

Published in final edited form as:

Mol Ecol. 2016 May ; 25(10): 2286–2301. doi:10.1111/mec.13633.

Microbial eukaryote plankton communities of high-mountain lakes from three continents exhibit strong biogeographic patterns

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Abstract

Microbial eukaryotes hold a key role in aquatic ecosystem functioning. Yet, their diversity in freshwater lakes, particularly in high-mountain lakes, is relatively unknown compared with the marine environment. Low nutrient availability, low water temperature and high ultraviolet radiation make most high-mountain lakes extremely challenging habitats for life and require specific molecular and physiological adaptations. We therefore expected that these ecosystems support a plankton diversity that differs notably from other freshwater lakes. In addition, we hypothesized that the communities under study exhibit geographic structuring. Our rationale was that geographic dispersal of small-sized eukaryotes in high-mountain lakes over continental distances seems difficult. We analysed hypervariable V4 fragments of the SSU rRNA gene to compare the genetic microbial eukaryote diversity in high-mountain lakes located in the European Alps, the Chilean Altiplano and the Ethiopian Bale Mountains. Microbial eukaryotes were not globally distributed corroborating patterns found for bacteria, multicellular animals and plants. Instead, the plankton community composition emerged as a highly specific fingerprint of a geographic region even on higher taxonomic levels. The intraregional heterogeneity of the investigated lakes was mirrored in shifts in microbial eukaryote community structure, which, however, was much less pronounced compared with interregional beta-diversity. Statistical analyses revealed that on a regional scale, environmental factors are strong predictors for plankton community structures in high-mountain lakes. While on long-distance scales (>10 000 km), isolation by distance is the most plausible scenario, on intermediate scales (up to 6000 km), both contemporary environmental factors and historical contingencies interact to shift plankton community structures.

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T.S. and R.S. conceived and guided the study. R.S. and I.V. conducted sampling. S.F. performed laboratory work. S.F. and T.S. analysed data. T.S. and S.F. wrote the first version of the manuscript, and R.S. and I.V. added to subsequent versions. All authors read and approved the final manuscript.

Data accessibility

Sequence reads have been deposited to National Center for Biotechnology Information (NCBI)'s Sequence Read Archive and can be found under the Accession No. SRP065150. Custom scripts are provided in Appendix S1 (Supporting information).

Keywords

alpine lakes; biogeography; diversity; fungi; next-generation sequencing; protistan plankton

Introduction

Protists are single-cell organisms, which in terms of cytological diversity and abundance (if not species diversity) dominate the kingdom Eukarya (Patterson 1999). Inhabiting our planet at least twice as long as multicellular life (Knoll *et al.* 2004; Berney & Pawlowski 2006), they have conquered nearly any habitat on earth and have evolved multiple modes of life. Protists include mixotrophs, autotrophs, heterotrophs and osmotrophs, and together with bacteria, they account for the majority of the biomass in aquatic environments: for example, the entire pelagic microbial food web, including protozoan microzooplankton, is typically five to ten times the mass of all multicellular aquatic organisms (Pomeroy *et al.* 2007). This points to the key role protists have in aquatic biogeochemical cycles (Sanders 2009). Traditionally, the description of protists has been microscopy-based and their structural diversity has been recorded since more than two centuries (Weisse 2008), resulting in an invaluable legacy. The recurrent observation of the same morphotypes in freshwater habitats has led some researchers to the conclusion that the global protistan diversity could be relatively low (Finlay & Clarke 1999; Fenchel & Finlay 2004). Furthermore, this assertion led to the concept of a cosmopolitan distribution of most, if not all, protists (Finlay 2002). However, results from more recent molecular-based studies on protistan diversity and distribution patterns (e.g. Bass *et al.* 2007a; Ryšánek *et al.* 2015) have prompted most ecologists to abandon the ubiquitous dispersal concept for protists (Gast 2015). Yet, studies with strong evidence for spatial structures in whole protistan communities are still scarce. Likewise, genetic diversity surveys showed that protistan diversity is still far from being described (Massana *et al.* 2015; de Vargas *et al.* 2015).

In particular, inland (fresh)water bodies are largely uncharted. Compared to the high number of studies targeting marine protistan communities (e.g. López-García *et al.* 2001; Lovejoy *et al.* 2006; Worden *et al.* 2006; Countway *et al.* 2007; Massana & Pedrós-Alió 2008; Alexander *et al.* 2009; Amaral-Zettler *et al.* 2009; Stoeck *et al.* 2010; Stock *et al.* 2012; de Vargas *et al.* 2015), studies describing genetic protistan diversity from freshwater habitats are rare (e.g. Šlapeta *et al.* 2005; Lepère *et al.* 2007; Triadó-Margarit & Casamayor 2012; Taib *et al.* 2013; Kammerlander *et al.* 2015; Oikonomou *et al.* 2015; Simon *et al.* 2015). Freshwater ecosystems are usually more heterogeneous than the marine realm and thus are expected to hold an even higher genetic protistan diversity than oceans (Logares *et al.* 2009a; Auguet *et al.* 2010; Barberán & Casamayor 2010; Barberán *et al.* 2011). Because marine–freshwater transitions are relatively rare among protists (Logares 2009b; Forster *et al.* 2012), freshwater communities are distinctively different from marine protistan communities.

Among the inland freshwater bodies, high-mountain lakes hold an exceptional position. Located remotely above the tree line, these ecosystems are traditionally considered as extreme for life (Catalan *et al.* 2006). Challenges for the biota of high-mountain lakes, such as protists, include in the temperate zone low availability of nutrients, strong changes in

incident light and low water temperature (Sommaruga 2001). This requires specific adaptations to osmoregulation and coping with nutrient limitation, which are not necessarily mandatory in the survival toolbox of protists in lowland lakes. The usually low density of organisms in such highly diluted waters (Catalan *et al.* 2006) entails low encounter rates. Low encounter rates not only are crucial in foraging theory (Jumars 1993), but also are an evolutionary force exerting specific selection pressure and new adaptive pathways (Catalan *et al.* 2006). Furthermore, high-mountain lake biota is subjected to significantly higher ultraviolet radiation (UVR) compared with lowland lakes, due to a thinner atmosphere and usually high water transparency (Sommaruga 2001). Being harmful to various lake inhabitants, including protists (Sommaruga *et al.* 1996), intense UVR requires further specific adaptations to prevent DNA damage. Strong UVR exposure alternates at least in the temperate zone with periods of limited light availability and snow/ice-cover time in winter, which may last for many months, or intense short rains in the Altiplano. Not surprisingly, such environmental changes cause pronounced microbial community shifts in those high-mountain lakes (Felip *et al.* 2002; Dorador *et al.* 2003; Márquez-García *et al.* 2009).

In view of these extreme environmental conditions in high-mountain lakes, it is reasonable to assume that these ecosystems raise a protistan genetic diversity that is different from the one found in other inland freshwater lakes. Further, it is highly likely that protistan communities in high-mountain lakes are extremely diverse because a high genomic potential would allow these organisms to buffer shifts in environmental conditions. The very few available genetic protistan diversity studies from high-mountain freshwater lakes support these assumptions, but are not conclusive because of data scarcity and low sample coverage (Triadó-Margarit & Casamayor 2012; Kammerlander *et al.* 2015). In this study, we therefore sampled 13 lakes from three different mountain regions (Austrian Alps, Chilean Altiplano and Ethiopian Bale Mountains) to analyse and statistically compare microbial eukaryote plankton diversity. Specific aims of the study were (i) to reveal the phylogenetic diversity of eukaryotic microbes to investigate their biogeographic patterns among high-mountain lakes, (ii) to uncover the environmental factors, which might be responsible for the partitioning of diversity in this three distant mountain ranges and (iii) to analyse the degree of genetic novelty within the plankton communities.

Materials and methods

Sample sites

The three selected high-mountain areas strongly differ in important environmental characteristics and temperature regimes. While the lakes in the Alps are ice-covered for several months and are typically dimictic (i.e. water column mix twice a year), those in the Altiplano present a very thin ice cover in winter developing only in the littoral zone during night-time and disappearing usually by midday. Those systems are described as cold polymictic (Mühlhauser *et al.* 1995). Similarly, the shallow systems in the Bale Mountains are also polymictic and eventually night-time freezing is also observed (Löffler 1978). Whereas lakes in the Chilean Altiplano have a negative water balance (Dorador *et al.* 2003), those in the Alps and Bale Mountains have a positive one, although in the latter area, rainfall is highly seasonal with a clear rainy season going from March to May and from October to

November (Löffler 1978). The lakes in the Chilean Altiplano and in the Bale Mountains are naturally more productive and have high phosphorus concentrations (Löffler 1978; Mühlhauser *et al.* 1995; Márquez-García *et al.* 2009), which strongly contrast with the oligotrophic character of the lakes in the Alps. Further, because of the different geology and hydrology, the lakes in the three areas have a strong gradient in salt content as indicated by the concentration of major ions and specific conductivity (Table 1). Thus, the endorheic character of the lakes in the Altiplano is paralleled by the highest conductivity values among the studied lakes (Table 1).

