Organic N Cycling at SPRUCE

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At the heart of microbial C-N cycling are microbial metabolism and extracellular enzymes. Amino acid release by microbial extracellular proteases is important for N turnover and the production of bioavailable N in forest soils. Amino acid production is particularly important in boreal systems, where N supply strongly influences both decomposition and plant primary productivity. Yet little is known about the abundance, potential activity, or diversity of the microbial extracellular protease encoding genes in peatland forests. To evaluate the overall enzymatic potential for decomposition we measured microbial biomass and extracellular enzyme activity at three depths (+10 cm, 0 cm and -10 cm relative to peat hollows) at the Spruce and Peatland Responses Under Climatic and Environmental Change (SPRUCE) experiment site in the Marcell National Forest, Minnesota, USA. Samples were collected from fresh peat in June and September 2013. In addition, fungal ingrowth cores filled with sterilized peat were incubated in situ from June to September to assess new microbial inputs. In both fresh peat and ingrowth cores enzymatic potential diminished with peat depth. Potential enzyme activity was lower and stratification of activity by depth was more pronounced in fungal ingrowth cores compared to native peat cores. Proteolytic microorganisms present in the SPRUCE bog were characterized by concurrent analysis of metagenomic data from 0-10 cm peat samples from February 2012. Microbial protease genes were abundant and diverse, with a total of 32,533 microbial extracellular protease genes in nine extracellular protease gene groups. Among identified proteases, sequences encoding for the enzymes aminopeptidase and trypsin were the most prevalent in all samples. The majority of genes resembled known proteases of bacterial origin, primarily of the Proteobacteria, Acidobacteria and Actinobacteria. Less abundant were fungal protease genes, which were predominantly from the Ascomycota, and Archeal protease genes most similar to Crenarchaeota origin. While both fungal and bacterial genes consistently diminish with depth, archaeal RNA polymerase and extracellular protease genes were more abundant at 25-75 cm than 0-10 cm. Our results indicate that peatland systems have a stratified microbial extracellular protease potential across depth. Although fungi are commonly considered to be central regulators of proteolysis, our analysis suggests that bacteria may be very important at the surface and archaea deeper in the profile. The low importance of fungal proteolysis, particularly at depth, presumably limits vertical nitrogen translocation via fungal hyphae and contributes to the long-term storage of N (and C) in unavailable pools below the aerobic zone.