WWTF Project VRG14-021

Understanding molecular host-microbe interactions in nature: Lucinid clams and their chemosynthetic symbionts

Zusammenfassung

Animal-microbe mutualisms are ubiquitous in nature and are powerful driving forces in the evolution of life on Earth. Most animal-associated microbial communities, including those on and within humans are enormously diverse, which poses an immense challenge to understanding the molecular mechanisms that underpin their establishment and maintenance. Many marine invertebrates have evolved intimate associations with just one or a few species of chemosynthetic bacteria. They are therefore ideal natural models for investigating the molecular mechanisms underpinning host-microbe associations. My Group investigates host-microbe mutualisms in lucind clams that host a specific species of sulfur-oxidizing bacteria in their gills. Lucinid clams are found worldwide in shallow marine habitats such as coastal seagrass sediments that are easily accessible for sampling. There are up to 500 known species of lucinid clams currently known, and each of these hosts its own specific symbiotic microbes. The symbiotic bacteria are chemosynthetic, which means they use chemical energy from the environment to synthesize sugars and other molecules needed by the host. This ancient and highly successful partnership has resulted in a reduction of the length and complexity of the clam's digestive tract over evolution, as it relies on its gill symbionts for nutrition.
We focus on two fundamental aspects of mutualistic interactions: Molecular host-microbe crosstalk, and fine-scale microbial genetic diversity. Molecular host-microbe crosstalk is the language used by symbiotic partners to recognize and communicate with one another. The innate immune system of bivalves allows them to interact specifically with their symbionts and to tell them apart from the diverse 'crowd' of bacteria in their environment. Many beneficial microbes are known to use similar molecular mechanisms to communicate with their hosts as pathogenic microbes use to 'hijack' their hosts. How these mechanisms evolved, and which factors determine whether they will be used for 'good' or 'evil' is currently not well understood. Our approach uses field experiments and laboratory experiments in aquaria at the University of Vienna. The goal of our work is to bring our understanding of the molecular basis of beneficial host-microbe associations to a level previously only achieved for model organisms in artificial surroundings, but so-far unmatched in natural systems. Our second focus is fine-scale microbial diversity and the individuality of the microbiome. Fine-scale diversity in bacteria is the diversity seen within traditionally accepted species boundaries. Recent studies have revealed a remarkable diversity of microbes in nature, and have provided insights into how fine-scale diversity emerges and how it is maintained in natural populations. Investigating the fine-scale diversity of host-associated microbes have revealed the remarkable individuality of these microbes, meaning that each individual animal, including each human being, hosts its own genetically unique microbiome. The next challenge is to understand how microbial fine-scale genetic diversity affects their function. Our research therefore relies on modern techniques for quantifying microbial activity in nature. Our goal is to understand how fine-scale diversity drives the functioning and evolutionary stability of host-microbe associations.

Wissenschaftliche Disziplinen:
106022 - Microbiology (50%) | 106014 - Genomics (30%) | 105904 - Environmental research (15%) | 106054 - Zoology (5%)

Keywords:
Symbiosis, chemosynthesis, sulfur-oxidizing bacteria, lucinid clam, genomics, transcriptomics

VRG leader:	Jillian Petersen
Institution:	University of Vienna
Proponent:	Michael Wagner
Institution:	University of Vienna

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Weiterführende Links zu den beteiligten Personen und zum Projekt finden Sie unter
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