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High habitat-specificity in fungal communities in oligo-mesotrophic, temperate Lake Stechlin (North-East Germany)

Christian Wurzbacher[1,2,3,4], Norman Warthmann[1,2,5], Elizabeth C. Bourne[1,2], Katrin Attermeyer[3,6], Martin Allgaier[2,3], Jeff R. Powell[7], Harald Detering[1,2,8], Susan Mbedi[2,9], Hans-Peter Grossart[3,10], Michael T. Monaghan[1,2]

1 *Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Department of Ecosystem Research, Berlin, Germany* **2** *Berlin Center for Genomics in Biodiversity Research, Berlin, Germany* **3** *Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Department of Experimental Limnology, Stechlin, Germany* **4** *University of Gothenburg, Department of Biological and Environmental Sciences, Gothenburg, Sweden* **5** *The Australian National University, Research School of Biology, Divison of Plant Sciences, Canberra, ACT, Australia* **6** *Uppsala University, Department of Ecology and Genetics, Limnology, Uppsala, Sweden* **7** *Hawkesbury Institute for the Environment, Western Sydney University, Penrith, NSW, Australia* **8** *University of Vigo, Department of Biochemistry, Genetics and Immunology, Vigo, Spain* **9** *Museum für Naturkunde Leibniz-Institute for Evolution and Biodiversity Science, Berlin, Germany* **10** *Potsdam University, Institute for Biochemistry and Biology, Potsdam, Germany*

Corresponding author: *Christian Wurzbacher* (christian@wurzbacher.cc)

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Abstract

Freshwater fungi are a poorly studied ecological group that includes a high taxonomic diversity. Most studies on aquatic fungal diversity have focused on single habitats, thus the linkage between habitat heterogeneity and fungal diversity remains largely unexplored. We took 216 samples from 54 locations representing eight different habitats in the meso-oligotrophic, temperate Lake Stechlin in North-East Germany. These included the pelagic and littoral water column, sediments, and biotic substrates. We performed high throughput sequencing using the Roche 454 platform, employing a universal eukaryotic marker region within the large ribosomal subunit (LSU) to compare fungal diversity, community structure, and species turnover among habitats. Our analysis recovered 1027 fungal OTUs (97% sequence similarity). Richness estimates were highest in the sediment, biofilms, and benthic samples (189–231 OTUs), intermediate in water samples (42–85 OTUs), and lowest in plankton samples (8 OTUs). NMDS grouped the eight studied habitats into six clusters, indicating that community composition was strongly influenced

by turnover among habitats. Fungal communities exhibited changes at the phylum and order levels along three different substrate categories from littoral to pelagic habitats. The large majority of OTUs (> 75%) could not be classified below the order level due to the lack of aquatic fungal entries in public sequence databases. Our study provides a first estimate of lake-wide fungal diversity and highlights the important contribution of habitat heterogeneity to overall diversity and community composition. Habitat diversity should be considered in any sampling strategy aiming to assess the fungal diversity of a water body.

Key words

Freshwater fungi, aquatic fungi, metabarcoding, LSU, GMYC, habitat specificity, Chytridiomycota, Cryptomycota, Rozellomycota, community ecology, lake ecosystem, biofilm, sediment, plankton, water sample, benthos, reed, fungal diversity

Introduction

Aquatic fungi play an important role in the cycling of carbon and nutrients in ecosystems (Gleason et al. 2008; Wurzbacher et al. 2010; Jobard et al. 2010; Grossart and Rojas-Jimenez 2016). Fungi may be involved in many stages of nutrient cycling, but can also be quite specific in their ecological functions. The degradation of recalcitrant plant, algal and animal residues may be carried out by a number of poorly known groups within the phyla Chytridiomycota and Rozellomycota (Corsaro et al. 2014, syn. Cryptomycota; Jones et al. 2011), and by ecological groups of aquatic hyphomycetes and yeasts (reviewed by Wurzbacher et al. 2010; Jobard et al. 2010). Parasitism by Chytridiomycota species facilitates the trophic transfer of nutrients from otherwise inedible phytoplankton to filter-feeding zooplankton (termed the "mycoloop"; Kagami et al. 2007, 2014). Aquatic fungi also form symbiotic relationships, such as endophytic or mycorrhiza-forming fungi (Kohout et al. 2012) or Chytridiomycota symbioses with algae (Picard et al. 2013). Despite their important functional role in lakes, the biodiversity of freshwater fungi remains poorly known.

Estimates of total fungal diversity currently range from 1.5–3 M species worldwide (Hawksworth 2012). Of these, roughly 100,000 species are described, with only ca. 3000 of these from aquatic habitats (Shearer et al. 2007; Tsui et al. 2016). The low diversity of aquatic compared to terrestrial (e.g., soil) fungi partly results from the fact that mycological studies in aquatic systems remain rare. Apart from a few well studied lotic ecosystems and wetlands (Wong et al. 1998; Shearer et al. 2007; Gulis et al. 2009; Krauss et al. 2011), the total diversity of aquatic fungi has not been linked to habitat heterogeneity. Most studies in freshwaters have focussed on marshlands (reviewed in Kuehn 2008) and examined the open water, leaf litter or emergent macrophytes (e.g., *Typha*, *Phragmites*). Studies in lakes have often concentrated on seasonal patterns in the water column (e.g., van Donk and Ringelberg 1983; Holfeld 1998; Lefèvre et al. 2012; Rasconi et al. 2012) or have compared different lakes (e.g. Zhao et al. 2011; Lefèvre et al. 2012; Taib et al. 2013). Several studies have found evidence for vertical and horizontal structuring of fungal communities in the water column (Lefèvre et al. 2007; Chen et al. 2008; Lepère et al. 2010), suggesting that there is an important spatial component of diversity. A recent

meta-analysis of global diversity found that aquatic fungi clustered in habitat-specific biomes, with freshwater biomes having the highest diversity at the phylum level (Panzer et al. 2015). The authors attributed this to the high substrate diversity and temporal dynamics of environmental parameters in freshwater ecosystems.

