

ORIGINAL ARTICLE

Metatranscriptomic census of active protists in soils

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The high numbers and diversity of protists in soil systems have long been presumed, but their true diversity and community composition have remained largely concealed. Traditional cultivation-based methods miss a majority of taxa, whereas molecular barcoding approaches employing PCR introduce significant biases in reported community composition of soil protists. Here, we applied a metatranscriptomic approach to assess the protist community in 12 mineral and organic soil samples from different vegetation types and climatic zones using small subunit ribosomal RNA transcripts as marker. We detected a broad diversity of soil protists spanning across all known eukaryotic supergroups and revealed a strikingly different community composition than shown before. Protist communities differed strongly between sites, with Rhizaria and Amoebozoa dominating in forest and grassland soils, while Alveolata were most abundant in peat soils. The Amoebozoa were comprised of Tubulinea, followed with decreasing abundance by Discosea, Varioseae and Mycetozoa. Transcripts of Oomycetes, Apicomplexa and Ichthyosporea suggest soil as reservoir of parasitic protist taxa. Further, Foraminifera and Choanoflagellida were ubiquitously detected, showing that these typically marine and freshwater protists are autochthonous members of the soil microbiota. To the best of our knowledge, this metatranscriptomic study provides the most comprehensive picture of active protist communities in soils to date, which is essential to target the ecological roles of protists in the complex soil system.

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Introduction

Soils harbour a spectacular microbial diversity. Among the least-studied soil microorganisms are single-celled protists. They display a high diversity of fundamentally different taxa, based on both morphological features and phylogenetic relatedness (Adl *et al.*, 2012; Pawlowski, 2013). Despite being microscopic, protist biomass in soils has been estimated to exceed that of most soil animal taxa (Schaefer and Schauerermann, 1990; Zwart *et al.*, 1994; Schröter *et al.*, 2003). Protists play important ecological roles in controlling bacterial turnover and community composition, recycling of nutrients and plant growth promotion (Clarholm, 1985; de Ruiter *et al.*, 1993; Bonkowski, 2004). However, we still lack basic knowledge of the protist

communities in soils, and therefore a comprehensive understanding about their distribution and ecological functions in different soil systems has not yet been achieved.

The pervasive lack of knowledge on soil protist communities is mainly caused by the need to establish enrichment cultures, as the majority of protist taxa are difficult to extract and cultivate from soils, and the opaqueness of soil particles that prevents direct microscopic observation of the majority of taxa (Foissner, 1987; Clarholm *et al.*, 2007). Expert knowledge is needed for the time-consuming microscopic identification (Foissner, 1987; Smirnov *et al.*, 2008; Fenchel, 2010; De Jonckheere *et al.*, 2012). Therefore, these traditional attempts to describe the full diversity of protist taxa in natural soils are rare and identification is usually only possible to a rather shallow taxonomic level (Finlay *et al.*, 2000; Bamforth, 2007; Geisen *et al.*, 2014a). Cultivation-based approaches also introduce bias, as different growth media select for different species, and only a subset of taxa is likely to be cultivable (Ekelund and Rønn, 1994; Foissner, 1999; Smirnov and Brown, 2004).

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The advent of molecular techniques along with a revised species concept that usually includes molecular information such as the universal protist barcode, the small subunit ribosomal RNA (SSU rRNA) gene (Pawlowski *et al.*, 2012), has fundamentally altered the view on the 'protist world'. Consequently, the classification of and relatedness between protist taxa are constantly being revised (Adl *et al.*, 2012; Pawlowski, 2013). Further, environmental sequencing studies based on the SSU rRNA gene have revealed a huge diversity of previously unknown protists (Bass and Cavalier-Smith, 2004; Berney *et al.*, 2004; Lara *et al.*, 2007; Lejzerowicz *et al.*, 2010; Bates *et al.*, 2013). Despite molecular tools having diminished some of the problems associated to deciphering the community structure of soil protists, they introduce new biases that still obscure the true protist diversity in soils. Fundamental problems include (i) the lack of SSU rRNA reference sequences for a substantial number of protist species and genera, (ii) numerous mislabelled sequences in public databases and (iii) a large seed bank of dormant protist cysts that may survive for decades (Goodey, 1915; Moon van der Staay *et al.*, 2006; Smirnov *et al.*, 2008; Epstein and López-García, 2008; Adl *et al.*, 2012; De Jonckheere *et al.*, 2012). Further biases are introduced by the PCR step of SSU rRNA gene studies (for example, Bachy *et al.*, 2013). The often applied 'general' eukaryotic primers to decipher the community structure of protists are in fact far from being truly universal (Adl *et al.*, 2014). Thus, a strongly biased view of the protist community in soils is being depicted as only a subset of its diversity can be recovered (Jeon *et al.*, 2008; Hong *et al.*, 2009), whereas, on the other hand, some taxa within this subset will be overrepresented because of preferential PCR amplification (Berney *et al.*, 2004; Medinger *et al.*, 2010; Stoeck *et al.*, 2014). Taxa of the common supergroup Amoebozoa as one of the dominant soil protists for instance, are notoriously underrepresented in molecular surveys because of long SSU rRNA sequences, frequent mismatches in primer regions and presence of introns (Berney *et al.*, 2004; Fiore-Donno *et al.*, 2010; Pawlowski *et al.*, 2012). Ciliates on the contrary are highly overrepresented because of their shorter SSU rRNA sequences that ease amplification, and the presence of extremely high SSU rRNA gene copy numbers (Gong *et al.*, 2013).

Most of these obstacles are avoided when directly targeting SSU rRNA transcripts instead of genes, especially by random hexamer-primed reverse transcription as in metatranscriptomic approaches. These rRNA transcripts are indicative of ribosomes and thus are likely derived from metabolically active cells and can be considered markers for living biomass (Urich and Schleper, 2011). The generated cDNA fragments originate from different regions of the SSU rRNA molecule unlike PCR-primed specific sites, and are therefore insensitive to the presence of

introns or primer mismatches (Urich *et al.*, 2008). These cDNA fragments can further be assembled into longer fragments, or even full-length SSU rRNA molecules for phylogenetic analyses (Urich *et al.*, 2014). However, metatranscriptomics also has biases; the reported community composition is influenced, for example, by the different accessibility of SSU rRNA regions to primers and reverse transcriptase and also the physiological status of cells resulting in varying ribosomal content. Using this approach, Urich *et al.* (2008) generated cDNA from the total extracted RNA of soil communities. The cDNA was subjected directly to high throughput sequencing without any SSU rRNA gene PCR steps. Although the fraction of SSU rRNA originating from protists is comparably small in metatranscriptomes, recent studies showed that the sequencing depth even with 454 pyrosequencing yielded sizable datasets of protist SSU rRNAs (Urich *et al.*, 2008; Turner *et al.*, 2013; Tveit *et al.*, 2013).

