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Anaerobic isoprene reduction from *Eucalyptus*-detritus in forest sediments by *Pelotomaculum* sp. and its impacts on methanogenesis

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Isoprene, the most abundantly produced biogenic volatile organic compound, shares a similar atmospheric prevalence with the potent greenhouse gas methane, making it a crucial climate-active gas. Isoprene's high reactivity in the atmosphere notably influences methane concentrations, contributing to adverse effects on climate, air quality, and human health. Until now, isoprene remains a neglected factor in addressing climate change. Despite being universally generated by organisms from all three domains of life, our understanding of its global biogeochemical cycle is severely lacking in contemporary data. The fate of isoprene and the potential microbial communities capable of metabolizing it in the environment, with potential implications for methane metabolism, is unclear. This knowledge gap emphasizes the need for comprehensive investigations to unravel the intricacies of isoprene's role in environmental dynamics and its interconnectedness with methane, further advancing our capacity to address critical climate challenges. In this study, we provide physiological evidence for anaerobic microbial isoprene degradation and evaluate the influence of isoprene abundance on microbial methane formation (methanogenesis) in *Eucalyptus*-leaf sediments. Anaerobic cultures amended with Eucalyptus-leaf sediment revealed the reduction of isoprene into three products: 3-methyl-1-butene, 2-methyl-1-butene, and 2-methyl-2-butene. Contrary to prior research identifying *Acetobacterium wieringae* as the sole anaerobic isoprene-reducing bacterium, our findings suggest that *Pelatomaculum sp*. is potentially responsible for anaerobic isoprene reduction as indicated by 16S rRNA analysis. Methanogenic isoprene-reducing cultures showed that anaerobic microbial isoprene-reduction inhibited methanogenesis. In cultures amended solely with isoprene, methanogenesis was completely inhibited, persisting even after the complete degradation of isoprene from the system. Conversely, in cultures supplemented with isoprene and carbon sources, only hydrogenotrophic methanogenesis was inhibited, indicating a competition between methanogens and isoprene degraders for hydrogen. Metagenomic analyses of the cultures, as well as the isolation of the potential anaerobic isoprene-degrader *Pelatomaculum* sp., are currently being carried out. Our study provides novel insights into the microbial dynamics of anaerobic isoprene degradation using a culture-based approach and metagenomic analyses.