Considering the multitude of available niches and fungal lifestyles in aquatic habitats (Karling et al. 1977; Wurzbacher et al. 2010), the actual species number of aquatic fungi is likely to be much higher than what is currently recognized. Freshwater systems contain a great diversity of habitats including the boundaries that connect them to terrestrial and groundwater ecosystems (Vadeboncoeur et al. 2002; Schindler and Scheuerell 2002). Temperate, stratified lakes encompass horizontal gradients from shallow (littoral zone) to open water (pelagic zone) habitats, as well as vertical gradients from the surface associated epilimnion (often photic, light) to the deeper hypolimnion (often aphotic, dark) and the sediment. Shore regions are transition zones between terrestrial and aquatic habitats, and include biogeochemical gradients and macrostructures such as aquatic macrophytes, animals, plant debris and biofilms. These shore regions may thus be "hot spots" of aquatic, amphibious and terrestrial fungal diversity (Wurzbacher et al. 2010). In contrast, pelagic habitats have little or no macrostructure, and pelagic fungi may be limited to planktonic substrates such as dissolved organic matter (DOM), phytoplankton and zooplankton (living or dead). In particular, accompanying the change of substrate from coarse particulate organic matter (CPOM) near the edges of the lake to fine particulate organic matter (FPOM) in the open water, filamentous Dikarya are expected to be replaced by less abundant single celled yeasts and flagellated Chytridiomycota (Wurzbacher et al. 2010). We hypothesize that such a change in "fungal morphotypes" to unicellular fungi is linked to a change in the abundance and size of substrates present in the various lake habitats.

We examined the fungal diversity of a temperate lake in North-East Germany (Lake Stechlin) using a high throughput sequencing and metabarcoding approach. Our first aim was to examine the effect of habitat specificity on the fungal community by measuring the extent to which different habitat types contained similar communities, or whether there was a pronounced taxa turnover among habitats. Our second aim was to test the morphotype hypothesis, specifically whether fungal groups present were related to the availability of major types of particulate organic matter (POM). We expected that the broad diversity of substrate size and structures sampled (e.g. plankton, macrophytes) would reveal a more heterogeneous fungal community than previously detected by traditional lake sampling strategies.

Methods

Sampling site

Lake Stechlin is a deep (maximum depth: 69.5 m), oligo-mesotrophic, dimictic hard-water lake in North-East Germany (53°10'N; 13°02'E). It has a surface area of 4.25 km^2 and is divided into three distinct basins (Figure 1). The lake has a littoral reed

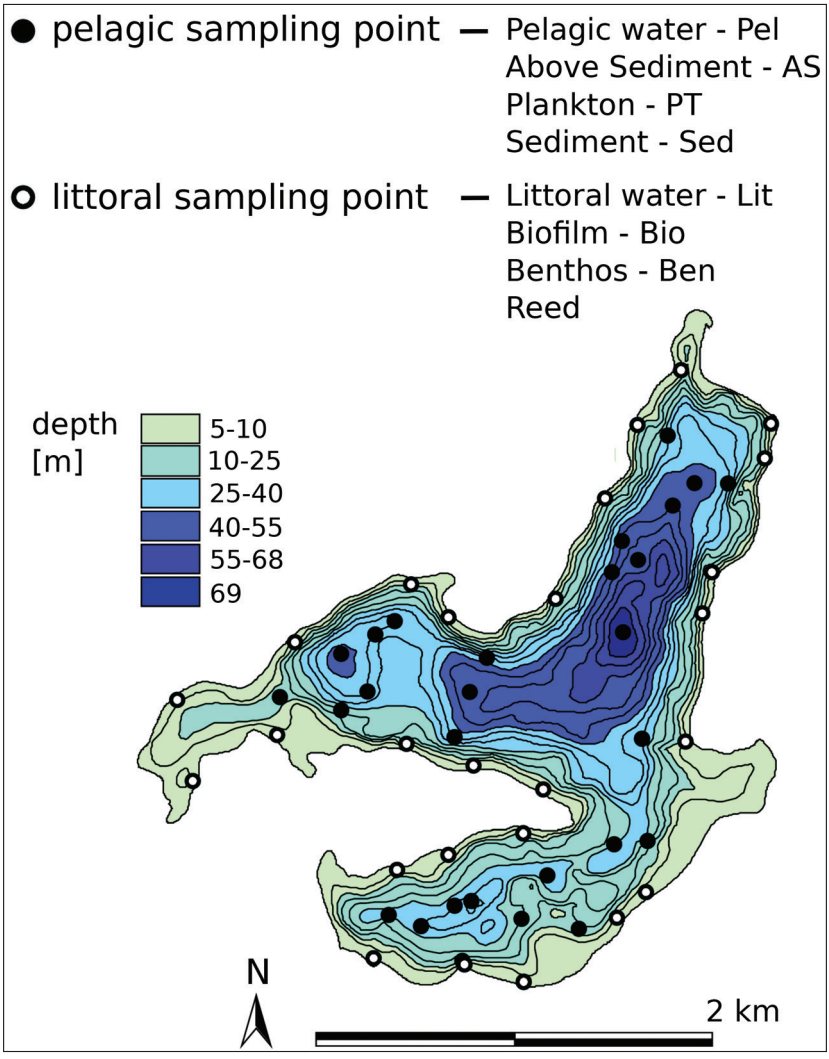

Figure 1. Sampling sites in Lake Stechlin. Integrated water samples, above-sediment water, plankton (> 55 µm), and sediment were taken from pelagic locations. Surface water samples, reed plants (*Phragmites australis*), biofilm samples (from stone, wood and macrophytes) and benthic samples (detritus, macrozoobenthos) were taken from littoral locations.

belt of *Phragmites australis* that is interspersed with areas of underwater macrophytes (mainly *Characea*). It is surrounded by mixed forest dominated by *Pinus sylvestris* and *Fagus sylvatica.* Lake Stechlin is part of the global lake ecological observatory network (GLEON) and has been monitored since 1959 (Casper 1985). Of the many publications from Lake Stechlin, few have examined the fungi (Casper 1965; Luo et al. 2011; Wurzbacher et al. 2014). This study thus represents the first attempt to characterize Lake Stechlin's mycobiota. During the course of our field sampling (April–June 2010),

Table 1. Overview of the total abundance of eukaryotic sequences and OTUs (97% similarity clustering) recovered for each lake habitat. Fungal contribution (reads, OTUs) was calculated as median percentage with standard deviation. Habitat abbreviations used in Figs 2 and 3 are indicated to the right of habitat names. POM mainly consisted of three types: fine (FPOM), coarse particulate organic matter (CPOM), or a mixture of both (MIX). Reported values were obtained from analysis of 3 samples in each habitat, except for Reed habitat which had only 1 sample. Each of these samples contained pooled DNA from three time points (April – June 2010). The shared Chao OTU richness is given as a range between a conservative and a non-conservative estimate (see Method section).

