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Data Descriptor

Testate Amoebae (Amphitremida, Arcellinida, Euglyphida) in *Sphagnum* Bogs: The Dataset from Eastern Fennoscandia

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Abstract: The paper describes a dataset, comprising 236 surface moss samples and 143 testate amoeba taxa. The samples were collected in 11 *Sphagnum*-dominated bogs during frost-free seasons of 2004, 2007, 2009, 2017, and 2022. For the whole dataset, the sampling effort was sufficient in terms of observed species richness (143 species in total), though a regional species pool is deemed to be discovered incompletely (143 species is its lower 95 % confidence limit using Chao's estimator). The local community composition demonstrated high heterogeneity in a reduced ordination space. It supports the opinion that the high versatility of bog ecosystems should be taken into account during ecological studies.

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Keywords: testate amoebae; species richness; *Sphagnum* bogs; community structure; community variation; community differentiation

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1. Summary

Testate amoebae are an important component of soil, wetland, and freshwater ecosystems, playing a crucial role in carbon and silicon cycles [1–3]. They are a convenient and popular proxy for water table depth reconstruction in palaeoecological studies [4–8]. This paper describes a dataset, which contains information about species structure of testate amoeba assemblages in 11 *Sphagnum*-dominated bogs, located in Eastern Fennoscandia (Republic of Karelia and Murmansk oblast, Russia) (Figure 1). The studied area is out-of-the-way, and it is characterized by severe climatic conditions and a low population density. For these reasons, peatlands in this territory are little disturbed by human activity, particularly, by peat mining. Therefore, these data can be treated as records on the natural state of peatland ecosystems.

The dataset originates from initially separate sample series (sample sets), collected for the unrelated original studies with different aims and research focuses in 2004, 2007, 2009, 2017, and 2022 in various bogs. Some parts of this dataset were previously reported in publications (the full list of the references is available in [9]). The community composition across all sample series was typical for peatland habitats [10–12] and confirmed common patterns of microspatial testate amoeba community variations [13–19]. Regarding seasonal variability (the data were available for 4 out of 11 bogs), no sufficient changes in the community composition were revealed in previous studies. The only evidence of seasonal dynamics in the community structure was the opposite trends in abundance changes of *Archerella flavum* and *Hyalosphenia papilio*, which are two common species of wetland testate amoeba communities. Most of the bogs (9 out of 11) were sampled only in a single year. Interannual variability of the community composition in the remaining two bogs cannot be assessed due to considerable differences in the sampling designs between the sampling years.