We used this PCR-free metatranscriptomic approach to reveal the diversity of the active soil protist communities within five different natural soil systems in Europe, including forest, grassland and peat soils as well as beech litter. We annotated all protist SSU rRNA sequences to a reference database consisting of manually curated, published protist SSU rRNA sequences and revealed high protist diversity, with communities strongly differing between sites. We show that Rhizaria and Amoebozoa are the most abundant protist groups and detect abundant potential plant and animal pathogens. Further, we perform for the first time an in-depth molecular analysis of the amoebozoan community structure. Finally, we report the widespread presence of protist clades that are usually associated with marine and freshwater environments, but not considered typical soil inhabitants.

Materials and methods

Soil sampling and processing

Arctic peat soils were sampled as described in the study by Tveit *et al.* (2013). The grassland site (Park Grass, untreated control plot 3d, Rothamsted) was sampled by coring, with intact cores being brought to the laboratory, topsoil (5–10 cm) sieved (5 mm mesh size) and subsequently flash-frozen in liquid nitrogen. Beech (*Fagus sylvatica* L) forest soils were sampled as described in the study by Kaiser *et al.* (2010), the top soil (5–10 cm) sieved (5 mm mesh size) and subsequently flash-frozen in liquid nitrogen. Beech litter from the same site was homogenized with a sterilised coffee grinder for 10 s and flash-frozen in liquid nitrogen.

Nucleic acid extraction, cDNA synthesis and sequencing

Nucleic acids were extracted from 5 g of mineral soil and 1.2 g of litter and peat and processed as

previously described (Urich *et al.*, 2008). cDNA synthesis was performed as described before (Radax *et al.*, 2012; Tveit *et al.*, 2013). 454-pyrosequencing was done either with FLX (forest soil and litter) or FLX Titanium (grassland, peat soil) chemistry. Sequencing was carried out at the CEES at the University of Oslo (Norway).

Sequence processing and analysis

Raw reads were processed as described in the study by Tveit *et al.* (2013). Sequences were first filtered using LUCY (Chou and Holmes, 2001), removing short (<150 bp) and low-quality sequences (>0.2% error probability). SSU ribosomal RNA sequences of eukaryotes were identified by MEGAN analysis of BLASTn files against a 3-domain SSU rRNA reference database (Lanzén *et al.*, 2011; parameters: min. bit score 150, min. support 1, top percent 10; 50 best blast hits). All identified eukaryotic SSU rRNAs were reanalysed with CREST (Lanzén *et al.*, 2012) using the Silvamod database and MEGAN with LCA parameters min bit score 250, top percent 2 (50 best blast hits) for classification of protist sequences. Correct taxonomic assignment of rRNA reads was verified by manual BLASTn searches against the NCBI GenBank nucleotide database. For the high-resolution taxonomic annotation of amoebozoan rRNA sequences, a custom-made database was constructed consisting of 1164 sequences from Silva (www.arb-silva.de) and sequences of in-house cultivated and newly described species (Geisen *et al.*, 2014b, c, d). The taxonomy was set according to the most recent taxonomy of Amoebozoa (Smirnov *et al.*, 2011; Adl *et al.*, 2012; Lahr *et al.*, 2013) to enable high-resolution taxonomic placement of sequences. Reference database and taxonomy were then generated with the CREST scripts (Lanzén *et al.*, 2012), and amoebozoan sequences were classified using the same parameters in MEGAN as described above. The database can be obtained from TU or SG upon request.

SSU rRNA sequences of Choanoflagellida and Foraminifera were assembled into ribo-contigs using CAP3 (Huang and Madan, 1999), performing two subsequent rounds of assembly with (i) a minimum overlap of 150 bp with a minimum similarity threshold of 99% and mismatch and gap scores of -130 and 150, and (ii) minimum overlap of 150 bp and minimum 97% similarity threshold, respectively (Radax *et al.*, 2012).

Phylogenetic analysis

Assembled Choanoflagellate contig sequences were subjected to BLASTn searches against the NCBI nucleotide database and manually aligned with their respective five best hits in Seaview 4 (Gouy *et al.*, 2010). Additionally, SSU rRNA sequences of described choanoflagellates were added to this alignment. For phylogenetic analyses,

1438 unambiguously aligned positions of a total of 71 unique sequences were retained, excluding ambiguous positions and several positions in variable regions especially in V4 (helix E23). Maximum likelihood phylogenetic analyses were run using RAxML v. 7.2.6 (Stamatakis, 2006) using the GTR+ γ +I model of evolution, as proposed by jModeltest v. 2.1.3 under the Akaike Information Criterion (Darriba *et al.*, 2012), γ approximated by 25 categories. A total of 1000 non-parametric bootstrap pseudoreplicates were performed. Subsequently, Bayesian phylogenetic analyses were run in Mr Bayes v. 3.2.1 with GTR+ γ +I model of evolution and eight categories (Huelsenbeck and Ronquist, 2001). Two runs of four simultaneous Markov chains were performed for 2 000 000 generations (with the default heating parameters) and sampled every 100 generations; convergence of the two runs (average deviation of split frequencies <0.01) was reached after 590 000 generations. Therefore, we discarded the first 5900 trees and built a consensus tree from the remaining 14 100 trees.

Unweighted Pair Group Method as a cluster analysis was applied to evaluate differences between the protist community composition in all samples (Sokal, 1961).

Data deposition

The sequence data generated in this study were deposited in the Sequence Read Archive of NCBI under accession number SRP014474 and SAMN03365922-24.