Habitat		POM type	n	Total reads/ total OTU	Fungal reads % ± SD	Fungal OTU % ± SD	Shared Chao (total)	Shared Chao (fungal)
Pelagic	Pelagic water - Pel	FPOM	3	19795/470	2.4 ± 0.4	5.8 ± 0.6	303–711	42–107
	Above Sediment -AS	FPOM	3	18701/592	2.2 ± 0.3	7.7 ± 2.5	467–1005	85–148
	Plankton - PT	FPOM	3	17902/165	0.4 ± 0.2	3.7 ± 0.5	151–294	8–8*
	Sediment - Sed	MIX	3	79190/1759	5.1 ± 1.2	23.5 ± 0.9	612–3219	189–853
Littoral	Littoral water - Lit	FPOM	3	29128/521	1.5 ± 0.2	6.8 ± 1.0	363–883	54–116
	Biofilm - Bio	MIX	3	26302/1053	11.0 ± 6.8	25.1 ± 2.6	541–1971	225–640
	Benthos - Ben	CPOM	3	59169/1070	63.1 ± 13.1	30.9 ± 8.4	580–2280	231–1323
	Reed	CPOM	1	4277/179	88.7	35.8	n.a.	n.a.

n.a. (non applicable)

* Chao estimate may be not reliable for small sample sizes

the phytoplankton community was dominated by diatoms and by filamentous cyanobacteria (*Dolichospermum flos-aquae*). The nutrient status of the lake during the sampling period is detailed in the Suppl. material 1.

Sampling

We sampled eight different habitat types (Table 1) at three time points encompassing spring and early summer 2010 (8–9 April; 11–12 May; and 9–10 June). Sampling was carried out relatively early in the year to avoid an over-representation of wood-degrading Basidiomycetes that are introduced as airborne spores from the surrounding forest between July to November (personal observation). Our sampling scheme was designed to cover for both pelagic (defined here as areas with > 20 m depth and > 100 m from shore) and littoral (< 10 m from shore) habitats (Figure 1). Habitats were defined as follows: "Pelagic" samples consisted of a 1 litre water sample integrated from three depths: 1 m below the surface, at mid-depth, and at 2–3 m above the sediment. These were collected using a Niskin-type water sampler (Hydro-Bios, Germany); "Plankton" was obtained from an integrated sample (surface to 2–3 m above sediment) from a plankton net (55 µm mesh; Hydro-Bios, Germany); "Above Sediment" was a water sample from 0–20 cm above the sediment that was retrieved together with "Sediment", which itself comprised 1 ml of the uppermost cm of the core, using a sediment corer (6 cm diameter; Uwitec, Austria). "Littoral" samples consisted of a 1 litre water sample taken from 0.5–1 m depth in the

littoral zone; "Reed" samples were taken from aerial, submerged, and rhizosphere parts of reed plants, following the physical removal of biofilm; "Biofilm" samples were taken from stones, woody debris, and reed stems (removed using a scalpel); and "Benthos" consisted of detritus and zoobenthos sampled from the littoral zone using a sediment grabber (Ekman-Birge bottom sampler, Hydrobios, Germany). Each of the eight habitat types was sampled at 3 locations in each of the 3 basins at each of the 3 time points (n = 27), for a total of 216 samples. Samples were pooled by combining one sample from each of the three basins, resulting in 3 representative samples of each habitat per time point. These were further pooled for sequencing analysis (see below). Water samples were filtered on a 0.22 µm Sterivex filter (Millipore, USA), plankton-net samples were filtered onto a 12 µm cellulose acetate filter (Sartorius AG, Germany), and 1 ml of sediment was transferred to a cryotube for storage. All samples and filters were stored at -80 °C until further processing. We categorized the typically predominant POM type for each habitat. Water samples were FPOM dominated and Reed and Benthos habitats were CPOM dominated, while Sediment and Biofilm was classified as a mixture of both POM types (Table 1).

DNA extraction

Total DNA was extracted using the Power Soil kit (MoBio Laboratories, Carlsbad, USA) for Sediment samples; the Qiagen Plant kit (Qiagen, Hilden, Germany) for Reed, Biofilm, and Benthos samples; and the Qiagen Blood & Tissue kit for Littoral, Pelagic, Above Sediment and Plankton samples. Manufacturers' instructions were followed with the following modifications: Reed and Benthos samples were homogenized with a mill (Pulverisette 9, rpm = self-optimize speed, 20 sec, Fritsch, Germany) and all other samples were subjected to a bead-beating step prior to extraction (MMX400, 2 × 2 min, f = 30 sec^{-1}, Retsch, Germany). We added 20 µl Proteinase K (Qiagen, Netherlands) to the lysis buffer for Sediment, Reed, Biofilm, and Benthos samples, and incubated these for 1 h at 56 °C. DNA concentrations were measured using a PicoGreen assay (Invitrogen, USA). Approximately 20 ng of DNA was used as template for PCR.

Library preparation for pyrosequencing

DNA metabarcoding was carried out on all samples using the D1/D2 variable region of the ribosomal LSU with the eukaryotic primers NLF184cw (TACCCGCTGAAYTTAAGCATAT; modified from Van der Auwera et al. 1994) and Euk573rev (AGACTCCTTGGTCCRTGT; modified from NLR818, Van der Auwera et al. 1994). After *in silico* tests using TestPrime (Klindworth et al. 2012) we found the primer pair covered 84% of all eukaryotes deposited in the SILVA database (LSU r123 version) when allowing for two mismatches, neither of which was in the last 3 bp of the 3' region. The primer pair potentially excludes single eukaryotic lineages within Amoebozoa, Excavata, Cercozoa. Within fungi it covers 93.4% of deposited sequences in all phyla, except Microsporidia. Oomycetes were covered at 76%. Among the fungal phyla, the

lowest coverage was 85% for Basidiomycota, followed by Zygomycota with 93%. Primers were modified with 5' sequencing adaptors (extended primer list in Suppl. material 2), consisting of barcodes recommended by Roche and Lennon et al. (2010) and Lib-L adapters (Roche). PCR was conducted with AccuPrime Taq Polymerase High Fidelity (Invitrogen, USA) in a 40 µl reaction with the following conditions: initial denaturation for 3 min at 98 °C followed by 32 cycles of 1 min denaturation at 94 °C and 2 min annealing/elongation at 60 °C. The quality and intensity of the amplicons were checked on an agarose gel to ensure semi-quantitative assumptions (Lindahl et al. 2013). PCR amplicons were purified using AMPure XP Beads (Beckman Coulter) and quality was verified by microfluidics electrophoresis (Bioanalyzer, Agilent). The 9 PCR products per habitat (3 replicates per sampling time) were then pooled into three final replicates for sequencing, each of which contained all 3 time points. As a result, the sequencing triplicates were representative for the habitat biota within the sampled timespan of April-June. Pooling also helps to ameliorate PCR bias and template stochasticity. We sequenced only one of the triplicates of the reed habitat. Afterwards all amplicons were pooled equimolar for emulsion PCR and subjected to pyrosequencing library preparation and sequencing following the manufacturer's recommendations (Lib-L, FLX titanium chemistry, Roche, Switzerland). The sequence data was deposited at ENA (http://www.ebi.ac.uk/ena) under following accession number: PRJEB14236.

