

Uncovering microbial species-specific effects on organic matter transformation through novel isotopic approaches

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The biogeochemical transformation and cycling of carbon is largely driven by the activity of complex and diverse microbial communities. Reactions initiated by microbial enzymes at the molecular scale drive the rate and extent of organic matter (OM) degradation to CO₂ and CH₄. A major unknown in carbon biogeochemistry is determining what controls the reactivity of OM to microorganisms. Recent studies have found that the ability to use different carbon sources varies among microorganisms, suggesting that the reactivity of certain pools of carbon can be specific to the taxa that utilize the pool. Here, we ask the question: to what extent is the reactivity and transformation of OM dependent on the species that are present and active in the environment. Using a novel bioreactor system (IsoCaRB), we carried out time-series incubations using bacterial isolates and sterilized organic-rich sediment collected from Guaymas Basin. The IsoCaRB system allows us to measure the production rate and natural isotopic ($\Delta^{14}\text{C}$ and $\delta^{13}\text{C}$) signature of microbially-respired CO₂ to constrain the type and age of organic matter that is accessible to each species. Separate incubations using marine bacterial isolates (*Vibrio* sp. and *Pseudoalteromonas* sp.) and sterilized sediment under oxic conditions showed that the rate and total quantity of organic matter metabolized by these two species differs. Approximately twice as much respired CO₂ was collected during the *Pseudoalteromonas* sp. incubations compared to the *Vibrio* sp. incubation. $\Delta^{14}\text{C}$ and $\delta^{13}\text{C}$ signatures of respired CO₂ show selective utilization of different carbon pools by the two species. These differences in OM degradation may be due to the physiological characteristics of each species and the gene copy number and substrate specificity of degradative enzymes. Our results suggest that organic matter transformation in marine environments may depend on the metabolic capabilities of the microbial populations that are present and active.