

ORIGINAL ARTICLE

Tree diversity and species identity effects on soil fungi, protists and animals are context dependent

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Plant species richness and the presence of certain influential species (sampling effect) drive the stability and functionality of ecosystems as well as primary production and biomass of consumers. However, little is known about these floristic effects on richness and community composition of soil biota in forest habitats owing to methodological constraints. We developed a DNA metabarcoding approach to identify the major eukaryote groups directly from soil with roughly species-level resolution. Using this method, we examined the effects of tree diversity and individual tree species on soil microbial biomass and taxonomic richness of soil biota in two experimental study systems in Finland and Estonia and accounted for edaphic variables and spatial autocorrelation. Our analyses revealed that the effects of tree diversity and individual species on soil biota are largely context dependent. Multiple regression and structural equation modelling suggested that biomass, soil pH, nutrients and tree species directly affect richness of different taxonomic groups. The community composition of most soil organisms was strongly correlated due to similar response to environmental predictors rather than causal relationships. On a local scale, soil resources and tree species have stronger effect on diversity of soil biota than tree species richness *per se*.

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Introduction

Plant interactions and feedbacks with soil biota determine ecosystem functioning and primary productivity in terrestrial habitats (Wardle *et al.*, 2004; van der Heijden *et al.*, 2006; Bagchi *et al.*, 2014; Wagg *et al.*, 2014). Soil microorganisms and meiofauna (that is, microfauna and mesofauna) have key roles in nutrient cycling. In particular, fungi act as obligate root symbionts, decomposers or pathogens of other organisms. Soil meiofauna and protists consume living organisms and dead organic material and disperse these degradation products as well as fungal and bacterial propagules in soil (Wardle, 2002; Adl and Gupta, 2006).

Greater taxonomic and functional diversity of plants promotes ecosystem services and enhances stability (Cardinale *et al.*, 2011; Gamfeldt *et al.*, 2013). The plant diversity effects on these functions are more pronounced in stress conditions (Steddel *et al.*, 2012)

and become stronger with time (Reich *et al.*, 2012). Through resource availability and niche differentiation, increase in plant biomass and species richness favours the accumulation of soil microbial and faunal biomass and abundance that accommodate greater number of species. Such bottom-up relationships among diversity of food-web organisms occur both aboveground and belowground and are reflected along the trophic cascades (Scherber *et al.*, 2010; Eisenhauer *et al.*, 2013; but see Porazinska *et al.*, 2003). Recent studies on natural grassland plants showed that plant species richness is positively correlated with that of several major fungal groups on a local scale (Hiiesalu *et al.*, 2014; Pellissier *et al.*, 2014). Richness of free-living protists, meiofauna and saprotrophic fungi may similarly benefit from specialization on different sources of food or substrate for decomposition.

Top-down relationships may also regulate ecosystem functioning. In experimental systems, more diverse communities of arbuscular mycorrhizal fungi promote plant diversity, productivity and nutrient uptake (van der Heijden *et al.*, 2006; Wagg *et al.*, 2011) that could be related to the mediation of interspecific competition (van der Heijden *et al.*, 2003) and

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differential benefits of phylogenetically distantly related fungi (Maherali and Klironomos, 2007). In ectomycorrhizal (EcM) symbiosis, fungal species provide differential benefits to their hosts (van der Heijden and Kuyper, 2003) and more diverse communities are more efficient in the uptake of organic phosphorus (Baxter and Dighton, 2005). Counterintuitively, greater diversity of pathogens may also enhance plant richness by specifically suppressing dominants (Bagchi *et al.*, 2014) and reducing the yield in monospecific agroforestry systems (Cardinale *et al.*, 2011).

In addition to taxonomic and functional richness, certain component species may determine the efficiency of ecosystem processes, a phenomenon termed as (taxonomic) sampling effect (Cardinale *et al.*, 2006, 2011). Many of the pioneering ecological studies failed to separate sampling effect from the diversity effect *per se*, which requires optimizing the experimental design (Huston, 1997; Wardle, 1999; Tedersoo *et al.*, 2014a). Sampling effect can be eliminated or accounted for by (i) comparing species performance in monocultures and polycultures (Wardle, 1999) or (ii) by using model selection or variation partitioning, incorporating component species as dummy variables (Healy *et al.*, 2008; Wagg *et al.*, 2011).

A vast majority of biodiversity studies have recorded short-term effects (but see Reich *et al.*, 2012) and focussed on grassland ecosystems. However, ecosystems naturally dominated by woody plants cover nearly half of the land surface on the Earth. Compared with grassland plants, tree individuals may live for several centuries and they are more widely spaced, creating heterogeneous patches via stem flow and accumulation of root and leaf litter (Nadrowski *et al.*, 2010). Tree species differ substantially in the quality of their litter that determine the chemical composition and microbial biomass directly or indirectly by stimulating earthworm activity (Frouz *et al.*, 2013). Soil and litter quality affect degradation rates and community composition of saprotrophic and EcM fungi (Aponte *et al.*, 2013; Prescott and Grayston, 2013) and meiofauna (Ayres *et al.*, 2009). Tree species richness has usually a neutral (including unimodal relationships) or slightly positive effect on ecosystem processes (Nadrowski *et al.*, 2010). Because of great differences in physiology and ecological properties, tree species drive many of the biochemical and ecological processes in soils (Nadrowski *et al.*, 2010; Gamfeldt *et al.*, 2013). The few available studies so far suggest that tree diversity has a neutral effect on richness of herbs and arthropods on a local scale, but the effects of tree species composition predominate (Vehviläinen *et al.*, 2008; Ampoorter *et al.*, 2014). Plant communities may also correlate with communities of soil organisms such as fungi (Bahram *et al.*, 2012; Peay *et al.*, 2013), but the statistical methods explicitly addressing community-wise relationships and their underlying mechanisms are poorly validated in ecological literature.

Nearly all previous biodiversity studies have used traditional morphology-based identification methods to determine the richness of consumers (but see Hiiesalu *et al.*, 2014; Pellissier *et al.*, 2014). This approach requires substantial taxonomic expertise and long processing time given the large number of samples and individuals (Scherber *et al.*, 2010). Many microscopic taxa are comprised of cryptic species that potentially exhibit different ecological requirements, but they remain undetected owing to the paucity of taxonomically informative morphological character states. The alternative DNA-based tools have been developed and increasingly used for identification of bacteria, protists and fungi since two decades ago. More recently, the massively parallel DNA metabarcoding technology has been adopted for large-scale community-level identification of fungi (Jumpponen and Jones, 2009), protists (Chariton *et al.*, 2010; Medinger *et al.*, 2010) and animals (Porazinska *et al.*, 2009). For meiofauna, metabarcoding studies have focussed on specific order to phylum-level groups such as nematodes or certain arthropods (Porazinska *et al.*, 2009; Hajibabaei *et al.*, 2011). The cytochrome I oxidase gene, the standard barcode for animals, has proven to be suboptimal for metabarcoding analyses owing to problems with primer coverage and large DNA insertions in certain taxa (for example, Creer *et al.*, 2010; de Wit and Erseus, 2010; Deagle *et al.*, 2014; Zhan *et al.*, 2014). It has been outlined that multiple taxonomic groups should be addressed simultaneously for better documenting their relative abundance (Soininen *et al.*, 2013) and understanding of ecological and biogeographic processes (Coleman, 2009; Soininen, 2014). For these reasons, the small subunit (SSU) of ribosomal DNA has been targeted following traditions in microbiology and kingdom-level phylogenetics (Bik *et al.*, 2012). However, there are multiple primer mismatches and/or this marker is too conservative for species-level resolution in nearly all groups of protists, fungi, plants and animals (Pawlowski *et al.*, 2012; Schoch *et al.*, 2012; Tang *et al.*, 2012; Bachy *et al.*, 2013; Lindahl *et al.*, 2013). As an alternative to these markers, the internal transcribed spacer 2 (ITS2) has been proposed as a common species-level metabarcoding marker in eukaryotes, although taxonomic groups differ somewhat in length and there is some intraindividual variation inherent to all nuclear markers (Coleman, 2009; Koetschan *et al.*, 2010; Yao *et al.*, 2010; Bengtsson-Palme *et al.*, 2013; Wang *et al.*, 2015). The ITS2 marker has been successfully used to target fungi (Clemmensen *et al.*, 2013), various protist groups (for example, Arif *et al.*, 2014) and plants (De Barba *et al.*, 2014) in metabarcoding studies. Although a large number of animal ITS sequences have been deposited in public databases, this region has been hitherto overlooked in the DNA metabarcoding of meiofauna.