Results

Community composition of protist supergroups

In total, 32 808 SSU rRNA transcripts of protists were obtained from 12 soil metatranscriptomes (Table 1). In all cases, the biological replicates of each site yielded a very similar community composition (Figure 1) and grouped together in a cluster analysis (Figure 2). All five protist supergroups according to Adl *et al.* (2012) were found at each site (Table 1; Figure 1). The SAR group, consisting of the formerly independent supergroups Stramenopiles, Alveolata and Rhizaria, dominated the active communities at all sites with sequences of Rhizaria being most numerous. We observed a clear dichotomy in protist community composition (Figure 2) with dominance of Alveolata in peat soils with their high moisture and high organic matter content, versus dominance of Rhizaria and Amoebozoa in grassland and forest soils, including forest litter (Figure 1).

The Rhizaria were almost exclusively comprised of Cercozoa (Figure 3a) with dominance of rRNAs of the small flagellates belonging to the class Filosa-Sarcomonadea (formerly combined into Cercomonadida) and both, flagellated and amoeboid Cercozoa in the class Filosa-Imbricatea (formerly Silicofilosea). Foraminiferan SSU rRNAs occurred in

Table 1 Soil sample description, protist SSU rRNA sequence numbers (\pm s.d.) and relative abundances obtained from each site

Sample name	Grassland soil (Gs)	Forest soil (Fs)	Forest litter (Fl)	Peatland soil 'Knutsen' (PsK)	Peatland soil 'Solvatn' (PsS)
# of replicates	2	4	2	2	2
pH	4.9	4.5–5.1	NA	7.3	7.6
Moisture (% soil dry weight)	33	43–64	18	1010	900
Substrate type/horizon	Mineral soil/ A horizon	Mineral soil/ A horizon	Litter/organic (L/F) horizon	Organic peat/ Top layer	Organic peat/ Top layer
Vegetation	Grassland	Beech forest	Beech forest	Fen wet land, moss dominated	Fen wet land, moss dominated
Climatic zone	Temperate	Temperate	Temperate	Arctic	Arctic
Location	Rothamsted, UK	Vienna woods, Austria	Vienna woods, Austria	Svalbard, Norway	Svalbard, Norway
# of Protist SSU rRNAs (%)	253 \pm 21 100%	961 \pm 470 100%	4862 \pm 2579 100%	2722 \pm 773 100%	6631 \pm 210 100%
SAR	163 \pm 15 64%	662 \pm 287 69%	3494 \pm 1735 72%	2058 \pm 844 76%	5265 \pm 187 79%
Stramenopiles	24 \pm 8 9.5%	77 \pm 26 8.0%	234 \pm 238 4.8%	294 \pm 71 10.8%	731 \pm 25 11.0%
Alveolata	24 \pm 1 9.5%	96 \pm 34 10.0%	870 \pm 542 17.9%	1295 \pm 756 47.6%	3797 \pm 144 57.3%
Rhizaria	115 \pm 7 46%	489 \pm 236 50.9%	2391 \pm 954 49.2%	470 \pm 160 17.3%	737 \pm 18 11.1%
Amoebozoa	65 \pm 4 26%	250 \pm 87 26%	1009 \pm 633 20.8%	322 \pm 6 11.8%	586 \pm 29 8.8%
Excavata	7 \pm 1 2.8%	25 \pm 11 2.6%	233 \pm 141 4.8%	148 \pm 20 5.4%	420 \pm 23 6.3%
Archaeplastida	12 \pm 6 4.7%	11 \pm 7 1.1%	47 \pm 19 1.0%	144 \pm 93 5.3%	222 \pm 10 3.3%
Opisthokonta	6 \pm 4 2.4%	19 \pm 10 2.0%	82 \pm 52 1.7%	50 \pm 7 1.8%	139 \pm 6 2.1%

Abbreviations: NA, data not available; SAR, Stramenopiles, Alveolata and Rhizaria; SSU rRNA, small subunit ribosomal RNA. In italics: eukaryotic supergroups.

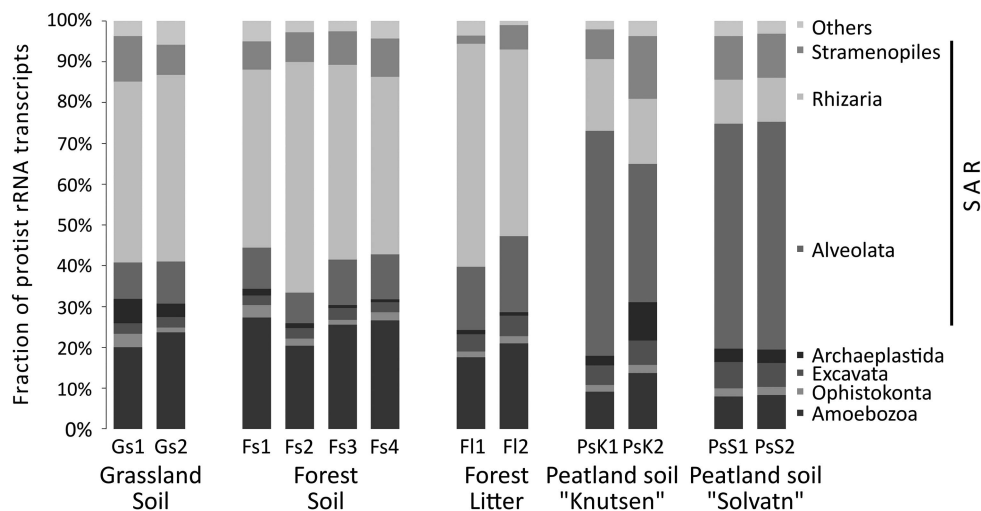


Figure 1 Community composition of protist supergroups in the investigated soils. For detailed information on soil parameters, see Table 1.

relatively constant, albeit low abundances in all samples (Figure 3a) except for the peatland site 'Knutsen', where they were more abundant and comprised 22% of all Cercozoa. Alveolate SSU rRNAs were quite variable among samples and dominated in the peat soils (Figure 1) with the phylum Ciliophora and its main orders Spirotrichea, Colpodea and Oligohymenophorea being most

abundant, whereas the exclusively parasitic Apicomplexa still represented up to 11% of all Alveolata (Figure 3b). The third group in SAR, Stramenopiles, was less abundant, with Oomycetes representing the dominant stramenopiles in forest soils (Figure 3c), while abundant transcripts of the photosynthetic Bacillariophyta were characteristic in the water-logged peatland soils. Chrysophyceae SSU rRNAs

