



## **Growth and element flux at fine taxonomic resolution in natural microbial communities**

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Microorganisms are the engines of global biogeochemical cycles, driving half of all photosynthesis and nearly all decomposition. Yet, quantifying the rates at which uncultured microbial taxa grow and transform elements in intact and highly diverse natural communities in the environment remains among the most pressing challenges in microbial ecology today. Here, we show how shifts in the density of DNA caused by stable isotope incorporation can be used to estimate the growth rates of individual bacterial taxa in intact soil communities. We found that the distribution of growth rates followed the familiar lognormal distribution observed for the abundances, biomasses, and traits of many organisms. Growth rates of most bacterial taxa increased in response to glucose amendment, though the increase in growth observed for many taxa was larger than could be explained by direct utilization of the added glucose for growth, illustrating that glucose addition indirectly stimulated the utilization of other substrates. Variation in growth rates and phylogenetic distances were quantitatively related, connecting evolutionary history and biogeochemical function in intact soil microbial communities. Our approach has the potential to identify biogeochemically significant taxa in the microbial community and quantify their contributions to element transformations and ecosystem processes.