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Microbial Response to Deep Peat Heating in SPRUCE Peatland Experiment

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Soil microbes are major drivers of soil elemental cycling, yet we lack an understanding of how temperature will affect microbial communities in situ. This is particularly pressing for ecosystems such as boreal peatlands because peatlands contain disproportionate amounts of carbon relative to the land area. Boreal regions are particularly vulnerable to changing temperature. We examined the response of peatland microbial communities to soil warming during the Deep Peat Heat experiment at the Spruce and Peatland Responses under Climatic and Environmental Change (SPRUCE) experimental research station. The Deep Peat Heat experimental design at SPRUCE includes ten 12 m-diameter enclosures that are warmed to five target temperatures (+0, +2.25, +4.5, +6.75 and +9 °C) at depths of 2–3 m. Warming was initiated between June 17 and July 2, 2014 as the electrical systems for each plot became available. Samples were collected June 3 prior to warming and September 9 after one season of warming. Bacterial community composition was studied using Illumina sequencing of the 16S and ITS primers to determine the response to deep peat warming of the total (DNA) and active (RNA) microbial communities.

Although temperature at depth (2 m) reached the target, surface warming was less intense, increasing on average < 2 °C. In general, soil bacterial and archaeal communities were more sensitive than fungi to warming manipulation. Microbial community composition significantly shifted with temperature for both the total (P= 0.009) and active (P = 0.001) prokaryotic communities. Generally, compositional changes for prokaryotes were greater in the 4.5 °C treatment than in the 9 °C treatment. Both Euryarchaeota and Firmicutes consistently decreased with warming, whereas Proteobacteria and Planctomycetes were sensitive to warming, but direction of response varied by genus. Taxa that consistently decreased in abundance with warming for both DNA and RNA included *Thermoanaerobacteraceae syntrophaceticus*, *Syntrophaceae smithella* and *Methanosarcina* sp. We did not detect changes due to warming in fungal community composition. The fungal genus *Suillus* responded strongly to warming in both active and total abundance, generally increasing in response. These results suggest sensitivity to small shifts of temperature can alter microbial populations. Ongoing studies are investigating the functional implications.