Sampling

Samples for three of the five lakes selected in the Austrian Alps were collected in July and October 2013 during the stratification and overturn period, respectively. The lakes Mutterbergersee (MUT II) and Schwarzsee ob Sölden (SOS II) were sampled only in October 2013 as they can only be reached by helicopter. The three lakes in the Chilean Altiplano were sampled in August 2013 (cold, dry season) and in March 2014 (warm after the rainy season) and those in the Bale Mountains, Ethiopia, were collected in October 2013 during the rainy season. In all lakes, a composite sample was collected to obtain representative information for the whole water column. For that, the same volume of lake water collected at different depths (number depended on lake maximum depth) was pooled. Depths close to the sediment were avoided. In all lakes, three replicated composite samples were obtained. Water samples for DNA extraction were filtered on the same day onto 0.65- μm Durapore membranes (Millipore) using a peristaltic pump until clogging was observed. Samples were prescreened to exclude zooplankton through a sieve with a 100- μm mesh size nylon net. Filters were immediately placed into cryovials with *RNAlater* (Qiagen) and stored as recommended by the manufacturer until further processing.

Measurement of environmental variables and geographic distances

A multiparameter probe (YSI) was used in the European Alps and in Chile to make profiles in the water column for temperature, conductivity, pH and oxygen. Because of the shallowness of the systems in the Bale Mountains, this was not possible and measurements were taken with single probes (Hach). From the same composite samples, several auxiliary parameters were also measured in the dissolved fraction. The dissolved fraction was defined as the filtrate passing through a glass fibre filter (GF/F Whatman), which was previously burned at 450 °C for 2 h. Dissolved organic carbon (DOC) was measured in acidified samples (pH = 2) with a total carbon analyser Shimadzu TOC-VCPH, while dissolved nitrogen (DN) was measured in a total nitrogen measuring unit (Shimadzu TNM-1). All these analyses were performed in Innsbruck. Ion concentrations in samples from the Alps and Bale Mountains were measured by ion chromatography in a Dionex ICS 1000 and 1010 system, whereas those from the Altiplano by atomic absorption spectrophotometry in a Shimadzu 6800 system with a GFA-EX graphite furnace.

Geographic distances were determined based on the longitude/latitude data using the ‘haversine’ formula as implemented in the script provided by Chris Veness (2002–2015) at <http://www.movable-type.co.uk/scripts/latlong.html>. The ‘haversine’ formula calculates the great-circle distance between two points on a sphere, that is the shortest distance over the

earth's surface. To account for altitude differences, the altitudes of the sample pairs were subtracted and the difference was added to the resulting value of the 'haversine' formula for the respective sample pair.

Nucleic acid extraction, PCR and sequencing

As described previously (Oikonomou *et al.* 2015), each filter was cut with a sterile scalpel into smaller pieces and transferred to a Lysis E Matrix tube (MP Biomedicals, Germany), followed by the addition of 600 μ L RLT buffer and 6 μ L β -mercaptoethanol. Filters were then shaken at 30 Hz for 45 s using a mixer mill (MM200, Retsch, Germany). The tubes were centrifuged (14 000 *g*, 3 min), the supernatant was retained, and DNA extraction was carried out using Qiagen's (Hilden, Germany) All Prep DNA/RNA Mini kit according to the manufacturer's protocol (after step 4). The concentration of bulk DNA was measured spectrophotometrically (NanoDrop 2000, Thermo Scientific, Wilmington, DE, USA). The hypervariable V4 region of the SSU rDNA was amplified using the primer pair TAREukV4F and TAREukREV (Stoeck *et al.* 2010), yielding ca. 500-base pair (bp) fragments. The polymerase chain reaction (PCR) mixture, containing 1 U of Phusion High Fidelity DNA Polymerase (New England Biolabs), was heated to 98 °C for 30 s, and the V4 region was amplified with a PCR protocol described in Stoeck *et al.* (2010). To minimize PCR bias, three individual reactions per filter were prepared. The three individual reactions were pooled during the PCR product purification using Qiagen's MinElute PCR purification kit. Paired-end sequencing of purified V4 amplicons was conducted on an Illumina MiSeq platform by SeqIT (Kaiserslautern, Germany). The paired-end reads generated from the same amplicon were merged using a custom script.

Sequence data processing and taxonomic assignment

Raw paired-end Illumina reads were quality-filtered using the `split_libraries.py` script implemented in QIIME v.1.8.0 (Caporaso *et al.* 2010). Only reads with exact barcodes and primers, unambiguous nucleotides and a minimum length of 300 bp were retained and subjected to a *de novo* chimera detection using `uchime` (Edgar *et al.* 2011). Nonchimeric reads were clustered with `SWARM` v1.2.6 (Mahé *et al.* 2014) using $d=1$. Other than popular *de novo* clustering methods, `SWARM` does not rely on arbitrary global clustering thresholds (as lineages evolve at variable rates, no single sequence similarity value can accommodate the entire tree of life) and input order dependency. Instead, it uses a local clustering threshold to assign amplicons to an operational taxonomic unit (OTU). OTUs grow iteratively by comparing each generation of assigned amplicons to the remaining amplicons. An OTU is closed when no new amplicon can be integrated in the OTU. This strategy produces robust and high-resolution OTUs that allow for accurate, meaningful and interpretable biological results. Using a custom script (Appendix S1, supporting information), an OTU contingency table was created based on the output files of `SWARM`. Representative sequences (i.e. the most abundant sequence) from each OTU were extracted and analysed with the software package `JAGUC` (Nebel *et al.* 2011) and GenBank's nr nucleotide database release 202 as reference database. The tabular taxonomic information and the OTU contingency table were then merged to the final OTU table. Nontarget OTUs (metazoans, embryophytes) as well as singletons and doubletons [unique/double amplicons that occur exclusively in only one sample are most likely erroneous sequencing products (Bokulich *et al.* 2013; Nelson *et al.*

2014)] were excluded. The resulting file was used as a basis for statistical and network analyses.

Diversity statistics

Indices of alpha -diversity and similarities among the samples (beta-diversity) were calculated in R (R-Team 2008) using the program package VEGAN (Oksanen *et al.* 2013). We used the Shannon entropy as an index, as it provides robust quantification and meaningful comparison of the microbial diversity in molecular data sets (Haegeman *et al.* 2013). Because the shannon index is biased towards the most abundant taxa (phylotypes), we used log-transformation to down-weight the most abundant taxa. For an interpretation of a diversity index, it was recommended to convert any given index into 'true diversity' as an equivalent, termed as effective number of species (=equally common species) (MacArthur 1965; Jost 2006, 2007). We conducted this conversion according to Jost *et al.* (Jost 2006).

The analysis of variance (one-way ANOVA) was calculated in R using the STATS package (R-Team 2008).

The Jaccard index was used as a measure of similarity between the samples. Here, we used the binary Jaccard index to avoid bias based on abundance values resulting from different gene copy numbers in protists and fungi (Casamayor *et al.* 2002; Zhu *et al.* 2005; Amaral-Zettler *et al.* 2009; Dunthorn *et al.* 2014). Prior to beta-diversity estimation, the number of sequences per sample was rarefied to the smallest sample size ($n = 36,744$). Jaccard similarity values were transformed to distance matrixes for a nonmetric multidimensional scaling (NMDS) analysis. Environmental vectors were fitted to the ordination using the envfit function of the VEGAN package in R. The fit (R^2) of each variable to the ordination using the envfit function was assessed with a Monte Carlo analysis of 10000 permutations.

