

MATES - Microbiome Assembly and Transfer under Ecological- and Sexual Selection

Bacteria, like animals, rely on transmission to spread and colonise new environments. In this context, the microbial communities that inhabit and/or transiently interact with animal hosts, collectively known as the "microbiome", are key to animal health and fitness. The assembly of the microbiome in the hosts begins at birth and later undergoes a variety of dynamic processes influencing its establishment, function and evolution. Newly, research has theoretically recognized the importance of the microbiome associated with reproductive organs and fluids in influencing a range of reproductive processes and outcomes in males and females. The study of such communities founding the "reproductive microbiome" and the ease with which they could be tracked between hosts' reproductive systems therefore offers key advantages for measuring the role of host-mediated transmission in microbiome assembly and variation. Still, we lack an understanding of the ecological mechanisms influencing such variation. Advances in meta 'omics are sparking interest in how microbiomes impacts physiology, propensity to disease and in turn natural and sexual selection. In addition, gnotobiotic organisms provide unique opportunities to study host-microbiota interplay with a level of experimental control that is not achievable in human studies. Coupling these two approaches should allow to pinpoint key mechanisms underlying this mutualistic relationship in a research field that is still in its infancy. In this light, we will make use of accurate observational systems that have been established to monitor interactions and mating events in the internally fertilising fish Poecilia reticulata, to measure the contribution of host contact to reproductive microbiome transmission and assembly, and how how this in turn shapes host-microbiome feedback effects on their mutual fitness. Here, we propose a research project that will fully address these challenges, providing a shift in host-microbiome research.

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