Glimpses of a Hidden Realm

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Charismatic they are not, but fungi have a vastly larger impact on the flow of essential elements through ecosystems than do most more appealing organisms. Gaining an understanding of their diversity and spatial variability, and the implications of these for fundamental ecological processes such as decomposition, has to be a high priority if biologists are to predict the consequences of habitat and climate change.

Only in recent years have techniques existed to allow the systematic exploration of patterns of fungal diversity, as Kabir Peay, Peter Kennedy, and Thomas Bruns explain in the 21st Century Directions in Biology article that starts on p. 799. The often microscopic size and the generally cryptic nature of fungi have typically made it necessary to use biochemical techniques to differentiate them. This requirement has in turn hobbled efforts to chart even the number of fungi in different environments, let alone to assess critical matters such as the resilience of their ecological functions. The knowledge gap is sobering, considering the critical role of fungi in so much of the biosphere (in the case of plants, as symbionts as well as pathogens).

New techniques based on DNA sequencing are now making possible major explorations of fungal diversity. The results are startling: even though fungal species are much more stable than are bacteria, soil samples reveal levels of diversity so high that it is impossible to put an upper limit on it. Moreover, fungi exhibit very high spatial variability, the explanation for which is unknown. Species composition responds to influences such as temperature and nutrient availability, but not in any straightforward way.

DNA analysis also offers potentially useful ways to use this new information with ecosystem management in mind. Conservation cannot be based on trying to preserve unique sequences of DNA: there are too many, and the majority of species identified in this way are probably not vital in terms of larger-scale effects. Yet it should be possible, through the use of new high-throughput sequencing techniques, to assess the occurrence of fungal functions that do have broader significance. As this information emerges, it will allow mycologists to grade the plausible future importance for ecosystems not only of specific species but also of species assemblages. Emergent properties of such assemblages seem likely, because fungi profoundly affect their environment. Comprehending such emergent properties becomes a challenge with practical as well as academic implications, because some of those properties are likely to be causally salient at large scales.

What then? The level of detail that DNA sequence information brings is revelatory but also challenging. Not only can we not preserve everything unique, we cannot even preserve everything that looks beneficial. But the number-crunching capability and data resources now becoming available might, together with laboratory and field experiments, make it feasible to identify those changes in fungal communities that look the most dangerous to ecosystems or human populations. As Peay and his coauthors stress, building a knowledge base that might allow such an endeavor has hardly begun. But it seems like a goal worth working toward.

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