In this study, we first describe the development of a DNA metabarcoding method for identification of

multiple eukaryotic organisms simultaneously at species-level resolution. We constructed multiple taxon-targeted primers for the ITS2 region in single PCR reactions to maintain ribosomal DNA-based proportions of organisms. By using the metabarcoding analysis of DNA extracted from pools of thousands of soil cores, we disentangled the relative roles of tree diversity, confounding sampling effects as well as spatial and edaphic variables on taxonomic richness and community composition of soil fungi, protists and meiofauna. We postulated the following alternative hypotheses: (1) tree diversity *per se* and taxonomic sampling effect influence microbial biomass and richness of soil biota; (2) the effect of these biotic variables is relatively stronger in biotrophic organisms compared with saprotrophs and trophically directly unrelated organisms; (3) vegetation has both direct effects, and indirect effects through altered soil chemistry and microbial biomass, on richness of soil biota; and (4) communities of soil biota shift in concordance mainly owing to similar responses to the environment.

Materials and methods

Experimental design and sampling

We selected two forest diversity experiments in Satakunta, Finland (61° N; 22° E) and Järvselja, Estonia (58° N; 27° E) to test our hypotheses. The Finnish experiment was established across three sites in a clear-cut boreal forest in 1999. We selected sites 1 and 3 for sampling, because these were the least damaged by moose (Ampoorter *et al.*, 2014). At the time of sampling, trees had reached a height of 5–11 m and formed a closed canopy in most of the plots. The soils are podzols with a silty or sandy texture on granite bedrock. Seedlings of *Pinus sylvestris* L., *Picea abies* (L.) H. Karst., *Larix sibirica* Ledeb., *Betula pendula* Roth. and *Alnus glutinosa* (L.) Gaertn. were planted as monocultures or equal combinations of two, three or five species in 400-m² square plots (Scherer-Lorenzen *et al.*, 2006). To avoid edge effects, we restricted our sampling to 300 m² in the centre of each plot by excluding the outermost row of trees.

Vegetation at the Estonian study system constitutes a remnant of a large-scale forest experiment established in early 1920 s on clear-cut forested land. The soils are formed on postglacial alluvial deposits and exhibit loamy or sandy texture. Certain forest quadrats were planted with trees, whereas others were left for natural regeneration. At the sapling stage, trees were selectively thinned and forest quadrats were deeply drained to stimulate tree growth and prevent waterlogging. In the second half of the twentieth century, intensity of management declined and forest development was subjected to natural succession that was affected by sporadic selective cutting and differential moisture regime owing to degradation of the ditch network.

The combination of these treatments and processes resulted in the development of vegetation with different dominant trees (*P. abies*, *P. sylvestris*, *B. pendula*, *A. glutinosa*, *Tilia cordata* Mill. or *Populus tremula* L.) and a range in tree richness (2–11 species; other subdominant EcM trees *Corylus avellana* L., *Quercus robur* L., *Salix caprea* L. and arbuscular mycorrhizal hosts *Ulmus glabra* Huds., *Fraxinus excelsior* L., *Acer platanooides* L. and *Sorbus aucuparia* L.). Because the original quadrats were of unequal size and shape, we established round 2500-m² plots in uniform patches of vegetation. For mature forests, greater plot size represents better the edaphic and floristic processes and the interacting biota (Bruehlheide *et al.*, 2014).

In each plot, we determined the basal area (BA) of all tree species and coverage of understorey vascular plant species. In Finnish plots, we estimated the relative amount of birch coppice (cut in spring, 2010) in 10 abundance classes based on the number and size of stumps. For Estonian plots, we obtained additional information about productivity, volume and height of trees from the State Forest Management Centre (www.rmk.ee).

In summer 2011, we collected samples from 43 Finnish plots (spread over two sites 10 km distant, each roughly 4 ha) and 41 Estonian (spread evenly across 1000 ha) plots. In Finland, we randomly selected 40 trees per plot to equally represent the composition of planted species. At ca. 0.5 m distance from the trunk of each tree individual, we collected a single soil core by hammering a PVC tube (5 cm diameter) to 5 cm depth. In Estonia, we similarly sampled 40 soil cores per plot, but we collected each pair of cores 1–1.5 m distant from each of 20 randomly selected trees (> 10 cm diameter at breast height) located at least 8 m distant from each other to account for spatial autocorrelation range in soil biota (Bahram *et al.*, 2013). For Finnish and Estonian study areas, information about plant species composition and other metadata is given in Supplementary Table S1, and Supplementary Data S1 and S2.

In both study areas, the cores nearly always comprised both the organic layer and top mineral soil and included roots. Although deep soil may comprise some unique organisms adapted to anoxic conditions and low nutrients, our sampling was limited to topsoil, because >50% of microbial biomass and its biological activity occurs in the topmost organic soil (Serna-Chavez *et al.*, 2013) and deeper sampling was impossible in Finnish soils owing to great abundance of rocks. All 40 soil cores per plot were pooled, thoroughly mixed and air-dried at 30–40 °C for 24 h. Drying was selected as an alternative to deep freezing or fresh extraction because of improved options for pulverization of large amounts of soil and necessity to standardize extractable material on a dry weight basis. Dried soil was stored air-tight in zip-lock plastic bags and ground into fine powder by heavy rubbing of the zip-lock bags followed by bead beating using 3-mm

tungsten carbide balls in Mixer Mill MM400 (Retsch GmbH, Haan, Germany) at 30 Hz for 10 min for subsequent soil nutrient and molecular identification analyses.

Soil nutrients, phospholipid fatty acids and ergosterol
Concentrations of C, N, ^{13}C and ^{15}N were measured from 2 to 70 mg of soil using an elemental analyser (Eurovector, Milan, Italy) coupled with an isotope ratio mass spectrometer (MAT 253; Thermo Electron, Bremen, Germany) according to Tedersoo *et al.* (2012). Total phosphorus was extracted using ammonium lactate and determined using flow injection analysis. Potassium concentration was determined from the same extract by the flame photometric method (AOAC956.01). Exchangeable magnesium and calcium content were determined in ammonium acetate extract (pH = 7.0).

Bacterial biomass was assessed using the phospholipid fatty acid analysis for which the samples were extracted with a mixture of chloroform–methanol–phosphate buffer (1:2:0.8; V/V) according to Bligh and Dyer (1959). Phospholipids were separated using solid-phase extraction cartridges LiChrolut Si60 (Merck, Whitehouse Station, NJ, USA), and the samples were subjected to mild alkaline methanolysis (Šnajdr *et al.*, 2008). The samples were analysed with gas chromatography–mass spectrometry (450-GC, 240-MS; Varian, Palo Alto, CA, USA). Methylated fatty acids were identified according to their mass spectra using a mixture of chemical standards (Sigma, St Louis, MO, USA). Actinobacterial biomass was estimated as the sum of 10Me-16:0, 10Me-17:0 and 10Me-18:0. Total bacterial biomass was determined on the basis of i14:0, i15:0, a15:0, i16:0, i17:0, a17:0, 16:1 ω 7, 18:1 ω 7, cy17:0, cy19:0, 16:1 ω 5, 10Me-17:0, 10Me-18:0 and 10Me-16:0 (Šnajdr *et al.*, 2011).

Fungal biomass was estimated based on ergosterol concentration. Total ergosterol was extracted and analysed as described previously (Šnajdr *et al.*, 2008). Samples (0.5 g) were sonicated with 3 ml 10% KOH in methanol at 70 °C for 90 min. Distilled water (1 ml) was added and the samples were extracted three times with 2 ml cyclohexane, evaporated under nitrogen, redissolved in methanol and analysed isocratically using an high performance liquid chromatography system with methanol as a mobile phase at a flow rate of 1 ml min⁻¹. Ergosterol was quantified by ultraviolet detection at 282 nm. Saprotroph and EcM fungal biomass was calculated based on the proportion of sequences corresponding to each functional group, assuming that these two groups have equal ergosterol-to-ribosomal DNA ratio on average (Štursova *et al.*, 2014).