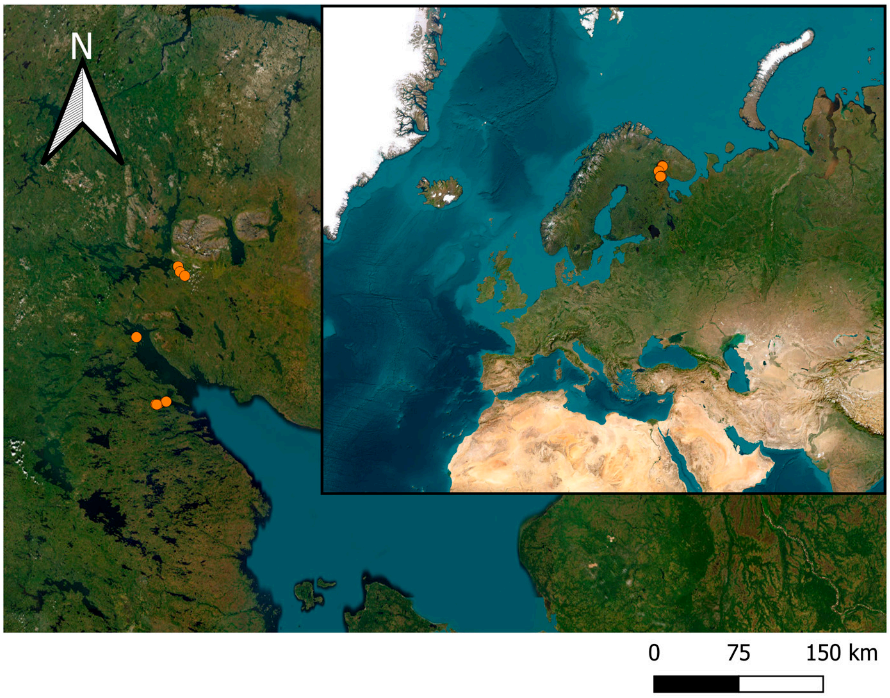

Figure 1. The study area (sampled bogs are marked with orange dots). Exact coordinates of studied bogs can be obtained from the dataset file. (Made with QGIS. Basemap: ESRI Satellite ©2023 ESRI).

The aim of this paper is to compile a joint dataset for the available community composition data and to assess its characteristics in two aspects. The first one is a completeness of the regional species pool detection in terms of the observed species richness against the estimated species richness. The second aspect is the heterogeneity extent of the joint dataset in terms of the community composition variation among individual bogs.

2. Data Description

2.1. The Dataset Structure

The dataset consists of 3019 occurrence entries for 143 testate amoeba taxa. These entries are gathered from 236 samples of surface mosses collected in 11 *Sphagnum*-dominated bogs at the shore area of the Kandalaksha Gulf (the White Sea). Among the observed taxa, 113 and 27 taxa were identified to the species and intraspecies levels, respectively, and three taxa were identified to the genus level only.

The general data structure corresponds with the Global Biodiversity Information Facility (GBIF) database requirements for "Occurrence Data" type [20], or more exactly, it follows the Darwin Core standard of Biodiversity Information Standards (historical "TDWG"—Taxonomic Databases Working Group) and uses terms of "Occurrence" and "Event" classes [21]. To clarify further, in Table 1 we provide meanings of the most important database fields (the dataset column titles) with an example of data entries.

Table 1. The database fields in the dataset.

Database Field	Standard Interpretation [1]	The Meaning in the Present Dataset	Example Entries (from the Single Row of the Dataset) [3]
occurrenceID	An identifier for the **occurrence**—the existence of a taxon at a particular place at a particular time	The presence of a particular **species** (taxon) in a particular **sample**	Bog1_2017-06-21_B1.1_Albm
eventID	An identifier for the **event**—the action that occurs at some location during some time	We treat "event" as **a sample**—a portion of moss material, processing as an entire item	Bog1_2017-06-21_B1.1
parentEventID	An identifier for the broader event that **groups** this and potentially other events	We treat "parent event" as **a sample series**—a set of samples ("events"), collected on one day ("eventDate") at a single bog ("locationID")	Bog1_2017-06-21
eventDate	The date when the event was recorded	The field sampling date	2017-06-21
locationID	An identifier for the information regarding a spatial region or named place where an event occurred	A designation of a specific bog. Identifiers are unique within the dataset [2] and might be presented as codes ("Bog1", "Bog2", "Uzkii", etc.)	Bog1 [2]
scientificName	The full scientific name, with authorship and date information if known.	The full scientific name of the **species** (taxon), with authorship and date information	*Alabasta militaris* (Penard 1890) Duckert, Blandenier, Kosakyan and Singer 2018
organismQuantity and organismQuantityType	A number for the quantity of organisms, and its units	Each taxon quantity is provided as taxon relative abundance (%) to the total testate amoeba counts per sample, rounded to two decimal places	0.99 percentageOfSpecies

[1] In according with [21]; [2] bogs can be also discerned by geographical coordinates ("decimalLatitude" and "decimalLongitude"); [3] the example represents a part of a single record (a row) of the dataset. OccurenceID "Bog1_2017-06-21_B1.1_Albm" consists of the sample designation "Bog1_2017-06-21_B1.1" and the species name abbreviation "Albm". The latter can be decoded from the taxon scientific name (scientificName dataset field) "*Alabasta militaris* <…>". In turn, the sample designation "Bog1_2017-06-21_B1.1" is combined from the site name "Bog1" (locationID), the sampling date "2017-06-21" (eventID), and the conditional sample number "B1.1". After conversion of GBIF data format to a common rectangular "species-in-samples" table, the organism quantity "0.99" becomes a cell entry at intersection of the sample row "Bog1_2017-06-21_B1.1" and the species column "*Alabasta militaris*".

