



The diversity of larger fungi in peatlands: ten years of plot-based monitoring complemented by barcoding and metabarcoding

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Peatlands are widespread around the world, with several highly paludified regions, one of which is the Western Siberian plain. Fungi are an important part of the decomposer community of peatlands, playing a critical role in the aerobic decomposition in the upper peat layer. The research of fungal diversity of peatlands globally, started over a century ago with microbiological approach, later complemented by mycologists working by direct observation of fruitbodies of larger fungi, and recently intensified by molecular approach, including metabarcoding of environmental DNA (1). The community of larger fungi of the raised bog “Mukhrino” in Western Siberia was studied using plot-based monitoring throughout a 10 year observation period. The revealed species diversity was represented by approximately 500 specimens in the Fungarium of Yugra State University collection (YSU-F) (2). Selected specimens were used for barcoding of the ITS region to reveal a total of 95 species from 33 genera and three classes. The barcoding effort confirmed morphological identifications for most specimens as well as revealed cryptic species and several potentially new taxa. Based on regular all-season observations, we described the phenology of the community fruiting. The quantitative community structure based on fruiting revealed difference in abundance of species by 4 orders of magnitude, the rare species representing near half of the species list. The inter-annual fruiting abundance varied several times by the total number of accumulated fruitbodies per year. In order to complement the direct observations of fruitbodies by environmental DNA sequencing, four major substrates were subjected to metabarcoding analysis: peat, bog plants litter, wood and mycorrhizal roots. Totally 192 samples were extracted during field summer of 2022 in order of cover spatial and temporal community variability, substrate features and some methodological questions and were sequenced on Illumina MiSeq (length of reads – 300 bp on both sides fragments). The sequences were analyzed by the pipeline QIIME2. The resulted taxonomic composition of fungi and quantitative community structure revealed by direct observation and metabarcoding generally coincide, but both approaches add a proportion of unique species. To make the comparisons with global studies, we created an open access database of literature-based observations of fungi in peatlands based on about 120 previously published papers (comprising about 5000 records of about 1300 species) (3). As a result, the study created an accurate representation of taxonomic and quantitative structure of the community of larger fungi in raised bogs in the region based on combination of methodological approaches (long-term monitoring of fruitbodies, specimens sequencing and metabarcoding). The raw data of plot-based counts was published as a sampling-event dataset (4) and the sequenced specimens with the sequence information as an DNA-derived extension dataset in GBIF (5).

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3) N. Filippova, E. Rudykina (2023) Literature occurrence database of global fungal diversity in peatlands. Version 1.7. Yugra State University Biological Collection (YSU BC). Occurrence dataset. <https://doi.org/10.15468/p8q8q4>

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5) N. Filippova, E. Rudykina, A. Dobrynina (2023) Plot-based observations of macrofungi in raised bogs in Western Siberia (2014-2022). Version 1.37. Yugra State University Biological Collection (YSU BC). Sampling event dataset. <https://doi.org/10.15468/e9g5ri>