Molecular analyses

DNA was extracted from 2.0 g of soil per sample using the PowerMax Soil DNA Isolation Kit (MoBio,

Carlsbad, CA, USA) according to the manufacturer's protocols. PCR was performed using a mixture of 11 forward primers (ITS3tagmix1-11 in equimolar concentration) analogous to ITS3 and a degenerate reverse primer ITS4ngs analogous to ITS4 (the original primers are described in White *et al.*, 1990; Tedersoo *et al.*, 2014b, 2015a). Both primers were shortened and modified to perfectly match >99.5% of all Fungi (except Tulasnellaceae and Microsporidia; Supplementary Table S2). The ITS3 primer mixes were designed to cover Cercozoa protists (amoebae from Rhizaria superkingdom), Ciliophora protists (Alveolata superkingdom), Chlorophyta (unicellular algae from Viridiplantae superkingdom), as well as soil animals (Acari, Nematoda, Collembola, Rotifera and Annelida (Metazoa)). Based on a wide range of studies, these groups are the most abundant and species-rich eukaryote taxa in soil. For primer design, we downloaded available sequences from the International Nucleotide Sequence Data-bases Consortium (INSDC) and aligned the conserved 5.8S and large subunit (LSU) regions by classes or phyla by using MAFFT ver. 7 (Katoh and Standley, 2013). The primer annealing sites for ITS3 and ITS4 were visually examined to distinguish true mismatches from low-quality sequences and mitochondrial LSU sequences. We further checked primer matching by running BLASTn searches against targeted organisms in INSDC, setting the number of comparisons greater than the number of species available for that taxonomic group. The ITS4ngs primer was tagged with one of the 110 identifier barcodes (10–12 bases) that were modified from those recommended by Roche (Basel, Switzerland) to differ by >3 bases, to start only with adenosine and to comprise the proportion of adenosine and thymidine between 0.3 and 0.7 to equalize their affinities in an adapter ligation step. The PCR cocktail comprised 0.6 μl DNA, 0.5 μl each of the primers (20 μM), 5 μl 5 \times HOT FIREPol Blend Master Mix (Solis Biodyne, Tartu, Estonia) and 13.4 μl double-distilled water. PCR was carried out in four replicates in the following thermocycling conditions: an initial 15 min at 95 °C, followed by 30 cycles of 95 °C for 30 s, 55 °C for 30 s, 72 °C for 1 min, and a final cycle of 10 min at 72 °C. PCR products (typically 350–400 bp) were pooled and their relative quantity was estimated by running 2 μl DNA on 1% agarose gel for 15 min. DNA samples yielding no visible band or a strong band were re-amplified using 35 and 25 cycles instead. We also used negative (for DNA extraction and PCR) and positive controls (*Hydnoplicata whiteii* specimen MURU5860) throughout the experiment. Amplicons were purified by use of exonuclease and Shrimp alkaline phosphatase enzymes (Fermantas, Kaunas, Lithuania) at 37 °C for 45 min and at 85 °C for 15 min. Purified amplicons were subjected to normalization of quantity by use of SequalPrep Normalization Plate Kit (Invitrogen, Carlsbad, CA, USA) following the manufacturer's instructions. Normalized amplicons

were divided into two pools that were each subjected to 454 adaptor ligation, emulsion PCR and 454 pyrosequencing using the GS-FLX+ technology and Titanium chemistry as implemented in Beckman Coulter Genomics (Danvers, MA, USA).

Pyrosequencing resulted in 625 074 reads with a median length of 412 bases. By use of Acacia 1.52 (Bragg *et al.*, 2012), these sequences were re-assigned to samples based on the barcodes, and quality trimmed (options: minimum average quality threshold = 30, maximum k-mer distance = 13; homopolymer significance threshold = -2) to exclude short and low-quality sequences. The resulting 564 305 sequences were subjected to removal of the flanking 5.8S and 28S rRNA genes for better resolution in clustering of ITS sequences and removal of chimeric sequences by use of the ITSx software (Bengtsson-Palme *et al.*, 2013). We retained sequences of > 99 bp in length to remove most of the partial sequences. We ran a second round of chimera checking using UCHIME (Edgar *et al.*, 2011). After these quality-filtering steps, the 401 762 retained sequences were further clustered at 98.0% sequence similarity as implemented in CD-Hit 4.6.1 (Fu *et al.*, 2012). Compared with the routinely used 97%, this threshold is a better proxy at species level in several groups of fungi (Kõljalg *et al.*, 2013), protists (Litaker *et al.*, 2007) and animals (Noge *et al.*, 2005). Of 16 437 clusters, 6823 (41.5%) were represented by a single sequence. These singletons were removed from further analyses, because these comprise a high proportion of technical artefacts (Tedersoo *et al.*, 2010). The longest sequence of each remaining 9614 clusters was selected as a representative for BLASTn sequence similarity search (word size = 7; penalties: gap = -1; gap extension = -2; match = 1) against the INSDC and UNITE (Abarenkov *et al.*, 2010a) databases. In addition, we ran BLASTn searches against reference sequences of fungi in 99.0% similarity species hypotheses that include third-party taxonomic and metadata updates (Kõljalg *et al.*, 2013) as implemented in the PlutoF workbench (Abarenkov *et al.*, 2010b). For each query, we considered 10 best-matching references to annotate taxa as accurately as possible. If no taxonomy was reliably revealed, we ran manual BLASTn searches against INSDC with 500 best-matching sequences as output. We followed the regularly updated INSDC and Index Fungorum (www.indexfungorum.org) for higher-level taxonomy of eukaryotes and up to class-level taxonomy of fungi, respectively. We assigned each fungal genus, family or order to functional categories. If different lifestyles were present in specific genera, we chose the dominant group (>75% of species assigned to a specific category) or considered its ecology unknown (<75%). Taxa were considered to be EcM if they best matched to any sequences belonging to EcM lineages (Tedersoo and Smith, 2013) and exhibited sequence length/blast scores above predetermined lineage-specific thresholds. Targeted groups of protists and soil animals were

too poorly represented in INSDC to allow reliable trophic categorization. We selected 98.0% sequence similarity to represent roughly species-level discrimination of operational taxonomic units (OTUs) in all taxa based on *post-hoc* determination of optimal metabarcoding thresholds (Põlme *et al.*, 2014; Tedersoo *et al.*, 2014c). Only for Collembola, we re-clustered all sequences at 94.0% sequence similarity, because this level distinguishes better among species (Anslan and Tedersoo, 2015).

Statistical analyses

We chose to analyse richness and community composition in groups that were represented by >50 OTUs (Cercozoa, Ciliophora, Chlorophyta, Collembola, Nematoda as well as EcM, saprotrophic, plant pathogenic fungi). For richness analyses of soil biota, we calculated the residuals of OTU richness in relation to square root of the number of obtained sequences to account for differences in sequencing depth. We excluded two outlier samples from Finland and four outliers from Estonia that were dominated by a few species of moulds (relative abundance of sequences belonging to Trichocomaceae >5%, Mortierellaceae >20% or Mucoraceae >20%, that exceeds three times the mean+3 s.d.), which is indicative of substandard sample preservation (Tedersoo *et al.*, 2014b). By use of vegan package of R, 'individual'-based rarefied OTU accumulation curves were constructed separately for functional groups of fungi and major taxa of animals and protists in the two study systems (Supplementary Figure S1).

Concentrations of soil nutrients and vegetation measurements were logarithm-transformed prior to analyses to improve the distribution of residuals and reduce non-linearity. To estimate taxonomic sampling effects, the relative BA of each tree species was log-ratio transformed (Szava-Kovats *et al.*, 2011). Besides species richness, we calculated both Shannon and Simpson indices of diversity for trees and understorey vascular plants (Magurran, 1988). To account for spatial autocorrelation that may arise from both spatially structured environmental factors and dispersal limitation, we calculated Principal Components of Neighbours Matrices (PCNM) spatial eigenvectors based on geographical coordinates of plots by using the vegan and packfor packages of R (R Core Development Team, 2014). These vectors represent spatial variation at different geographical scales over the study area and are used to control for spatial autocorrelation in ecological data sets (Legendre, 2008). To disentangle the effects of edaphic, floristic and spatial variables on residual richness of soil biota and biomass estimates, individual variables were subjected to multiple regression model selection based on the corrected Akaike information criterion. The components of best models were forward-selected to determine their

adjusted coefficients of determination as implemented in the packfor package of R.

We used Structural Equation Models (SEM) to determine the direct and indirect paths between environmental predictors, biomass and richness of EcM fungi and saprotrophs. We also included bacterial biomass in these models for comparison. The initial SEM models were constructed based on the best models for these variables using Amos ver. 22 (SPSS, Chicago, IL, USA). We tested all direct and indirect relations among exogenous and endogenous variables, together with their error terms. Then the fit of models was maximized based on both chi-square test and root mean square error of approximation and Comparative Fit Index. We followed a backward stepwise elimination approach to remove non-significant links to maximize model fit.

The relative effects of edaphic, spatial and floristic variables on communities of soil organisms were determined based on Hellinger dissimilarity, exclusion of OTUs occurring in a single sample and a multivariate model selection procedure as implemented in DISTLM function of Permanova+ (Anderson, 2005). To obtain coefficients of determination (cumulative R^2_{adjusted}) and statistics (F_{pseudo}) for each variable, the components of best models were forward selected. We prepared Global Non-metric Multidimensional Scaling graphs in parallel, using the same options. Significant variables were fitted into the ordination space using the envfit function in the vegan package of R.

