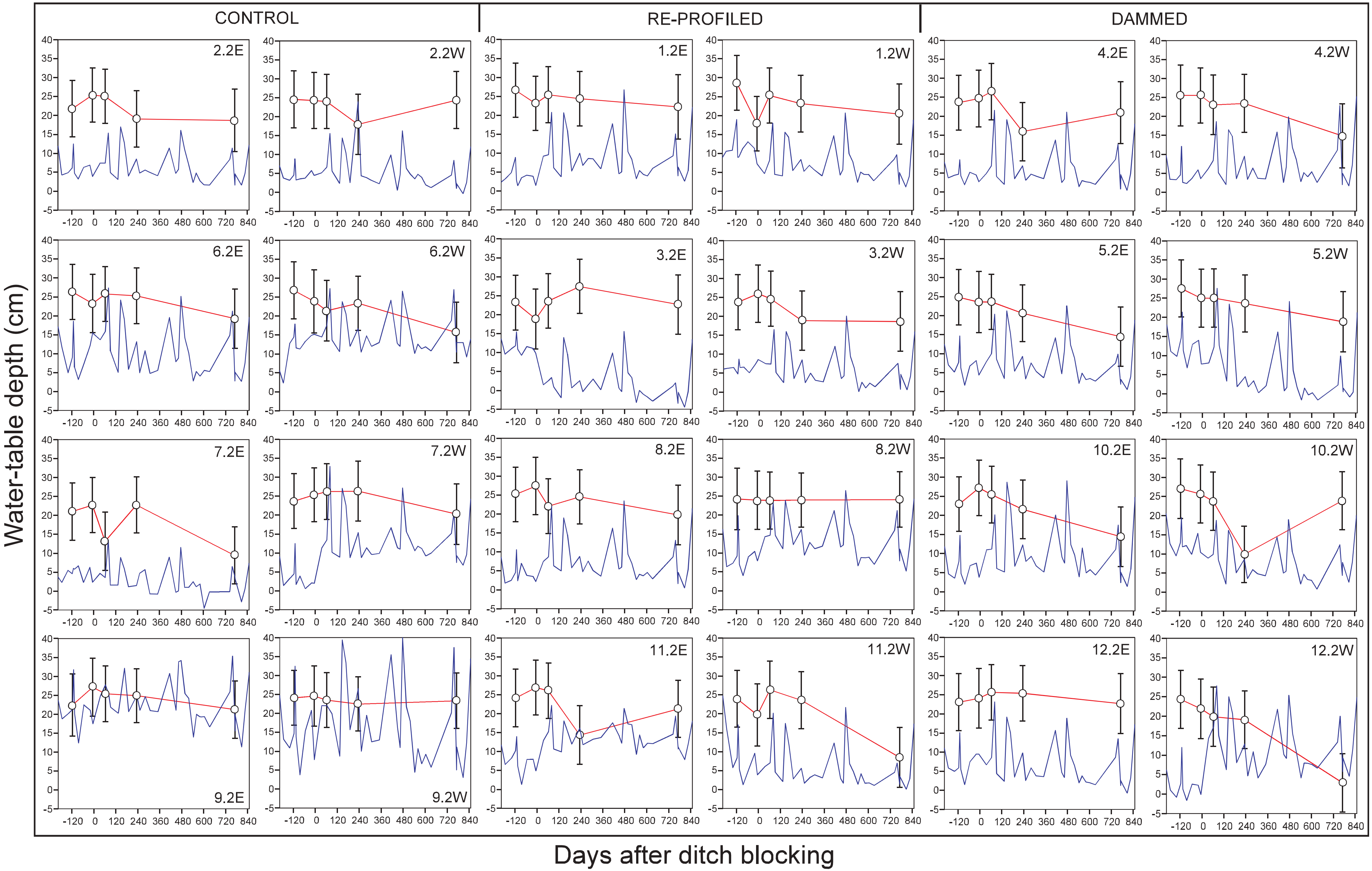
Treatment	Time	Mean monitored water table depth (cm)	Mean predicted water table depth (cm)	Shannon Diversity Index
Control	t_0	8.10 (± 1.8)	23.9 (± 1.3)	2.21 (± 0.11)
	t_1	5.24 (± 1.8)	24.6 (± 1.3)	1.95 (± 0.11)
	t_2	7.15 (± 1.8)	23.1 (± 1.3)	2.15 (± 0.11)
	t_3	9.80 (± 1.8)	22.8 (± 1.3)	2.52 (± 0.11)
	t_4	1.09 (± 1.8)	19.0 (± 1.3)	2.49 (± 0.11)
Reprofiled	t_0	10.5 (± 1.8)	24.9 (± 1.3)	2.16 (± 0.11)
	t_1	7.21 (± 1.8)	24.7 (± 1.3)	1.93 (± 0.11)
	t_2	14.9 (± 1.8)	24.1 (± 1.3)	2.26 (± 0.11)
	t_3	14.6 (± 1.8)	19.9 (± 1.3)	2.63 (± 0.11)
	t_4	5.84 (± 1.8)	16.6 (± 1.3)	2.57 (± 0.11)
Dammed	t_0	8.61 (± 1.8)	25.0 (± 1.3)	19.7 (± 0.11)
	t_1	7.18 (± 1.8)	23.0 (± 1.3)	2.12 (± 0.11)
	t_2	12.0 (± 1.8)	24.7 (± 1.3)	2.10 (± 0.11)
	t_3	10.7 (± 1.8)	22.5 (± 1.3)	2.50 (± 0.11)
	t_4	4.58 (± 1.8)	19.7 (± 1.3)	2.67 (± 0.11)

