

Identifying the factors that determine robustness of bacterial cross-feeding networks to ecological disturbance

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Microbial communities drive many ecosystem processes and are vital for maintaining plant and animal health. To understand and manipulate these communities, it is necessary to unravel the principles that structure microbial communities. Previous analyses revealed that microorganisms likely exist within highly integrated interaction networks, within which the survival of cells depends on an exchange of essential metabolites with other community members. However, a major puzzle is how these networks can persist despite changing environmental conditions. This project will address this fundamental question by using both synthetic and natural bacterial communities. Bacteria that differ in their ability to produce one or several amino acids will be obtained by deleting different genes from the genome of three bacterial species or by isolating strains from soil microbial communities. Cocultivating bacterial strains will yield different interaction networks, whose robustness to ecological disturbance will be experimentally verified. The project takes advantage of a technique to simultaneously analyze many different bacterial communities and builds upon previous theoretical work, which identified key factors determining the stability of cross-feeding networks. These predictions will be experimentally tested by determining the stability of networks that differ with regards to critical parameters. The expected results will identify principles that organize microbial communities.

Projektbeteiligte

Prof. Dr. Christian Kost

Universität Osnabrück
Fachbereich Biologie
Abteilung für Ökologie
Osnabrück

Dr. Jonathan Friedman

Hebrew University
Rehovot
Israel