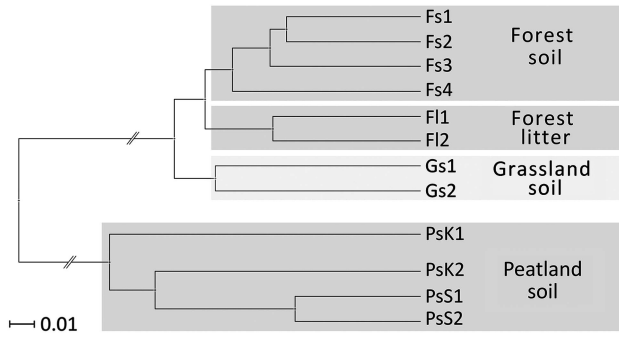


Figure 2 Unweighted Pair Group Method (UPGMA) clustering analysis to evaluate differences between soil protist communities. For detailed information on soil characteristics and abbreviations, see Table 1.

were abundantly found in grassland soils and litter, as were transcripts of the Bicosoecida. The supergroup Amoebozoa represented up to 30% of SSU rRNAs, with highest abundances in the grassland and forest soil samples (Figure 1 and Table 1). The other protist supergroups, that is, Excavata, Archaeplastida and Opisthokonta (excluding fungi and animals) were generally less abundant (Figure 1 and Table 1; see Supplementary Table 1 for more information).

SSU rRNA transcripts of protist clades highly represented in cultivation-based approaches were analysed to evaluate whether these clades were also recovered in our metatranscriptomes. Among the clades targeted were flagellates of the supergroups SAR (Glissonomadida and Cercomonadida (Sarcomonadea; Rhizaria), Chrysophyceae and Bicosoecida (Stramenopiles) and Excavata (Bodonidae and Euglenida), as well as amoebae in the supergroup Excavata (Heterolobosea). All clades were found at each location, with cercomonads being highly abundant in grassland and forest habitats. Glissonomads were abundant especially in grasslands (5% of all protists). Bodonids were also common (1.9% of all protists) whereas euglenids, chrysophytes, bicosoecids and heteroloboseans comprised only about 1% of all protist transcripts (Supplementary Table 1). Exhaustive analyses of the most abundant clades of amoebae are presented in the next section.

Community composition of amoebozoa

The supergroup Amoebozoa was of particular interest, as no comprehensive molecular taxonomic analysis of this protist supergroup in soil exists to date because of PCR-primer biases (Baldwin *et al.*, 2013; Bates *et al.*, 2013). For this purpose, we constructed a high-resolution reference database and taxonomy of Amoebozoa (see Table 2 and Materials and Methods for details). Using this taxonomic assignment approach, the rather short SSU rRNA sequence reads could reliably be classified at least to the order, often even to the genus level. Amoebozoa were highly diverse at each

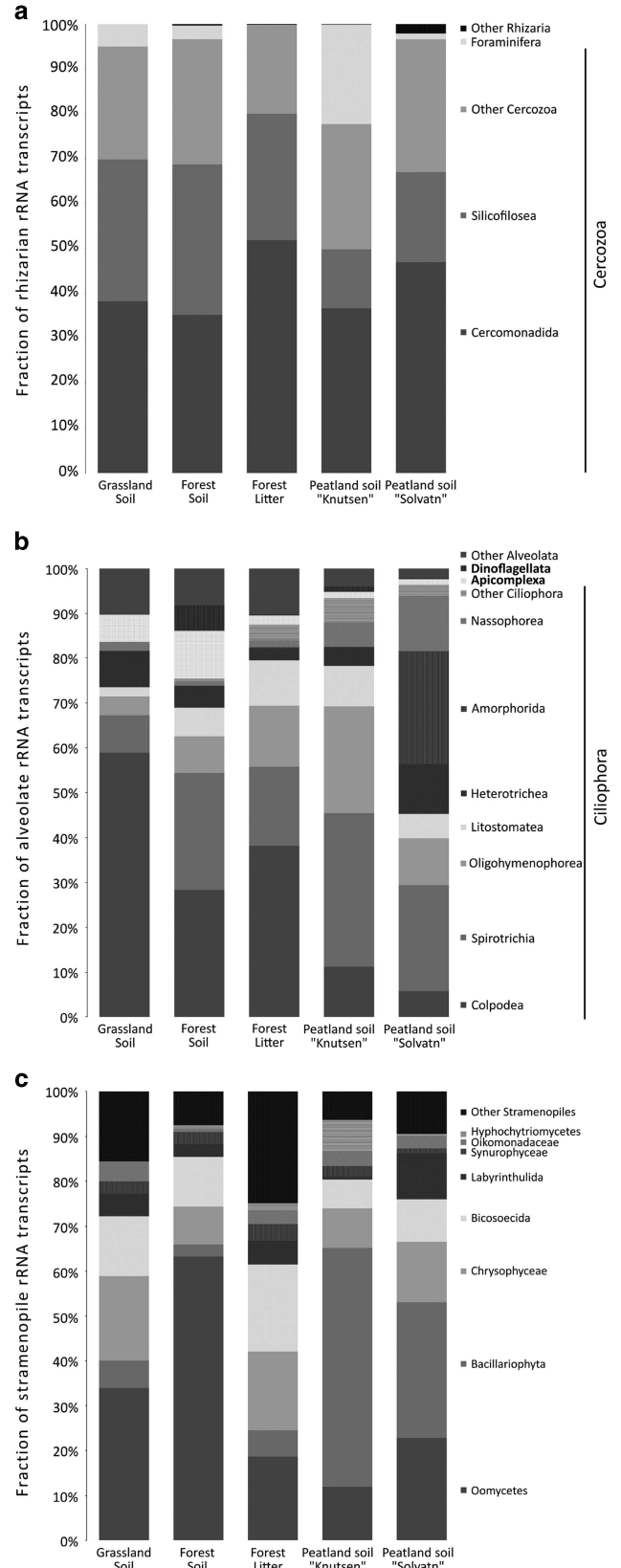


Figure 3 Community composition within the SAR supergroup independently showing the community compositions within the individual clades of SAR, i.e., Rhizaria (a), Alveolata (b) and Stramenopiles (c). Shown are means of biological replicates. Labels and sites as described in Table 1 and Figures 1 and 2.

