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Identification of key microbial players in biogeochemical processes by stable isotope probing of nucleic acids

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The turnover of carbon compounds in the environment is mediated by diverse microbial communities. Despite the progress in cultivation-independent surveys using the phylogenetic marker 16S rRNA, we are still unable to define, which microorganisms (structure) do what (function) actively in their environments. More recently, approaches have been developed that link structure‑function relationships of uncultured microorganisms more directly, one of which is stable-isotope probing of nucleic acids (SIP). This approach is based on the incorporation of 13C-labeled substrate into cellular biomarkers, density gradient separation of 13C-labeled and unlabeled nucleic acids, and molecular identification of active populations. SIP has been used to define structure‑function relationships of microorganisms in a number of different habitats targeting functional guilds involved in C1-metabolism, the turnover of simple carbon substrates, and in pollutant degradation. Moreover, SIP allows even tracking of microbial guilds thriving on complex substrates such as whole microbial cells as part of a food web. Recent advances have set the stage for SIP studies with a higher sensitivity, shorter incubation times, and more relevant substrate concentrations than used previously.