



Microbial Ecology at the Spatial, Temporal, and Phylogenetic Scales

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Abstract

Agriculture, bioremediation, disease, and biogeochemical cycling are all heavily influenced by microbial communities. However, it has been challenging to separate the varying impacts of the ecological processes that control the assembly of microbial communities. Microbial systems are being studied at various spatial, temporal, and phylogenetic scales, according to our hypothesis here. We argue that microbial community assembly can be better understood by taking into account spatial, temporal, and phylogenetic grains and extents, which are the two components of scale, more explicitly. This will allow us to demonstrate that distinct processes dominate at various scales. By focusing on taxa area relationships, nastiness, legacy effects, and the application of ecological scale concepts to microbiology, we demonstrate the value of doing so. The long-standing debates in microbial ecology regarding the processes that determine the assembly of microbial communities will be resolved by these proposed scale conditions, and they will serve as organizing principles for the development of hypotheses and theories.

Keywords: Agriculture, Bioremediation, Microbial community, Phylogenetic scale, Phylogenetic scales, Microbial ecology

INTRODUCTION

The most numerous and diverse organisms on Earth are called microbes, which are here referred to as bacteria, archaea, viruses, fungi, and protists. More than 1029 million living microbial cells can be found in soil alone, which contributes to a global biomass of approximately 400 billion tons of carbon. Microbes have a huge amount of biodiversity, probably several orders of magnitude more than animals and plants. The impact that microbes have is proportional to their wide spreaders: Agriculture, health, bioremediation, and other ecosystem services all greatly benefit from microbes, which play a crucial role in the pathogenesis of disease in both animals and plants and play a role in biogeochemical cycling. It is becoming increasingly clear that these effects are caused by emergent properties of microbial communities as a whole as well as individual microbe strains and taxa acting on their own. For example, Crohn's infection and other gastrointestinal problems have been connected to dysbiosis of the human micro biome, while parts of general wellbeing have been

attached to soil microbial biodiversity. The structure of microbial communities can be linked to carbon and nitrogen cycling. In farming frameworks, soil microbial biodiversity can encourage further developed environment working with direct advantages to agro ecosystem action (Whitman W, 1998).

DISCUSSION

Mechanism

The formation of microbial communities, as well as the formation of ecological communities for all organisms, is generally understood to be governed by four mechanisms. First, selection can shape communities. Predation and competition, for example, can influence which species occur (biotic selection), and the physical environment can also filter taxa (abiotic selection). Second, communities' composition can be determined by neutral assembly processes. Communities' composition can change and be neutrally determined through processes similar to genetic drift. Thirdly, dispersal restriction may be crucial: Taxa

that are present in a community but do not belong to it may be those that are unable to reach it. Lastly, mutation may be involved. Microbial genomes can undergo *de novo* mutations to alter community composition and increase diversity. Naturally, these mechanisms can interact with one another and are not entirely distinct from one another (Locey K, 2016) (Yarza P, 2014).

The roles of these four processes have been the subject of extensive microbial ecology research. Selection, neutral processes, dispersal limitation, and other mechanism have all been suggested to play a role in the formation of microbial communities in the human micro biome. Selection and the absence of a dispersal restriction can be significant in marine communities. Abiotic selection has also been used in polluted environments (Schloss P, 2016).

The diversity of microbial community assembly mechanisms, including selection, neutral processes, dispersal limitation, and mutation, is demonstrated by these and other examples. There could be a number of reasons for this heterogeneity, like different mechanisms that work in different environments, different methods for figuring out mechanisms, and taking into account different groups of microbial taxa. Here, we propose that a factor has largely been overlooked in microbial ecology is to blame for much of this heterogeneity: scales of time, space, and phylogeny. We contend that a comprehensive comprehension of the mechanisms underlying the assembly of microbial communities can only be achieved by explicitly taking scale into account (Mora C, 2011) (Joossens M, 2011).

Consideration scale

Microbial ecology studies require the explicit or implicit specification of three scales. First, research identifies a scale of space. Are samples taken from a single location, a city, state, continent, or the entire world? Second, a temporal scale is specified. Are all samples collected over an hour, a day, a season, or a decade? How do these lengths relate to replication rates and asynchronous properties like dormancy? Finally, a phylogenetic scale is specified (Carding S, 2015).

For instance, are all microbes taken into consideration, only bacteria, archaea, or fungi, and are they identified down to the Operational Taxonomic Unit (OTU) level or at a coarser taxonomic resolution? There are two parts to each of these spatial, temporal, and phylogenetic scales: extent and grain. The breadth of the individual units of observations is what is referred to as grain. The spatial grain, for instance, is 10 meters if multiple soil cores from within 10 m quadrats are mixed prior to sequencing. The temporal grain, on the other hand, is 12 hours if ocean water is filtered for 12 hours before being sequenced. Also, the phylogenetic grain is at the OTU level if reads cluster there (but not at the strain level, for example). In contrast to grain, extent refers to the entire study's scope. A study of human gut microbiomes from the contiguous United States would span approximately 4000

kilometers. A study of airborne microbes that were sampled in 2012 and 2013 would span two years. A study that only took into account archaea would be restricted to the domain of archaea. Scale is defined by grain and extent.

It is well known that different mechanisms control community assembly at various grains and scales in macro organisms. Interspecific interactions (biotic selection), on the other hand, frequently take center stage at smaller spatial scales, while environmental filtering (abiotic selection) frequently does so at larger ones. At smaller spatial scales, neutral processes dominate in other systems, while processes like dispersal limitation dominate at larger scales (Wall D, 2015) (Graham E, 2017).

Anthropogenic disturbances can also have effects that are highly scale-dependent. For both spatial and temporal scales, there are numerous additional examples. Scale dependence and heterogeneity of mechanisms are the norm rather than the exception. The role of scale in generating this variability in microbes' mechanisms of community assembly remains largely unexplored (Luo G, 2017) (Siles J, 2018).

CONCLUSION

Future research should focus on the explicit consideration of spatial, temporal, and phylogenetic grain and extent in order to gain a better understanding of how microbe communities form. An understanding of this kind would make it easier to design interventions to microbial systems that would improve human health, agriculture, and the environment in addition to predicting microbial systems and their functions. Macro organism ecology has a long history of explicitly considering scale, which microbial ecology can benefit greatly from.

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CONFLICT OF INTEREST

None

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