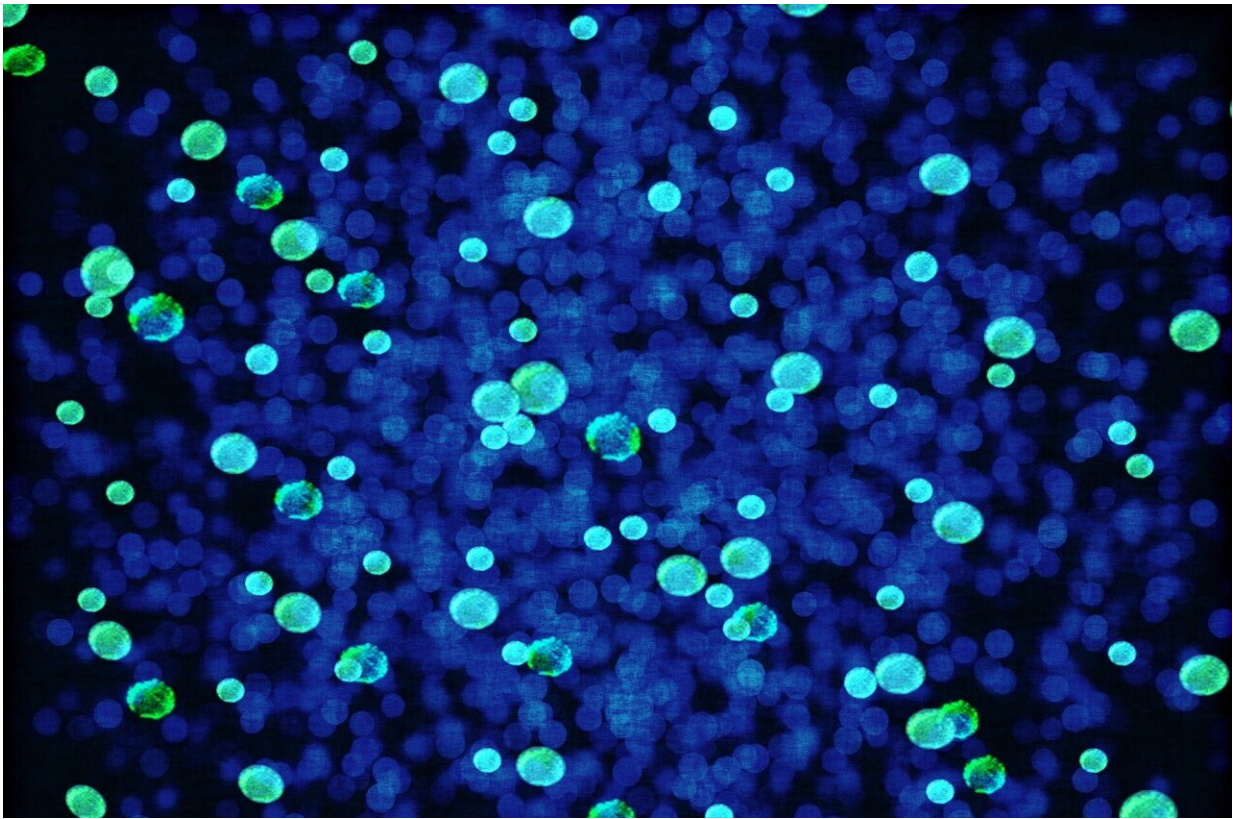# Researchers identify potential microbes and genes that impact forever chemicals

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Credit: Pixabay/CC0 Public Domain

A new study identifies microbes that potentially play important roles in breaking down harmful per- and polyfluoroalkyl substances (PFAS) chemicals—also known as forever chemicals—and points to functional

genes that may be involved in biologically transforming these compounds.

Although microorganisms are known to facilitate PFAS transformation, the key microorganisms and genes responsible for these processes have been largely unknown.

[The paper](link) published in the *Environmental Science & Technology* journal pioneers the employment of bioinformatic tools conventionally used in medical fields and applies them for the first time to the study of PFAS biotransformation.

"The goals are to help other researchers understand which microbes may impact PFAS fate in the environment and develop microbial transformation technologies to treat these contaminants like we do other contaminants," said Natalie Cápiro, assistant professor in the Department of Biological and Environmental Engineering in the College of Agriculture and Life Sciences and senior author of the study.

"Biological treatment of contaminants doesn't require much infrastructure, it's more economical and it can be applied to hard to access locations," Cápiro said. It is best used for areas that won't be developed soon because microbes are slow relative to physical-chemical methods, she said.

"The study provides clues for the next scientists who are working in the area of PFAS biotransformation to help them hone in on what they're trying to target," said Sheng Dong, a postdoctoral researcher in Cápiro's lab and the paper's lead author.

Other researchers conducting [experimental work](link) may now use this information to verify that some of these genes are associated with these transformation pathways, Dong said.

Scientists have previously documented environmental microbial communities capable of transforming human-made PFAS chemicals, which are found in food packaging, water-resistant clothing, nonstick cookware and foams that extinguish fuel-based fires.

Once they get into the environment, including water, they bio-accumulate in organisms, and rise up the food chain in increasing concentrations. They have been linked to lower fertility, development issues in children, high cholesterol and a variety of cancers.

Currently, forever chemicals can be removed from water using activated carbon filters and other sequestration treatment techniques. In soils, current technologies include physical methods such as high temperature thermal and excavation to remove these compounds from the environment. Some microbes can break extremely strong carbon to fluorine bonds found in PFAS chemicals, which may then transform the compounds.

"These compounds are manmade and the analogs in nature are not so widespread, and they don't have the same complexity," Cápiro said.

People began using PFAS chemicals less than 100 years ago. Since then, exposure to the chemicals has possibly given microbes opportunities to adapt and develop pathways for transforming them.

In the study, the researchers collected soil samples from contaminated sites where microbial communities have been exposed to the compounds for many decades.

First, Dong and colleagues used network analysis methods based on the relative abundances of microbial community members in samples, where PFAS biotransformation was observed, to determine relationships between the microorganisms.

"We believe that the microbes are working in a team, it's not just one," Dong said. "We looked for patterns, and if certain microbes were always present." They also considered distinct soils collected from different geographical locations and the presence of various PFAS compounds.

In a second part of the study, the researchers used a metagenome prediction tool, based on marker gene sequencing to explore potential functional genes (and enzymes they express) that contribute to PFAS biotransformation. Marker gene sequencing targets a small section of the genome that is unique to each microbial taxonomical group, and Dong and colleagues then applied bioinformatic approaches to predict the rest of the genome.

Co-authors include Peng-Fei Yan, a postdoctoral researcher in Cápiro's lab.

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