



Microbial responses to multifactorial climate change factors in heathland soil revealed by ^{13}C tracing of added glycine and FACE CO_2

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Understanding microbial responses in soils is the key to understand the potential impacts of predicted climate changes on soil C dynamics. Microbial utilization of carbon sources represents a gateway in the routing of carbon incorporation and respirational release.

After one year of accumulated ecosystem effects from multifactorial climate change treatments ('CLIMAITÉ'), microbial activity was investigated by addition of the ^{13}C labelled amino acid ($^{13}\text{C}_2$ -glycine; 99 at.%) to a factorial design of: elevated temperature (T), summer drought (D) and elevated atmospheric carbon dioxide (510 ppm [CO_2]), and combined treatments (TD, TCO_2 , DCO_2 and TDCO_2) at an undisturbed temperate heathland dominated by *Calluna vulgaris*.

The integrated microbial long-term responses to treatments were identified by analysis of PLFA in full concentrations in the top soil and the accumulative indirect labelling by the ^{13}C -depleted FACE CO_2 air. The short-term microbial response was directly assessed by quantification of incorporation of ^{13}C -glycine into biomarker PLFA of specific microbial groups one day after injection, using gas chromatography-combustion-stable isotope ratio mass spectrometry (GC-C-IRMS). Bacteria were more opportunistic in utilization of the added glycine substrate: i.e. ^{13}C from the labelled glycine was incorporated into Gram positive bacteria (i15:0, i17:0) in all treatments, whereas in contrast the fungi had minor or no glycine derived ^{13}C -enrichment.

The direct short-term response was a more active microbial biomass both incorporating and respiring ^{13}C from the added glycine in treatments with elevated CO_2 . However, as response to the long-term climate treatment, warming decreased the concentration of PLFAs in general.

The integrated ^{13}C -depleted labelling obtained via plant use of ^{13}C -depleted CO_2 and subsequent root exudation of ^{13}C -depleted labile carbon, illustrated the intimate links between microbial incorporation of carbon and plant CO_2 assimilation. Hence, the response suggests future climatic conditions may increase bacterial utilization of free amino acids from labile root exudates.