Testing for geographic distance effects

The Mantel test was used to evaluate the relationship between genetic distance and geographic distance (Mantel 1967), which is the most commonly used method to address spatial processes driving population structures (Diniz-Filho *et al.* 2013). Analyses were conducted with the IBD program package (<http://ibdws.sdsu.edu>, Jensen *et al.* 2005) running 5000 randomizations of the rows and columns of the genetic community and geographic distance matrixes to generate the distribution of correlations under the null hypothesis. The community distance was calculated as the Sørensen distance between two samples. Positive Mantel correlations and significant P -values are conclusive that nearby communities tend to be more similar than expected by chance and that (genetic) differences in communities increase with geographic distance (Diniz-Filho *et al.* 2013). Because zero distances are invalid in the Mantel test, the data set(s) used for this analysis included each lake only once. Therefore, Mantel tests were conducted with different data sets, one of them including the data from summer samplings (DRA, OPL, GKS, COT, PIA, CHU and all Ethiopian lakes) and one from winter samplings (DRA II, OPL II, GKS II, MUT II, SOS II, COT II, PIA II, CHU II and all Ethiopian lakes). Details of samples included in a specific analysis are given in the respective figure legends. Furthermore, a variation of the Mantel test (Mantel correlogram) was applied. While the simple Mantel test shows the overall relationship

between the geographic and community distance matrices, the Mantel correlogram allows the analyses of relationships between community distances and specific geographic distances across space (Diniz-Filho *et al.* 2013). Therefore, the geographic distance matrix was divided into three submatrices, each one describing pairs of communities within a bounded interval of geographic distances. This strategy is useful to identify possible variations in the correlation between community distance and geographic distance classes. Our data sets were subdivided into the following distance classes: class 1 – up to 50 km, corresponding to ‘short distances’ (local scale); class 2 – up to 6000 km, corresponding to ‘intermediate distances’; and class 3 – up to 12 000 km, corresponding to ‘large distances’. Three Mantel correlations were then obtained by performing a Mantel test between the community distance matrix and the three geographic distance matrices. The Mantel correlogram was constructed by plotting Mantel correlations between the community distance matrix and each geographic distance class matrix against the mid-point of the respective distance class (Oden & Sokal 1986; Legendre & Legendre 2012).

Identification of novel diversity

The construction of novel diversity networks followed the description of Filker *et al.* (2015). To infer genetically divergent diversity in the three biogeographic regions, data sets from individual lakes within a specific biogeographic region were pooled. All sequences were truncated to the same length (300 bp) and dereplicated using a custom script (Appendix S1, Supporting information). Unique reads were clustered using SWARM v1.2.6 (Mahé *et al.* 2014) with $d = 1$. To build the network, the representative reads from the 200 most abundant OTUs were extracted and subjected to BLASTN analyses (Altschul *et al.* 1990) against GenBank’s nr nucleotide database (release 202) to identify their taxonomic affiliation. The seed reads were then aligned in Seaview (Galtier *et al.* 1996), followed by the calculation of sequence similarities between each pair of seed sequences using PAIRALIGN (see Appendix S1, Supporting information). The network was built using the IGRAPH R package (Csárdi & Nepusz 2006) and was based on the sequence similarity values. In the network, two nodes were connected by an edge if they shared a sequence similarity of at least 90%. The resulting network was visualized and modified with GEPHI v.0.8.2-beta (Bastian *et al.* 2009) according to the OTU taxonomic affiliation and BLAST hit value.

Results

Replicate sequencing of the same sample from Drachensee, Austria (DRAa and DRAb), produced nearly identical results (Fig. S1, Supporting information). For further comparative analyses, we therefore used only one of the two replicate samples (DRAa), for which we obtained nine more phylotypes (n phylotypes DRAa = 284) compared to the replicate sample DRAb.

Microbial eukaryote diversity at local scale (alpha-diversity)

For the 20 samples (including the replicate sequenced sample DRAb) analysed in this study, we obtained between 36 744 and 184 273 high-quality protistan (including fungal) V4 amplicons after Illumina sequencing and data cleaning (Table 2). The number of distinct OTUs for each sample varied from 99 to 1166. Rarefaction analyses predicted that all

samples were sampled to near saturation (Fig. S2, Supporting information). Shannon entropy-based effective number of species varied from 1.9 in the Austrian DRA lake to 71.5 in the Ethiopian KOR lake (Fig. 1). One-way ANOVA revealed a significant difference in the effective number of species among the three geographic regions ($P < 0.05$, for details of ANOVA results, see Fig. S3, Supporting information).

Taxonomy of phylotypes

Austrian Alps—In terms of phylotype diversity (measured as OTU richness), there was little variation among the different lakes when considering high taxonomic levels (phylum level). All lakes in this region were strongly dominated by dinoflagellates (Fig. 2). This group accounted for up to 86% (531 phylotypes (OTUs), in Gossenköllesee, GKS II) of the total phylotype diversity in these lakes. The second most diverse taxon group was Heterokontophyta (mostly Chrysophyceae and Synurophyceae) accounting for up to 33% (112 phylotypes, in Oberer Plenderlessee, OPL II). Fungi and nonpigmented protist phylotypes such as ciliates and heterokont flagellates were underrepresented in terms of diversity. Seasonal variations in higher taxon diversity patterns were observed, but not pronounced. For example, in OPL, the number of ciliate phylotypes increased from 5 to 13 from OPL (July) to OPL II (October). Such minor discrepancies could, however, be a result of patchy distribution during sampling or of undersampling.

Chilean Altiplano—In this region, phylotype diversity was more variable among the three lakes and seasons than in the Alps. In general, lakes from this region were characterized by a high diversity of chlorophytes, cryptophytes and Heterokontophyta. In individual lakes (PIA II), also ciliates accounted for up to 21% of the observed phylotype diversity. Dinoflagellates accounted for a maximum of 11% in COT II.

Ethiopian Bale Mountains—Similarly to the lakes in the Altiplano, they showed unique diversity signatures at the phylum level. Even though the higher-rank taxon diversity in these lakes was also largely coined by pigmented lineages (with the exception of lake KOR), also nonpigmented taxon groups were remarkably diverse. These include bicosoecid flagellates, oomycetes, centroheliozoans, cercozoans and fungi (ascomycetes and chytridiomycetes). Variation among the lakes in the relative proportions of different higher-rank taxon orders was pronounced. For example, while KOR and TOG harboured a relatively high proportion of nonpigmented flagellates (bicosoecids accounting for 42% of the observed phylotypes in KOR and 37% in TOG), chlorophytes dominated the lakes HaLu (59%) and CRA (55%).

Partitioning of diversity among biogeographic regions

The pronounced differences in microbial eukaryote community composition in the distinct geographic regions on higher taxonomic ranks were statistically confirmed at the phylotype level. In a nonmetric multidimensional scaling (distance measure: Jaccard), geographic plankton community clusters with their 95% confidence intervals did not overlap (Fig. 3). The biogeographic clusters followed a gradient along axis 1. Within each of the geographic regions, the individual lakes were arranged along a gradient of axis 2. The 2D stress (Kruskal) of the NMDS analysis was 0.11.

Environmental effects on diversity partitioning

Because the lakes in the different geographic regions were significantly different in a number of environmental parameters, we tested whether the observed partitioning of diversity was due to biogeography or to environmental selection, or a combination of both. Although ANOVA also revealed significant differences in altitude, pH, all ions measured, DOC and DN ($P < 0.01$ in all cases) among the lakes in the three geographic regions, none of these parameters correlated significantly with the effective number of species (Pearson R for all comparisons > -0.3 or < 0.3). Fitting environmental variables into the NMDS analyses revealed that all but water temperature ($P > 0.5$) have a significant effect on the observed diversity partitioning patterns (Table 3). Interestingly, the vast majority of environmental parameters showed a much stronger affinity to NMDS axis 2. Only altitude correlated strongly with NMDS axis 1. Thus, altitude was the only factor, which was meaningful for the observed gradient along NMDS axis 1 (separation of geographic regions). The remaining environmental variables contributed to explaining the detected differences in microbial eukaryote community structures within each of the individual biogeographic regions.

Geographic distance effects on diversity partitioning

To evaluate the effect of geographic distance on (genetic) community structure, we used variations of the Mantel test. The correlation between community distance and geographic distance (Fig. 4) showed a spatial pattern. The Mantel correlation between the two matrices was equal to 0.739 when using log geographic distances. This showed an increase in community distance with geographic distance. None of the values from 5000 randomizations was larger than the observed value of 0.739, so that the chance of obtaining a value as large as the observed is smaller than 1/5000. This resulted in a highly significant P -value of < 0.0002 for this Mantel test, suggesting a significant increase in community distance with geographic distance. Further, when using the natural distances (nonlog) in the Mantel test, the P -value was < 0.0002 at a Mantel correlation r of 0.536.

To test whether distance effects are more or less pronounced at different distance scales (as suggested by a nonlinear relationship between geographic distance and community distance, Fig. 4 and Fig. S4, Supporting information), we used a Mantel correlogram, which considers nonoverlapping distance classes. In the first distance class (0–50 km), microbial eukaryote communities tend to be more similar ($r_m = 0.478$; $P < 0.01$ with 5000 permutations) than in the second distance class (5235–5278 km; $r_m = 0.315$; $P = 0.05$ with 5000 permutations) (Fig. 5). In the third distance class (10 741–12 270 km), Mantel correlation decreased to -0.469 ($P = 0.016$). This negative correlation value indicates that communities that are located at such high distances apart tended to be more dissimilar than communities of the first (up to 50 km) and second (up to 5278 km) distance classes.

