Playing scales in the methane cycle: From microbial ecology to the globe

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Two of the great challenges in understanding the planet’s climate system are that (i) biogeochemical cycles (e.g., carbon, water, energy, etc.) are tightly coupled, and (ii) important drivers of those cycles occur at all scales of biogeochemical organization. At the largest scale of space and time are phenomena such as the “Great Ocean Conveyor” (1), which circulates water (plus chemicals and heat) through the oceans of the planet, or the Hadley convection cells (2), which produce the latitudinal climate belts. At the smallest scales of organization, however, there are equally critical processes. For example, in atmospheric chemistry, the kinetics of hydroxyl radical formation and consumption regulate the redox chemistry of the atmosphere (3), whereas the adsorption of nitrogen oxides to ice crystals in stratospheric clouds regulates ozone destruction (4). In biology, global models increasingly find that they must capture the physiology of plant photosynthesis to get the overall C cycle “right” (5).

Microbes and Global Cycles
At the smallest scale of life are microorganisms: bacteria, fungi, and unicellular algae. Microbial processes dominate global biogeochemistry, accounting for roughly half of global photosynthesis and almost all organic matter decomposition, nitrification, denitrification, methane production, etc. (6). Microbial processes, however, are regularly treated as a simplistic black box, although the details of microbial physiology can have large impacts on global biogeochemical cycles and the planet’s climate system, as illustrated in the article by Gauci et al. (7) in this issue of PNAS. The article evaluates the importance of industrial S emissions on the global methane cycle, an interaction that results from the competition for substrates between two groups of anaerobic microbes, and thus highlights an important linkage between the smallest and largest scales of biogeochemical organization on the planet.

Methane is a critical gas in the atmosphere; it currently accounts for >20% of the anthropogenically enhanced greenhouse effect, it is important in regulating the concentration of hydroxyl radicals (the atmosphere’s primary “scrubbing” agent), and its oxidation is a major source of the water vapor in the stratosphere that is critical in forming polar stratospheric clouds, which play an important role in ozone depletion (8).

About 70% of the total global methane source [~600 Tg (9)] is biological production by methanogens. Methanogens are strictly anaerobic members of the Archaea; they are single celled and functionally similar to bacteria, but are actually a distinct third line of evolution along with Bacteria and Eukarya. There are two distinct groups of methanogens: one uses H\(_2\) + CO\(_2\) to form CH\(_4\), and the second splits acetate to form CH\(_4\) and CO\(_2\). The compounds used by both groups are products of anaerobic decomposition (Fig. 1). In all terrestrial ecosystems, decomposition starts with depolymerization, in which extracellular enzymes break down plant polymers into monomers [e.g., simple sugars and amino acids (10)]. In wetlands, where flooding blocks oxygen diffusion into the soil, these monomers are then used by fermenting bacteria that produce H\(_2\) and acetate (as well as other simple organic acids and alcohols) as waste products. These compounds can then be used by methanogens, but they can also be used by sulfate-reducing bacteria. Sulfate reducers use H\(_2\) or acetate as electron donors in anaerobic respiration, using SO\(_4^{2-}\) as an electron acceptor and producing H\(_2\)S as a final product (11).

Largely because SO\(_4^{2-}\) reduction is energetically favorable compared to methanogenesis, sulfate-reducing bacteria are able to outcompete methanogens for substrates. Thus, SO\(_4^{2-}\) is a powerful natural inhibitor of methanogenesis. That is why salt marshes are extremely weak CH\(_4\) sources compared to freshwater wetlands; ocean water flushing provides a constant supply of SO\(_4^{2-}\).

Sulfur, Wetlands, and Methane
Because they lack external sources of electron acceptors (nitrate, sulfate, etc.), natural freshwater wetlands have been...
strong CH₄ sources, accounting for >25% of the total flux to the atmosphere (9). With increases in CO₂ and temperature, and the associated increases in wetland productivity, CH₄ fluxes would be expected to increase (7, 12). However, SO₄²⁻ deposition (from industrial combustion) has the potential to divert substrate flow away from methanogenesis and thereby inhibit CH₄ flux to the atmosphere (Fig. 1 and ref. 13). Even relatively small external inputs of SO₄²⁻ can be powerful agents in redirecting C flow in freshwater wetlands (14).

The relationship between SO₄²⁻ supply and CH₄ production in wetlands shows a hyperbolic relationship with a maximum inhibition of ≈45% (7, 15). The question raised by this result is how much does this interaction affect global-scale CH₄ fluxes? The actual strength of the interaction depends not only on the specific interactions of fermenters, methanogens, and sulfate reducers, but also on the global distributions of freshwater wetlands, of SO₄²⁻ deposition, and of how they relate to regional climate and industrial activity.

Gauci et al. (7) estimated the global impacts of the interaction between methanogens and sulfate reducers. They started with a spatially explicit model of CH₄ flux from natural wetlands to project CH₄ flux out to 2100 under two scenarios of climate change; one included only the warming effects of trace gases emissions on global CH₄ fluxes. According to their estimate, SO₄²⁻ emissions have already reduced the natural wetland CH₄ source by 5 Tg below preindustrial levels. With warming, but ignoring the SO₄²⁻ effects, the natural CH₄ source is predicted to increase by 30 Tg by ≈2050 (7). However, fully accounting for SO₄²⁻ effects reduces that increase by 50% to only 15 Tg. Of course, a global shift to cleaner technology would reduce SO₄²⁻ emissions and the associated inhibition of CH₄, and so the nature of the interactions between the SO₄²⁻ and CH₄ cycles is highly sensitive to human decisions.

Thus, Gauci et al. (7) have made several important contributions. The simple and obvious one is identifying and quantifying the importance of an interaction among the global sulfur and methane cycles. Industrial emission of S gases is having an important effect on the natural global CH₄ cycle, and through this on global warming and atmospheric chemistry. Integrating such second-order effects into global models is important for developing the most reliable possible models of the Earth’s climate system. The less obvious contribution, however, is in the exercise of “playing scales” with a globally important interaction that is grounded in the fine-scale details of microbial physiology and interspecies resource competition. Identifying critical microbial physiology and community dynamics and developing effective modeling approaches to characterize them at large scale remains an important area of research in earth and climate system modeling (16, 17). Technical and intellectual approaches are still being developed to accomplish this goal. The article by Gauci et al. (7) develops an approach that captures a critical microbial interaction, but in a way that makes the mathematical expression of that interaction simple enough, or perhaps even simplistic enough, to effectively integrate it into a global-scale model of CH₄ dynamics.

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