Sequence data processing

Sequences were processed as briefly outlined in Suppl. material 3. Raw 454 sequencing data were transformed by coding any nucleotide with a Phred score < 11 as N. We removed all reads shorter than 300 nt and trimmed reads with trailing Ns. The D1 region is highly variable and has a pronounced length polymorphism, which renders an accurate alignment difficult. We therefore defined an end position to serve as an alignment anchor by screening the SILVA reference database (v123) for a conservative eukaryotic region located within our amplicon. We identified a conserved 42-nt sequence (GAGNCCGATAGNNNACAAGTANNGNGANNGAAAGWTGNAAAG) located after the D1 region as being suitable to serve as a stable 3' end for the alignment by using the probe design tool of ARB (Ludwig et al. 2004). We subsequently clipped all filtered reads (fastq format) after the last nucleotide using Shore oligo-match: a sequence context-aware clipping tool (Ossowski et al. 2008). This normalized the length of the reads to a fixed position in a global alignment (average read length: 360 ± 13, n = 596k). We allowed for mismatches by scoring each match with 3, mismatches with -1, and gaps with -4. The threshold for clipping was set to $score_{MAX} > 0.5$ and the effect on the size-frequency distribution can be found in Suppl. material 3. Unclipped sequences were rejected and analysed separately (Suppl. material 3).

Clipped reads were processed in Mothur following 4-5-4 SOP (Schloss et al. 2009, accessed in August 2012). Quality filtering was achieved by using the sliding-window option (quality threshold of 25). For the alignment-based procedure, we constructed a reference dataset with long, high-quality reads processed with pyrotag-

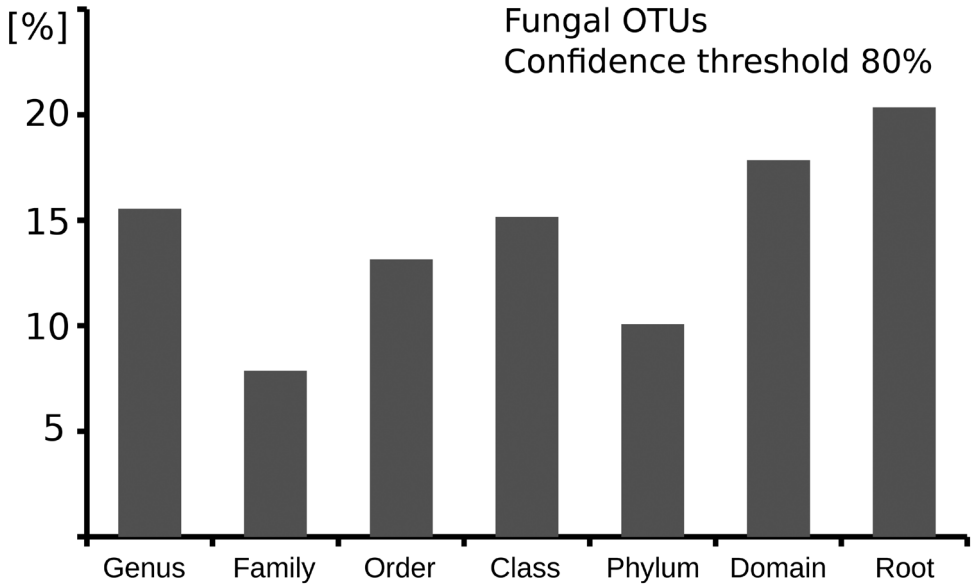

Figure 2. Classification of fungal OTUs by the RDP classifier to the different taxonomic levels as a percentage. Classification cutoff was a confidence level of 0.8.

ger (http://pyrotagger.jgi-psf.org) using a cutoff at > 500 nt. These were aligned to the eukaryotic backbone provided by the SILVA database LSURef (version 111; www.arb-silva.de) using the SINA aligner (Pruesse et al. 2012). This reference alignment was used to align our reads in Mothur. After clustering at 97% sequence similarity (average neighbour algorithm), the OTU abundance matrix was imported into R (www.r-project.org, version 3.3.1.) for further analysis (see below). As a comparison to a fixed 97% sequence similarity cutoff, we employed a coalescent-based clustering analysis as implemented by the gmyc model (Powell et al. 2011; Fujisawa and Barraclough 2013) with an UPGMA tree for the early diverging lineages (456 OTUs). OTUs were classified by the RDP classifier using the RDP fungal LSU training dataset with a confidence level of 80% (version 11; Liu et al. 2011; Figure 2; see Suppl. material 4 for classifications).

Habitat richness and statistics

OTU count was positively correlated with read count (Pearson's r = 0.90), thus we avoided single sample based richness estimates. For richness estimates of the habitats we applied a shared corrected Chao index (Chiu et al. 2014). More specifically, we provided a range for the Chao estimates based on a lower conservative OTU filtering and an upper overestimate based on unfiltered OTUs. In the former case all OTUs that occurred only in one sample of the dataset (independent of the absolute OTU

frequency) were removed while in the latter case all OTUs including singletons were kept. Supporting rarefaction curves displaying the sampling effort for Eukarya and Fungi based on a singleton filtered OTU matrix are provided in the Suppl. material 5).

POM and habitat types were compared by employing parametric statistics (ANOVA and Tukey honest significant difference) on "logit" transformed proportional read (read counts) or OTU (OTU counts) data. Plankton samples were excluded due to their skewing effect on the distribution caused by their low fungal proportion (including Plankton samples will still lead to a significant Kruskal-Wallis test, $p<0.001$, but renders PostHoc tests difficult to apply). Normality and homogeneity of variances were confirmed by Shapiro-Wilk tests and Levene's Tests, respectively.

Multivariate analyses

For all subsequent β-diversity analyses, an OTU table without singletons was used to account for noise in the data (e.g., Reeder and Knight 2009). Differences among habitats within the fungal sub-community were examined with a non-metric multidimensional scaling (NMDS) ordination plot based on the Cao distance (Cao et al. 1997), which accounts for variable sampling intensity. Ellipses correspond to the standard deviation around the habitat group centroids. Stress values below 0.1 can be considered as a very good fit. We additionally tested for significance when separating habitats (excluding Reed) and POM type and using a PERMANOVA (1000 permutations) on the distance matrices. The robustness of the results were evaluated by comparing them with a presence/absence transformed OTU matrix using Jaccard distances, as well as with a classified taxonomy abundance table generated with SILVA NGS (see below) using Cao distance. Both additional analyses resulted in similar outcomes (Suppl. material 6).

