

# New research shows soil microorganisms could produce additional greenhouse gas emissions from thawing permafrost

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As the planet has warmed, scientists have long been concerned about the potential for harmful greenhouse gases to seep out of thawing Arctic

permafrost. Recent estimates suggest that by 2100 the amount of carbon dioxide and methane released from these perpetually frozen lands could be on par with emissions from large industrial countries. However, new research led by a team of Colorado State University microbiome scientists suggests those estimates might be too low.

Microorganisms are responsible for the process that will generate [greenhouse gases](#) from thawing northern peatlands, which contain about 50% of the world's soil [carbon](#). For now, many of the microbes in this environment are frozen and inactive.

But as the land thaws, the microbes will "wake up" and begin to churn through carbon in the ground. This natural process, known as microbial respiration, is what produces the carbon dioxide and methane emissions forecasted by climate modelers.

Currently, these models assume that this community of microorganisms—known as a microbiome—will break down some types of carbon but not others. But the CSU-led work published this week in the journal *Nature Microbiology* provides new insight into how these microbes will behave once activated. The research demonstrates that the [soil microbes](#) embedded in the permafrost will go after a class of compounds previously thought to be untouchable under certain conditions: polyphenols.

"There were these pools of carbon—say, donuts, pizza and chips—and we were comfortable with the idea that microbes were going to use this stuff," said Bridget McGivern, a CSU postdoctoral researcher and the paper's first author.

"But then there was this other stuff, spicy food; we didn't think the organisms liked spicy food. But what our work is showing is that actually there are organisms that are eating it, and so it's not going to just stay as

carbon, it's going to be broken down."

More carbon being broken down by microbial respiration will produce additional greenhouse gas emissions. But this new finding has other implications, too. Some scientists had previously theorized that adding polyphenols to the thawing Arctic permafrost could potentially "turn off" these microorganisms altogether, effectively trapping a massive cache of potentially problematic carbon in the ground. The concept is known as the enzyme latch theory.

That no longer appears to be a viable option, said Kelly Wrighton, associate professor in the College of Agricultural Sciences' Department of Soil and Crop Sciences, whose lab led the work.

"Not only did we think these microbes didn't eat polyphenols," Wrighton said, "we thought that if the polyphenols were there it was like they were toxic and would lock the microbes into inactivity."

The soil microbiome has often been considered something of a black box due to its complexity. Wrighton hopes this new information about the role of polyphenols in permafrost helps shift that perception.

"I'd like to move past these black box assumptions," she said. "We can't engineer solutions if we don't understand the underlying wiring and plumbing of a system."

## **Probing the permafrost in Sweden**

Unlocking the relationship between soil microbes and polyphenols has been years in the making for McGivern, who began examining this topic while working on her doctoral degree in Wrighton's lab in 2017.

McGivern started with a simple question. Scientists presumed that

without oxygen, soil microbes could not break down polyphenols. Gut microbes, however, don't need oxygen to churn up the compound—that's how humans extract healthy antioxidant benefits from [polyphenol](#)-rich substances such as chocolate and red wine.

McGivern wondered why the process would be different in soils, a question that is particularly relevant to permafrost or waterlogged lands that contain little or no oxygen.

"The motivation for a lot of my Ph.D. was how could these two things exist?" McGivern said. "Organisms in our gut can breakdown polyphenols but organisms in the soil can't? The reality was that nobody in soils had really ever looked at it."

McGivern and Wrighton successfully tested the theory in a lab experiment and published a proof of concept study in 2021. The next step was testing it in the field. The team gained access to core samples from a research site in northern Sweden, a place that scientists have used for years to examine questions related to permafrost and the soil microbiome.

But before McGivern could look for evidence of polyphenol degradation in the core samples, she first had to create a database of gene sequences that corresponded to polyphenol metabolism. McGivern mined thousands of pages of existing [scientific literature](#), cataloging the enzymes in cattle, the human gut, and some soils that were known to be responsible for the process.

Once she built the database, McGivern compared the results to the gene sequences expressed by the microbes in the [core samples](#). Sure enough, she said, polyphenol metabolism was happening.

"What we found was that genes across 58 different polyphenol pathways

were expressed," McGivern said. "So, we're saying not only can the microorganisms potentially do it, but they actually are, in the field, expressing the genes for this metabolism."

Still, more work is needed, McGivern said. They don't know what might constrain the process or the rates at which the metabolism is happening—both important factors for eventually quantifying the amount of additional greenhouse gas emissions that could be released from permafrost.

"The whole point of this is to build a better predictive understanding so that we have a framework we can actually manipulate," Wrighton said. "The climate crisis we're facing is so fast. But can we model it? Can we predict it? The only way we're going to get there is to actually understand how something works."

**More information:** Bridget McGivern et al, A cache of polyphenol metabolisms discovered in peatland microbiomes, *Nature Microbiology* (2024). [DOI: 10.1038/s41564-024-01691-0](https://doi.org/10.1038/s41564-024-01691-0)

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