To test the correlation in community composition among soil biota, trees and herbs, we calculated the bidirectional Procrustes correlation coefficient using 4999 permutations as implemented in protest function in the vegan package of R. False discovery rate associated with multiple testing was reduced using the sharpened false discovery rate procedure (Benjamini and Hochberg, 2000). To test whether intimately associated communities display more similar beta diversity and to recover any sampling biases (size of matrices, connectance), we added the relatively small communities of trees, herbs and fungal subgroups belonging to mycoparasites, flagellates (Chytridiomycota) and white rot decomposers to the correlation matrices. The effects of association intimacy as well as the size of matrices and connectance on $R_{\text{Procrustes}}$ were tested using multiple regression analyses separately for Estonian and Finnish data sets. To further test whether the correlations among communities are potentially causal or related to the shared driving mechanisms of environmental variables, we calculated partial Procrustes association metrics accounting for the environmental and spatial predictors (Lisboa *et al.*, 2014).

Variation partitioning analyses were conducted on standardized biomass and OTU richness data and Hellinger-transformed community data using the packfor and vegan packages of R. Because of the limits of variation partitioning, we generated four components of variance, including richness (tree and

understorey richness and Shannon index), sampling effect (log ratio-transformed proportions of tree species), other floristic as well as edaphic characters (total BA, tree volume, productivity, herb and ericoid cover, soil pH and nutrients) and space (PCNM vectors). By using one-way analyses of variance, we further tested whether the groups of different mobility (mobile: actively moving organisms excluding amoeboid groups), body size (average cell diameter and organism diameter) and trophic strategies (biotrophic and non-biotrophic) exhibit significant differences in the relative importance of tree richness, individual tree species and space.

Results

Identification of soil biota

The metabarcoding approach enabled us to recover all targeted groups of eukaryotes from composite soil samples and identify them at different taxonomic levels (Supplementary Data S1). Across study systems, kingdom-level assignment of 1.0% of the recovered sequences and 3.9% OTUs remained unknown. Sequences and OTUs (98% similarity threshold) assigned to Fungi (81.1% of taxa), Alveolata (4.8%, mostly Ciliophora), Metazoa (4.8%, mostly Nematoda and Collembola) and Viridiplantae (4.0%, mostly Tracheophyta, Bryophyta and Chlorophyta) dominated among the soil eukaryote kingdoms both in Finland and Estonia (Figure 1). Saprotrophs, EcM mutualists and plant pathogens comprised 47.5, 17.7 and 3.5% of all fungal OTUs, respectively. The higher-level taxonomic distribution of soil organisms was remarkably similar in Finnish and Estonian samples (Figure 1). One of the negative controls produced two fungal sequences, whereas the two positive controls yielded six different fungal and oomycete sequences in addition to *H. whiteii*.

Richness and biomass

Tree species richness was positively correlated with richness of soil fungal groups in Estonia and EcM fungi in Finland, but it was poorly correlated with richness of protists and meiofauna (Supplementary Figure S2). Taxonomic sampling effect of plants and edaphic variables were usually among the best predictors of belowground richness depending on organisms and study systems (Figures 2 and 3; Supplementary Figure S3; Supplementary Table S3). Richness of all fungi was most strongly affected by herb cover (positive effect: $F_{1,35} = 17.30$; $R^2_{\text{adj}} = 0.289$; $P = 0.001$) and tree BA (negative effect: $F_{1,35} = 17.30$; $R^2_{\text{adj,partial}} = 0.108$; $P = 0.007$) in Finland. In Estonia, *P. sylvestris* BA ($F_{1,32} = 63.29$; $R^2_{\text{adj}} = 0.644$; $P < 0.001$) and tree species richness ($F_{1,32} = 25.21$; $R^2_{\text{adj,partial}} = 0.149$; $P < 0.001$), respectively, had a negative and positive effect on fungal richness. Richness of EcM fungi was negatively

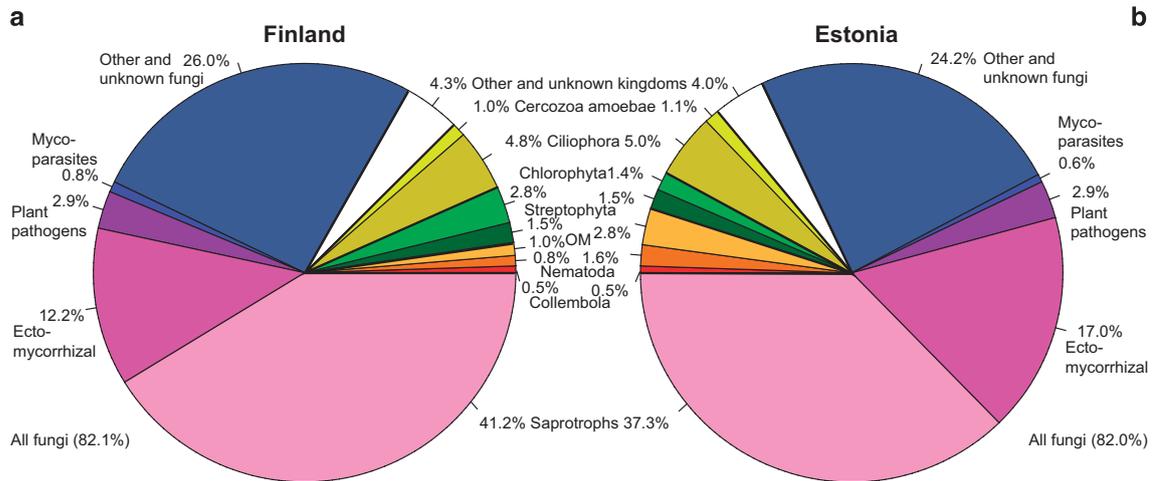


Figure 1 Proportion of 98% sequence similarity-level OTUs belonging to the fungal, protist and animal groups in (a) Finland and (b) Estonia. OM, other Metazoa.

affected by *A. glutinosa* BA ($F_{1,34} = 14.60$; $R^2_{\text{adj}} = 0.289$; $P = 0.003$) but positively by increasing soil pH ($F_{1,34} = 16.98$; $R^2_{\text{adj,partial}} = 0.217$; $P = 0.001$) and tree diversity (Shannon index: $F_{1,34} = 13.05$; $R^2_{\text{adj,partial}} = 0.127$; $P = 0.002$) in Finland. In Estonia, BA of *P. sylvestris* ($F_{1,32} = 40.28$; $R^2_{\text{adj}} = 0.522$; $P < 0.001$) and BA of *A. glutinosa* ($F_{1,32} = 11.35$; $R^2_{\text{adj,partial}} = 0.109$; $P < 0.003$) had a strong negative effect on EcM fungal richness, explaining 63.1% of variation, but there was no significant tree diversity effect. Herb cover enhanced ($F_{1,34} = 30.16$; $R^2_{\text{adj}} = 0.422$; $P < 0.001$), but increasing C/N ratio reduced ($F_{1,34} = 10.61$; $R^2_{\text{adj,partial}} = 0.114$; $P = 0.002$), plant pathogen richness in Finland. Similarly, soil C/N ratio had a strong negative effect on plant pathogen richness in Estonia ($F_{1,30} = 40.28$; $R^2_{\text{adj}} = 0.627$; $P < 0.001$). Richness of saprotrophic fungi was negatively influenced by total BA of trees ($F_{1,35} = 18.25$; $R^2_{\text{adj}} = 0.301$; $P = 0.001$) and BA of *P. abies* ($F_{1,35} = 9.94$; $R^2_{\text{adj,partial}} = 0.117$; $P = 0.004$) in Finland. In Estonia, however, tree species richness *per se* had a strong positive effect on saprotroph richness ($F_{1,32} = 25.60$; $R^2_{\text{adj}} = 0.406$; $P < 0.001$).

Richness of the Cercozoa amoebae was most strongly enhanced by herb cover ($F_{1,34} = 8.72$; $R^2_{\text{adj}} = 0.162$; $P = 0.006$) and soil pH ($F_{1,34} = 9.46$; $R^2_{\text{adj,partial}} = 0.149$; $P = 0.010$) in Finland but negatively affected by C/N ratio ($F_{1,33} = 17.75$; $R^2_{\text{adj}} = 0.318$; $P = 0.001$) and soil Ca concentration ($F_{1,33} = 17.75$; $R^2_{\text{adj,partial}} = 0.151$; $P = 0.003$) in Estonia. Chlorophyta richness was reduced by increasing total tree BA in Finland ($F_{1,37} = 21.12$; $R^2_{\text{adj}} = 0.335$; $P < 0.001$) but promoted by *A. glutinosa* BA in Estonia ($F_{1,31} = 5.41$; $R^2_{\text{adj}} = 0.109$; $P = 0.022$). Ciliophora richness was favoured by the relative amount of cut birch coppice ($F_{1,35} = 32.57$; $R^2_{\text{adj}} = 0.441$; $P < 0.001$) and understorey richness ($F_{1,35} = 12.05$; $R^2_{\text{adj,partial}} = 0.123$; $P = 0.004$) in Finland but by soil Ca concentration in Estonia ($F_{1,31} = 52.90$; $R^2_{\text{adj}} = 0.590$; $P < 0.001$).

