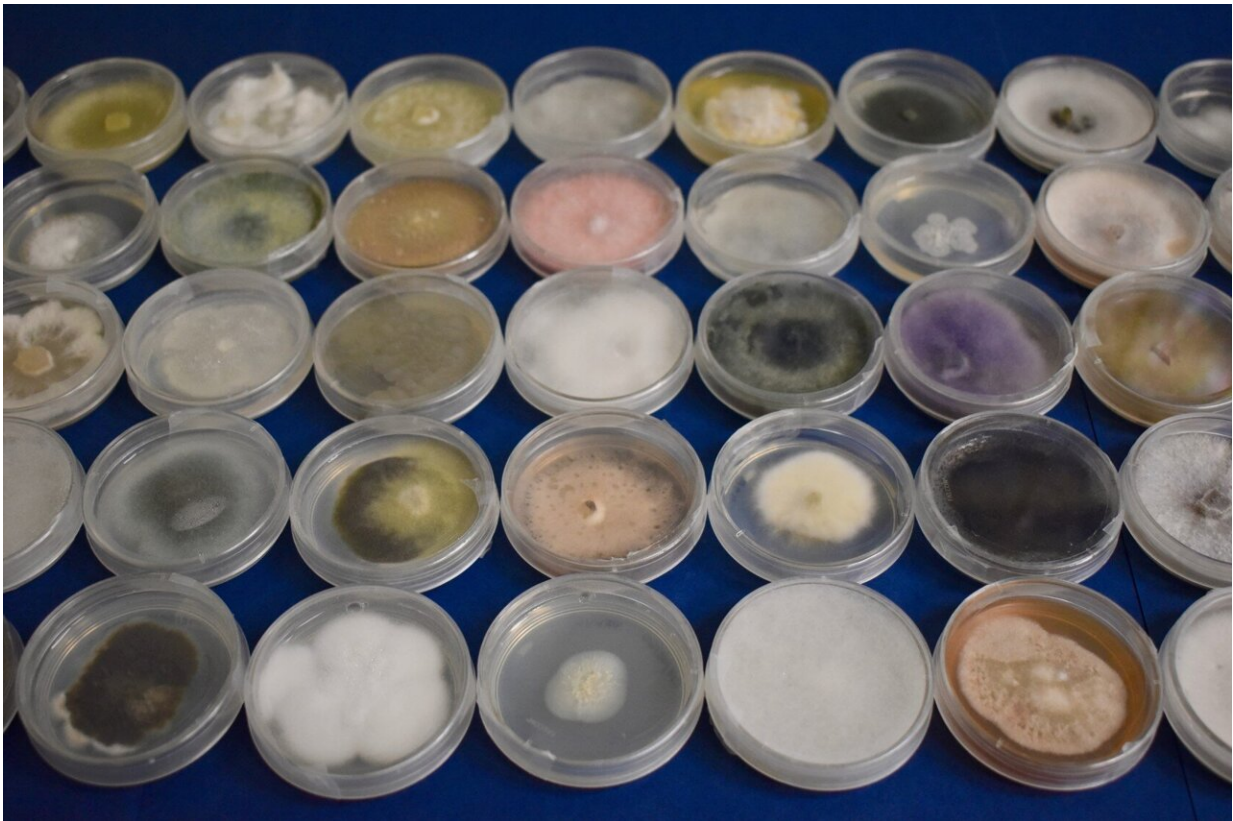


Bacteria, fungi interact far more often than previously thought

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A diverse culture collection of fungal isolates obtained from around the world has been screened by researchers at Los Alamos National Laboratory for potential bacterial associates. Credit: Los Alamos National Laboratory

In a novel, broad assessment of bacterial-fungal interactions, researchers

using unique bioinformatics found that fungi host a remarkable diversity of bacteria, making bacterial-fungal interactions far more common and diverse than previously known.

"Until now, examples of bacterial-fungal interactions were pretty limited in number and diversity," said Aaron Robinson, a biologist at Los Alamos National Laboratory and lead author of a new paper describing the research in Nature's *Communications Biology* journal. "It had been assumed that bacterial-fungal associations might not be that common. But we found a lot of diverse bacteria that appear to associate with fungi, and we detected those associations at a frequent rate."