Degree of novel diversity

Austrian Alps: The 200 most abundant phylotypes detected in the alpine lakes were relatively well represented in NCBI's nucleotide database (Fig. 6a). The mean sequence similarity of all 200 phylotypes to previously deposited sequences was 96.5%. Only 16 phylotypes had a sequence similarity of $< 90\%$ to previously deposited sequences. Specifically, several pigmented heterokonts (stramenopiles) (mean sequence divergence to

previously described sequences: 94.8%) as well as all bicosoecid flagellates (mean sequence divergence to previously described sequences: 88%), one katablepharid and one mucoromycote phylotype among the most abundant 200 phylotypes were highly divergent to previously deposited sequences. Among the dinoflagellates, which accounted for the largest proportion of diversity in the 200 most abundant phylotypes, only few phylotypes were highly divergent to previously deposited sequences (mean sequence divergence to previously described sequences: 97.4%).

Chilean Altiplano: The mean sequence similarity of the 200 most abundant phylotypes to previously deposited sequences was 96.5% (Fig. 6b). Of these phylotypes, 22 have a sequence similarity of <90% to previously deposited sequences. Ciliates have a mean sequence divergence of 95.8% to previously deposited sequences, and for dinoflagellates, this value is even lower (94.7%). Sequences assigned to heterokontophyts are on average 96.9% divergent to described sequences and bicosoecids even 90.4%. Further, highly divergent fungi (Ascomycota, Chytridiomycota), Cryptophyta and a katablepharid were detected. Within the most diverse group (Chlorophyta), most of the detected phylotypes were closely related to previously deposited sequences.

Ethiopian Bale Mountains: These lakes harboured the largest proportion of hitherto undescribed diversity (Fig. 6c). The mean sequence similarity of the 200 most abundant phylotypes to previously deposited sequences was only 94.2%. Of these phylotypes, 52 have a sequence similarity of <90% to previously deposited sequences. All of the numerous bicosoecid phylotypes were <92.6% similar to previously described sequences. The mean sequence divergence in the detected ascomycote sequences was as low as 81.9%, and even within the dinoflagellates, half of the detected phylotypes have a remarkably high divergence to described sequences. Our analyses even identified a whole group of unclassified alveolates (with loose affiliation to dinoflagellates), which were very divergent (mean: 87.7%, $n = 9$) to previously deposited sequences. All detected ciliate phylotypes ($n = 7$) and the vast majority of the detected chlorophyte phylotypes were relatively closely related to previously deposited sequences (mean divergence ciliates: 98.1%; mean divergence chlorophytes: 98.3%).

Discussion

The protistan and fungal diversity of inland water bodies have received relatively little attention compared with coastal and open ocean ecosystems. Specifically, freshwater lakes located above the tree line or at high altitude are largely uncharted in this respect (Triadó-Margarit & Casamayor 2012; Kammerlander *et al.* 2015). Therefore, understanding the planktonic diversity of high-mountain lakes and its geographic distribution patterns is fundamental. This is particularly relevant because different global changes strongly affect high-mountain lakes. Knowledge about the diversity of high-mountain lake biota (and subsequently their functions) will help to model the effect of such contemporary environmental change on these sensitive ecosystems and to develop conservation strategies.

Triadó-Margarit & Casamayor (2012) analysed the 18S rDNA gene of protistan plankton obtained from 11 high-mountain lakes in the central Pyrenees. They observed that high-

mountain lakes even within the same lake district can be so heterogeneous that highly distinct protistan plankton communities evolve in adjacent lakes. Their analyses included only 953 18S rDNA sequences. Even though these data are very valuable, they left the majority of the protistan diversity undetected because of a low sampling (sequencing) depth. Kammerlander *et al.* (2015) analysed protistan plankton (including fungi) in two adjacent high-mountain lakes in the Austrian Alps and two more in the Himalaya region. The authors used ultra-deep Illumina sequencing of the V4 fragment of the 18S rDNA as taxonomic marker and revealed a much higher diversity than reported earlier from high-mountain lakes. In agreement with Triadó-Margarit & Casamayor (2012), also Kammerlander *et al.* (2015) reported a high genetic divergence between microbial eukaryote plankton communities in adjacent lakes. However, these authors showed that interregional genetic differences in plankton communities are much more pronounced than intraregional differences. This tentatively suggested a biogeographic pattern of microbial eukaryote plankton communities in high-mountain lakes. However, the four lakes analysed by Kammerlander *et al.* (2015) were insufficient to draw more solid conclusions regarding biogeographic distribution patterns.

The higher-rank taxon groups (phylum level) detected in the lakes under the present study were largely the same and also corroborated well previous molecular diversity studies of high-mountain lakes in the central Pyrenees (Triadó-Margarit & Casamayor 2012). Yet, the diversity patterns of these higher-rank taxon groups were vastly different in the three mountain regions (interregional differences). In fact, the protistan and fungal communities in high-mountain lakes are fingerprints, which are specific for each of the three mountain regions. Thus, our study provides strong support for biogeographic patterns in high-mountain lakes. Even though intraregional microbial eukaryote communities were distinct from each other (as observed in Triadó-Margarit & Casamayor 2012 and in Kammerlander *et al.* 2015), the differences were more pronounced on an interregional scale (Fig. 2). Interestingly, high-mountain lakes in the central Pyrenees have yet again a different community fingerprint than the three mountain regions analysed in our study. In the Pyrenean lakes, stramenopiles, in particular chrysophytes, account for the most diverse phylotypes. To the best of our knowledge, no study has been published that analysed whole microbial eukaryote community structures in high-mountain lakes using microscopy. Most, if not all, microbial ecologists meanwhile agree that at least some single-celled organisms have limited distribution patterns at least on a high-resolution molecular scale (Gast 2015) and literature within (but see Finlay 2002 and Finlay & Fenchel 2004). Mostly, the ‘moderate endemism hypothesis’ (Foissner 2006) finds support in (both genetic and morphological) studies on individual taxa across the eukaryotic tree. These include, just to mention a few examples, the planktonic testate amoeba *Diffugia tuberspinifer* (Gomaa *et al.* 2015), some chrysophyte species (Stoeck *et al.* 2008), the green algae *Klebsormidium* (Ryšánek *et al.* 2015), diverse ciliates (Foissner *et al.* 2003; Katz *et al.* 2005; Dolan *et al.* 2012; Dunthorn *et al.* 2012), the cercozoans *Eocercomonas* and *Paracercomonas* (Bass *et al.* 2007b), diatoms (Van de Vijver *et al.* 2005) and the synurophyte *Mallomonas* (Rezácová & Neustupa 2007). At the whole-community level, relatively few studies have analysed the effect of (large-scale) geographic distance on protistan and fungal community genetic distance. Bates *et al.* (2012) analysed a pyro-sequenced 18S rDNA fragment (including the

V4 region) from 40 soil samples collected along a north–south gradient (North and South America and Antarctica). The analyses of these samples rejected the global dispersal hypothesis because none of the observed phylotypes was found in all samples across the latitudinal gradient. Instead, 84% of the observed phylotypes occurred in five samples or less. However, statistical analyses of the obtained community profiles revealed that distance is not a very strong predictor of community dissimilarity. Instead, shifts in soil protistan community structure are significantly correlated to annual soil moisture availability. Despite the high value of this study by Bates *et al.* (2012), the obtained data has to be interpreted with caution, because of severe undersampling. For statistical analyses of all samples, the authors had only 150 sequences available for each of the 40 samples. Thus, the full extent of protistan diversity was far from being uncovered.

In our study of high-mountain lake microbial eukaryote communities, we found predictable beta-diversity patterns: geographic distance had a significant effect on shifts in plankton community structures. On a local scale, environmental factors could be identified as structuring components for plankton communities. Heterogeneous community structures on a regional scale resulting from differences in environmental factors were reported in previous studies on protistan communities in high-mountain lakes in Tibet (Wu *et al.* 2009) and the Pyrenees (Triadó-Margarit & Casamayor 2012). Specifically, the concentration of ions, pH and also nutrients (Wu *et al.* 2009; Triadó-Margarit & Casamayor 2012) was identified as structuring factors on local scales. Studies in lakes of the Pyrenees showed that cryptophytes are associated with lakes with higher phosphorus concentrations, whereas chrysophytes are characteristic for oligotrophic and ultra-oligotrophic lakes (Catalan *et al.* 2006). Other algal groups did not show any correlation with nutrients. Furthermore, altitude seems to be a decisive factor for the structuring of high-mountain lake protistan communities (Wu *et al.* 2009). A critical factor changing with increasing altitude is the increase in harmful UV-B radiation (Sommaruga 2001), which requires specific adaptive mechanisms for inhabitants of high-mountain lakes.