Of soil animals, the richness of Collembola was affected by soil C/N ratio ($F_{1,37} = 9.93$; $R^2_{\text{adj}} = 0.182$; $P = 0.002$) and spatial eigenvectors in Finland ($F_{2,37} = 17.34$; $R^2_{\text{adj,partial}} = 0.250$; $P = 0.001$) but driven only by spatial variables in Estonia ($F_{2,34} = 15.17$; $R^2_{\text{adj,cumul}} = 0.288$; $P = 0.001$). Nematoda richness responded positively to *L. sibirica* BA in Finland ($F_{1,38} = 9.93$; $R^2_{\text{adj}} = 0.072$; $P = 0.047$), whereas soil C/N ratio had a negative effect on roundworms in Estonia ($F_{1,34} = 9.64$; $R^2_{\text{adj}} = 0.196$; $P = 0.003$).

Although the Estonian and Finnish soils differed considerably in nutrient concentrations (Supplementary Figure S4), the biomass of microbial groups in both study systems was positively related to soil macronutrients (Figure 2). Model selection indicated that the total microbial biomass and bacterial biomass were positively influenced by soil P concentration both in Finland and Estonia (Supplementary Table S3). The biomass of Actinobacteria increased with soil P concentration in Finland ($F_{1,38} = 45.55$; $R^2_{\text{adj}} = 0.527$; $P < 0.001$), but it responded positively to increasing proportion of *A. glutinosa* BA ($F_{1,33} = 14.43$; $R^2_{\text{adj}} = 0.272$; $P = 0.001$) and soil Ca concentration ($F_{1,33} = 8.84$; $R^2_{\text{adj,partial}} = 0.133$; $P = 0.011$) in Estonia. Fungal biomass, including that of saprotrophs and EcM fungi, was largely determined by N concentration in both study systems. The ratio of saprotrophs to EcM symbionts increased with the relative BA of *A. glutinosa* in both systems (Supplementary Table S3). In addition, soil Ca concentration negatively affected the relative proportion of saprotrophs in Estonia ($F_{1,33} = 14.85$; $R^2_{\text{adj,partial}} = 0.254$; $P = 0.001$).

Structural equation modelling revealed that site (PCNM1) had a strong effect on soil pH, N and P concentrations in Finland (Figure 4a). All these variables as well as tree diversity (Shannon index) had a direct positive effect on EcM fungal richness, whereas *A. glutinosa* BA had a direct negative effect on both EcM fungal biomass and richness. Soil

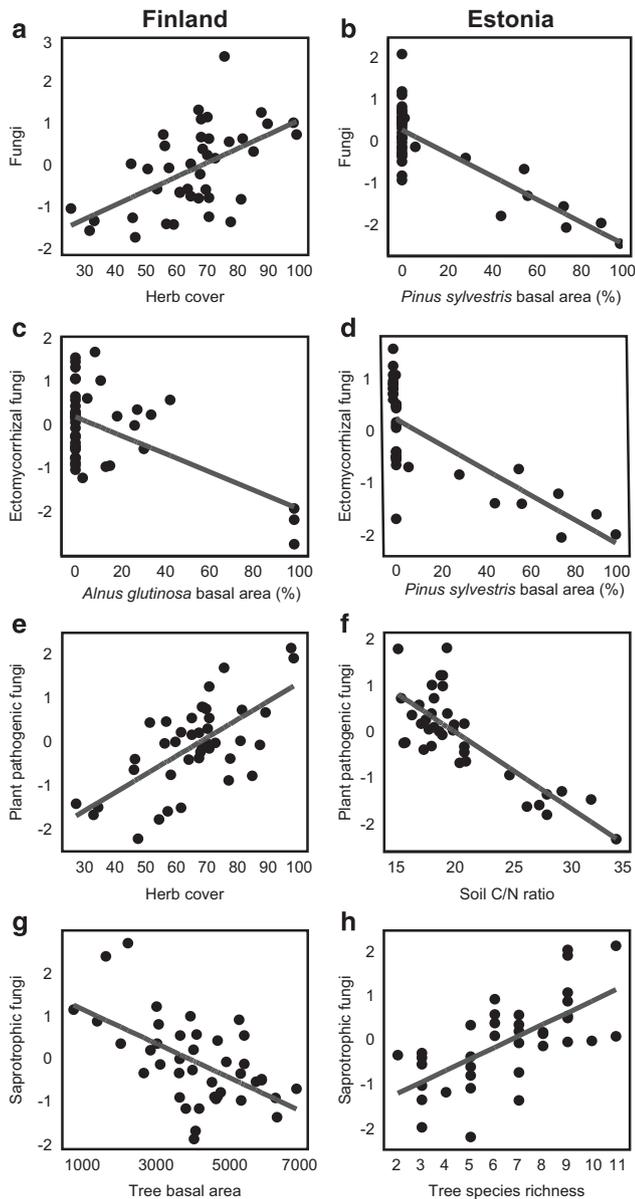


Figure 2 Linear regressions between the standardized residuals of richness of soil fungi and the strongest predictors as revealed from the best multiple regression models (Supplementary Table S2): (a, b) all fungi; (c, d) EcM fungi; (e, f) plant pathogens; (g, h) saprotrophs.

nitrogen concentration and total BA had, respectively, a direct positive and negative effect on the richness of saprotrophs. Saprotroph biomass positively influenced saprotroph richness and EcM fungal biomass, but the opposite paths were of minor importance ($P > 0.1$). Similarly for the Estonian data set, SEM largely confirmed the results of model selection, emphasizing the direct positive effect of tree richness and EcM fungal biomass but negative effects of *A. glutinosa* and *P. sylvestris* BAs on EcM fungal richness (Figure 4b). According to SEM, EcM fungal biomass and richness had strong positive

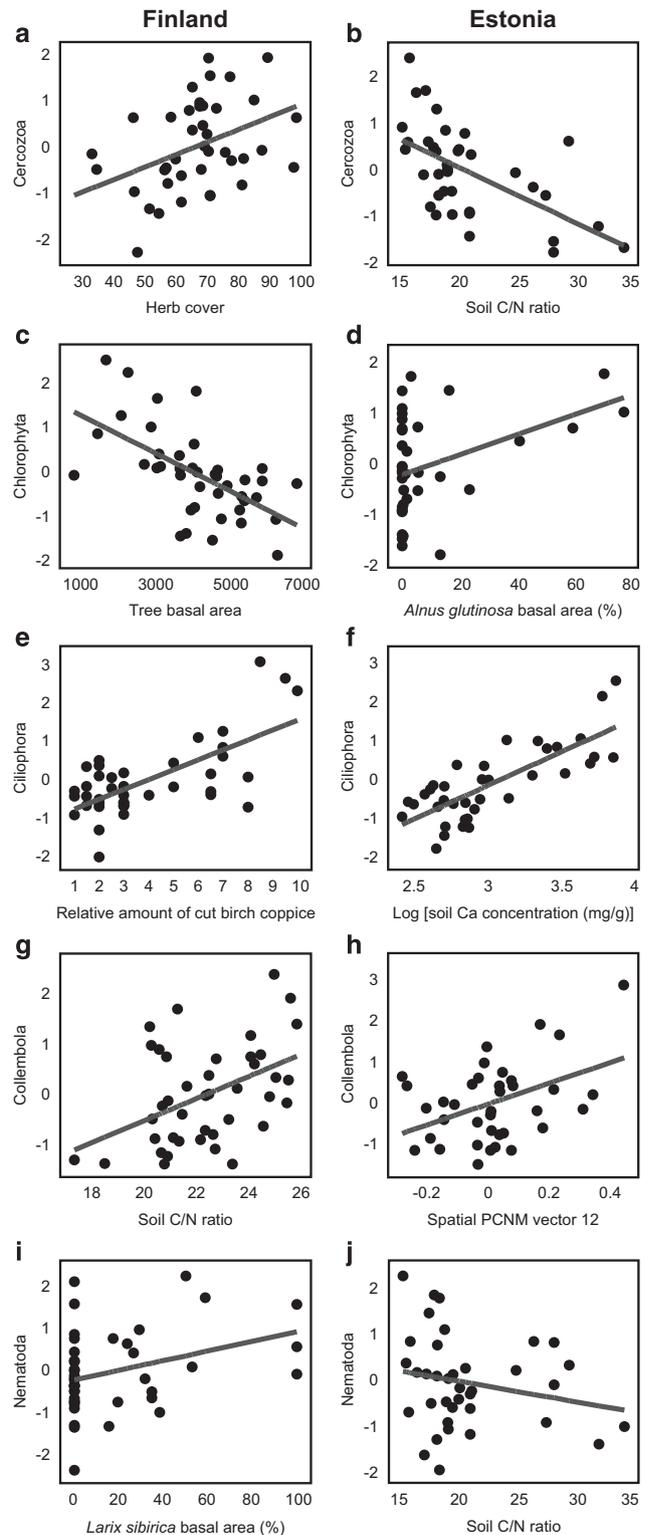


Figure 3 Linear regressions between the standardized residuals of richness of soil protists or animals and the strongest predictors as revealed from the best multiple regression models (Supplementary Table S2): (a, b) Cercozoa; (c, d) Chlorophyta; (e, f) Ciliophora; (g, h) Collembola; (i, j) Nematoda.