Table 3

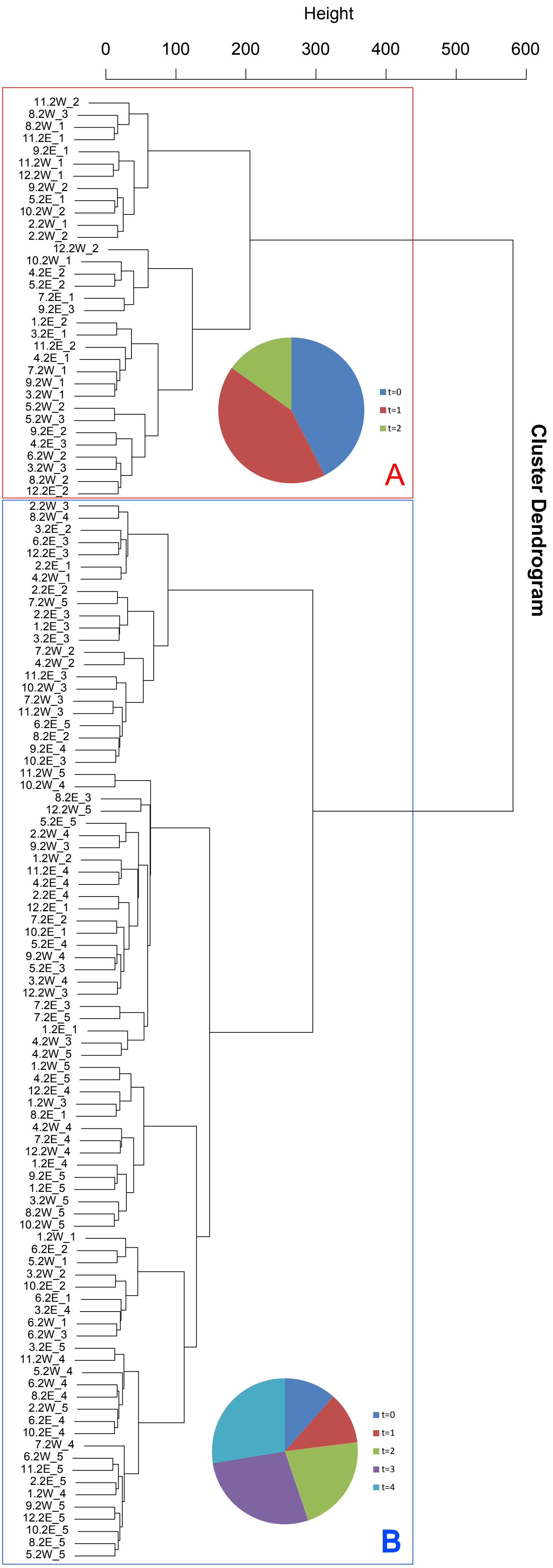
Number	Grip_Time	Number	Grip_Time	Number	Grip_Time	Number	Grip_Time	Number	Grip_Time	Number	Grip_Time
1	2.2E_0	21	10.2E_0	41	4.2E_1	61	8.2E_2	81	1.2E_3	101	7.2E_4
2	2.2W_0	22	10.2W_0	42	4.2W_1	62	8.2W_2	82	1.2W_3	102	7.2W_4
3	6.2E_0	23	12.2E_0	43	4.2E_1	63	11.2E_2	83	3.2E_3	103	9.2E_4
4	6.2W_0	24	12.2W_0	44	4.2W_1	64	11.2W_2	84	3.2W_3	104	9.2W_4
4	7.2E_0	24	2.2E_1	44	10.2E_1	64	4.2E_2	84	8.2E_3	104	1.2E_4
6	7.2W_0	26	2.2W_1	46	10.2W_1	66	4.2W_2	86	8.2W_3	106	1.2W_4
7	9.2E_0	27	6.2E_1	47	12.2E_1	67	4.2E_2	87	11.2E_3	107	3.2E_4
8	9.2W_0	28	6.2W_1	48	12.2W_1	68	4.2W_2	88	11.2W_3	108	3.2W_4
9	1.2E_0	29	7.2E_1	49	2.2E_2	69	10.2E_2	89	4.2E_3	109	8.2E_4
10	1.2W_0	30	7.2W_1	40	2.2W_2	70	10.2W_2	90	4.2W_3	110	8.2W_4
11	3.2E_0	31	9.2E_1	41	6.2E_2	71	12.2E_2	91	4.2E_3	111	11.2E_4
12	3.2W_0	32	9.2W_1	42	6.2W_2	72	12.2W_2	92	4.2W_3	112	11.2W_4
13	8.2E_0	33	1.2E_1	43	7.2E_2	73	2.2E_3	93	10.2E_3	113	4.2E_4
14	8.2W_0	34	1.2W_1	44	7.2W_2	74	2.2W_3	94	10.2W_3	114	4.2W_4
14	11.2E_0	34	3.2E_1	44	9.2E_2	74	6.2E_3	94	12.2E_3	114	4.2E_4
16	11.2W_0	36	3.2W_1	46	9.2W_2	76	6.2W_3	96	12.2W_3	116	4.2W_4
17	4.2E_0	37	8.2E_1	47	1.2E_2	77	7.2E_3	97	2.2E_4	117	10.2E_4
18	4.2W_0	38	8.2W_1	48	1.2W_2	78	7.2W_3	98	2.2W_4	118	10.2W_4
19	4.2E_0	39	11.2E_1	49	3.2E_2	79	9.2E_3	99	6.2E_4	119	12.2E_4
20	4.2W_0	40	11.2W_1	60	3.2W_2	80	9.2W_3	100	6.2W_4	120	12.2W_4