Alternative sequence data processing

As an alternative to the OTU-based RDP classification of our sequences, we performed two additional analyses with the aim to gain resolution for the taxonomic classifications of our sequences (see also Suppl. material 3). First, clipped sequences were demultiplexed and quality trimmed in Mothur as described above and then submitted to SILVA NGS (www.arb-silva.de/ngs/) (Quast et al. 2013) for classification at the minimum similarity level of 85% against the LSU reference database (version 123). This resulted in 57 fungal taxonomic paths (unique taxonomic names, hierarchical, see Quast et al. 2013; Suppl. material 4). Second, we performed an analysis, in which we pooled all clipped sequences of one habitat and then subjected these to a blast search (Blast+) against the nt database (GenBank, accessed January 2015) for eukaryotes. Sequences were then classified using the LCA classifier implemented in Megan5 (Huson et al. 2011) using the following parameters: Min. Score = 100,

Max. Expected = 0.01, Top % = 5.0, Min. Support % = 0.01, Min. Support = 2, LCA = 75 %, Min. Complexity = 0. Habitats were compared based on square root normalization (Suppl. material 7).

Phylogenetic inference

We recovered several Neocallimastigales (rumen fungi) sequences, as classified by SILVA NGS and also by the RDP classifier with a low probability (< 55%). We took 26 representative sequences and constructed a phylogenetic tree with an extension of the reference dataset from James et al. (2006) in order to confirm or reject this potential classification. A matrix was aligned using the SINA aligner (Pruesse et al. 2012) followed by manual inspection. For tree reconstruction, we used MrBayes (v3.2.6; Ronquist et al. 2012) with 10 million generations and an "invgamma" model.

Results

A total of 54 sampling stations, representing eight habitat types, were sampled at three time points in spring of 2010 and analysed using pyrosequencing of the large ribosomal subunit (LSU) as a universal eukaryotic marker. Across all habitats, the total number of eukaryotic OTUs was 3695, as estimated using alignment-based clustering at 97%, 47% of which were singletons. The lower limit of shared estimated OTUs (shared corrected Chao index) varied considerably among habitats, with the highest values found in Sediment, Benthos and Biofilm habitats, and the lowest in Plankton and water samples (Table 1). Of the total OTUs, 1027 (27%) were classified as fungi by RDP (48% of which were singletons). The gmyc method of OTU delimitation for the non-Dikarya taxa (mainly aquatic lineages that comprised 52% of the fungal OTUs in our data) resulted in 65% of OTUs with more than one occurrence, compared with 68% of units defined by gmyc clustering. The ability of each type of taxonomic unit to predict habitat (97%: adj. $r^2 = 0.59$; gmyc: adj. $r^2 = 0.61$) was very similar and we thus decided, to hereafter use the more conservative OTUs based on the 97% criterion. The shared lower estimated OTUs were following similar trends as for all eukaryotes with Benthos and Biofilm ranking highest (231 and 225 estimated OTUs, respectively) and markedly lower ranks for the water samples (42–85 estimated OTUs) and only 8 estimated OTUs for Plankton samples (Table 1). Both, the fungal proportions (fungal reads) as well as the proportional fungal diversity (fungal OTUs) were significantly different for each POM type (reads: ANOVA, $F = 104.4$, $p = 6.6^{-10}$, Tukey Post Hoc Test $p < 0.001$ (Figure 3); OTUs: ANOVA, $F = 132.9$, $p = 1.08^{-10}$, Tukey Post Hoc Test $p < 0.01$).

Fungal community composition was significantly structured into different habitats according to the NMDS clustering of OTUs (Figure 4, stress = 0.08; PERMANOVA, $r^2 = 0.71$, $p < 0.001$) and POM types (PERMANOVA, $r^2 = 0.36$, $p < 0.001$). The three wa-

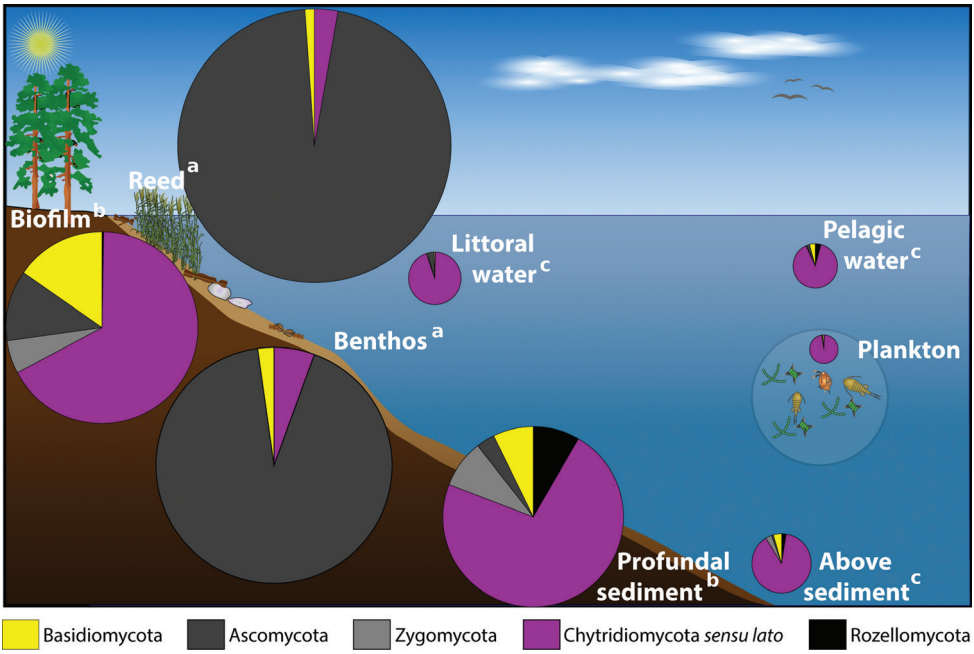

Figure 3. Contribution of fungal phyla within each of the lakes habitat. Pie chart diameters are scaled by the contribution of fungal diversity to the total eukaryotic diversity in each habitat. Lower case letters group significantly different POM types in terms of OTU diversity and fungal reads (Tukey Post-Hoc tests, $p < 0.01$).

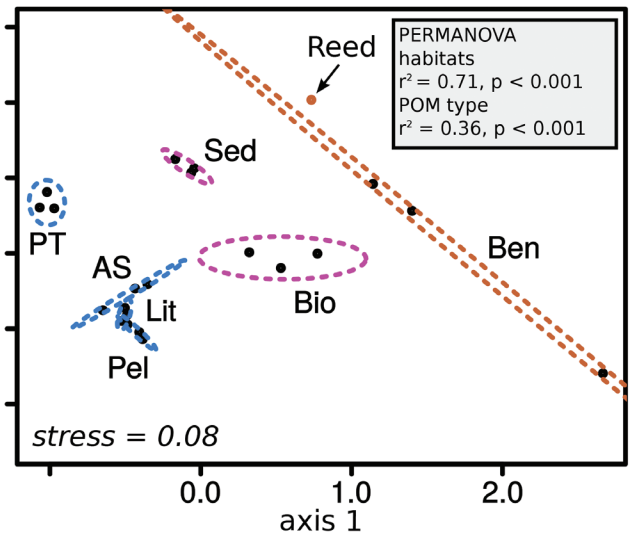

Figure 4. Habitat specificity of the fungal community in Lake Stechlin. NMDS plots based on the fungal OTU matrix (1027 OTUs). Ordination is based on Cao distances (Cao et al. 1997), which are insensitive to differences in sampling effort. Ellipses are based on standard deviations around habitat centroids (based on a confidence level of 0.95) and are coloured according to their POM type: FPOM (blue), MIX (magenta), CPOM (brown). Habitat codes and POM categories are taken from Table 1.

