

OS - oral session

Plot-based macrofungi monitoring in taiga zone of West Siberia and sampling event data publishing

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The protocols for sampling macrofungi using fixed-sized plots have begun to converge in recent years (O'Dell et al. 2004) thus making possible comparison of different project results and allowing extrapolation of data. On the other side, development of integrated biodiversity information facilities has opened the possibility of standardized data storage and open access to the accumulated quantitative data.

Following the standard plot-based protocol (10.17504/protocols.io.z2xf8fn) for sampling macrofungi, we initiated the long-term monitoring program in major ecosystem types in middle taiga zone of West Siberia, nearby Khanty-Mansiysk. The goal is to describe the quantitative and qualitative structure and spatial variation of the community of macromycetes, to follow its dynamics seasonally and inter-annually. A series of plots was established in a raised bog ecosystem and in different forest types following after-logging and paludification successions (about 560 micro-plots totaling 1700 m²). The plots were visited weekly during seasons 2014-2018 and carpophores of different fungal taxa were counted in each micro-plot.

The sampling-event dataset type of Global Biodiversity Information Facility allows publication of data on quantitative community assessments. The assessments of macrofungi community are still absent or rare in GBIF, despite the importance of such data for ecological monitoring. Thus, the resulting monitoring data were organized as sampling-event datasets and published in GBIF to provide open access to the data (10.15468/e9g5ri; 10.15468/ge1hkl). The datasets include about 17000 plot-based observations (=sampling events) with corresponding about 6500 occurrence records. About 60% of plot-based observations contain zero records (absence data).