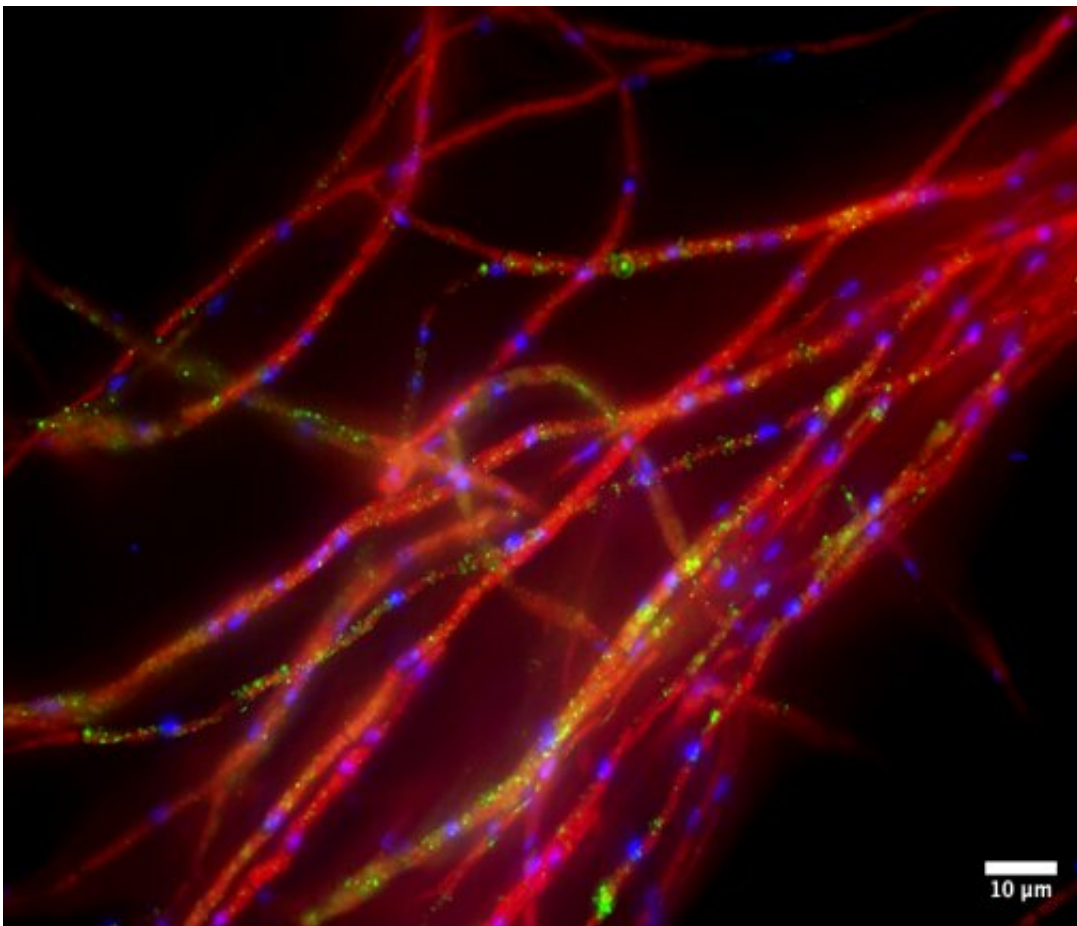
The research contributes to an emerging understanding of the fungal bacteriome, the existence of bacteria both within and in close association with a fungal host, opening up possibilities for studying the interactions more intimately and connecting that research to issues such as ecosystem functioning and [climate change impacts](#).

"This is a starting point to investigate mechanisms of bacterial-fungal interactions at a more intimate level," said Robinson. "That research will be valuable for understanding what allows bacteria to associate with fungi, and how to best leverage that insight to accomplish goals for the Laboratory, for the Department of Energy, and for society in general. Understanding how these organisms interact with each other and contribute to larger systems is highly valuable in everything from modeling things like [climate change](#) to societally beneficial activities such as agricultural or industrial utilization of microbes."

Researchers screened a total of 294 diverse fungal isolates from four culture collections from Europe, North America, and South America for potential bacterial associates. Collaborations with the Center for Integrated Nanotechnologies at Los Alamos allowed researchers to visually examine several of these associations using fluorescence in situ

hybridization techniques.

These fluorescence microscopy examinations complemented the screening and confirmed the widespread and variable presence of bacterial associates among diverse fungal isolates and even within the hyphae (fungal tissue) of a single fungal host.



A visualization of potential bacterial associates (green) in fungal hyphae using fluorescence in situ hybridization (FISH), performed in collaboration with the Center for Integrated Nanotechnologies. Credit: Los Alamos National Laboratory

In addition to screening the culture collections, the research team also screened 408 fungal [genome](#) sequencing projects from the MycoCosm portal, a repository of fungal genome projects developed and maintained by the Department of Energy Joint Genome Institute.

Bacterial signatures were detected in 79 percent of the examined fungal genome projects. In multiple cases, the authors recovered complete or nearly complete genomes of these bacterial associates. Recovery of these fungal-associating bacterial genomes allowed for comparisons between fungal-associating and free-living bacteria.

Of the 702 total fungal isolates examined by the research team, bacterial associates were found in 88 percent—an unexpected detection rate relative to previous, more limited studies. The results shed light on the complexity and diversity of the fungal bacteriome across the fungal tree of life.

The study's overview and description of diverse fungal-bacterial associations provides a path forward for understanding the associations in more depth. Continued analysis of the interactions will aid in a more complete understanding of environmental microbiome processes, particularly fungal and bacterial contributions to nutrient cycling, plant health and climate modeling.

Within the context of changing [climate conditions](#), understanding how bacterial-fungal interactions impact plants, animals, and general ecosystem functioning in diverse environments and under diverse conditions, such as drought and warming, will also help predict and potentially manipulate the impacts of these interactions.

More information: Aaron J. Robinson et al, Widespread bacterial diversity within the bacteriome of fungi, *Communications Biology* (2021). [DOI: 10.1038/s42003-021-02693-y](https://doi.org/10.1038/s42003-021-02693-y)

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