As the twenty-first century progresses, ecosystems and humans are facing several major challenges. Soil microorganisms are central both to understanding these challenges and solving them. While it is understandable how organisms that live underground and cannot be observed by the human eye can escape notice, these microbes are the most abundant organisms in terrestrial ecosystems. For example, one coffee cup of soil may contain approximately 200 billion bacteria, 20 million protozoa, and 100,000 meters of fungal hyphae (long, branching filamentous structures). These microorganisms feast on dead plants and animals, building new microbial cells and releasing important nutrients that are taken up by growing plants. As such, microbes are often referred to as the engines that drive ecosystems, turning over dead material and feeding new growth. Recently, emerging technologies have made it possible for scientists to directly observe soil microbial communities and their activities, providing critical knowledge about these communities.

It is vital to learn which microbial players are important in each ecosystem. First, we must identify the microbial species present in an environment. Because microbes are microscopic and often only a single cell, there are few morphological differences that can be observed to distinguish species; therefore, microbial species are most easily determined through DNA analysis. Fortunately, we now have the ability to rapidly and cheaply extract all DNA from an environment. The extracted DNA can be sequenced and the sequences grouped together based on similarity. These sequences can be compared to a database of sequences from known organisms to match taxonomic groups of bacteria and fungi, producing a list of which organisms make up the microbial community.
While many microbes look similar, the diversity of stuff microbes can digest is astounding! As such, microbial diversity is often described as a metabolic diversity instead of the morphological diversity we are used to in macro-organisms. Some microbes are extremely good at breaking down components of dead plants, such as cellulose and lignin. Other microorganisms specialize in transforming nutrients like nitrogen and phosphorus into forms that plants can easily use. Even still, some metabolic processes require multiple species of microorganisms to complete! Linking which microbes and groups of microbes perform certain metabolic functions in ecosystems is a rapidly expanding area of research.

Microbial ecology researchers at the Illinois Natural History Survey (INHS) study how ecosystems and soils can be conserved and managed to retain nutrients and carbon. Our research investigates how soil microbial communities and activities shift temporally across the growing season in tallgrass prairie. Temporal fluctuations in microbial activity may alter resources available to plants at different times in the year. For example, microbial interactions may modify competitive interactions between plant species, driving plant diversity. These temporal shifts could affect the persistence of plant species with different growth patterns. INHS research is targeting soil microbial communities under “cool-season” plant species, which emerge and mature early in the growing season, and “warm-season” plant species to determine which microbial species and activities may facilitate co-existence of these plant species. These findings could lead to new approaches for prairie restoration and management to promote plant diversity.

Plants fix carbon dioxide from the atmosphere to form leaves, stems, and roots. When these tissues decompose, microorganisms can assimilate that carbon into microbial biomass, or respire it as carbon dioxide back into the atmosphere. Understanding which microbes under which conditions assimilate more carbon and integrate into soil could help diminish adverse global climate change by moving carbon from the atmosphere to belowground.

As we confront existing and emerging environmental challenges, new insights and solutions might be right under our feet.

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