Table 2 Overview of taxa and taxonomic classification of Amoebozoa in the CREST reference database and taxonomy

Supergroup	Subphylum	Class	Subclass	Order	Suborder	Family	Genus		
Amoebozoa	Lobosa	Tubulinea		Euamoebida		Unresolved			
				Arcellinida	Arcellina Diffflugina Phryganellina	Unresolved Unresolved Unresolved			
				Nolandida		Nolandellidae	<i>Nolandella</i>		
				Echinamoebida		Vermamoebidae Echinamoebidae	<i>Vermamoeba</i> <i>Echinamoeba</i>		
				Leptomyxida		Leptomyxidae	<i>Leptomyxa</i> <i>Rhizamoeba</i>		
				Flabellinia	Vannellida		Vannellidae	<i>Vannella</i>	
					Himatismenida		Cochliopodiidae	<i>Cochliopodium</i>	
					Dactylopodida		Vexilliferidae Paramoebidae	<i>Vexillifera</i> <i>Korotnevela</i>	
					Discosea	Thecamoebida		Thecamoebidae	<i>Stenamoeba</i> <i>Thecamoeba</i>
						Longamoebia	Dermamoebida		Mayorellidae Dermamoebidae
	Centramoebida		Acanthamoebidae Balamuthiidae				<i>Acanthamoeba</i> <i>Balamuthia</i>		
	Conosa	Variosea		Varipodida		Filamoebidae	<i>Filamoeba</i> <i>Flamella</i>		
				Schizoplasmodiida		Unresolved	Unresolved		
				Mycetozoa			Unresolved		
							Unresolved		

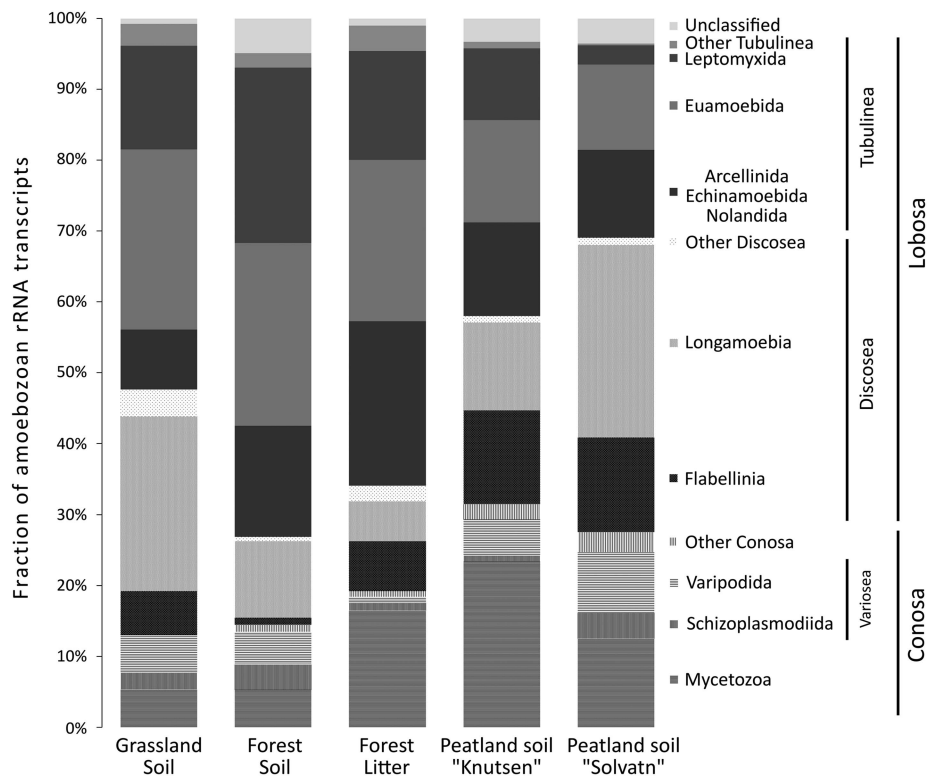


Figure 4 Community composition within the supergroup Amoebozoa in the investigated soils. Shown are means of biological replicates. Labels and sites as described in Table 1 and Figures 1 and 2.

sampling site, with rRNAs assigned to four classes, that is, Tubulinea, Discosea, Variosea and Mycetozoa with major orders Euamoebida, Leptomyxida, Arcellinida and Centramoebida (Smirnov *et al.*, 2011) (Figure 4). The community composition

within Amoebozoa differed significantly between sites. For instance, sequences assigned to the dominant class Tubulinea made up between 27.4% and 69.2% in Solvatn peat and forest soils, respectively, and were inversely related to Discosea with

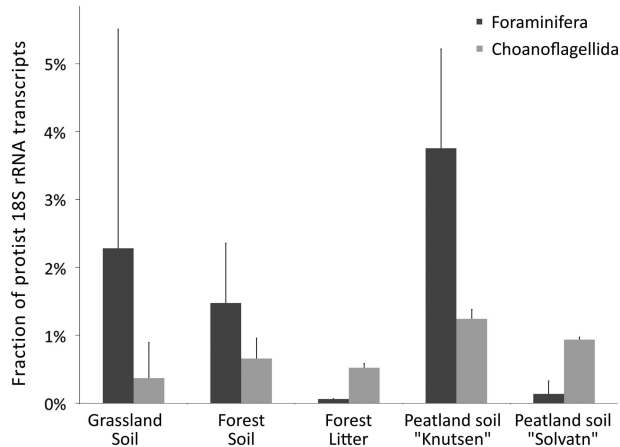


Figure 5 SSU rRNA transcript abundance \pm s.d. of Foraminifera and Choanoflagellida in the soil metatranscriptomes. Labels and sites as described in Figure 2 and Table 1.