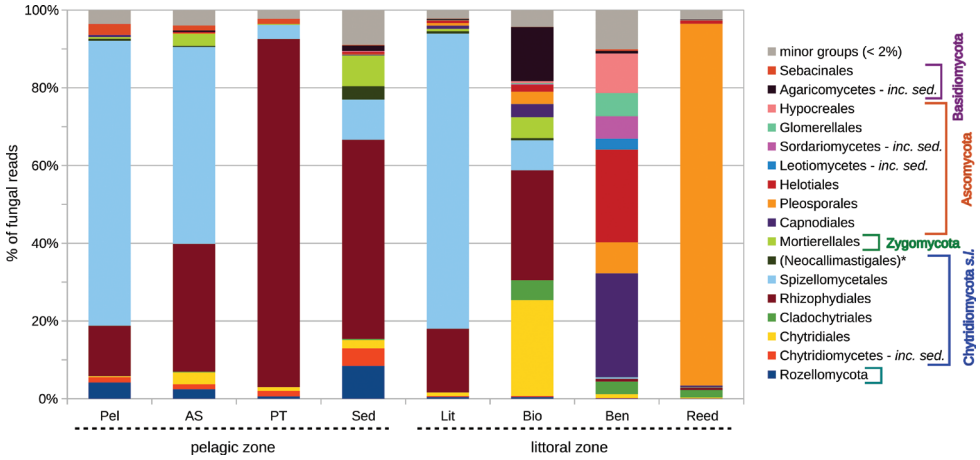

Figure 5. Distribution of fungal orders in Lake Stechlin habitats based on the mean percentages as determined with SILVA NGS. Fungal phyla are highlighted with brackets. Habitat codes are taken from Table 1. (*) marks the false classified Neocallimastigales as clarified by phylogenetic inference (see discussion paragraph on sediments).

ter samples (Pelagic, Littoral, and Above Sediment) appeared to be very similar, whereas all other habitats were distinct (Figure 4). Comparable results were found by NMDS clustering of the presence/absence OTU matrix or by clustering the fungal taxonomic paths generated by SILVA NGS, indicating that the habitat clustering was robust and took place at even higher taxonomic levels (phylum to order level; Suppl. material 6).

Only 23% of the fungal OTUs could be classified to the family or genus level, and around 20% of the sequences could not be assigned to the kingdom level at 0.8 confidence threshold (Figure 2). RDP classifier seem to provide limited classification success when certain early diverging lineages are targeted (e.g., see "Pel" sample in Suppl. material 4). Thus we decided to also evaluate other alternatives. By using Blast against the nucleotide database of NCBI most fungal sequences could only be classified as "fungi" or "environmental samples" (mean: 70.2% of sequences; range: 36.5–89.7% of sequences in a given habitat; see Suppl. material 7). Then by processing the sequences by SILVA NGS we obtained a classification on the order level. Hence, we will use RDP to discuss the fine scale resolution and the SILVA classification for overall comparisons on the order or phyla level (Figure 3, 5). The orders Spizellomycetales and Rhizophydiales (both Chytridiomycetes) comprised the majority of fungal sequences in the four pelagic habitats and the Littoral water sample, with a greater proportion of Spizellomycetales in the three types of water samples compared to more Rhizophydiales in the Plankton and Sediment habitats (Figure 5). In contrast, the Biofilm habitat harboured a good representation of all major fungal phyla (Figure 3) with Chytridiales, Rhizophydiales (both Chytridiomycetes), and Agaricomycetes (Basidiomycota) forming the most prominent orders (Figure 4). Capnodiales and Helotiales (both Ascomycota) were the most prominent orders in the Benthic habitat whereas the Reed habitat was dominated by Pleosporales (Ascomycota) (Figure 4).

Only a small proportion of fungal sequences (0–6%) could be assigned to what we assume are forest taxa (Agaricales, Auriculariales, Boletales, Cantharellales, Gleophyllales, Hymenochaetales, Polyporales, Russulales; Suppl. material 1). This proportion was significantly different among habitats (Kruskal-Wallis test, df = 5, p = 0.023), being highest in the Sediment samples (mean = 4.9%, SD = 0.9). From all habitats, we recovered sequences from oomycetes (i.e. *Albugo*, *Aphanomyces*, *Phytophthora*, *Pythium*, *Saprolegnia*), a group that was formerly related to aquatic fungi and that occupied similar ecological niches (Sparrow 1960). They have a Chytridiomycota-like life cycle and serve as parasites (e.g., agent of the European cray-fish plague) and saprophytes in aquatic systems. These sequences were 1–3 orders of magnitude lower in abundance compared to the fungal sequences, with maxima in Benthos and Sediment samples (Suppl. material 1).

Discussion

In the following discussion, we first address methodological considerations and then discuss fungal diversity separately for the major habitats.

Methodological considerations

The occurrence of early diverging fungal lineages as well as members of the Dikarya renders a comprehensive assessment of the aquatic mycobiota challenging. This is due to the difficulty in finding a universally suitable marker (i.e., "DNA barcode") with both sufficient coverage of evolutionary distant groups and meaningful resolution within any of the individual groups. We employed the D1 region of the LSU as a marker because of its high variability while still being conservative enough to amplify across the fungal kingdom (Porter and Golding 2012). Both D1 and D2 regions were formerly used as molecular markers for fungi, especially yeast (Kurtzman and Robnett 1997) and perform almost as well as the commonly used ITS region in discriminating fungal groups (Schoch et al. 2012). The LSU is an established phylogenetic marker for Chytridiomycota (Letcher et al. 2006) and, unlike the ITS region, it can be used to delimit distant aquatic fungal lineages (Lefèvre et al. 2012; Wurzbacher et al. 2014). The small ribosomal subunit (SSU) is also well established for early diverging lineages (e.g., Jobard et al. 2012; Ishii et al. 2015); however, it is less suitable for fungal groups within Dikarya (Lindahl et al. 2013; Tedersoo et al. 2015) and would fail to generate meaningful OTUs for a broad spectrum of simultaneously occurring fungal phyla, such as in our biofilm habitat. Currently, the major disadvantage of using LSU regions as taxonomic markers for aquatic fungi is the lack of reference sequences that allow assignment. Although the RDP classifier identified at least two aquatic hyphomycetes genera in our dataset (*Spirosphaera* and *Tetracladium*) most previous work on this ecological group was done with ITS (Duarte et al. 2014). The ITS region may pose a

