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Patterns and processes of microbial community assembly.

Nemergut DR, Schmidt SK, Fukami T, O'Neill SP ... Darcy JL, Lynch RC, Wickey P, Ferrenberg S

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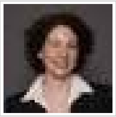

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Although this is a review article, and not primary literature, it is nevertheless an important summary of some important issues to consider when evaluating microbial communities and "microbiomes". While the authors' intent was to help unify some of the language and concepts used when describing microbial community assembly, they also raised several key points about the biases and misunderstandings inherent in microbial community sampling and analyses. As the field of microbiome analysis is blossoming exponentially (no pun intended), we must pay attention to these issues as we attempt to compare across studies, and even within a study. Drawing conclusions without fully appreciating all of the ecological "rules" can lead scientists down a dangerous path. This is especially true as we attempt to link microbiomes to human health and disease, and more attempts are made to identify the "most important" microbes for curing particular disbioses. For example, the authors highlight that dormant components of microbial communities (i.e. spores) potentially represent a vast reservoir of genetic diversity, and this reservoir is not subject to selection the same way that vegetative/growing organisms are. However, they are treated similarly in surveys, depending upon the sampling method. The authors also point out that by sampling even a gram of soil (or stool, skin, etc.), "we are averaging across all of this variation and attempting to uncover patterns between community structure and bio(geo)chemistry at a large scale relative to the size of an organism.". Because we need to focus on traits, as these are the functional components of community members, 16s rRNA sequencing of a relatively "large" sample area (e.g. one gram of soil or stool or skin) makes it more difficult to link traits and taxonomy for microbes than for macrobes. There are many other examples of important considerations as one attempts to survey and interpret microbial communities - too many to summarize in this review. One last example, however, seems critical for the expanding fields of microbiome study: "while communities are not restricted to taxonomic groups (e.g. plants, animal, or microbes), they are often studied in this manner because of logistical constraints... what we refer to as "microbial communities" are often just bacterial communities, as our understanding of membership is typically restricted to the use of certain molecular probes..." I recommend reading this review of community studies as one forms hypotheses in the study of microbial communities.

Disclosures
None declared

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Abstract:

SUMMARY Recent research has expanded our understanding of microbial community assembly. However, the field of community ecology is inaccessible to many microbial ecologists because of inconsistent and often confusing terminology as well as unnecessarily polarizing debates. Thus, we review recent literature on microbial community assembly, using the framework of Vellend (Q. Rev. Biol. 85:183-206, 2010) in an effort to synthesize and unify these contributions. We begin by discussing patterns in microbial biogeography and then describe four basic processes (diversification, dispersal, selection, and drift) that contribute to community assembly. We also discuss different combinations of these processes and where and when they may be most important for shaping microbial communities. The spatial and temporal scales of microbial community assembly are also discussed in relation to assembly processes. Throughout this review paper, we highlight differences between microbes and macroorganisms and generate hypotheses describing how these differences may be important for community assembly. We end by discussing the implications of microbial assembly processes for ecosystem function and biodiversity.

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