

EGU21-13734

<https://doi.org/10.5194/egusphere-egu21-13734>

EGU General Assembly 2021

© Author(s) 2022. This work is distributed under the Creative Commons Attribution 4.0 License.



Microbial community composition is linked to *Sphagnum* acclimation to warming

Tatjana Živković^{1,2}, Alyssa A Carell¹, Gustaf Granath³, Mats B Nilsson⁴, Manuel Helbig⁵, Denis Warshan⁶, Ingeborg Jenneken Klarenberg⁷, Daniel Gilbert⁸, A. Jonathan Shaw⁹, Joel E Kostka¹⁰, and David J Weston¹

¹Oak Ridge National Laboratory, Oak Ridge, USA

²McGill University, Montreal, Canada (tatjana.prsa@mail.mcgill.ca)

³Uppsala University, Uppsala, Sweden

⁴Swedish University of Agricultural Sciences, Umea, Sweden

⁵Dalhousie University, Halifax, Canada

⁶University of Iceland, Reykjavík, Iceland

⁷University of Akureyri, Akureyri, Iceland

⁸Université de Franche-Comté, Montbéliard, France

⁹Duke University, Durham, USA

¹⁰Georgia Institute of Technology, Atlanta, USA

Peatlands store about third of the terrestrial carbon (C) and exert long-term climate cooling. Dominant plant genera in acidic peatlands, *Sphagnum* mosses, are main contributors to net primary productivity. Through associative relationships with diverse microbial organisms (microbiome), *Sphagnum* mosses control major biogeochemical processes, namely uptake, storage and potential release of carbon and nitrogen. Climate warming is expected to negatively impact C accumulation in peatlands and alter nutrient cycling, however *Sphagnum*-dominated peatland resilience to climate warming may depend on *Sphagnum*-microbiome associations. The ability of the microbiome to rapidly acclimatize to warming may aid *Sphagnum* exposed to elevated temperatures through host-microbiome acquired thermotolerance. We investigated the role of the microbiome on *Sphagnum*'s ability to acclimate to elevated temperatures using a microbiome-transfer approach to test: a) whether the thermal origin of the microbiome influences acclimation of *Sphagnum* growth and b) if microbial benefits to *Sphagnum* growth depend on donor *Sphagnum* species.

Using a full-factorial design, microbiomes were separated from *Sphagnum* "donor" species from four different peatlands across a wide range of thermal environments (11.4–27°C). The microbiomes were transferred onto germ-free "recipient" *Sphagnum* species in the laboratory and exposed to a range of experimental temperatures (8.5 – 26.5°C) for growth analysis over 4 weeks.

Normalized growth rates were maximized for plants that received a microbiome from a matched "donor" and with a similar origin temperature ($\Delta T_{\text{treatment-origin}}$: $0.3 \pm 0.9^\circ\text{C}$ [\pm standard error]),

$p = 0.73$). For non-matched “donor-recipient” *Sphagnum* pairs, $\Delta T_{\text{treatment-origin}}$ was slightly negative with $-4.1 \pm 2.1^\circ\text{C}$ ($p = 0.06$). The largest growth rate of the “recipient” was measured when grown with a microbiome from a matching “donor” *Sphagnum* species and was 252% and 48% larger than the maximum growth rate of the germ-free *Sphagnum* and the non-matched “donor-recipient” *Sphagnum* pairs, respectively.

Our results suggest that the composition of the *Sphagnum* microbiome plays a critical role in host plant temperature acclimation. We found that microbially-provided benefits to the host plant were most pronounced when: 1) the thermal origin of the microbiome is similar to experimental temperatures, and 2) when donor and recipient *Sphagnum* species are the same. Together, these results suggest that *Sphagnum* temperature acclimation can be modulated, in part, by microbial interactions and may potentially play a role in peatland resilience to climate warming.