better solution for those lake habitats that were dominated by Dikarya, however, as of 2014 only 26% of described aquatic hyphomycetes species had an ITS database record (Duarte et al. 2014). The RDP database had also problems with classifying Chytridiomycota (and Rozellomycota) from the water samples and similar problems may arise with freshwater Chytridiomycota for ITS data (currently there are 1121 Chytridiomycota sequences in UNITE version 7.0, excluding Batrachochytrium sequences) pointing to larger gaps in the reference datasets for aquatic species. The UNITE species hypothesis concept introduced by Kõljalg et al. (2013) might be a good interim solution for dealing with undocumented species; however, the LSU offered alternatives here, namely (i) it was possible to employ species delimitation methods for clustering (GMYC) and classification (see below) and (ii) it allowed the multivariate analyses for using evolutionary (or trait based) based diversity indexes such as UniFrac, which is frequently used in microbial ecology (Lozupone et al. 2011).

Water and large plankton

All three water habitats (Pelagic, Littoral, and Above Sediment) had a low proportion of fungal sequences. Each were characterised by a predominance of Chytridiomycota. This was also the case for the habitats directly connected to processes in the open water (Plankton and Sediment). The proportion of fungal sequences in all samples classified as FPOM was significantly lower (Figure 3). Previous results from Lake Stechlin also reported a low proportion of fungi in water samples (Luo et al. 2011), which may be related to the fact that we did not enrich for fungi by prefiltration or by primer selection. Lefèvre et al. (2012) provided a summary of fungal and chytrid percentages ranging from 1–50% in water samples, relating these observations to prefiltration and primer pair used. Like Monchy et al. (2011), we observed similar communities in all of the water samples (Littoral, Pelagic, and Above Sediment). The greater number of OTUs per read abundance may originate from a rare fungal parasite community (Mangot et al. 2013), whereby parasitic chytrids can recruit for temporally variable infection opportunities such as may occur over time scales of a few weeks (e.g., Ibelings et al. 2004; Alster and Zohary 2007).

There was a limited number of fungal taxa associated with water borne zoo- and phytoplankton samples (Plankton; > 55 µm), which presumably should represent attached or infective stages of fungi. 84–93% of these fungi belonged to Rhizophydiales, a group of well described phytoplankton parasites. By contrast, Rhizophydiales accounted for only 14–17% in the pelagic (open) water samples. This is insofar important because most microscopic studies on chytrids refer to infected algae of approximate the size of 50 µm or larger (e.g., Hohlfeld 1998; Ibelings et al. 2004; Rasconi et al. 2012). However, in an unbiased water sample (i.e. not fractionated by filtration or enriched by a plankton net), they were replaced as dominant group by the order Spizellomycetales, which are common saproptrophs in soil and may underline to the importance of saprotrophic chytrids in aquatic environments (Wurzbacher et al. 2014).

This may establish the mycoloop (Kagami et al. 2014) as a trophic link during times with low prevalence of algal infections, based on the mineralization of detritus (cf. Gleason et al. 2008). Finally, there was a low proportion of Rozellomycota in the large plankton. Rozellomycota are discussed as *inter alia* attached algal parasites (Jones et al. 2011); however, their under-representation in Plankton samples indicates that they were not relevant parasites of the larger plankton in Lake Stechlin, where Chytridiomycota occupied this niche. Due to the small size of Rozellomycota, they may rather have a specialization towards smaller hosts, which do not provide enough resources for Chytridiomycota to complete their life cycle.

Sediment

The profundal sediment temperature in Lake Stechlin remains *ca.* 4 °C year-round while the upper sediment surface (~ 5 mm) is usually oxic. The sediment has a high water content (> 95%) and high organic matter content at the sampled sites because it receives sinking matter from pelagic organisms. Thus the sediments serve as a fungal spore bank. We therefore expected to observe elevated proportions of forest fungi that had probably blown in or been washed in as spores. The dominant fungal group was the Rhizophydiales (Chytridiomycota), as also found in the large plankton samples. Similar to their hosts, parasitic chytrids develop thick-walled resting spores (cysts), which can be found in sediment, while other parasitic species can actively infect algal resting stages in sediments (Canter 1948, Canter 1968). The few studies that have investigated lake or pond sediments reported Chytridiomycota and Rozellomycota (at that time referred to as LKM11 & LKM15) to be the dominant fungal phyla (Luo et al. 2005; Slapeta et al. 2005). Rozellomycota species appear to occur in the hypolimnion of lakes (Lepère et al. 2010) and also in anoxic habitats (Jones et al. 2011), but their ecological function remains unclear (Grossart et al. 2016). Similarly enigmatic was the appearance of Zygomycota (Mortierella) at the sediment surface in our study. Some of them can grow at low temperatures under oxic conditions, e.g. under snow packs in sub-alpine regions (Schmidt et al. 2008). Very surprising was the appearance of Neocallimastigomycota, which are by definition obligate, mutualistic, anaerobic rumen fungi. They are exceptional in that they break down a broad variety of plant polymers under anaerobic conditions (Solomon et al. 2016). These fungi must have had an environmental ancestor and it is possible that anoxic sediments may represent such an ancestral habitat. However, the sequences were only approx. 90% similar to *Orpinomyces* and the RDP classifier assigned a low probability to this classification (< 0.55). Lefèvre et al. (2012) also described sequences from lake plankton samples that may support such a new environmental lineage of "rumen fungi". Our test of whether those sequences clustered within the Neocallimastigomycota in a phylogenetic tree (Suppl. material 8) found no support for this. The sequences resembled unknown fungal lineages or belonged to Rozellomycota or Zygomycota lineages with a moderate probability.