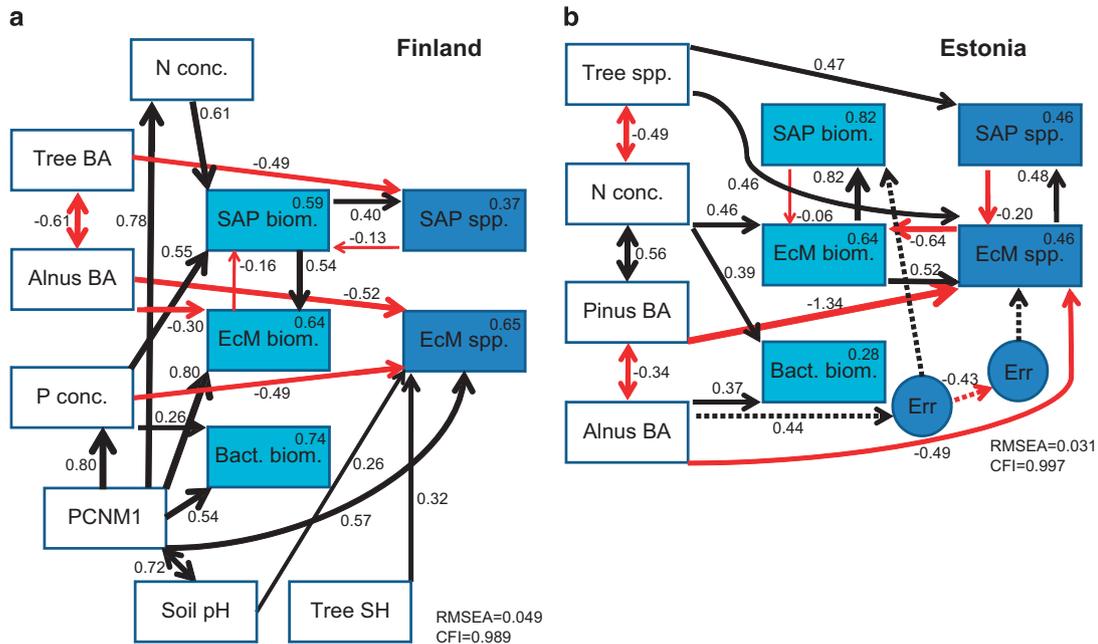


Figure 4 Structural equation models demonstrating the direct and indirect effects of spatial, environmental and floristic variables on biomass and species richness of EcM and saprotrophic fungi in (a) Finland and (b) Estonia. Black and red arrows indicate positive and negative relationships, respectively. Dashed arrows indicate connections through error terms (Err). Numbers above arrows indicate standardized path coefficients. Numbers above variables indicate proportion of variation explained. SH, Shannon diversity index.

effects on saprotroph biomass and richness, respectively.

The variation partitioning analysis was generally consistent with model selection (Supplementary Table S4; Supplementary Figure S3). There were no general differences in the relative strength of tree diversity or individual species effects on organisms with different mobility, body size or biotrophic associations ($P > 0.2$). Variation partitioning analysis ascribed much of the environmental variation to a shared effect among space, soil and vegetation (Supplementary Table S4), confirming the SEM results that much of the floristic effects are spatially and edaphically structured. Across all data sets, the effect of space was significantly greater in Finland than in Estonia ($F_{1,42} = 7.90$; $P = 0.007$). This could be ascribed to the arrangement of plots in two distinct blocks (sites) in Finland as opposed to a more uniform plot distribution in Estonia. Furthermore, the Estonian experiment was subjected to natural regeneration that may have been influenced spatially structured soil parameters.

Community composition

Communities of soil biota were generally driven by spatial vectors and soil variables in Finland and Estonia, respectively (Supplementary Table S5; Figures 5 and 6). According to the best multivariate model, the total fungal community was driven by spatial variation in Finland ($F_{1,37} = 8.09$; $R^2_{\text{adj}} = 0.151$; $P < 0.001$) but by soil C/N ratio ($F_{1,33} = 7.08$; $R^2_{\text{adj}} = 0.144$; $P < 0.001$) and Ca concentration ($F_{1,33} = 3.90$; $R^2_{\text{adj,partial}} = 0.086$; $P = 0.001$) in Estonia. The

community composition of EcM fungi was mostly affected by spatial structure ($F_{1,36} = 4.31$; $R^2_{\text{adj}} = 0.076$; $P = 0.001$) and BA of *B. pendula* ($F_{1,36} = 4.37$; $R^2_{\text{adj,partial}} = 0.073$; $P = 0.001$) in Finland. In Estonia, the EcM fungal community was mostly affected by the cover of Ericaceae ($F_{1,33} = 5.44$; $R^2_{\text{adj,partial}} = 0.110$; $P < 0.001$). The community structure of plant pathogens was driven by spatial variation ($F_{1,38} = 4.10$; $R^2_{\text{adj,partial}} = 0.072$; $P = 0.001$) in Finland. Pathogen community was most strongly influenced by soil N ($F_{1,34} = 5.37$; $R^2_{\text{adj}} = 0.108$; $P < 0.001$) and Ca ($F_{1,34} = 3.87$; $R^2_{\text{adj,partial}} = 0.068$; $P = 0.001$) concentration in Estonia. Finnish saprotroph communities were primarily affected by spatial distance ($F_{1,38} = 11.47$; $R^2_{\text{adj}} = 0.207$; $P < 0.001$), whereas Estonian saprotroph communities were influenced by soil C/N ratio ($F_{1,33} = 8.96$; $R^2_{\text{adj,partial}} = 0.181$; $P < 0.001$), N concentration ($F_{1,33} = 4.20$; $R^2_{\text{adj,partial}} = 0.069$; $P = 0.001$) and pH ($F_{1,33} = 4.12$; $R^2_{\text{adj,partial}} = 0.063$; $P = 0.001$).

In protists, community composition of Cercozoa was strongly influenced by soil pH both in Finland ($F_{1,39} = 3.33$; $R^2_{\text{adj}} = 0.055$; $P = 0.001$) and in Estonia ($F_{1,34} = 4.88$; $R^2_{\text{adj}} = 0.097$; $P = 0.001$), whereas the community structure of Chlorophyta was mainly affected by space in Finland ($F_{1,39} = 4.01$; $R^2_{\text{adj}} = 0.071$; $P = 0.001$) and by herb cover in Estonia ($F_{1,35} = 2.71$; $R^2_{\text{adj}} = 0.076$; $P = 0.001$). Community structure of Ciliophora responded most strongly to soil Ca concentration ($F_{1,36} = 7.83$; $R^2_{\text{adj}} = 0.146$; $P = 0.001$) in Finland but to Ericaceae cover in Estonia ($F_{1,34} = 5.05$; $R^2_{\text{adj,partial}} = 0.101$; $P < 0.001$).