41.6–12.7% in Solvatn peat and forest soils. Similar to the patterns observed at the class level, the proportional distribution within classes differed between sites. Among Tubulinea, the dominant order Euamoebida reached highest relative abundances in grasslands and forest mineral soils, while testate amoebae of the order Arcellinida became more abundant in organic rich substrates of litter and peat soils, and Leptomyxida were characteristic of forest habitats. The remaining tubulinean orders Echinamoebida and Nolandida were generally rare. Among the class Discosea, SSU rRNAs assigned to the subclass Longamoebia were almost entirely (96.1%) composed of the order Centramoebida. Sequences of the discosean subclass Flabellinia were generally less abundant (7.0% oas) and mostly derived from the order Vannellida (50.1% of flabellinian SSU rRNAs). Sequences assigned to the subphylum Conosa could only reliably be assigned to the class level, as taxonomy and the phylogenetic affiliations, especially of protists in the class Variosea, are still largely unresolved (Adl *et al.*, 2012). Variosea was the dominant conosan class in grassland, forest and the Solvatn peat soil, while Mycetozoa were more abundant in forest litter and Knutsen peat soil (Figure 4).

Widespread were amoebozoan SSU rRNA sequences with high sequence identity to potential parasites. At all sites occurred diverse sequences related to facultative human pathogens of the genus *Acanthamoeba* ($\geq 97\%$ sequence identity; 1.1–4.4% oas) while sequences most closely resembling *Balamuthia* were discovered in low relative abundance (0.1–0.5% oas) in all except the grassland soils. Transcripts related to groups of non-Amoebozoan parasitic taxa were also found, such as sequences most closely resembling the human pathogen *Naegleria fowleri* (Heterolobosea in the supergroup Excavata; $\geq 97\%$ sequence identity) in all four arctic peat samples. Further, opisthokonta Ichthyosporea

(mainly animal parasites) were ubiquitously found (0.4–3.3% oas; Supplementary Table 1) as well as predominantly plant-parasitic plasmodiophorans (up to 0.8% oas).

Widespread presence of foraminifera and choanoflagellida in soils

SSU rRNA transcripts of the typically marine groups Foraminifera and Choanoflagellida revealed their general presence and activity in all samples (Figure 5), and for the first time, allowed to estimate the relative abundance of these taxa in soils. They comprised between 0.1% and 3.5% of all protist SSU rRNAs.

To enable better taxonomic assignment and phylogenetic placement of these enigmatic soil protist groups we, assembled larger SSU rRNA sequences from the short 454 reads. Three assembled SSU rRNA contigs of Foraminifera (742–890 bp length) were quite similar ($\geq 91\%$) to sequences obtained in a recent focused PCR-based molecular survey targeting soil Foraminifera (Lejzerowicz *et al.*, 2010), but showed substantial sequence dissimilarity to described species (maximum SSU rRNA sequence identity of $\leq 76\%$). Several unassembled SSU rRNA sequences, however, closely matched sequences typically obtained from freshwater and marine environments, such as the genera *Astrammia*, *Bathysiphon*, *Allogromia* and diverse uncultured species (Supplementary Table 2).

Many Choanoflagellida-affiliated SSU rRNA sequences closely matched (with $\geq 99\%$ maximum identity) published sequences of uncultivated choanoflagellates (for example, with GenBank accession numbers HQ219439 (freshwater), EF024012 (soil), JF706236 and GQ330606 (peat soil)) while others reached similarities of $> 95\%$ with uncultivated choanoflagellate sequences among typical freshwater and marine genera, such as *Monosiga*, *Codonosiga*, *Salpingoeca*, and more rarely with *Lagenoeca*, *Stephanoeca*, *Didymoeca*, *Diaphanoeca*, *Desmarella* and *Acanthoeca*. Five assembled long SSU rRNAs (763–1163 bp) had high sequence similarities of 96–99% to uncultivated freshwater choanoflagellates (Figure 6), but the closest hit to a formally described species was $< 92\%$.

Discussion

Metatranscriptomics-enabled census of active soil protists

Cultivation-based studies have shown that soil protists are diverse, abundant and ecologically important (Ekelund and Rønn, 1994; de Ruiter *et al.*, 1995; Bonkowski, 2004; Pawlowski *et al.*, 2012), but fail to detect a majority of taxa (Epstein and López-García 2008). In contrast, cultivation-independent PCR-based SSU rRNA gene sequencing studies have revealed a much higher diversity of soil protists than previously anticipated (Lara *et al.*,

