Geophysical Research Abstracts
Vol. 20, EGU2018-1066, 2018
EGU General Assembly 2018

Responses of peatland micro-eukaryotic community structure and diversity to warming - a field experiment

Monika Reczuga (1,2), Christophe V.W. Seppey (3,4), David Singer (3), Amandine Pillonel (3), Anna Basińska (5), Dominika Łuców (1,6), Radosław Juszczak (5), Edward A.D. Mitchell (3,7), Mariusz Lamentowicz (1), and Enrique Lara (3)

(1) Laboratory of Wetland Ecology and Monitoring & Department of Biogeography and Palaeoecology, Faculty of Geographical and Geological Sciences, Adam Mickiewicz University, Krygowskiego 10, 61-680 Poznań, Poland, (2) Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, (3) Laboratory of Soil Biodiversity, University of Neuchâtel, Rue Emile-Argand 11, 2000 Neuchâtel, Switzerland, (4) Department of Arctic and Marine Biology, Faculty of Biosciences Fisheries and Economics, Biologibyget Framstredet 39 9037 Tromsø, Norway, (5) Department of Meteorology, Poznan University of Life Sciences, Piątkowska 94, 60-649 Poznań, Poland, (6) Department of Environmental Resources and Geohazards, Polish Academy of Sciences, Twarda 51/55, 00-818 Warszawa, Poland, (7) Jardin Botanique de Neuchâtel, Chemin du Perthuis-du-Sault 58, CH-2000 Neuchâtel, Switzerland

Peatlands store approximately one third of the global terrestrial carbon stock on 3% of the land surface. On-going climate change threatens peatlands in their structure (biotic communities) and function (Carbon sink). Micro-eukaryotes including protists and fungi are key actors of soil carbon cycling but their diversity and response to climate change are still not well known.

We assessed the influence of warming and reduction of precipitation on the structure and diversity of micro-eukaryotic communities using a high-throughput sequencing (HTS) of the V4 region of the 18S ribosomal RNA gene.

We identified 754 different Operational Taxonomic Units (OTUs) related to micro-eukaryotes, among which Rhizarians (189 OTUs) and Alveolates (180 OTUs) were dominant. Community structure and inferred function changed significantly in response to the manipulations as shown by constrained analysis of principal coordinates. Potential indicators of peatland warming identified by IndVal analysis, include an OTU related to the desmid genus Actinotaenium.

By identifying indicators of environmental changes and inferring the functional significance of these changes, HTS of micro-eukaryotes is a useful approach to better understand how the functioning of peatland ecosystems changes in response to ongoing climate change.

Project financed by a scientific grant from the Polish National Science Centre (NCN, No. 2015/19/N/NZ8/00172, Principal Investigator: Monika Reczuga) and the Polish-Norwegian Research Programme operated by the National Centre for Research and Development under the Norwegian Financial Mechanism (No. Pol-Nor/203258/31/2013, WETMAN).