CO2 reduction independent of hydrogen drives methanogenesis in five temperate lakes

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Methane produced by microorganisms in lake sediments is the second largest natural source of this greenhouse gas to the atmosphere. Rates of methane production in lake sediments are often thought to be limited by competing respiration reactions and organic carbon inputs. The latter have increased in lakes worldwide due to anthropogenic nutrient inputs leading to eutrophication. In this study we examine the influence of eutrophication on the abundance and community structure of methanogenic microorganisms and methanogenic pathways across sedimentary records of five temperate lakes that differ in trophic histories. Despite higher methanogenic activity in sediments of eutrophic lakes, abundances of methanogens were highest in sediments of oligotrophic lakes. Moreover, while methanogenic community structure varied significantly at the species (operational taxonomic unit) level in relation to trophic state at the time of sediment deposition, the presence of competing respiration reactions had no apparent impact on methanogenic community structure. Surprisingly, even though CO₂-reduction dominated methanogenesis in sediments of all lakes based on analyses of carbon isotopic compositions and the community structure and genomes of resident methanogens, methanogenic CO_2 -reduction with hydrogen (H_2) was thermodynamically unfavorable under *in situ* conditions. Based on correlations between genomic abundances of syntrophic bacteria with potential for extracellular electron transfer and CO_2 -reducing methanogens, we propose that methanogenic CO_2 reduction in the lakes studied is largely fueled by electrons that are directly transferred from syntrophic bacteria, and is thus independent of H₂ as an electron shuttle.