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Microbial community assembly and the microbiome revolution

Microbial communities (i.e. groups of potentially interacting microbial populations that co-exist in space and time) most commonly represent complex and highly diverse assortments of microbial populations, each possessing different genomic features that reflect on their specific life strategies. These communities play preponderant roles in most ecosystems, account for a large fraction of the Earth's biomass and most of its biodiversity, drive global biogeochemical cycles and thus the life-support processes of our planet, and develop intimate relationships with plants and animals with a significant impact on their wellbeing.

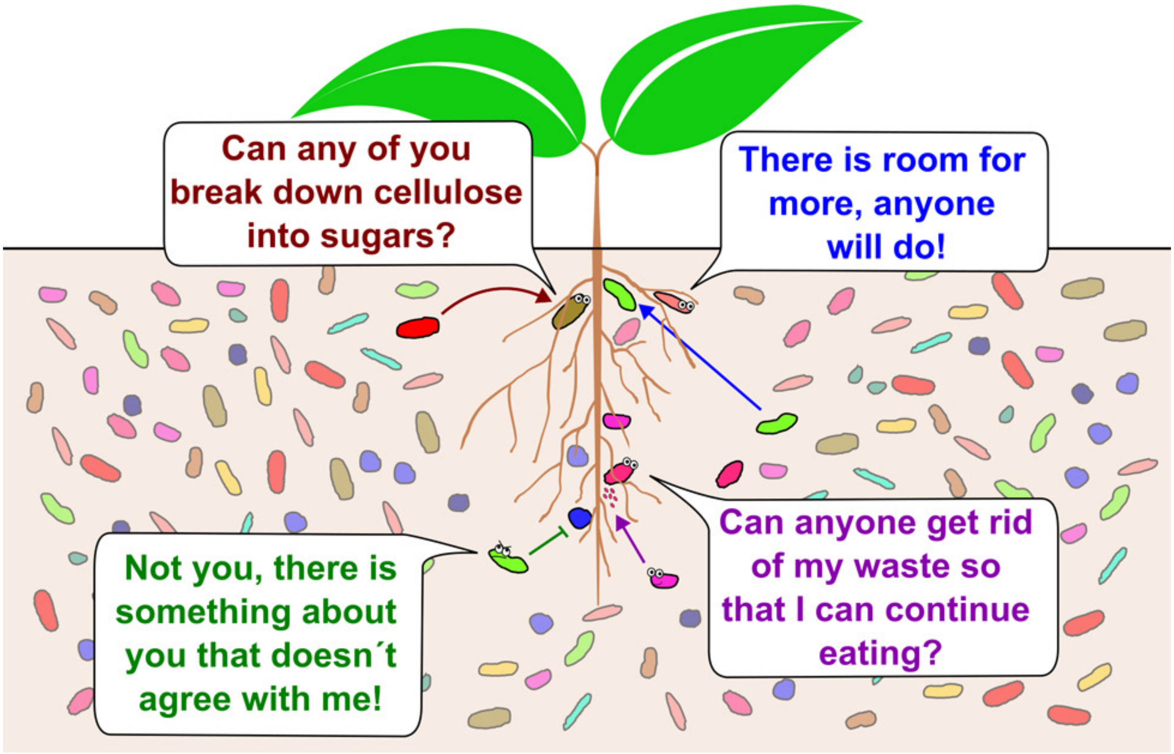

Fig. 1. Multiple, often seemingly conflicting mechanisms jointly determine microbial community assembly.

Microbial ecology is hard to study; microbes are invisible to the naked eye and, even under a microscope, most of them cannot be precisely identified since most microbial species lack characteristic morphological traits. Moreover, it is technically very difficult to know what they are doing at any given time, and how they are interacting with other members of the community. Notwithstanding these drawbacks, the development and subsequent reduction of costs of high-throughput sequencing technologies over the last decade has prompted a golden age in microbial ecology since they allow the unambiguous identification and genomic characterization of members of a given microbial community. Thanks to these technologies, we now possess a wealth of knowledge on the composition, distribution, and, to a certain extent, function of microbial communities from a myriad of ecosystems.

Significantly, we have learnt that microbial communities commonly present shared characteristics; they are highly diverse, show large species richness, and feature the coexistence of populations that should theoretically exclude one another attending to their genomic features. Also, trait-based selection seems to play an important role in determining community composition, microbial ecosystems show remarkable functional stability over time despite large species turnover, and most commonly microbes tend to co-occur with evolutionarily closely related populations (a phenomenon termed phylogenetic clustering). All these shared characteristics lead to the idea of a set of common principles that govern microbial community assembly.

Unfortunately, these principles are still poorly understood, even though they could spur a scientific, technological, and economic revolution. Indeed, the scientific consensus indicates that the domestication of relevant microbial communities has a great potential to provide nature-based solutions to many societal challenges faced in biotechnology, health, and agriculture. Far from being an abstract scientific quest, many economic actors are increasingly moving to the development of microbiome-based products, with both the human and agricultural microbiome markets projected to surpass the billion dollars threshold before the end of the decade.

Our own published conceptual framework for the phylogenetically constrained assembly of microbial communities is grounded on well-known microbial community and genomic characteristics, supported by the recent literature and dedicated results, and able to recapitulate the characteristics most commonly observed in microbial communities. Although the framework presents known limitations and cannot be understood as an all-encompassing model for community assembly, we contend that the analysis of phylogenetic clustering signals in a given microbial ecosystem, together with the ever-increasing microbial genomes repositories, can help unravel its inner workings and assembly rules, and thus the use of the framework offers a helpful route towards understanding and managing the ecosystem. Significantly, the framework presents predictions that can be useful in the production of biotechnologically relevant functional microbial consortia.

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