Our analyses showed, however, that the effects of environmental variables as structuring factors for plankton communities at a local scale were much less pronounced than the distance effect on an interregional scale (Fig. 3, Table 3). This corresponds well with the hypothesis of Martiny *et al.* (2006) on the biogeography of bacteria that at local scales, spatial variation in community structures is largely due to contemporary environmental factors, while at large distance scales, variations in community structures are largely due to historical contingencies. At intermediate scales, a mixture model of both parameters applies. This is supported by the Mantel correlogram, which did not show a linear decrease of community similarity with increasing geographic distance (Fig. 5). Our study is the first to confirm this hypothesis for microbial eukaryote communities. For soil ciliates, Foissner *et al.* (2008) showed tentative evidence that the split of Pangaea into Laurasia and Gondwana may have been an important historical contingency to relate contemporary ciliate distribution patterns.

Although the dispersal of freshwater protists over very long (intercontinental) geographic distances seems difficult (Ryšánek *et al.* 2015), one potential vector of dispersal is migratory land- and waterbirds (e.g. Maguire 1963; Figuerola & Green 2002). The Bale Mountains in

particular has a large number of migratory birds, and lakes in the Altiplano have important populations of waterbirds. Both, however, are less important in the case of high-altitude lakes in the Alps (Boere *et al.* 2006). Further, although an African/west Eurasian migratory waterbird flyway is known, it is uncertain how strong this dispersal mechanism can be between the Alps and Bale Mountains. In addition, apparently no bird migratory flyways are known that will connect the three study areas (Boere *et al.* 2006). Another dispersal mechanism for protists may be transportation by wind. This vector is known to transport microorganisms even between continents (Smith *et al.* 2013), and for example, dust from areas such as the Sahara has been identified as an important source of fungi, bacteria and even algae (Favet *et al.* 2013). In particular, this vector could be relevant for lakes near the tropics (Bale Mts. and Altiplano) where an ice cover occurs only on a daily basis. However, airborne dispersal seems more common among terrestrial protists, which can be picked up with dust particles from dry soil, rather than for freshwater protists (Atkinson 1971; Foissner 2006, 2008). Thus, although we cannot totally exclude the importance of these vectors, we argue that isolation by distance seems a more plausible explanation for the observed long-distance patterns in high-mountain lake microbial eukaryote community structures (Fig. 4).

At least on regional scales, it seems likely that the most abundant organisms (large population sizes) have the highest chances of regional dispersal (Fenchel & Finlay 2004; Finlay & Fenchel 2004) (Fig. 5), corroborating with Hubbell's unified neutral theory of biodiversity and biogeography (Hubbell 2001). This may explain the low degree of novel diversity detected in the two hundred most abundant phylotypes of the high-mountain lake microbial eukaryote consortia of the Alps Fig (Fig. 6a). Compared with the Chilean Altiplano lakes and the African Bale Mountain lakes, protistan morphotypes in European mountain lakes are much better studied (e.g. Stoeck *et al.* 2014, Kammerlander *et al.* 2015). Therefore, abundant species in European mountain lakes have better chances of being picked up and sequenced previously compared with abundant protists and fungi in the Altiplano and Bale Mountain regions. Protistan diversity in the latter two regions is largely uncharted resulting in a lack of gene data from these regions in public databases. This may be the most plausible explanation for a notably higher degree of novel diversity among the most abundant phylotypes of the Altiplano and Bale Mountain lakes (Fig. 6b,c) compared with the alpine lakes. This result further supports the finding that different geographic regions hold different sets of protistan and fungal diversity. Further diversity surveys in previously largely unexplored biogeographic regions would show how far we are indeed from uncovering earth's diversity of microbial eukaryote life.

Supporting information

Refer to Web version on PubMed Central for supplementary material.

Acknowledgements

We thank Josef Franzoi, Gry Larsen and Salvador Morales-Gomez (Austria) and Vilma Barrera (Chile) for water chemical analyses and Anna Waibel, Birgit Stenzel, Hannes Peter, Artur Hepberger (Austria), Eyasu Shuba (Ethiopia), Sergio Scott, Jose Carvajal, Juan Pablo Oyanedel and Ignacio Tobar (Chile) for helping during sampling. Furthermore, we thank four anonymous reviewers, who were extremely helpful and constructive with their comments and notably improved a previous version of this manuscript. Sampling in Chile was supported by a grant

from CONICYT 1140543 to I.V., in Ethiopia by the APPEAR program to R.S. and in Austria by the Austrian Science Fund (FWF, Project BACK-ALP P24442-B25) to R.S.

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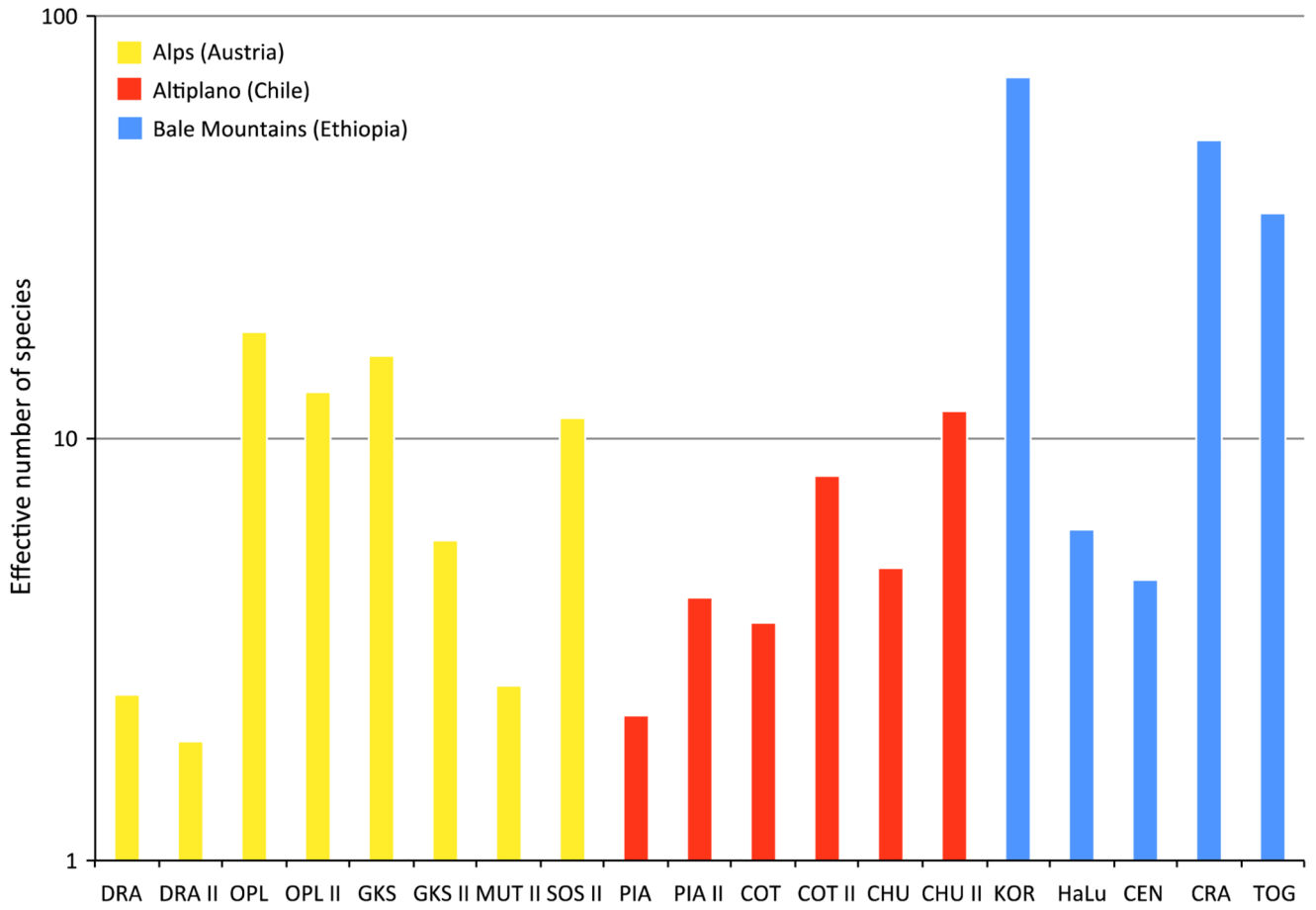


Fig.1. Shannon-based effective number of species (alpha-diversity) between the sampled lakes in the European Alps, the Chilean Altiplano and the Ethiopian Bale Mountains. Results are based on normalized data sets ($n = 36\ 744$).

