

Background:

Microbial communities provide diverse ecosystem functions in a wide range of fields such as medicine, industry, and agriculture. In stably managing those microbial functions, forecasting of microbial community processes is of particular importance. However, predicting microbiome dynamics is notoriously difficult because communities often show abrupt structural changes, such as “dysbiosis” observed in human-gut and aquaculture microbiomes. Elucidating the mechanisms and factors driving community structural changes is one of the key challenges in microbial ecology. In this thesis, I focus on the predictability and controllability of microbiomes by quantifying community-scale stability as well as by exploring core species driving community dynamics.

Methods:

I examined the predictability of microbial community dynamics by estimating population dynamics of constituent microbial species based on quantitative DNA metabarcoding (Chapter 2). I monitored 48 experimental microbiomes for 110 days and observed that various community-level events, including collapse and gradual compositional changes, occurred according to a defined set of environmental conditions. I then applied analytical frameworks of statistical physics and nonlinear mechanics to examine whether community-stability indices could allow us to forecast major shifts in microbial community structure.

I next investigated how community dynamics are driven by species interactions within the microbial communities (Chapter 3). I compiled microbial community data from two types of aquatic ecosystems, namely, fish aquaculture and experimental paddy ecosystems. I then inferred dynamics of causality relationships between microbial species based on a machine-learning framework. By examining changes in the structure of the species interaction networks, I assessed potential roles of “phase-specific” species (or indicator species) that show characteristic population growth in limited periods of time through community dynamics.

Results:

I found that the abrupt community changes observed through the microbiome time-series could be described as shifts between “alternative stable states” or dynamics around complex attractors (Chapter 2). I then showed that collapses of microbiome structure were successfully anticipated by means of the diagnostic threshold defined with the “energy landscape” analysis of statistical physics or that of a stability index of nonlinear mechanics. The results indicate that abrupt microbiome events in complex microbial communities can be forecasted by extending classic ecological concepts to the scale of species-rich microbial systems.

In the analysis of microbial interaction networks, I found that indicator species occupied most upstream positions within the inferred interaction networks and that they could impose causative impacts on many other species. Moreover, indicator species had much more positive than negative impacts on the population dynamics of other species. I further found that such positive interactions were condensed and strengthened within limited periods of time, reinforcing abrupt alternations of dominant species sets. These findings suggest that indicator species involved in time-varying webs of positive interactions are keys to managing and controlling catastrophic shifts in microbial communities and ecosystems.

Conclusion:

In this thesis, the predictability of microbial communities was empirically demonstrated for the first time, to the best of my knowledge. I then explored the possibility of anticipating and thereby preventing large community structural shifts based on monitoring of community stability indices. Moreover, the reconstruction of ecological network architecture provided insights into the potential mechanisms by which alternations of dominant species sets could be promoted by dynamically changing species interactions. Further empirical studies on experimental and field ecosystems are necessary to deepen our understanding of the predictability and controllability of biological community processes.