Of soil animals, the community of Collembola was affected by spatial structure in Finland ($F_{2,38} = 5.53$; $R^2_{\text{adj,cumul}} = 0.083$; $P = 0.001$) but by soil pH in Estonia

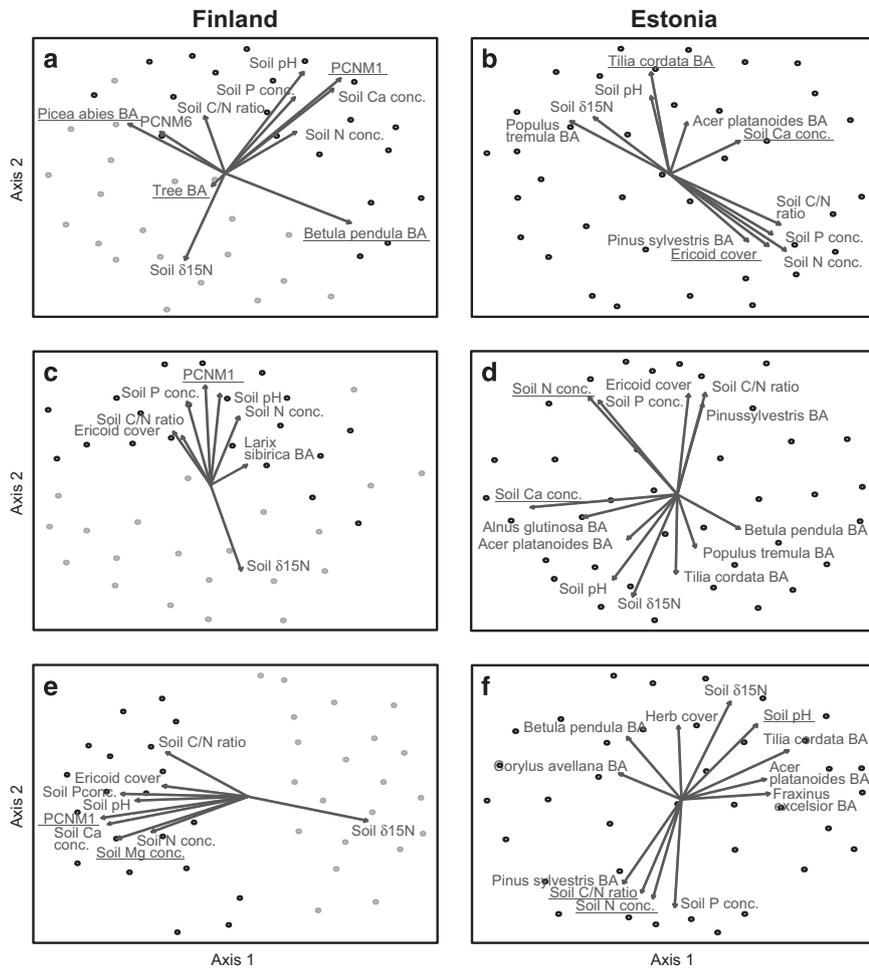


Figure 5 Non-metric Multidimensional Scaling graphs of communities of soil fungal functional groups: (a, b) EcM fungi; (c, d) plant pathogens; and (e, f) saprotrophs. Left panes, Finland (different shades depict sites); right panes, Estonia. Only those variables with significant fit ($P < 0.05$) are indicated. Variables included in the best community models are underlined.

($F_{1,34} = 3.27$; $R^2_{\text{adj,partial}} = 0.059$; $P = 0.001$). Nematode communities were weakly affected by soil P concentration in Finland ($F_{1,39} = 2.66$; $R^2_{\text{adj}} = 0.040$; $P = 0.005$) but by soil N concentration in Estonia ($F_{1,32} = 4.78$; $R^2_{\text{adj}} = 0.095$; $P = 0.001$).

Procrustes analysis revealed that communities of nearly all soil organisms and those of trees and herbs significantly correspond to each other in both study systems (Supplementary Table S6). Further analysis revealed that $R_{\text{Procrustes}}$ was strongly linearly related to the logarithm of the size of the community matrix (Finland: $t = 10.6$; $R^2_{\text{adj}} = 0.634$; $P < 0.001$; Estonia: $t = 7.9$; $R^2_{\text{adj}} = 0.446$; $P < 0.001$), indicating that the Procrustes statistic may have inherent biases related to sampling depth and richness. Partial Procrustes tests revealed that strong and highly significant correlations between communities were lost after accounting for environmental and spatial predictors (Supplementary Table S6). Consistent with our past hypothesis, these results suggest that the same spatial or environmental variables drive the community composition of different organisms

convergently with no causal relationships among these groups.

Discussion

Taxonomic richness and biomass

Diversity and identity of trees exhibited context-dependent effects on taxonomic richness of soil biota, depending on the study system and taxonomic group, which only partly supports our first hypothesis. Nonetheless, tree diversity was an important driver of the richness of EcM fungi in Finland and saprotrophic fungi in Estonia, suggesting that richness of both mutualistic and free-living organisms may benefit from greater producer diversity in certain conditions. Consistent with previous research on understory richness (Ampoorter *et al.*, 2014) and ecosystem services (Nadrowski *et al.*, 2010; Gamfeldt *et al.*, 2013), neutral effects of tree diversity prevailed in plant–soil biota relationships in both study systems.

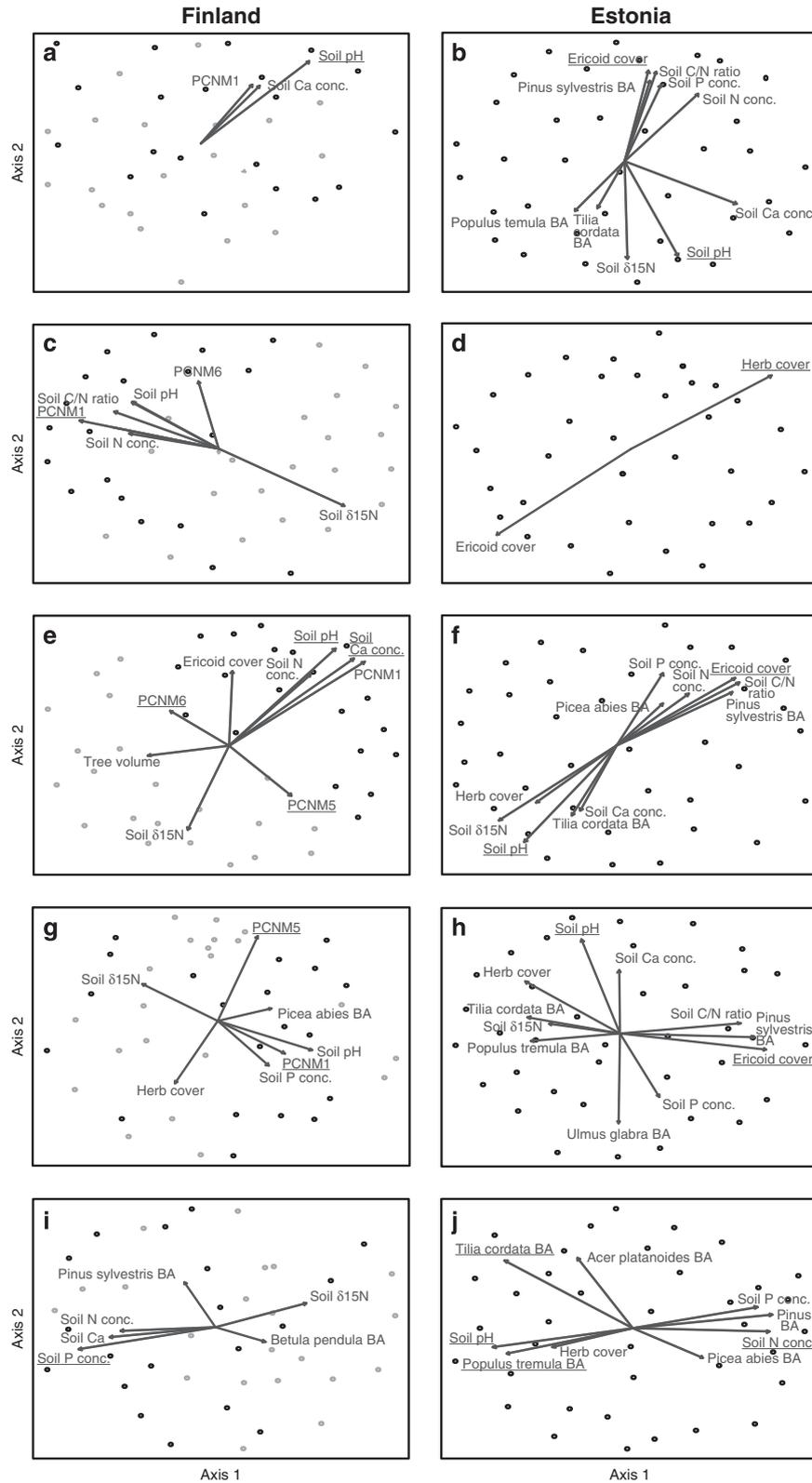


Figure 6 Non-metric Multidimensional Scaling graphs of communities of soil protists and animals: (a, b) Cercozoa; (c, d) Chlorophyta; (e, f) Ciliophora; (g, h) Collembola; (i, j) Nematoda. Left panes, Finland (different shades depict sites); right panes, Estonia. Only those variables with significant fit ($P < 0.05$) are indicated. Variables included in the best community models are underlined.

The low tree diversity impact contrasts with implications from grasslands, in which richness effects on functioning increase with ecosystem's age (Hooper *et al.*, 2012; Reich *et al.*, 2012).

