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Soil microbial communities in a CO2-enriched and 13C-labelled treeline ecosystem with different tree species

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The aim of this study was to estimate the responses of soil microbial communities at the alpine treeline to elevated CO2 and to gain insight into the C cycling through microbial groups under two tree species by tracking 13C signatures into phospholipid fatty acids (PLFA). In alpine treeline ecosystems, we exposed 30 year-old larch and pine trees growing on undisturbed thick mor-type organic layers to five years of elevated CO2 (+200 µmol CO2 mol-1) being depleted in 13C. Results showed that elevated CO2 increased soil respiration particularly under pine trees. However, we found negligible CO2 effects on the biomass and community structure of soil microorganisms, which might be due to small plant growth responses, and a comparatively small input of new plant-derived C into the thick organic layers with large C stocks. The tracing of 13C-depleted CO2 revealed that only a small portion of the microbial community actively metabolized new C (25%). The 13C label in individual PLFA indicated that mainly fungi were involved in the use of new substrate. Tree species affected soil microbial communities in the organic layer with a significantly higher ratio of fungal to bacterial fatty acids under pine than under larch trees. Under pine, fungal PLFA of the organic layer carried a stronger 13C label which strongly suggests a greater mycorrhizal activity that might also lead to the 60% greater input of new plant-derived C into soil organic matter under pine than under larch. In conclusion, our results show that significant responses of microbial communities in these treeline ecosystems if any would require more drastic and long lasting effects than five years of elevated CO2. Tree species have a major impact on the cycling of new plant C through soil microbial communities.