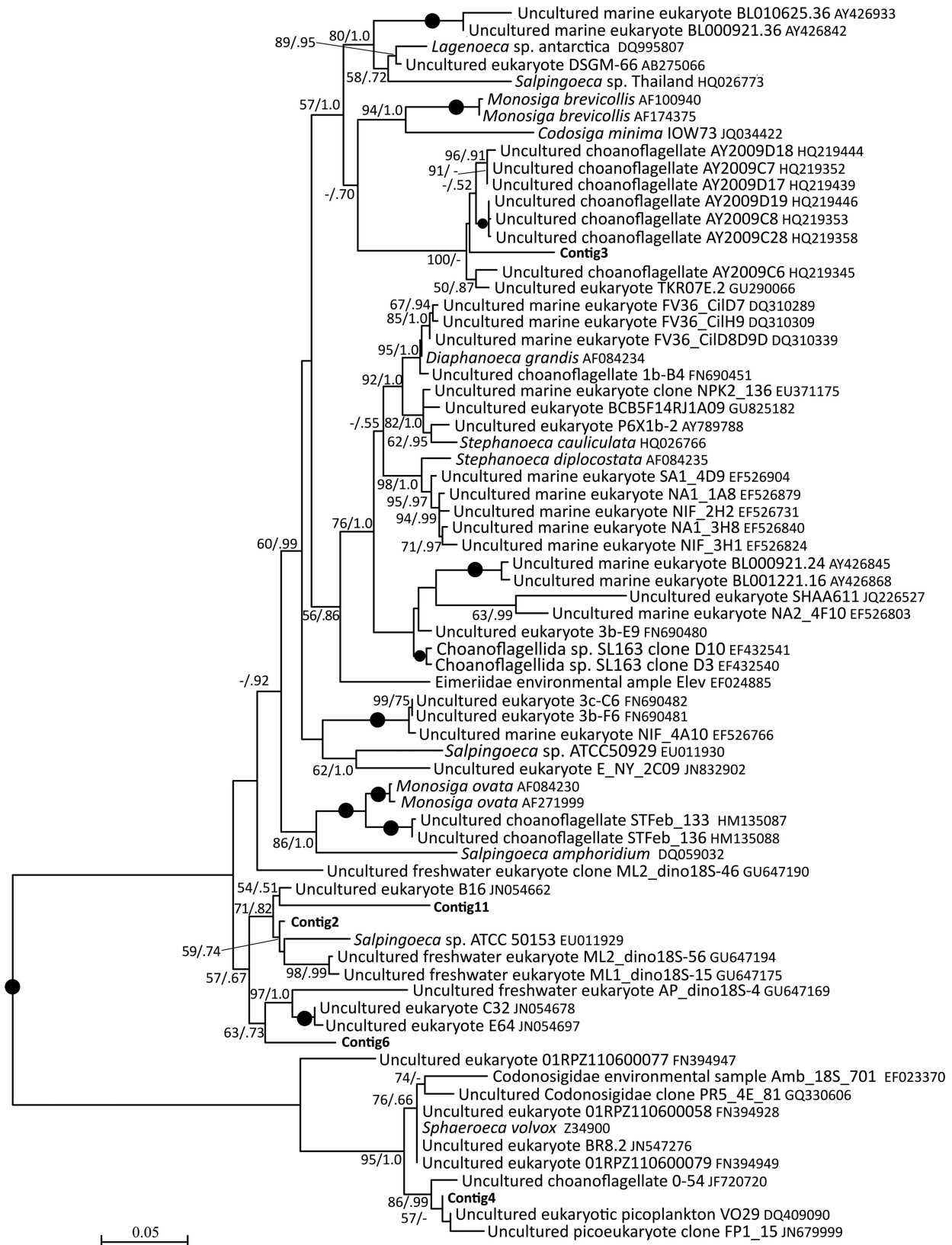


Figure 6 Maximum likelihood tree of Choanoflagellida placing assembled long SSU rRNA contigs (red) with sequences of described and uncultivated choanoflagellates. Seventy-one sequences with 1232 unambiguously aligned positions were used; the tree is unrooted; values higher than 50 for maximum likelihood analyses (left) and 0.50 for Bayesian analyses (right) shown. Black circles indicate full support.

2007; Lejzerowicz *et al.*, 2010; Bates *et al.*, 2013); however, they still fail to amplify the SSU rRNA genes of a wide range of protists and provide a highly skewed picture of protist communities (Epstein and López-García, 2008; Weber and Pawlowski, 2013; Stoeck *et al.*, 2014). This is exemplified by the negative selection of amoebozoan sequences in PCR-primer-based approaches (Berney *et al.*, 2004; Amaral-Zettler *et al.*, 2009), explaining the virtual absence of nearly the entire supergroup in high throughput sequencing surveys (Baldwin *et al.*, 2013; Bates *et al.*, 2013), whereas the high rRNA gene copy numbers in ciliates (Gong *et al.*, 2013) generally lead to their over-proportional representation.

Through the usage of metatranscriptomics, we avoided some of the above-mentioned issues to gain a more accurate picture of the protist diversity in soil systems. In fact, this study and earlier metatranscriptomes have revealed a different soil protist community structure than suggested before (Urich *et al.*, 2008; Baldwin *et al.*, 2013). The only similarity to primer-based high throughput sequencing surveys is merely the dominance of the supergroup SAR, which was because of high sequence abundances of Rhizaria (and Alveolata in arctic peat soils) (Baldwin *et al.*, 2013; Bates *et al.*, 2013). However, SSU rRNA sequences of Amoebozoa dominated over those of Alveolata in all non-peat soils. This is in line with cultivation-based studies, which show that small flagellates, especially cercozoans and glissomonads (Rhizaria) (Finlay *et al.*, 2000; Ekelund *et al.*, 2001; Howe *et al.*, 2009) and amoebae represent the numerically dominant soil protists (Schaefer and Schauer mann, 1990; Finlay *et al.*, 2000; Robinson *et al.*, 2002). Similarly, other taxonomically highly divergent heterotrophic protist taxa especially abundant in cultivation-based studies such as bodonid and euglenid euglenozoans (Finlay *et al.*, 2000; Geisen *et al.*, 2014a), chrysophytes (Finlay *et al.*, 2000; Boenigk *et al.*, 2005; Chatzinotas *et al.*, 2013), bicosoecids (Ekelund and Patterson, 1997; Lentendu *et al.*, 2014) and heteroloboseans (Geisen *et al.*, 2014a) were identified, but contributed relatively little to the entire protist community.

It should be noted here that metatranscriptomics also has several biases and shortcomings. For example, the reported community composition can be biased by different accessibilities of SSU rRNA regions to primers and enzymes owing to RNA secondary structure. Further, the number of ribosomes can vary dependent of the physiological status of the cell. The higher costs related to cDNA synthesis and missing specificity as compared with PCR-amplicons make this approach rather low-throughput.

Diversity of Amoebozoa: the neglected supergroup in soil

In addition to the above-mentioned negative biases of Amoebozoa in high throughput sequencing

approaches, a lack of molecular data and SSU rRNA reference sequences until now prevented thorough molecular diversity analyses of this supergroup. Therefore, the diversity of Amoebozoa in terrestrial samples is still largely unknown (Smirnov *et al.*, 2005; Smirnov *et al.*, 2008). Applying the most recent taxonomy and a newly built reference database allowed us to detect a large diversity within all amoebozoan classes. The general dominance of the classes Tubulinea and Discosea confirmed former cultivation-based studies (for example, Finlay *et al.*, 2000; Bass and Bischoff, 2001), whereas the high abundance of Variosea is novel. This class was only constructed in 2004, hosting mostly large plasmodial, branching or reticulate amoebae (Cavalier-Smith *et al.*, 2004; Smirnov *et al.*, 2008; Smirnov *et al.*, 2011). To date, only few variosean species have formally been described, and molecular information on those taxa is even more limited (Berney *et al.*, in press). Recent cultivation studies specifically targeting Variosea confirm the results obtained here and revealed an unprecedented diversity of these large amoebae in soils (Geisen *et al.*, 2014a). The addition of several of these recently published variosean SSU rRNA sequences (Geisen *et al.*, 2014a) to our reference database resulted in improved sequence assignments of variosean-specific SSU rRNAs and confirmed that this group of amoebae has been entirely overlooked in earlier studies.

