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PROJECT

Adaptation of Microbial Communities: When Some of the Parts Rely on the Sum of the Parts

Microbiomes (the microorganisms living in/on eukaryotes) critically shape the evolution, ecology, and disease epidemiology of host populations, influencing everything from disease susceptibility, to metabolism and growth, to an organism's ability to adapt to human-mediated change. The advent of "next-generation" sequencing has offered unprecedented insight into the complex and dynamic nature of microbiomes, but we still understand little of how these diverse, multi-kingdom communities function. Much like actors in a play, protists, bacteria, fungi, and viruses all interact in ways that can benefit themselves directly, but also benefit other members of their community, including the host. In this way natural selection, which we typically think of as acting on individual organisms, can act on the level of the "holobiont" (the host and its microbiome). For such selection to result in (co)evolution (whereby each species influences the evolution of the other via imposed reciprocal selection pressure), host-microbiome associations must remain relatively stable over time, and there is to date very limited evidence that this is the case. During my fellowship, I plan to synthesize the history of multi-level selection in evolutionary theory and to use this synthesis to bring together recent data from across systems with the goal of identifying when and how we might predict selection on host-microbiome interactions to result in (co)evolutionary change.

Recommended Reading

Koskella, Britt, Lindsay J. Hall, and C. Jessica E. Metcalf (2017). "The Microbiome beyond the Horizon of Ecological and Evolutionary Theory." *Nature Ecology & Evolution* 1, no 11: 1606-1615. <https://doi.org/10.1038/s41559-017-0340-2>.

Koskella, Britt, and Joy Bergelson (2020). "The Study of Host-Microbiome (Co)Evolution across Levels of Selection." *Philosophical Transactions of the Royal Society B* 375, no. 1808: 20190604. <https://doi.org/10.1098/rstb.2019.0604>.

Morella, Norma M., Francis Chen-Hsuan Weng, Pierre M. Joubert, C. Jessica E. Metcalf, Steven Lindow, and Britt Koskella (2020). "Successive Passaging of a Plant-Associated Microbiome Reveals Robust Habitat and Host Genotype-Dependent Selection." *Proceedings of the National Academy of Sciences* 117, no. 2: 1148-1159. <https://doi.org/10.1073/pnas.1908600116>.

Evolution of the Host and its Microbiome

Biology textbooks are undergoing a great revision as we expand our appreciation of how critical the host-associated microbiome (the community of microorganisms that lives in and on eukaryotes) is to the physiology, health, ecology, and evolution of eukaryotic organisms on this planet. It follows that there is also great interest in learning if, when, and how we can leverage existing host-microbiome interactions or engineer new ones in order to increase human health, sustainable agriculture, and conservation efforts. But key to doing so is acquisition of basic knowledge about how these communities form and function. This includes asking: 1) which species are inside of and which are outside of the microbiome (i.e. where does it begin and end?); 2) how selection can act efficiently to eliminate problematic microbes while allowing for growth of beneficial ones (i.e. how do we 'know' who is good?); 3) whether there exists an optimal amount of diversity in light of host organismal health and fitness (i.e. how much is enough?); and ultimately 4) how hosts and their microbiomes have and continue to influence one another's evolution.

Many in the field are calling for new evolutionary theory in order to parameterize these complex interactions in a way that allows us to predict – and ultimately control – their dynamics. There is now an active debate as to whether we need to rewrite our understanding of evolutionary principles in order to accommodate “the Holobiont” (i.e. the host and its microbiome). Indeed, there has been a push to consider the holobiont as the meaningful unit of selection during adaptive evolution and to consider the genes of the host and those of all of the microbes in and on us as a ‘hologenome.’ However, this seemingly elegant solution has (at least) two key problems: First, it ignores decades of work on multi-level selection that may well be sufficient to explain host-microbiome interactions; and second, it relies on assumptions that are typically vague or undefined and which are often biologically unrealistic. As such, the introduction of a new evolutionary framework (and lexicon) for the microbiome might in fact do more harm than good as the field matures.

In this talk, I will explore how the outcome of natural selection that is imposed simultaneously on genes across different genomes (e.g. on genes from multiple species within a microbiome or on microbial genes and those of the host genome) relates to classical natural selection that acts on genes within the same genome. I will (re)introduce the basic principles of evolution by natural selection in order to hypothesize how diversity is optimized within genomes, and ask whether similar mechanisms could explain diversity of the whole microbiome. Along the way, I will introduce aspects of existing theory (e.g. multi-level selection) that work and those that may not, and will consider if and where the introduction of new terminology in the field is warranted. I will use recent results from my own research to exemplify how these interactions are currently being studied and where I hope this field can contribute to human health, agricultural sustainability, and ecosystem function.

Koskella, Britt (Palo Alto, Calif.,2022)

Understanding the impacts of bacteriophage viruses : from laboratory evolution to natural ecosystems

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=183322471X>

Koskella, Britt (Chichester,2022)

Hosts, microbiomes, and the evolution of critical windows

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=1830584669>

Koskella, Britt (Cold Spring Harbor,2022)

Early phyllosphere microbial associations impact plant reproductive success

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=1830578987>

Koskella, Britt (Cold Spring Harbor,2022)

Leaf side determines the relative importance of dispersal versus host filtering in the phyllosphere microbiome

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=1830553577>

Koskella, Britt (Washington, DC,2020)

Successive passaging of a plant-associated microbiome reveals robust habitat and host genotype-dependent selection

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=1764087569>

Koskella, Britt (London,2017)

The microbiome beyond the horizon of ecological and evolutionary theory

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=1764086554>

Koskella, Britt (2013)

The origin of specificity by means of natural selection : evolved and nonhost resistance in host-pathogen interactions

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=104328205X>

Koskella, Britt (2009)

Evidence for negative frequency-dependent selection during experimental coevolution of a freshwater snail and a sterilizing trematode

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=757170277>

Koskella, Britt (2007)

Advice of the rose : experimental coevolution of a trematode parasite and its snail host

<https://kxp.k1oplus.de/DB=9.663/PPNSET?PPN=75717065X>