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Microbial processing of leaf- and root-derived organic matter in the boreal forest

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Soil microbial composition may vary in response to changes in organic matter inputs or stand compositions. Boreal soils from Alberta, Canada, support a canopy cover of aspen (Populus tremoloides Michx.), white spruce (Picea glauca (Moench) Voss) or a mixing of these two species. These soils also reflect different biogeochemical processing of organic matter degradation. This study sets out to determine if a simple labelled compound (13C glucose) and more complex labelled litter (13C leaves, or roots) are processed differently by forest floors from these two dominant stand types (aspen and spruce).

To examine these effects, we put in place a lab incubation experiment, and added labelled substrates (glucose, roots or leaves) to a small quantity of moistened aspen or spruce forest floor. We measured soil respiration throughout the 67-day incubation, and used phospholipid fatty acids (PLFA) analysis to identify the soil microbial structure. By quantifying the incorporation of 13C into different PLFAs, we were also able to identify functional groups responsible for the metabolism of labelled compounds. The measure of 13C-CO_2 gave some information about the percent of CO_2 coming from each added substrate.

Preliminary results indicate that daily respired CO_2 fluxes were more important from spruce than from aspen forest floor; this was true for all added substrates. For the spruce samples, CO_2 fluxes decreased very rapidly during the first four days, and stayed relatively constant during the remainder of the incubation. For the aspen samples, fluxes also decreased very rapidly during the first four days, and decreased more gradually for the rest of the incubation. Results also show that both soils rapidly incorporated and respired the simple labelled carbon; indeed, after two days between 40 and 60 % of the added glucose had been respired against only 20 to 30 % for the more complex substrates (roots and leaves).

The two soils maintained a distinct microbial community structure throughout the 67-day incubation. While the microbial structure changed during incubation, there was no measurable shift in response to substrate addition (labelled glucose, leaves or roots). Finally, results show that the percent of substrate incorporated into microbial PLFAs was more important for the labelled roots than for the other two labelled substrates (glucose or leaves).