The dataset csv-file can be downloaded from the GBIF web site as the "long" data format which is different from a more common "wide" format of rectangular matrix comprising, in our case, 236 rows (samples) and 143 columns (taxa). "OccurrenceIDs" are unique identifiers of each row in the long format data file and are compiled from the sample identifier and taxa scientific name abbreviation (Table 1). Sample IDs ("eventID") and taxa names ("scientificName") should be used to restore a common form of data as a rectangular "species-in-samples" table. Additional guidelines on navigation across the dataset can be found in the dataset description in the GBIF repository [9].

2.2. Dataset Performance

To assess the sufficiency of the sampling effort in terms of observed species richness for the whole dataset and separately for each sample series ("parent" sampling event in terms of GBIF), we implemented Chao's incidence-based richness estimator [22–24] coupled with a species accumulation curve [25] for the whole dataset (Figure 2).

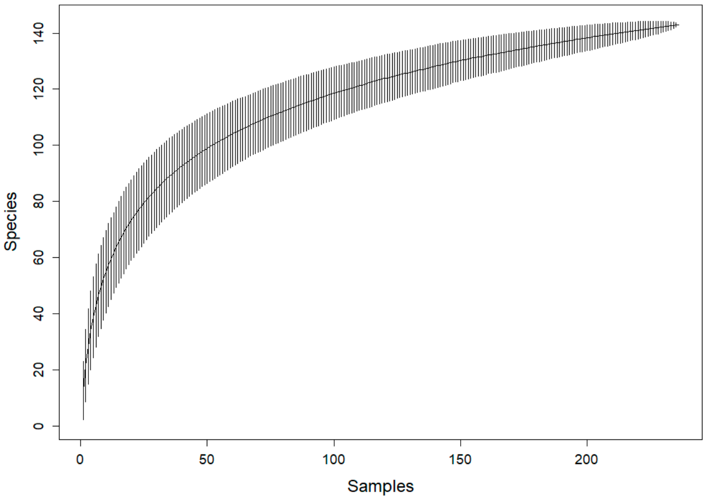

Figure 2. Sample-based species accumulation curve for the entire dataset. The solid curve is a mean species number. The vertical lines are 95% confidence intervals for the means. Produced with R [26] "vegan" package, v. 2.6-4 [27].

The species accumulation curve for the entire dataset indicates that the regional species pool was not discovered completely. However, the observed species number (143 species) lies on the lower 95% confidence limit of the estimated regional species number (175.2 species) (Table 2). For all sample series, their observed species numbers also fell within the 95% confidence intervals (Table 2). Nevertheless, a sample series with a lower number of samples and with a greater range of confidence intervals must be treated with caution when they are used as descriptors for a particular bog.

Table 2. The whole dataset and sample series characteristics.

Sample Series	Number of Samples	Observed Species Richness	Estimated (Chao's) Species Richness ± SE
The whole dataset	236	143	175.2 ± 16.0
Bog1_2017-06-21	10	26	28.8 ± 3.3
Bog2_2017-06-21	8	27	48.9 ± 21.3
Bog3_2017-06-22	19	27	27.9 ± 1.4
DorogaBBS_2004 *	10	53	56.3 ± 3
Peschanii_2004 *	9	30	37.4 ± 6.2
Peschanii_2009	30	55	60.9 ± 5.9
Riazhkov_2009	59	51	61 ± 8.9
Rodnik_2004 *	15	72	89.9 ± 9.6
Uzkii_2004 *	14	39	58.6 ± 15.3
Uzkii_2022-06-12	30	58	80.4 ± 14.3
Verkhnee_2017-06-24	16	25	28.8 ± 3.8
Vodoprovodnoe_2017-06-25	10	21	28.2 ± 10.5
ZabolLes_2007-07-30	6	22	28.7 ± 6.3

* Merged sample series. Due to small number of samples in original series, for each bog in 2004 sampling year, original sampling series, collected by months, were merged into joint sample series.