Table 4

Samples		Wet indicators %						Diversity								
Treatment	Dipwell	ARFL	AMST	ARDI	DIBA	DIBM	Σ Wet indicators	SDI t_0	SDI t_4	Δ SDI	Richness t_0	Richness t_4	Δ Richness	Evenness t_0	Evenness t_4	Δ Evenness
Control	2.2E						0.00	1.97	2.43	0.46	15	21	6	0.48	0.54	0.06
Control	2.2W			3.49			3.49	1.68	2.60	0.92	16	23	7	0.33	0.58	0.25
Control	6.2E	0.61					0.61	2.38	2.18	-0.20	17	19	2	0.64	0.47	-0.17
Control	6.2W	2.87					2.87	2.40	2.54	0.13	18	22	4	0.61	0.57	-0.04
Control	7.2E			0.48			0.48	2.54	2.59	0.04	18	25	7	0.71	0.53	-0.18
Control	7.2W						0.00	2.23	2.35	0.12	16	19	3	0.58	0.55	-0.03
Control	9.2E			5.85			5.85	2.24	2.74	0.49	20	23	3	0.47	0.67	0.20
Control	9.2W						0.00	2.21	2.49	0.28	15	21	6	0.61	0.57	-0.03
Summary							13.29			2.25			38			0.06
Reprofiled	1.2E			0.56			0.56	2.16	2.78	0.62	15	27	12	0.58	0.60	0.02
Reprofiled	1.2W						0.00	1.70	2.70	1.00	14	27	13	0.39	0.55	0.16
Reprofiled	3.2E						0.00	2.34	2.59	0.25	18	27	9	0.58	0.49	-0.08
Reprofiled	3.2W						0.00	2.13	2.73	0.60	14	26	12	0.60	0.59	-0.01
Reprofiled	8.2E						0.00	2.57	2.69	0.12	19	21	2	0.69	0.70	0.01
Reprofiled	8.2W			1.28			1.28	1.60	2.43	0.83	11	22	11	0.45	0.52	0.07
Reprofiled	11.2E			3.43			3.43	1.62	2.62	1.00	14	25	11	0.36	0.55	0.19
Reprofiled	11.2W			22.47	3.93	1.69	28.09	1.68	2.82	1.15	11	26	15	0.49	0.65	0.16
Summary							33.36			5.57			85			0.52
Dammed	4.2E			0.63			0.63	1.95	2.46	0.51	16	24	8	0.44	0.49	0.05
Dammed	4.2W						0.00	2.14	2.46	0.32	14	17	3	0.61	0.69	0.08
Dammed	5.2E	2.06					2.06	1.79	2.79	1.00	14	30	16	0.43	0.54	0.12
Dammed	5.2W	2.49					2.49	2.22	2.52	0.30	17	21	4	0.54	0.59	0.05
Dammed	10.2E						0.00	2.54	2.77	0.24	19	21	2	0.67	0.76	0.10
Dammed	10.2W			26.67			26.67	2.29	2.46	0.17	15	19	4	0.66	0.62	-0.04
Dammed	12.2E						0.00	2.53	2.64	0.11	21	24	3	0.60	0.59	-0.01
Dammed	12.2W	36.14	2.41	0.60			39.16	1.86	2.43	0.56	15	24	9	0.43	0.47	0.04
Summary							71.00			3.22			49			0.38


CONTROL
RE-PROFILED
DAMMED
2.2E
2.2W
1.2E
1.2W
4.2E
4.2W
6.2E
6.2W
3.2E
3.2W
5.2E
5.2W
7.2E
7.2W
8.2E
8.2W
10.2E
10.2W
9.2E
9.2W
11.2E
11.2W
12.2E
12.2W
Water-table depth (cm)
Days after ditch blocking
-120 0 120 240 360 480 600 720 840
-5 0 5 10 15 20 25 30 35 40

Supplementary Material 2



Supplementary Material 3