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High-throughput screens to identify selective controls on methane fluxes from aquatic sediments

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Both terrestrial and marine aquatic sedimentary systems offer possible sinks for carbon sequestration and account for nearly 50% of global methane emissions. However, we lack a robust and quantitative understanding of how complex biogeochemical parameters influence the fate of carbon between stable terrestrial reservoirs and carbon dioxide or methane in the atmosphere nor have we identified reliable, potent chemical interventions to control this partitioning of carbon fluxes. Currently known inhibitors of microbial methanogenesis are limited in number, non-specific and require high concentrations to be effective. Using high-throughput cultivation and high-throughput spectrophotometric assays we our working to establish the first high-throughput screening methodology to identify potent and selective inhibitors of methanogenesis. At the same time, we are developing high-throughput assays to measure the partitioning of carbon between gaseous products (e.g. CO_2 and CH_4) versus biomass and recalcitrant carbon. Using these methodologies, we are able to use high-throughput laboratory incubations assess how complex gradients of carbon sources and inorganic ions influence carbon and electron flow in methanogenic microbiomes. Through this work we have identified several previously overlooked potent and selective inhibitors of methanogenesis from our compound collections. Ultimately, we anticipate that we can identify actionable mechanistically informed strategies to predictably perturb the carbon cycle towards minimizing methane fluxes into atmospheric reservoirs and de-risk targeted chemical interventions to aid in efforts to maximize carbon sequestration in dynamic aquatic ecosystems responsible for the majority of methane fluxes.