The effects of individual tree species were usually stronger than diversity effects on richness and biomass of soil biota, corroborating the relatively strong sampling effects on ecosystem services (Cardinale *et al.*, 2006; Nadrowski *et al.*, 2010; Gamfeldt *et al.*, 2013). Our results indicate that the magnitude and directionality of individual species effects are system specific. For example, the increasing proportion of *P. sylvestris* strongly suppressed richness of all fungi and in particular that of saprotrophs in Estonia, but it had a slight but significant positive effect on these groups in Finland. The richness of Cercozoa and Chlorophyta responded to different tree species in the two study systems. By contrast, the relative abundance of *A. glutinosa* consistently suppressed EcM fungal richness in both study systems that corroborates with the low mycobiont range in *Alnus* spp. worldwide (Pölme *et al.*, 2013).

Taken together, negative and positive sampling effects were nearly equally represented, suggesting that both stimulating and suppressive species effects are common in tree–soil biota richness relationships. The positive effects are probably related to the abundance of a particularly suitable substrate or facilitation, whereas the negative effects may stem from low palatability, poor compatibility with mutualistic partners or strong defence mechanisms (such as allelochemicals) against soil biota. Variation partitioning further revealed that tree diversity and sampling effects did not differ between biotrophic (pathogens, mutualists) and free-living organisms, providing no support to our second hypothesis.

Both SEM and model selection revealed that soil pH and nutrient concentration were generally the strongest direct or indirect predictors for richness of soil biota in spite of great differences in vegetation. Consistent with the third hypothesis, soil N and P concentrations determined the biomass of bacteria and fungi, especially that of saprotrophs; biomass was the strongest direct predictor of saprotrophic fungal richness in Finland and EcM fungal richness in Estonia. The positive biomass effects are in agreement with studies in grasslands, in which the abundance of individuals or their biomass determines taxonomic richness of particular groups of meiofauna both aboveground and belowground (Scherber *et al.*, 2010; Borer *et al.*, 2012). Soil nutrient concentration or lower C/N ratio had a strong positive effect on richness of Ciliophora in Finland and that of plant pathogenic fungi, Cercozoa amoebae, Ciliophora and Nematoda in Estonia. Apart from nutrients, richness of EcM fungi and Cercozoa responded positively to increasing soil pH in Finland, which is consistent with the substantial

pH effect on phylogenetic composition of soil microbes (Rousk *et al.*, 2010).

Community composition

Plant biodiversity experiments carried out so far have seldom addressed community composition of the responding biota. Understanding whether species composition of organisms in one trophic level affects the community structure of organisms in a linked trophic level enables ecologists to further shed light into biological processes shaping the communities of interacting organisms and into the stability of the interaction networks (Nuismer *et al.*, 2013). In our study systems, community composition of most groups of soil biota were related to edaphic variables, especially soil pH and Mg concentration in Finland but to soil pH, C/N ratio, Ca and N concentration in Estonia. Individual tree species had a minor effect at the community level, except that of *T. cordata* on EcM fungi and Nematoda, and ericoid plant cover on EcM fungi, Cercozoa, Ciliophora and Collembola in Estonia. Such sampling effects were fewer in Finland, but it could be due to the absence of *T. cordata* and paucity of Ericaceae in the Finnish plots. These two taxa transform the soil environment into extremities in terms of pH and C/N ratio (Read *et al.*, 2004; Frouz *et al.*, 2013).

Our results indicate that different environmental variables drive biomass, richness and community composition of soil organisms. Only site effect and soil pH were among the statistically significant shared determinants of both richness and community composition for groups of soil biota in Finland, whereas soil pH and soil Ca concentration sometimes determined both richness and community composition in Estonia. These results suggest that soil pH is universally related to both environmental filtering and niche differentiation that underlie richness and community development, respectively (Pärtel, 2002; Lauber *et al.*, 2009; Tedersoo *et al.*, 2014b).

Methodological advances

This is the first study to address organisms from multiple eukaryotic kingdoms simultaneously using a molecular marker with species-level resolution. The mixture of 11 forward primers designed to perfectly match Fungi, Viridiplantae, Ciliophora, Cercozoa, Straminipila and selected groups of Metazoa enabled us to recover the identity of all these target organisms in a metabarcoding analysis of a single PCR template. Our approach allows addition of further primer variants to capture additional taxonomic groups. Alternatively, different groups can be targeted in separate PCR reactions or using different markers followed by estimation of biomass or individuals by subsampling or quantitative PCR (Fierer *et al.*, 2005; de Barba *et al.*, 2014; Lentendu *et al.*, 2014). Multiple pairs of MID-tagged primers and preparing several metabarcoding libraries per

sample dramatically enhance requirements for time and analytical costs. Our approach of simultaneous identification of multiple organism groups from soil offers a relatively cheap and powerful alternative. The drawback of this method is that it renders cost-effective MID-tagging only the more conserved primer, but updated technologies exist for adding unique identifiers to templates before amplification (Lundberg *et al.*, 2013). With further increase in sequence length (>700 bp), the full ITS region could be targeted as there are more universal eukaryote primer sites in the end of SSU (Tedersoo *et al.*, 2015a). Adding further degenerate positions to the ITS4ngs primer (5'-TCCTSSGCTTANTDATATGC-3') would render it universal to nearly all eukaryotes.

Previous studies have used ribosomal DNA SSU genes to target taxonomic composition of various protist kingdoms in soil and water (Moon-van der Staay *et al.*, 2001; Bates *et al.*, 2013). However, SSU offers poor species-level resolution in most eukaryote groups (Pawlowski *et al.*, 2012; Schoch *et al.*, 2012; Tang *et al.*, 2012), and the 'universal' SSU primers exhibit several mismatches to many large and important eukaryote kingdoms (Pawlowski *et al.*, 2012; Tedersoo *et al.*, 2015a, b). Although SSU and cytochrome I oxidase have additional problems with multiple introns in several taxonomic groups, there is also considerable variation in the length of ITS sequences (for example, Acari, many Insecta; Wang *et al.*, 2015). These biological phenomena cause exclusion of a small fraction of taxa from any metabarcoding data sets using a single marker (de Barba *et al.*, 2014).

Ecologists may argue that our strategy of metabarcoding composite soil samples is better suited to detect immobile organisms. Other studies of soil animals have typically relied on identification of organisms obtained from specifically extracted pools of individuals (Porazinska *et al.*, 2009; Hajibabaei *et al.*, 2011). That approach is more labour intensive and enables to address only specific group(s) of soil biota, usually resulting in capturing the most mobile subset of the target species that respond to light or bait. Nonetheless, inclusion of only the active community members rather than eggs, dormant stages and pieces of cuticle may pose an advantage of that approach in certain cases. Alternatively, inactive community members can be discriminated against by targeting RNA instead of DNA (Baldrian *et al.*, 2012).

Based on our analysis of DNA and microbial biomass, the amount of cells and ribosomal DNA molecules of soil animals is in minority compared with that of bacteria and fungi, which is in agreement with previous studies targeting SSU and LSU (Baldwin *et al.*, 2013; Ramirez *et al.*, 2014; Tedersoo *et al.*, 2015a). The fungal dominance could be related to the actual differences in the number of cells and/or copies of ribosomal DNA (Medinger *et al.*, 2010; Vetrovsky and Baldrian, 2013). One gram of organic forest soil may comprise >10⁹ m of hyphae that

roughly translates into 10⁸ cells (Leake *et al.*, 2004). The same amount of soil harbours thousands of nematodes that altogether comprise 10⁶–10⁷ cells (Wardle, 2002). The estimated cell numbers of protists generally fall into the same orders of magnitude (Adl and Gupta, 2006). Deeper sequencing using the Illumina (San Diego, CA, USA) or forthcoming ultra-high-throughput platforms are likely to provide more accurate richness estimates by exhaustively capturing taxonomic groups that are common but exhibit a relatively low biomass or marker gene content (Smith and Peay, 2014).

Conclusions

Compared with the effects of individual species and soil parameters, tree diversity *per se* has generally relatively low influence on taxonomic richness of soil biota. Our results outline that biodiversity effects are context dependent and that experiments and field studies should be replicated to secure representativeness and understand system specificity (Vehviläinen *et al.*, 2008; Bruelheide *et al.*, 2014). Corresponding changes in beta diversity among vegetation and soil biota are largely explained by the convergent effect of environmental predictors, indicating that these variables must be accounted for in addressing community-wise relationships.

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgements

The data are available as Supplementary Data S1 and S2. Raw sequence data have been deposited in Short Read Archive under accession no. SRP043706. We thank I Jussila, M Mett and V Veldre for assistance during sampling, M Haugas for isotope sample preparation and L Neuenkamp for discussion about Procrustes analysis. This project received support from the Estonian Science Foundation grants 9286, 171PUT, EMP265, RMK and FIBIR.

Author contributions

LT and JK designed the experiments; LT, MB, SP, SA and IH performed sampling; HH, TC, FB and KP did part of the molecular work; LT, MB, KA and SP analysed the data; LT wrote the manuscript with input from other authors.

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