To evaluate the heterogeneity of the dataset, we involved a common and popular in ecological studies method of non-metric multidimensional scaling (nMDS) [28]. This method is broadly used for the visualization of community composition variation in low-dimensional ordination space (e.g., in two axes) [29]. The relative positions of sample points in the plot space are defined by pair-wise distances between all pairs of communities (samples). The distances can be calculated using a variety of methods, e.g., from community pair-wise similarity (or dissimilarity) measures [28]. We used the quantitative Bray–Curtis percentage difference distance [30] and qualitative (absence–presence) Jaccard dissimilarity measure [28]. Both distances yielded similar results in reduced ordination space, so we present only the site ordination plot, based on qualitative (Jaccard) distances owing to its better readability (Figure 3). The nMDS routine was conducted in the R "vegan" package, v. 2.6-4 [27]. Distances were calculated with the R "adespatial" package, v. 0.3-20 [31].

Figure 3. Site ordination plot of nMDS results, based on Jaccard distance. Each point represents a single sample. Samples with similar species composition are plotted nearer to each other. The plot is produced with R "ggplot2" package, v. 3.4.0 [32].

In the reduced ordination space (Figure 3), samples demonstrated high heterogeneity of taxonomical composition both within and between individual bogs. In the scatterplot (Figure 3), samples from each bog did not come together in distinct groups (except Riazhkov bog). Moreover, samples from 10 out of 11 bogs formed a smooth gradient in the space of two nMDS axes. Nevertheless, along the gradient, non-overlapping bog-specific areas are discerned, which indicates that the high versatility of bog ecosystems should be taken into account during ecological studies concerning testate amoeba assemblages [33].

3. Methods

3.1. Study Area and Sampling Designs

Samples were collected in 11 *Sphagnum* bogs from Eastern Fennoscandia (Republic of Karelia and Murmansk district, Russia) in the area of the Kandalaksha Gulf shore (the White Sea). Field work was conducted in 2004, 2007, 2009, 2017, and 2022 during summer months (June–August), i.e., during a surely frost-free period of a short local vegetation season. Not every bog was sampled in each sampling year.

At each bog, sample points of a sample series either encompassed a complete microtopographical gradient (hummocks, lawns, and hollows) or represented a gradient "open bog—forest" through the uniform microrelief conditions, except for the sample series "Riazhkov_2009", where both factors of spatial heterogeneity (i.e., microrelief and gradient position) were considered.

For each sample, the surface moss layer from the plot ca. 10 × 10 cm^2 was collected to the depth of 5–10 cm [9]. Field material was stored in plastic bags in a refrigerator for laboratory treatment.

3.2. Laboratorial Sample Processing and Taxonomical Identification

Laboratory sample preparation was carried out using standard techniques [9,34] of testate amoeba investigations. Species identification and counting was conducted by means of light microscopy [9,35]; both alive and dead shells were counted.

Taxa scientific names are reported according to generally used identification keys and recent taxonomical reviews [36–39]. Due to uncertainty of infraspecific level designations [28], taxon ranks except "species" are not reported. Classification at higher taxonomical levels is reported in accordance with Ruggiero et al., 2015 [40].

3.3. Data Processing

After taxonomical validation of the initial data, they were merged into a joint dataset. Since the initial data were designed by various researchers, data representation differed between them: some sample series represented absolute densities of testate amoeba populations and the others represented raw counts of taxa. To keep a consistency in data representation across the dataset, taxa abundances were transformed to relative abundance (%) of a particular taxon to the total counts per sample.

4. User Notes

The dataset is a sufficient source of data on species distribution and can be used in studies on biogeography and macroecology. When using the dataset as a source for community composition data in the scale of a bog, we recommend that researchers treat the sample series ("parent events") with a low number of samples with caution. Due to the same reasoning, we recommend merging the sample series from 2004, collected during different months (June and August) in a particular bog, into a joint bog-specific subset, when the focus of interest is on the community composition data for an individual bog.

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