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Seasonal changes of microbial activity and community structure in a tundra ecosystem in Western Siberia, Russia

H. Meyer (1), A. Haslinger (1), O. Rusalimova (2), C. Biasi (1), C. Kaiser (1), N. Lashchinsky (3), P. Barsukov (2), A. Richter (1)

(1) Institute of Ecology, University of Vienna, Austria, (2) Institute of Soil Science and Agrochemistry, Russian Academy of Sciences, Novosibirsk, Russia, (3) Central Siberian Botanical Garden, Novosibirsk, Russia

(arichter@pflaphy.pph.univie.ac.at / Fax: +43-1-4277-9542)

Erect dwarf-shrub tundra is the zonal vegetation on acidic soils in the Low Arctic (bioclimate subzone D). The lichen-rich variant of this dwarf-shrub tundra is common on drier, sandy soils throughout the Arctic. This study aimed at elucidating seasonal pattern of biogeochemical cycling and linking them to microbial community structure. Towards this goal we examined the soil nutrient status, microbial community structure (phospholipid fatty acid pattern), heterotrophic respiration and gross mineralization rates in four different soil horizons of a dwarf-shrub tundra near Yamburg (67°55'N, 78°08'E) over the growing season (June to September 2003). All investigated parameters exhibited significant changes over the course of the season. Ammonium and dissolved organic nitrogen were highest shortly after snow melt, while nitrate peaked at the mid season. Microbial biomass was highest in spring and decreased significantly when plants started to grow. While the relative abundance of gram+ and gram-bacteria and actinomycetes increased, the abundance of fungi decreased with soil depth. The fungi/bacteria ratio also increased significantly during the growing season in all soil depths (e.g. from 0.16 to 0.28 in upper organic horizons). However, we were unable to link changes in community structure to changes in microbial activity rates. Heterotrophic respiration was highest in early spring followed by a sharp decrease with the onset of plant nutrient uptake. In contrast, gross N mineralization rates peaked at the end of July during the peak growing season, but were low at the early season. We conclude that the seasonal pattern of heterotrophic respiration mainly reflect competition between plants and microbes and availability of easily decomposable dissolved organic carbon shortly after snow-melt, while pattern of nitrogen mineralization seem to be controlled by other factors, presumably nutrient limitations and temperature. Our study demonstrates that a better link between microbial community structure and function is needed to explain the complex pattern of seasonal changes in biogeochemical cycling.