Adenovirus and Astrovirus infections perturb the gut microbial community of non-human primates and bats

Non-human primates represent an excellent natural model system for studying host-pathogen-microbiome interactions, since they harbour an important source of several crucial viruses of humans and livestock, including Adenoviruses AdV - a major cause of diarrhoea in children. As in humans, a remarkably high AdV-prevalence, and inferred zoonotic potential has been reported for mouse lemurs. We examined the influence of AdV on the gut microbiome of naturally infected Malagasy mouse lemurs (Microcebus griseorufus). Our study shows that enteric AdV indeed disturbed the gut microbial community composition. Beneficial genera decreased, whereas pathogen-containing genera increased after AdV-infection leading to pathobiont-like shifts in the gut microbiome. This shows that in apparently healthy lemurs, AdV infections disturb the gut bacterial homeostasis, which can increase previously suppressed health risks by promoting co-infections. Interestingly, we observed similar effects also in a neotropical bat species (Artibeus jamaicensis) infected with Astroviruses, also causing diarrhoea in young and immune-compromised humans, supporting the idea that virus-microbiome interactions have important, largely neglected implications for host health. If similar processes are present in humans, the effects of enterovirus infections would cause longer-term impacts and go beyond the directly observed symptoms.


Unraveling the skin microbiome of endangered and rediscovered Costa Rican amphibians

Some amphibians that were thought to be “extinct” have been rediscovered decades after population declines in the late 1980s. These species appear to have evolved resistance to the pathogen Batrachochytrium dendrobatidis (Bd), the likely causative agent of their declines and offer a unique opportunity to improve our understanding of the selection and diversity of Bd-protective skin microbiomes in endangered neotropical amphibians. Our study showed that the skin microbiome of surviving species (Lithobates vibicarius, Craugastor escoces, Isthmohyla rivularis and I. pseudopuma) possess putatively Bd-inhibitory activity across species (e.g., by the presence of Pseudomonas veronii and Acinetobacter johnsonii), which
could be involved in resistance against Bd. We also studied the variation of the skin microbiome across the life stages of *L. vibicarius* and observed that life stage is a strong predictor of the diversity of the skin microbiome, suggesting a dynamic skin microbiome through development. With this study, we have begun to fill the gap in our knowledge of the skin microbiome, particularly from those species that are susceptible to *Bd* and have relict populations that persist and recover after dramatic *Bd*-associated declines.


**Extreme MHC diversity in bats with wide geographic ranges**

Different hypotheses may explain extreme MHC variability. One is that such variability is attributable to adaptation to a wide geographic range and a diverse array of habitats, as found in passerine birds. Here we show that MHC class I diversity in Seba’s short-tailed bats (*Carollia perspicillata*), a widely distributed, generalist, neotropical species, shows a remarkable individual and population-level diversity and length-polymorphism comparable with that reported in passerine birds. Investigation of the details of the underlying adaptive processes and the role of the high MHC diversity in pathogen resistance are important next steps for a better understanding of the role of bats in viral evolution and as carriers of several deadly zoonotic viruses.


**How low is functional MHC diversity in cheetahs?**

Species that experienced a population bottleneck, a sharp reduction in the size of a population, often show a low genetic variability, also in adaptive immune relevant genes required to defend against parasites and pathogens. Free-ranging Namibian cheetahs (*Acinonyx jubatus*), however, despite being a textbook example of depleted genetic variability due to habitat loss, human-wildlife conflicts and historic bottlenecks, show no signs of impaired immunocompetence or health - thus contradicting the theoretical assumptions. How are cheetahs able to defend themselves against diseases? This study revealed that free-ranging Namibian cheetahs indeed possess only a low number of immune gene alleles at the major histocompatibility complex (MHC) comparable to other bottlenecked (endangered) cat species. However, these remaining alleles are functionally very divergent and might (currently) be sufficient in terms of pathogen recognition and initiation of the immune defence. Moreover, the allelic composition of cheetahs influences the level of MHC expression (so far only known from human research) which could add to functional variation and, thus, might play a role in the ability to defend against pathogens. This offers an explanation as to how bottlenecked cat species might have avoided impaired immuno-competence, despite showing low MHC allelic diversity.

Corridor effects on the genetic diversity of mouse lemurs

Corridors rank top among the recommendations to counteract the effects of habitat modification and reduce the vulnerability of small populations to environmental variation and stochastic processes, such as genetic drift. Our study focuses on the effect of the establishment of corridors on neutral (microsatellites) and adaptive (MHC) genetic diversity in *Microcebus ganzhorni*, a recently discovered primate species restricted to a few patches of littoral forest in southeastern Madagascar. While we find similar patterns of neutral and adaptive individual diversity as suggested from estimates of heterozygosity and allelic richness between sampling periods, we provide evidence that after the establishment of corridors a larger number of shared private alleles are found at microsatellite loci. Furthermore, our results confirm the role of selection as a main driver of MHC II diversity in *M. ganzhorni*. We argue that corridors, even for animals that appear to be robust to fragmentation, might play an important role in population dynamics. This work highlight the relevance of long-term genetic monitoring providing insights into the evolutionary history and patterns of gene flow of wild populations and the possibility to tease apart the effects of drift from selection maintaining MHC adaptive variability.


Microplastics and the gut microbiome: how chronically exposed species may suffer from gut dysbiosis

Since the mass production of plastics began in the 1950s, we have become inundated in plastic. Although this development brought with it advantages (imagine what might happen if you dropped a mobile phone made out of glass), it also started a massive and uncontrolled experiment since it takes centuries for plastics to degrade. In this review, we identified three mechanisms through which microplastics could harm one of animals’ greatest symbionts, the gut microbiome, and thus, because of its vital standing in host health, how microplastics could harm wildlife health: 1) by mechanically damaging the gut lining, an essential component in maintaining homeostasis between host and the gut microbiome; 2) by acting as a pathogen vector, allowing potential pathogens to hitchhike on the surface of microplastics and thus disturbing the gut microbial community; and 3) by leaching chemicals that can interfere with normal host hormone signaling, another major regulator of the gut microbiome.

Gut microbiome as indicator of heavy metal pollution in soil

Gut microbiomes are becoming recognized as important players in organism health, with comprehension of their perturbations in the polluted environment offering new insights into the nature and extent of heavy metal effects on the health of soil biota. Earthworms are essential species in soil, which carry out the soil biological regulation by mixing organic matter and mineral particles inside their gut. Through their intimate contact with soil, earthworms are exposed to the variety of pollutants and are important indicators of soil quality. In this research we investigated the effect of heavy metal cadmium (Cd) on the earthworm (Lumbricus terrestris) gut microbiota. Cd exposure led to perturbations of earthworm gut microbiota with an increase in bacteria previously described as heavy metal resistant or able to bind heavy metals, revealing the potential of the earthworm-gut microbiota system in overcoming human-caused heavy metal pollution. Furthermore, we defined several bacterial genera as bacterial indicators of exposure to Cd which could serve as biomarkers in soil biomonitoring practices. The results of this study help to understand the impact of anthropogenic disturbance on soil fauna health and will have implications for environmental monitoring and protection of soil resources.