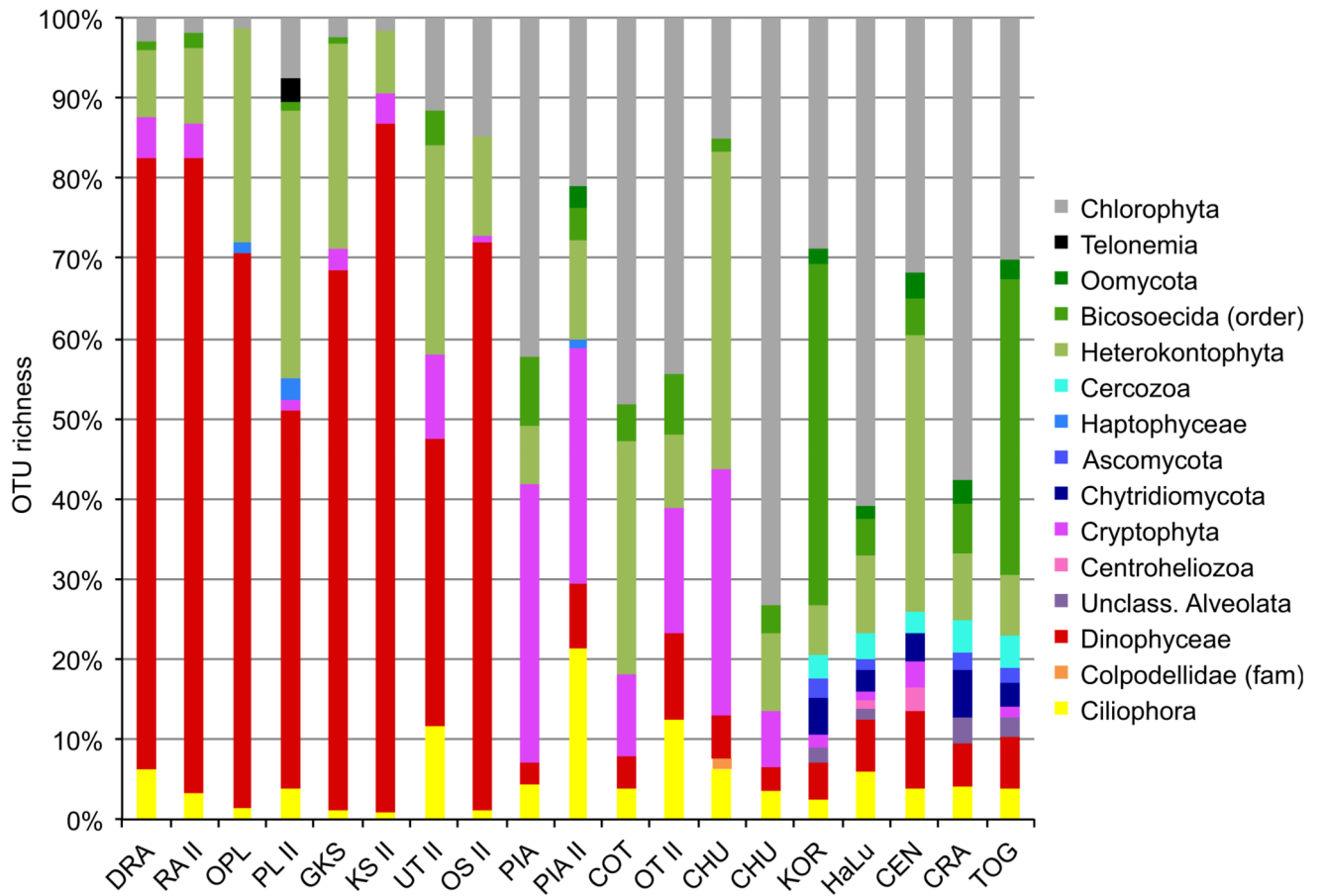


Fig. 2. Distribution of the protistan and fungal communities among the analysed lakes in the European Alps, the Chilean Altiplano and the Ethiopian Bale Mountains. The bars display the relative number of distinct operational taxonomic units (OTUs) per taxonomic group (i.e. OTU richness). Only those taxonomic groups (phylum level) were considered that contain at least 1% of the total number of OTUs per sample.

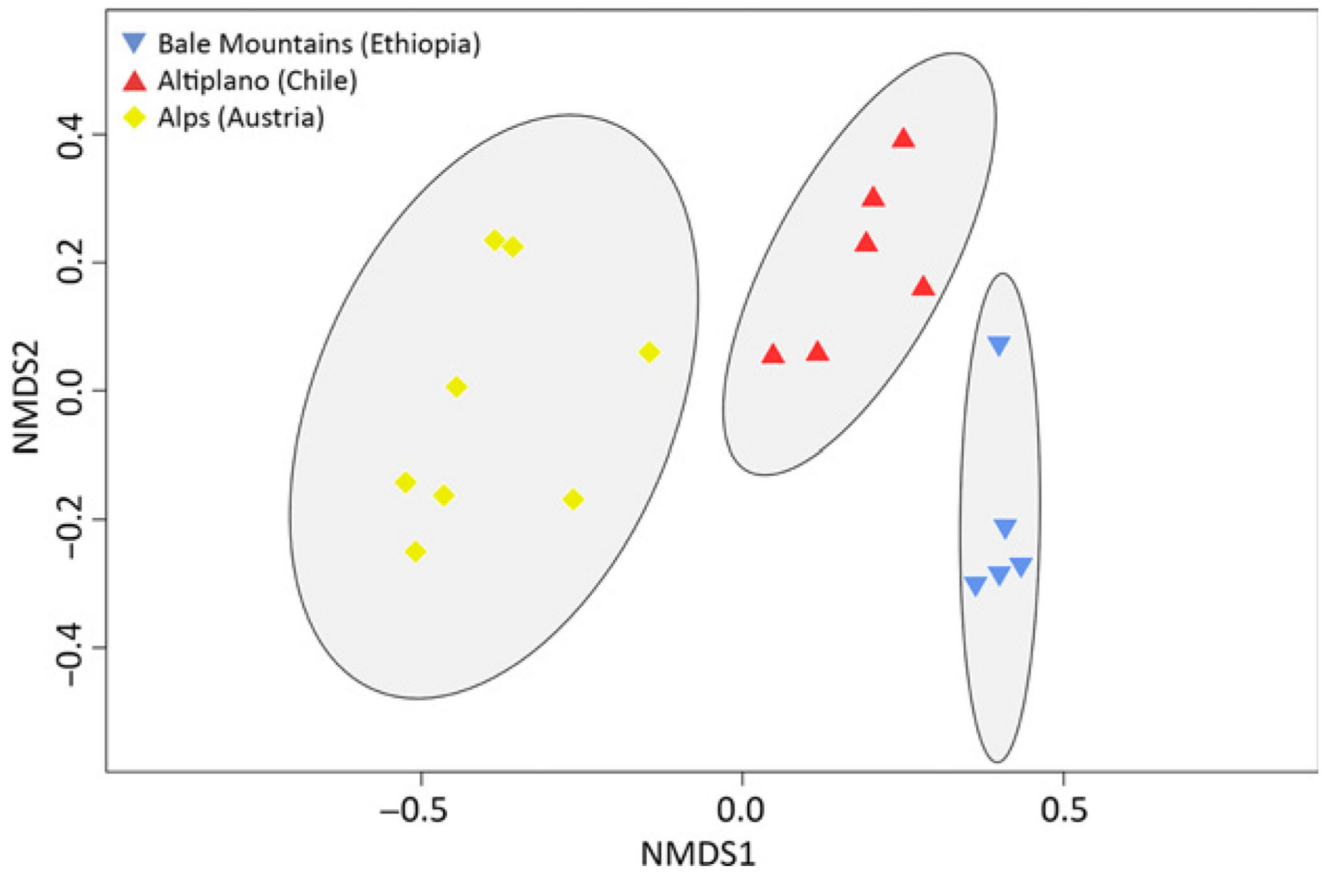


Fig. 3. Nonmetric multidimensional scaling analysis of the European, Chilean and Ethiopian high-mountain lake samples under study based on Jaccard similarities. For each community cluster, the ellipses represent 95% confidence intervals.

