

How to Use Ecological Tools to Synchronize Microbiomes Based on Single Cell Analyses

Ruyu Gao¹, Shuang Li^{1,2}, Susann Müller¹

¹Department of Environmental Microbiology, Helmholtz Centre for Environmental Research - UFZ, 04318 Leipzig, Germany.

²Faculty of Resources and Environmental Sciences, Hubei University, Wuhan, Hubei 430062, China.

Ubiquitous in ecosystems and human life, natural microbial communities play significant roles and exhibit high complexity in terms of microbial interactions and environmental dependencies. However, complex microbiomes are prone to varying and stochastic fluctuations in composition and function. Few works have been done on assembling and controlling stable complex natural microbial communities with the exception of a looped mass transfer design that shown the ability to stabilize microbiomes over long periods of time (Li et al., 2022).

In this study we want to explore to which degree the rescue effect can be re-established. The looped mass transfer design setup was replicated using the same original environmental sample. Five local microbial communities were continuously grown in parallel, connected by a regional pool with a constant mass transfer rate. The dynamics of these communities were monitored using quantitative high-throughput flow cytometry. Complex microbiome structure variations were evaluated through automatic gating, with the resulting data analyzed using bioinformatic pipelines based on microbial ecology theory.

Results showed that we confirmed the repeatability and feasibility of the looped mass transfer design setup. We observed a repeatedly similar trend attributed to the rescue effect. To explore the ability to synchronize the assembly of microbial communities, the rescue effect was interrupted two times by experimental design. Each time the rescue effect was re-established within the same round but rebuilt to a different structure among rounds. Ecological analysis revealed that both stochastic and deterministic processes play significant roles in our microbial community assembly.

This study is connected to our further aim to gain deeper insights into stabilization and controllability of microbial communities based on this looped mass transfer design and ecological theory, such as constituting artificial microbial communities by bottom-up approaches.

Reference

Li, S., Abdulkadir, N., Schattenberg, F., Nunes da Rocha, U., Grimm, V., Muller, S., & Liu, Z. (2022). Stabilizing microbial communities by looped mass transfer. *Proc Natl Acad Sci U S A*, 119(17), e2117814119. <https://doi.org/10.1073/pnas.2117814119>