Protist parasites

Terrestrial Oomycetes, distinguished for containing diverse and devastating plant-pathogens (Latijnhouwers *et al.*, 2003) such as *Phytophthora infestans*, the causative agent of potato blight (Martin *et al.*, 2012), also include a variety of pathogens of other organisms (Benhamou *et al.*, 1999; Phillips *et al.*, 2008). Oomycetes in soil have been targeted with little success (Coince *et al.*, 2013). Our metatranscriptome approach revealed that Oomycetes were ubiquitous, abundant and active members among soil protists, suggesting a significant role as structuring elements of natural plant communities. Unlike in the study of Urich *et al.* (2008), plant parasitic plasmodiophorids were little abundant in this study.

Apicomplexa are common parasites of soil invertebrates and may potentially play a comparable role in structuring soil food webs (Altizer *et al.*, 2003; Field and Michiels, 2005). Similar to a recent DNA-based study (Bates *et al.*, 2013), we found Apicomplexa in all samples. However, we found higher relative abundance in the dry grassland and forest habitats, in contrast to Bates *et al.* (2013), who detected apicomplexan SSU rRNA genes with higher relative abundance in the wet soils. As the detected sequences were derived from RNA, they probably did not originate from encysted apicomplexans (Ruiz *et al.*, 1973), but most likely from parasitized soil invertebrates.

Most ichthyosporean taxa are animal parasites and have been described as inhabitants of aquatic

organisms, but have recently been found as parasites in terrestrial animals (Glockling *et al.*, 2013). We support these recent findings as we detected Ichthyosporea in significant abundances in all habitats studied.

Protist sequences closely resembling potential human pathogens were detected in all soils. Similar to cultivation-based studies (Page, 1988; Geisen *et al.*, 2014b), *Acanthamoeba* spp. were common, some of which might be causative agents of amoebic keratitis and amoebic encephalitis. However, as the SSU rRNA sequences never showed perfect sequence matches with described species and only functional studies on cultivated species allow drawing reliably conclusions on potential pathogenicity, we can only state that these could potentially act as pathogens. Amoebic encephalitis can also be caused by *Balamuthia mandrillaris* and *Naegleria fowleri* (Excavata, Heterolobosea) (Visvesvara *et al.*, 1993; Schuster and Visvesvara, 2004; Visvesvara *et al.*, 2007; Siddiqui and Ahmed Khan, 2012). The finding of related SSU rRNA sequences support recent studies showing the presence of both *B. mandrillaris* (Lares-Jiménez *et al.*, 2014) and *N. fowleri* in soil (Moussa *et al.*, 2015).

Unexpected presence of typically marine and freshwater protists

The surprising finding of several typically aquatic protist groups corroborates the notion that a plethora of soil protist taxa have formerly been missed in both, cultivation- and PCR-primer-based studies. For example, we detected Choanoflagellida in all samples; these protists are typically marine and only a few taxa are known from freshwater systems (Tong *et al.*, 1997; Arndt *et al.*, 2000; Stoupin *et al.*, 2012). Mostly, anecdotic evidence from few cultivation-based studies exists on the existence of the choanoflagellate genera *Monosiga*, *Codosiga* and *Salpingoeca* in soils (Ekelund and Patterson, 1997; Finlay *et al.*, 2000; Ekelund *et al.*, 2001; Tikhonenkov *et al.*, 2012), and only a few molecular soil surveys have reported choanoflagellate SSU rRNA sequences (Lesaulnier *et al.*, 2008; Lara *et al.*, 2011), several of which closely resemble SSU rRNA sequences obtained in this study. However, other sequences, among them our assembled rRNA contigs (Figure 5), more closely resembled sequences obtained in freshwater surveys (Chen *et al.*, 2008; Monchy *et al.*, 2011; Stoupin *et al.*, 2012). As most transcripts showed highest similarity with SSU rRNAs of uncultivated species, the future linkage of sequence information with morphological and functional information on the respective protist species in soil will be essential (Bachy *et al.*, 2013).

Foraminifera are another group of typically marine protists commonly not associated with the soil environment, with *Edaphoallogromia australica* representing the only foraminiferan species reported from soil (Meisterfeld *et al.*, 2001). Our study is the

first to assess their relative abundance among active soil protists. Although Foraminifera appeared to comprise a small fraction of the active protist community, they were diverse and present at all sites. This is supported by a recent targeted DNA survey that detected diverse foraminiferan SSU rRNA genes in 17 out of 20 soils samples (Lejzerowicz *et al.*, 2010). Most sequences and SSU rRNA contigs closely matched the sequences obtained by Lejzerowicz *et al.* (2010), but several non-assembled transcripts more closely resembled the typically marine genera *Astrammmina*, *Bathysiphon* and *Allogromia*.

The presence of rRNA transcripts of Choanoflagellida and Foraminifera in soil has important implications. First, these taxa are genuine autochthonous, active inhabitants of soils and not simply dormant states accidentally dispersed to soil by wind or water. Second, there is a need to cultivate these protists, because this will provide information about their ecological roles, morphology and adaptations to the terrestrial habitat, as well as enable comparative studies with their marine relatives that may provide insights in the evolutionary origin of soil protists.

Conclusions

Our study demonstrates the power of metatranscriptomics for obtaining a census of soil protist communities by circumventing major biases commonly associated with cultivation and molecular studies. Still, significant gaps in the taxonomic information prevail in all soil protist supergroups, especially in Amoebozoa where reliable assignment of several SSU rRNA sequences beyond order or even class level was still impeded. Cultivation-based approaches (for example, Geisen *et al.*, 2014c, d) are necessary to fill these gaps. Furthermore, taxonomic expertise remains a crucial prerequisite to interpret protist SSU rRNA data and is as indispensable as a reliable reference database for the correct assignment of taxa. Taking the high sequence coverage into account, we are confident that our study provides the most detailed and potentially closest picture of the true composition of active protist communities in soils so far.

Conflict of Interest

The authors declare no conflict of interest.

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Author Contributions

TU, SG and MB designed research. TU, AT, MS and IC collected the soil samples. Metatranscriptomes were generated by TU and AT. TU processed metatranscriptome data, analysed by SG and TU. SG and TU generated Amoebozoa-CREST. SG, TU and MB wrote the manuscript, aided by all authors.

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