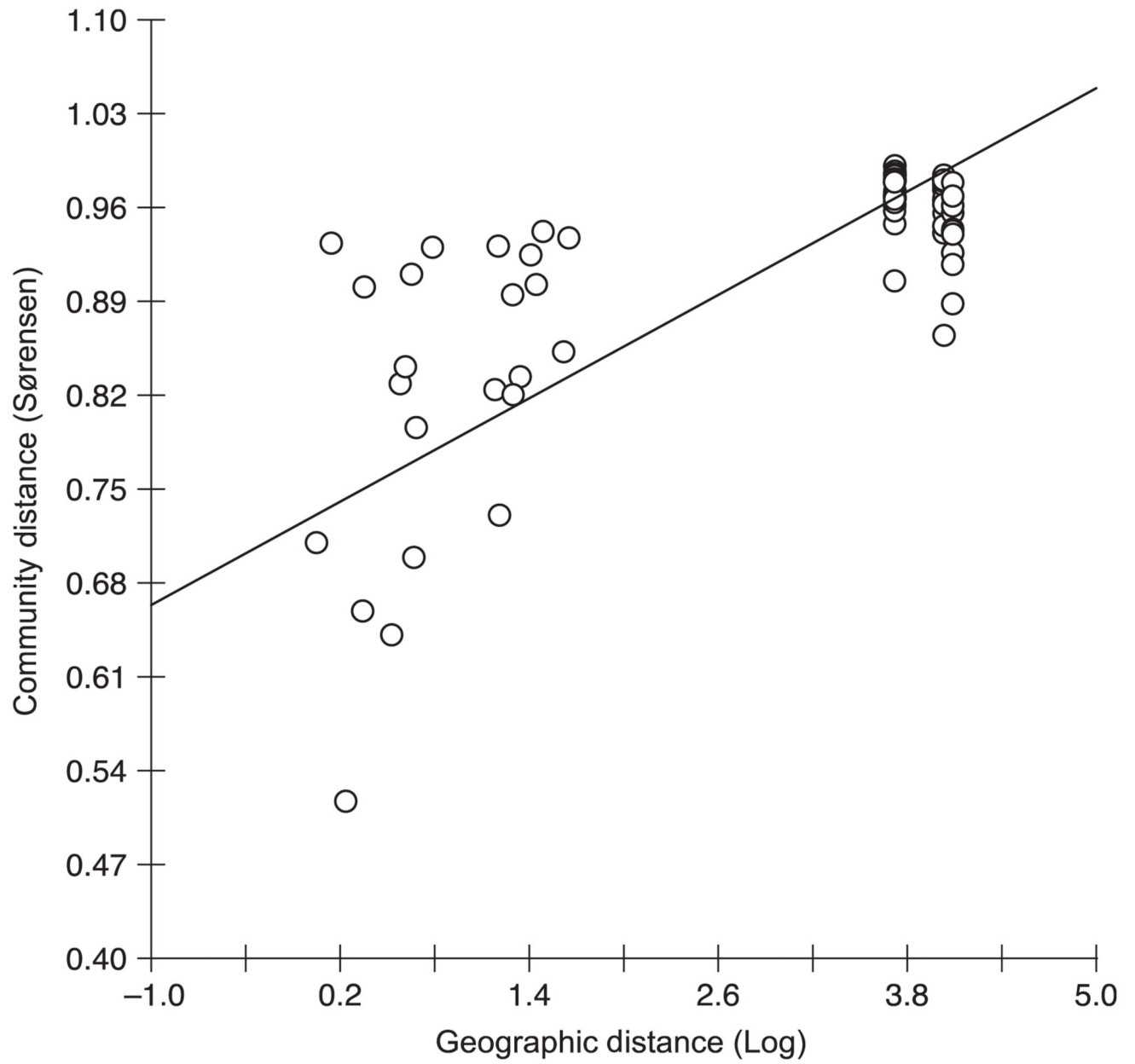


Fig. 4. Relationship between the pairwise community (Sørensen distance) and geographic distances (log-transformed) for the analysed high-mountain lakes (including winter samples).

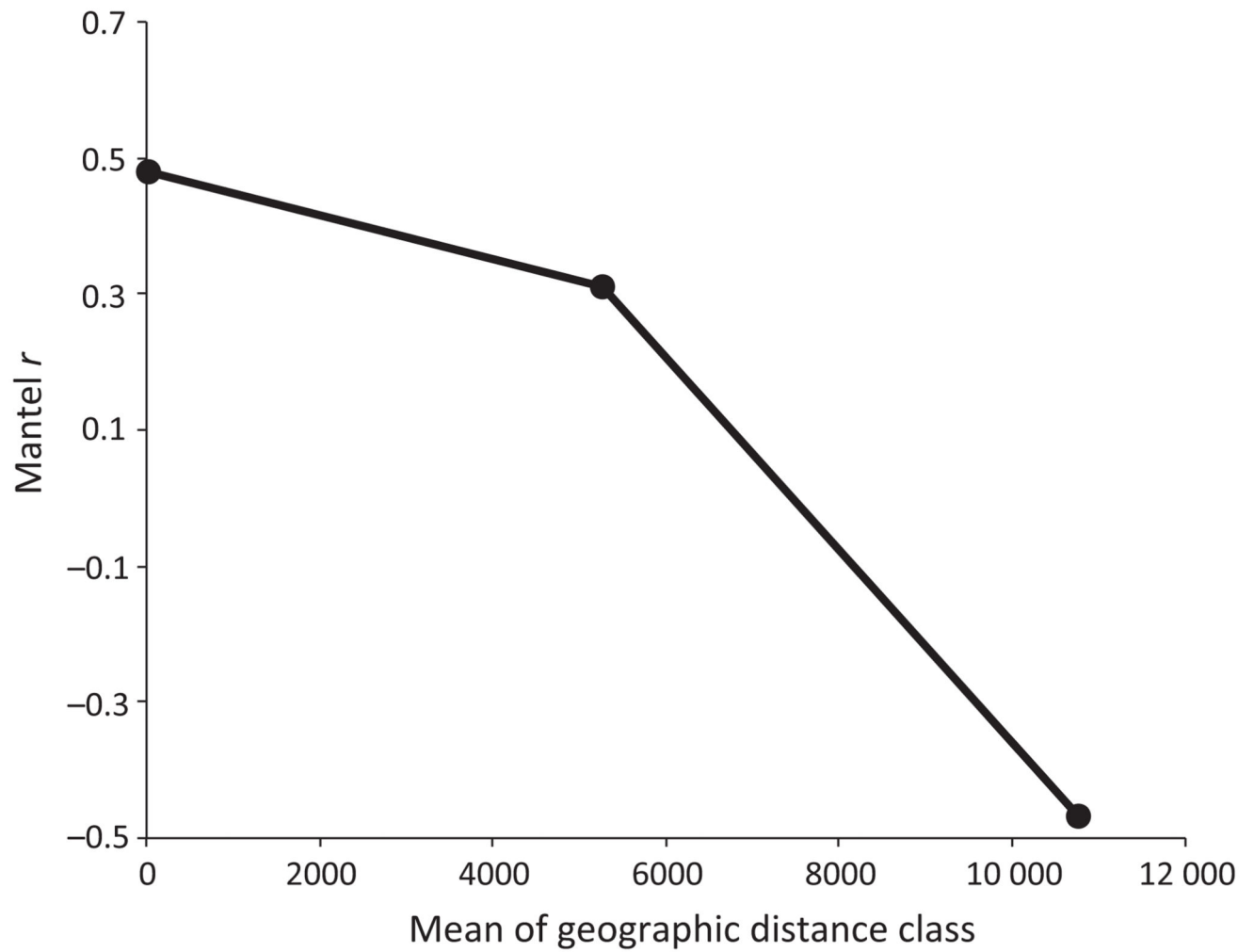


Fig. 5. Mantel correlogram displaying spatial structuring of the high-mountain lake communities within the following nonoverlapping distance classes: 0–50 km, 5235–5278 km and 10 741–12 270 km.

