

Wildlife microbiomes

Institute research is advancing our understanding of the complex microbial communities essential to the health of species and ecosystems.

Microscopic organisms are found everywhere on Earth: in soils, oceans and living in association with animal and plant hosts. Complex microbial communities, known as the ‘microbiome’, play an essential role in maintaining the health of both individual species and entire ecosystems.

In animals, the microbiome underpins a myriad of physiological processes critical to host health, including metabolism, digestion, optimal immune system function and protection from pathogens. Understanding the links between the microbiome and animal health can help us to tackle a broad range of global conservation challenges. Institute scientists are conducting groundbreaking research into the fundamental science of host-microbiome interactions, how these principles can be applied to issues such as global population declines caused by wildlife disease, and how best to manage threatened populations.



and what consequences this variation has for disease resistance.

New research led by the Institute has revealed that common frogs (*Rana temporaria*) living in habitats with greater bacterial diversity in turn had more diverse skin microbiomes. More importantly, frogs with more diverse microbiomes were less susceptible to the lethal pathogen ranavirus.

In a separate study, we have shown that midwife toads (*Alytes obstetricians*) in populations suffering more severe outbreaks of *Bd*, characterised by rapid population declines, exhibited lower microbiome diversity compared to populations suffering milder *Bd* infection dynamics. Thus, microbiome diversity appears to be a critical trait in predicting host resistance to disease and disease dynamics, and colonisation

of the host by bacteria living in the environment may be a crucial process determining that diversity. Future research will probe the mechanistic basis of these links between microbiome diversity and disease resistance. For example, we will use both shotgun metagenomics and metabolomics to understand whether increased microbiome diversity also results in a greater diversity of bacterially derived metabolites that may directly attenuate the pathogen.

Bacterial probiotics to mitigate wildlife disease

A novel tool for the mitigation of wildlife disease involves the augmentation of the host microbiome with bacteria known to inhibit the growth of the pathogen. The Institute plays a leading role in the development of probiotic treatments

for wildlife disease. Previous work has demonstrated that the ability of a single probiotic bacterium to inhibit *Bd* is not consistent across multiple variants of chytrid isolated from separate geographic locations.

By adopting a community-level approach to probiotic development, we have demonstrated that using a combination of multiple bacterial isolates as a single ‘consortium probiotic’ yields broader-spectrum inhibition of *Bd* compared to single bacteria. This research highlights the possibility that bacterial consortia may offer a more robust tool for the probiotic inhibition of wildlife diseases, such as chytridiomycosis, in the wild.



Linking gut microbiome to nutrition and physiology

Bacteria living in animal digestive tracts have enormous potential to impact host health and physiology by controlling the efficiency of energy metabolism from food. There is now growing interest in the idea that differences among individuals in their gut microbiomes may underpin the differences we observe in the wild in animal body condition and health, and the extent to which individuals are able to specialise on different food resources.

The Institute is leading a novel research programme to understand the links between gut microbiome and nutritional health, using the light-bellied brent goose (*Branta bernicla*

hrota) as a model system. Migratory brent geese use fat reserves stored during the spring staging period in Iceland to finance the energetic cost of reproduction in the Canadian Arctic. Thus, geese able to liberate more energy from food can store more fat and lay more eggs. This study will probe the mechanistic link between gut microbiome composition and ability to maximise energy metabolism, and how differences in microbiome may



allow individuals to specialise on different food sources by providing a pre-adapted metabolic toolkit digestion of specific nutrients. Results from this study will have marked implications for our management of wildlife populations.

For example, we may be able to improve the health of animals translocated to new areas by administering probiotics that will optimise their ability to digest local food/prey items.