Molecular and compound-specific stable C isotope investigation of the fate of dung C in a temperate grassland soil

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Establishing the potential of soils to sequester C and elucidating the mechanisms whereby this is achieved is vital in order to understand the capacity of terrestrial ecosystems to act as sinks for anthropogenic C. Significant quantities of cattle dung are applied to temperate grassland annually and traditional long-term use of manures as soil improvers has been proven to increase SOM (Haynes and Naidu, 1998). This project applied molecular and compound-specific stable C isotope methods to investigate the fate of cow dung in a temperate grassland soil, utilising the $\Delta^{13}C_{(con\text{-}trt)}$ values of compounds from natural abundance ^{13}C-labelled C_4 dung ($\delta^{13}C$ = -12.6‰) and C_3 soil ($\delta^{13}C$ = -30.3‰). The 0-5 cm horizon of dung-treated soils were sampled at 0, 7, 14, 28, 56, 112, 224 and 372 d. Bulk $\delta^{13}C$ values estimated that a maximum of 12% dung C was incorporated at 56 d (Dungait *et al*., 2005) with compound-specific determinations estimating that 19% dung C was incorporated at this time. Differences between degradation rates of major organic components of C_4 dung were revealed. C_4 dung comprised 80% carbohydrate, 5% lignin and <1% lipid. Percentage incorporation of xylose accounted for 10% dung C at 56 d, compared with 3% for glucose; signficant concentrations of dung carbohydrates remained in the soil at the end of the experiment. Dung-derived lignin 4-hydroxyphenols displayed a range of degradation rates in the soil, but appeared to be more labile than expected and did not contribute significantly to dung-derived C later in the experiment. Faecal biomarker 5β-stanols and free fatty acids suggested that concepts of recalcitrance might not rely on individual chemistry but on the potential of certain compound classes to escape degradation or leaching; very long chain fatty acids were appeared to be the most resistant dung compound class.

References

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Investigation of the 'Trigger Molecule Response' using ^{13}C stable isotope probing of microbial membrane fatty acids

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The 'Trigger Molecule Response' is a hitherto unrecognised mechanism in soil microorganisms that provides a strategy for survival in a relatively substrate-poor environment. Previous respiration experiments have shown that the additions of 'trigger molecule' concentrations of low molecular-weight compounds to soils induce two- to five-fold greater expenditure of energy by the soil microbial biomass than that provided by the added substrate (De Nobili *et al*., 2001). Thus, we investigated the hypothesis that soil microorganisms maintain metabolic alertness in anticipation of a food event through application of ^{13}C-labelled substrates at 'trigger molecule' concentrations, using compound-specific ^{13}C isotope analysis of microbial biomarker PLFAs (Evershed *et al*., 2006). This paper presents results from recent experiments with soils from Rothamsted Classical Experiments that show: a) significant increases in the $\delta^{13}C$ values of individual PLFAs without signficant increases in abundance at four concentrations (0, 25, 83 and 416 μg ^{13}C g^{-1} soil) after 120 h, and, b) differential uptake of ^{13}C over a 240 h time course in individual microbial PLFAs extracted from soils treated with 15 μg ^{13}C g^{-1} soil. Additional evidence for the 'Trigger Molecule Response' from concurrent experiments using CO_2 respiration, nucleic acid and RNA-SIP methodologies will also be discussed. The significance of these findings in the context of the role of the soil microbial biomass in C cycling in soils will be considered.

References

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