Biofilm (Periphyton)

Biofilm samples appeared to represent an intermediate fungal habitat between sediments and benthic samples by including a high diversity of early diverging lineages as well as elevated proportions of Dikarya (16–36%, Figure 3). Fungi formed a significant proportion of the overall eukaryotic biofilm community recovered (28% of the OTUs recorded in the habitat were identified as fungi), dominated by biofilm-forming algae (the ratio of fungi to periphyton/epilithic algae was roughly 1:5, see Suppl. material 4, SILVA NGS). Biofilms represent a complex environment (exhibiting the highest eukaryotic taxon richness of all eight habitats) and this is also reflected by a broad range of fungal groups and taxa. Along with Rhizophydiales and Spizellomycetales, we found other chytrids of the orders Chytridiales and Cladochytridiales. The spatial proximity of host cells in periphyton could be ideal for chytrid species, facilitating a high encounter rate with potential hosts and substrates. In contrast to the water samples, the RDP classifier was able to classify more Chytridiomycota to genus level: *Nowakowskiella*, *Chyridium* and *Betamyces*. The RDP classifier also identified the earlier mentioned aquatic hyphomycetes. However a large part of sequences was only classified to phylum level (Suppl. material 4). These autotrophic lake biofilms seem to be a rich source of fungal biodiversity and pose promising target habitats for future studies. Biofilms (in our case mainly littoral periphyton and epilithic biofilms) have been rarely examined for fungi, and only a few studies on stream ecosystems have investigated the fungal occurrence (measured as ergosterol) on substrates other than leaves (Tank and Dodds 2003; Artigas et al. 2004; Aguilera et al. 2007; Frossard et al. 2012). In lakes and streams, periphyton can contribute substantially to the primary production of the whole ecosystem (Lalonde et al. 1991; Vadeboncoeur et al. 2007 and references therein; Vis et al. 2007) and can be the primary food source for macrozoobenthic grazers (Cattaneo and Mousseau 1995). Our findings suggest that it is not only a rich source of widely divergent fungal lineages, but that fungi might play an important ecological role in periphyton, turning over a significant amount of algal carbon and thus total carbon in the lake.

Benthic and reed samples (CPOM)

In contrast to water samples, fungal sequences were dominant in CPOM (Benthos, Reed) samples and their relative proportions were significantly elevated in this POM type. Samples consisted mainly of submerged plant residues in addition to algae and benthic animals. Mitosporic ascomycetes lineages were predominant, followed by a small percentage of chytrids (mainly Cladochytridiales) and very few Basidiomycota. This appears congruent with our initial "morphotype hypothesis". Mitosporic ascomycetes are effective plant decomposers in freshwater systems (Gessner et al. 2007), where they are ecologically grouped together as aquatic hyphomycetes (e.g. *Spirosphaera*, a potential aero-aquatic hyphomycete increased to 12% in Benthos samples). The Ben-

thos habitat had a high proportion of fungal OTUs and fungal reads and is probably home to those fungi responsible for the breakdown of submerged plant remains. Interestingly, the importance of aquatic hyphomycetes for plant litter breakdown has thus far only been demonstrated in lotic environments, with lakes not yet investigated in detail (see Chauvet et al. 2016). In contrast to the benthic samples, the Reed sample exhibited a dominance of the fungal order of Pleosporales (93%). Early molecular work has already established the high diversity of reed endophytes (Neubert et al. 2005, Angelini et al. 2012) and we could confirm their presence. The reed sample can be seen as an outgroup in our study, as it comprised the emergent parts of plants. Sequences of the order Pleosporales were largely restricted to the reed and, to a lesser extent, benthic samples.

Conclusions

Fungi play an important role in the cycling of carbon and nutrients in a wide range of freshwater habitats (Bärlocher and Boddy 2016). While much of our understanding of their diversity and ecological roles stems from research in the terrestrial realm, there is increasing interest in their taxonomic and functional diversity in freshwater systems (Grossart et al. 2016; Grossart and Rojas-Jimenez 2016). We examined fungal community composition in eight different habitats of a single lake, in contrast to most studies which have compared water samples among seasons or lakes (e.g., Monchy et al. 2011; Taib et al. 2013). We found pronounced differences in diversity and community composition among the sampled habitat types, and conclude that the habitat heterogeneity within a single lake offers a wide range of fungal niches. The results extend previous research of fungal diversity and distribution in freshwaters and clearly indicate that lake biofilms can be hotspots for aquatic fungi. Most of the fungi from the water samples were rather homogeneous in their community composition, with a clear dominance of Chytridiomycota. This may be due to the predominance of FPOM in the sampled habitats. Our study highlights the importance of habitat heterogeneity and we hope will stimulate further research on under-sampled lake habitats, such as sediments, biofilms, and submerged macrophytes. A more holistic approach in evaluating fungal diversity, using a more comprehensive inclusion of habitat types and taxonomic markers, should provide deeper insights into the multiple ecological roles of fungi in diverse freshwater environments.

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Supplementary material 1

Accompanying data tables

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: Two additional tables stating 1) the physicochemistry of the lake during the sampled time span, 2) the proportions of fungal-like organism and terrestrial fungi (“forest fungi”, see main text).

Supplementary material 2

List of pyrosequencing primers.

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: List of employed pyrosequencing fusion primers.

Supplementary material 3

Detailed results of the clipping procedure

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: ZIP file

Explanation note: File archive in "zip" format. Decompress with e.g., "unzip" for inspecting individual files. Files describing the bioinformatic processing and the effects of the clipping procedure.

Supplementary material 4

Krona charts of classified OTUs (RDP) and sequences (SILVA NGS).

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: ZIP file

Explanation note: File archive in "zip" format. Decompress with e.g., "unzip" for inspecting individual html files. Open html files with an internet browser (network connection must be enabled). Krona charts presenting the classified sequences based on a) OTUs classified by the RDP classifier, and b) based clipped reads processed by the SILVA NGS pipeline.

Supplementary material 5

Rarefaction analysis

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: Rarefaction curves based on the OTU table without OTU singletons for all eukaryotes (left panel) and for fungal OTUs (right panel).

Supplementary material 6

Alternative ordinations based on binary data and taxonomy

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: Two alternative NMDS accompanied by corresponding PERMANOVA statistics based on a) the presence/absence of OTUs (left panel) and the Jaccard index, and b) the taxonomic classification of SILVA NGS and the Cao index. The ellipses (coloured to POM type) are based on standard deviations around centroids with a confidence level of 0.95.

Supplementary material 7

Comprehensive Blast analysis

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: Blast results against the NCBI nt database (June 2015) for all eukaryotes presented in a Megan5 plot.

Supplementary material 8

Phylogenetic tree of Neocallimastigales sequences

Authors: Christian Wurzbacher, Norman Warthmann, Elizabeth Bourne, Katrin Attermeyer, Martin Allgaier, Jeff R. Powell, Harald Detering, Susan Mbedi, Hans-Peter Grossart, Michael T. Monaghan

Data type: PDF file

Explanation note: Phylogenetic bayesian tree based on 10 million generations. Sequences that were classified as Neocallimastigales in the manuscript are coloured in red with the frequency of sequences in the dataset in black. The name corresponds to the representative read identifier in the dataset (accessible at ENA nucleotide archive: PRJEB14236). Node labels are posterior probabilities above 0.8. Statistically supported branches have an probability of 0.95-1.