ENVIRONMENTAL CONTROL OF GROSS PROTEIN DEPOLYMERIZATION IN DECAYING PLANT DETRITUS

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The microbial decomposition of senescent plant tissue is a crucial ecosystem process that regulates the cycling of carbon (C) and nitrogen (N). Microbes release extracellular enzymes that deconstruct plant macromolecules and ultimately liberate soluble substrates for microbial uptake. These soluble substrates are used as microbial energy source and for biomass production. While senescent plant litter often provides excess carbon for microbial metabolism, N is an essential nutrient for all organisms and N limitation often regulates the productivity of terrestrial ecosystems (Mooshammer et al., 2014). The depolymerization of plant proteins is the rate-limiting step for N cycling. This process yields smaller peptides or amino acids that are taken up by microorganisms and are either used to build up microbial proteins or are further mineralized to NH_4^+ and released to the environment (Schimel & Bennett, 2004).

Despite its importance in N-cycling, the protein depolymerization step is analytically difficult to target as a varying fraction of the free amino acids is directly incorporated into microbial biomass, i.e. used for microbial protein synthesis (Wanek et al., 2010). Here we describe a new approach to discriminate the plant and the microbial protein fractions in decomposed leaf litter using Fourier transform infrared spectroscopy (FTIR). FTIR spectra of microbial biomass containing high abundances of nucleic acids and proteins show a distinct absorption pattern compared to spectra of vascular plant tissue, which is dominantly composed of carbohydrates and lignin (Naumann, 2000). In a 75-day anaerobic litter decomposition experiment in three peat soils, FTIR spectroscopy readily revealed decreasing concentrations of vascular plant biomolecules and increases of microbial biomass. While the detected changes in protein content (Amide I and Amide II bands) reflect simultaneous changes in microbial and plant protein concentration, increases of nucleic acid bands (i.e., symmetric and asymmetric phosphodiester stretch bands) dominantly originate from microbial biomass alone as these bands are absent in the undecomposed vascular plant tissue. The microbial protein contribution to the total protein pool could therefore be estimated by using increases of the nucleic acid bands in the litter as a reference. Experimental results at different nutrient conditions indicates that plant protein depolymerization is highly site-dependend and, in the case of decomposition in the nutrient poor oligotrophic peatland, can lead to plant N losses that exceed the bulk C losses by as much as a factor of 2 (Fig. 1), regardless of the initial litter N content. This process causes a gradual depletion of plant N content during decomposition. The formation of microbial protein, on the other hand, showed less variation, indicating that all leaf litters provided excess N for microbial growth.

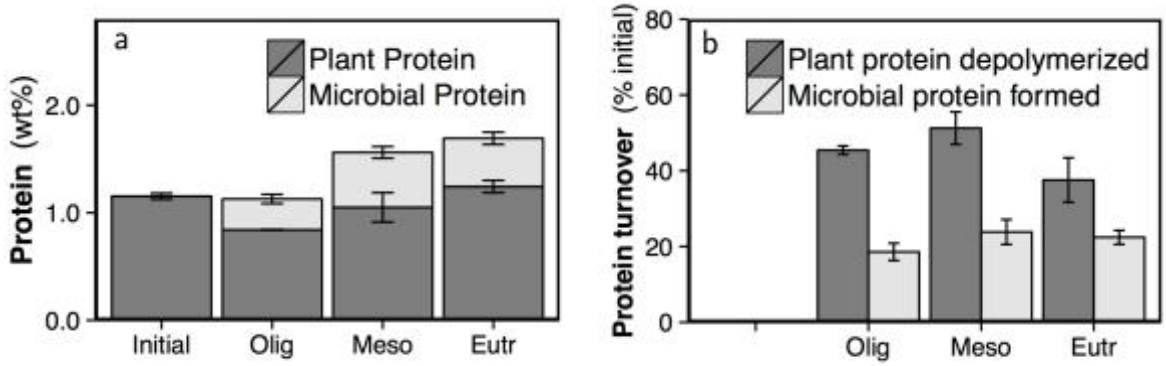

Figure 1 *Leaf litter protein content (a) and protein turnover (b) after 75 days of anaerobic decomposition in an oligotrophic, mesotrophic and eutrophic peatland.*

References

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