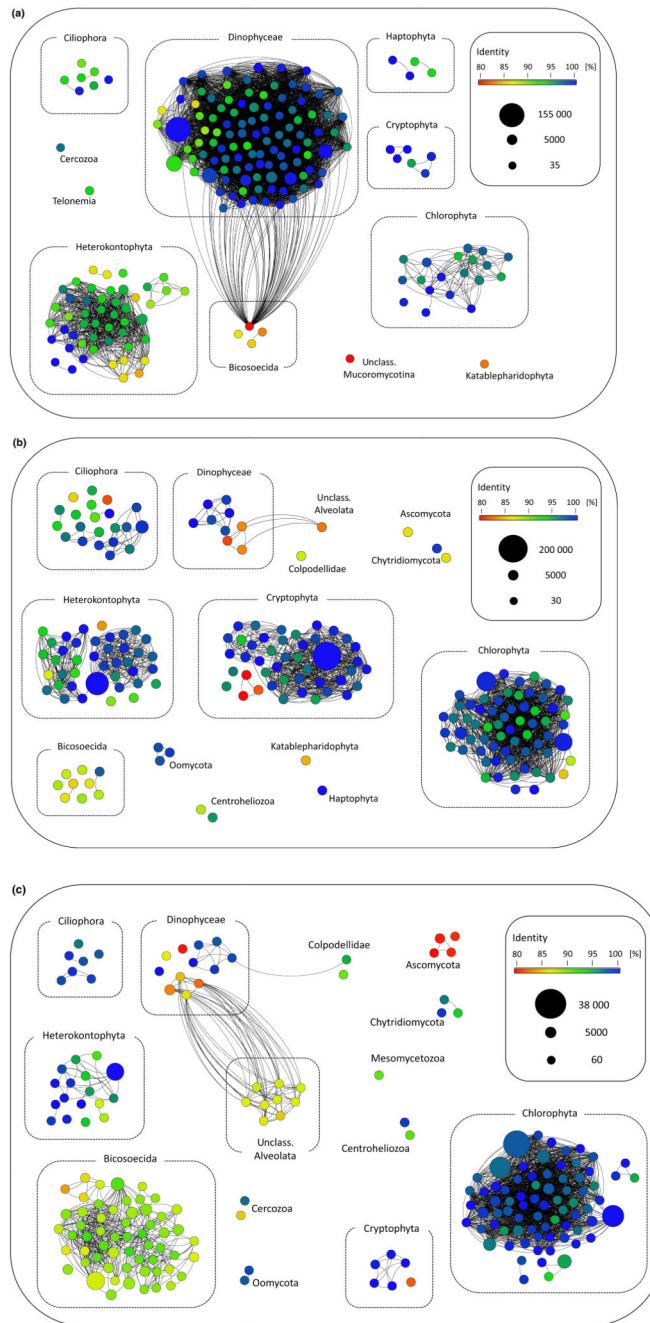


Fig. 6. Analyses of the novel diversity within the protistan (and fungal) communities in the European Alps lakes (a), the Chilean Altiplano lakes (b) and the Ethiopian Bale Mountain lakes (c). Each dot represents one operational taxonomic unit (OTU), the different colours indicate the level of sequence similarity to a deposited reference sequence, and the size of on OTU indicates the number of included V4 sequences. An edge weight (sequence similarity) of 90% was chosen to discriminate between the different OTUs.

Table 1
 Geographic properties (coordinates, altitude) and lake characteristics of the European Alps, Chilean Altiplano and Ethiopian Bale Mountain lakes

Lake	Lake code	Coordinates	Altitude (m)	Water temperature (°C)	pH	Conductivity (µS/cm)	SO ₄ ²⁻ (mg/L)	Cl ⁻ (mg/L)	Na ⁺ (mg/L)	K ⁺ (mg/L)	Mg ²⁺ (mg/L)	Ca ²⁺ (mg/L)	DOC (µg/L)	DN (µg/L)
European Alps														
		N	E											
Drachensee	DRA	47°21'36"	1874	7.48	8.3	146	1.06	0.23	0.09	0.12	2.59	25.84	356	284
Oberer Plenderlessee	OPL	47°12'11"	2417	11.25	7.35	22.3	3.35	0.06	0.38	0.23	0.29	3.52	290	187
Gossenköllesee	GKS	47°14'0"	2344	7.69	7.26	43	11.44	0.06	0.54	0.72	0.79	5.42	178	178
Drachensee	DRA II*	47°21'36"	1874	7.45	8.33	145	1.03	0.33	0.08	0.11	3.224	25.25	551	253
Oberer Plenderlessee	OPL II*	47°12'11"	2344	5.07	7.2	59.5	17.09	0.11	0.67	0.79	1.227	7.58	237	217
Gossenköllesee	GKS II*	47°14'0"	2417	7.21	7.36	22.1	3.32	0.2	0.39	0.24	0.282	3.65	384	170
Mutterbergersee	MUT II*	47°0'58"	2483	5.37	6.18	5.08	0.95	0.1	0.18	0.19	0.102	0.59	575	68
Schwarzsee ob Sölden	SOS II*	46°57'53"	2796	3.78	6.24	35.1	12.66	0.1	0.88	0.19	0.808	3.58	325	50
Chilean Altiplano														
		S	W											
Cotacotani	COT	18°12'08.6"	4550	10.5	9.8	840	58.27	46.11	63.64	9.16	57.78	28.69	6920	644.9
Piacota	PIA	18°11'49.8"	4400	12.6	9.3	660	44.53	40	60.22	13.6	30.96	22.32	8436	704
Chungara	CHU	18.14°	4600	9.9	9.22	1543	94.53	76.23	142.9	28.1	104.18	40.73	10904	969
Cotacotani	COT II*	18°12'08.6"	4550	5.7	8.96	849	59.15	51	62.34	8.45	59.52	36.71	6725	567
Piacota	PIA II*	18°11'49.8"	4400	6.4	9.9	640	44.54	47	55.6	9.32	42.52	20.74	8966	364.1
Chungara	CHU II*	18.14°	4600	4.8	9.12	1400	119.39	85	144.86	26.66	113.26	39.12	10486	794
Ethiopian Bale Mountains														
		N	E											
Koromi	KOR	06°53.561'	3917	8.4	7.57	21.2	1.8	0.46	0.9	0.25	0.65	3.04	3025	169
Hara-Lukas	HaLu	06°51.498'	4121	13.4	8.82	50.9	2.98	1.29	1.61	0.85	1.85	6.37	7121	406
Central	CEN	06°51.107'	4123	5.8	7.74	39	3.44	1.12	1.36	0.82	1.36	5.1	7318	350
Crane	CRA	06°51.285'	4047	10.1	8.85	49.5	2.47	0.88	1.58	0.53	1.79	6.31	5709	273
Togona	TOG	06°53.095'	4029	10.9	9.51	21.1	1.33	0.5	0.81	0.21	0.61	2.93	3552	170

II indicates sampling during October (Alps) or March (Chile).

Table 2

Number of sequences and operational taxonomic units generated after Illumina data processing. Target sequences comprise eukaryotic unicellular organisms and fungi

Sample ID	Raw sequences	Cleaned sequences	Cleaned OTUs	Target sequences	Target OTUs	Target sequences without singletons/doubletons	Target OTUs without singletons/doubletons
DRAa	70 147	65 788	4899	62 746	4723	58 156	284
DRAb	93 303	71 466	5322	67 873	5119	62 817	275
OPL	115 640	98 252	15 404	98 199	15 397	82 450	395
GKS	103 724	89 716	12 787	89 689	12 772	76 820	532
OPL II	95 449	69 823	6990	61 216	6603	54 681	348
GKS II	125 219	110 538	18 646	110 505	18 632	91 449	630
DRA II	127 949	124 754	8160	124 643	8139	116 526	336
MUT II	99 639	95 503	5627	89 124	5139	81 154	99
SOS II	87 461	79 774	9479	78 713	9332	69 293	382
COT	172 037	168 199	6518	164 832	6349	158 571	210
PIA	168 593	161 554	5449	160 981	5383	155 628	263
CHU	213 932	200 024	9406	193 343	9045	184 273	388
COT II	71 666	61 887	5896	61 732	5840	56 027	420
PIA II	147 042	135 163	7697	109 392	5620	103 945	353
CHU II	69 328	56 699	5378	54 399	5245	49 252	340
KOR	130 088	108 526	13 069	96 414	12 206	84 439	1166
HaLu	87 025	84 689	5750	82 505	5457	77 261	467
CEN	54 105	52 530	2331	50 670	2177	48 624	186
CRA	173 658	166 489	9843	69 801	6775	63 409	934
TOG	125 227	114 330	9469	42 606	6217	36 744	692

Table 3
Environmental variables fitted into nonmetric multidimensional scaling analysis. *P*-values <0.05 are considered as significant effect

	NMDS1	NMDS2	R^2	Pr ($>r$)
Altitude	0.9399	0.3412	0.76	0.0002
Water temperature	0.3384	-0.9410	0.28	0.0748
pH	0.7812	0.6243	0.43	0.0134
Conductivity	0.2489	0.9685	0.57	0.0020
SO ₄ ²⁻	0.2401	0.9708	0.51	0.0038
Cl ⁻	0.2885	0.9575	0.58	0.0019
Na ⁺	0.2795	0.9602	0.53	0.0025
K ⁺	0.2852	0.9585	0.48	0.0037
Mg ²⁺	0.2647	0.9643	0.56	0.0019
Ca ²⁺	0.1122	0.9937	0.71	0.0002
DOC	0.7299	0.6836	0.73	0.0003
DN	0.3844	0.9232	0.49	0.0041