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Linking microbial assimilation of carbon and microbial biomarkers to soil organic matter persistence

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Soils are a significant component of the Earth's carbon (C) cycle, yet a mechanistic understanding of what controls the turnover of this large C pool remains elusive. One major driver of C loss from soil is microbial processing, accounting for roughly half of total soil CO_2 respiration. However, limited options exist for accurately identifying the source of C assimilated by microbial communities and linking the persistence of organic matter to microbial community composition. We developed and applied methods to a grassland site in California which allow for the direct radiocarbon (^{14}C) analysis of microbial biomass and total lipids extracted from soil. These data are paired with fatty acid biomarker analysis of the same extracts and the ^{14}C analysis of microbially-respired CO_2 from soil incubations. We find that in the upper 50 cm soil depths, the $\Delta^{14}C$ of CO_2 from incubations is indistinguishable from that of extracted microbial biomass. Below 50 cm, the $\Delta^{14}C$ of the microbial biomass is more depleted (older) than that of the incubation CO_2, likely due to the inclusion of biomolecules from non-living cells (necromass) in the biomass extracts, or differences in C used for assimilation vs respiration. The $\Delta^{14}C$ of the total lipid extracts followed a similar pattern to that of the microbial biomass, with the exception of more depleted (older) C in the 20-50 cm depth, suggesting the biomass extract represents a more active C pool at this depth. Fatty acid biomarkers are being used to "fingerprint" the microbial community composition and link this to the ^{14}C age of the different extracts. Work is ongoing to isolate targeted, short-lived biomolecules such as RNA, in order to unambiguously determine the ^{14}C age of organic molecules being assimilated by active microbial communities.