

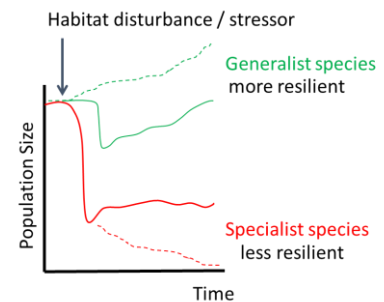
## Research Outline



### Understanding the effects of anthropogenic impact on ecology, genetic diversity and population health of wildlife

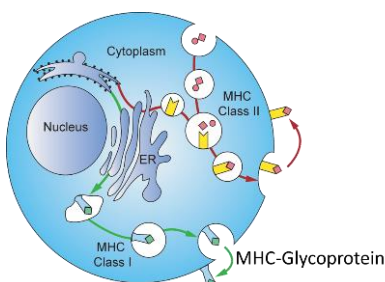


Changes in land use usually cause shifts in species composition, and alter species abundance and their genetic diversity. However, wildlife species reactions to anthropogenic disturbance are not alike. While species with a small ecological-niche are frequently more sensitive to environmental perturbation and decline after anthropogenic disturbance, species that have a high plasticity are more resilient and increase in numbers and density, and frequently become dominant in local species assemblages. These so-called generalist species often thrive in or at edges of altered landscapes and/or use the matrix surrounding the habitat fragments, often leading to closer contact to humans, livestock and domesticated animals. As a consequence, generalist species might turn into potential pathogen reservoirs and act as vectors of zoonotic diseases, despite appearing phenotypically healthy.



While there is strong awareness of the direct negative consequences of habitat loss, invasive species, environmental pollution, overexploitation and climate change on biodiversity, wildlife health was only recently recognized as an emerging cause of species decline. Changes in parasite and pathogen pressure due to microclimatic shifts and increased contact rates between wildlife, humans and their livestock potentially affect the prevalence and transmission rates of pathogens and might be one reason for the increasing number of novel infectious and zoonotic diseases threatening our biodiversity and personal well-being.

One fundamental question in evolutionary and functional ecology as well as applied conservation measures is to understand what drives and limits a species' ability to adapt to current environmental and climatic changes and how might this affect the dynamic interplay between pathogens and hosts. Pathogens and parasites form a natural part of our ecosystems and represent one of the major selective forces shaping host evolution, as they generally depend on ecological conditions of their host's habitat. On the other side, the ability of a host population to resist pathogens depends, to a large extent, on its immunogenetic constitution and its microbial symbionts.



In vertebrates, genes of the major histocompatibility complex (MHC) play a key role in the host's adaptive immune response and are of central importance in pathogen and parasite defense. When MHC diversity in a population is lost (owing to human or natural disturbance), the ability to present pathogen antigens to the immune system is strongly impaired. In addition, MHC variation in mammals is intrinsically related to an individual's unique odor, which plays an important key role in social behavior and mate choice influencing the genetic make-up of offspring. For instance, the MHC can directly

shape olfactory cues (e.g. through the urinary presence of its gene products), which many mammals (but also other vertebrates) use for individual recognition. Moreover, aside from direct involvement in mounting adaptive immune responses, the MHC is assumed to regulate gut commensal bacterial

diversity and shape the production of immune-modulatory substances by microbes, indirectly affecting host pathogen susceptibility.

Vertebrates are inhabited by vast numbers of microorganisms that are increasingly emerging as key players in their host's biology and evolution. These microbial communities carry orders of magnitude more genes than their hosts and support functions that are not encoded in the host's genome. The gut bacterial community provides essential nutritional services to its host, is an important driver of mucosal immunity maintaining gut homeostasis, and provides protection against gut-invading pathogens. Thus, the gut microbiome is functionally essential to host homeostasis and health but may also embody a source for potential pathogens. The microbiome is likely, to varying degrees, under host genetic control – and evolutionary partnership that benefits both parties and possibly enables the host to cope with disturbances. Shifts in the microbiome's diversity beyond the normal range of variation may, however, lead to dysbiosis, which might cause an increasing susceptibility to enteric pathogens, which, in turn, may cause diseases. Especially, zoonotic enteric viral infections might pose a serious threat to gut bacterial homeostasis, increasing health risks by promoting co-infections.

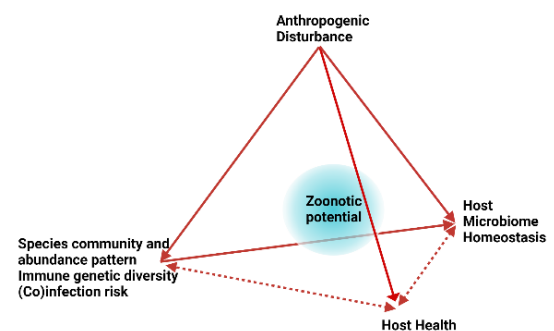


[https://www.youtube.com/watch?v=sfGJ\\_PwxrTA](https://www.youtube.com/watch?v=sfGJ_PwxrTA)



In our research, we combine ecological field work with laboratory analyses (genetics, pathogen and parasite screening) in a wide range of different wildlife taxa, such as rodents, marsupials, lemurs, bats, lagomorphs, carnivores, birds, amphibians and reptiles, and in order to understand the effects of anthropogenic impact, changes in land use and associated shifts in animal communities on wildlife health and emerging zoonotic diseases. We have ongoing projects in Africa, Central and South America, Canada and Europe. We apply genomic approaches using high throughput sequencing technologies (Illumina®) to investigate the mechanisms by which neutral (microsatellite, genome-wide

SNPs) and adaptive genetic diversity (MHC, TLR) act on evolutionary and behavioural processes, and investigate trace-amine associated olfactory receptor genes (TAARs). We study the gut and skin microbiomes of different wildlife hosts in order to understand the effects of ecological, genetic and environmental factors but also the implication of viral, bacterial and fungal (co)infections on the 'normal' range of bacterial variation, and the implications of a microbiome dysbiosis on wildlife health and as driver of zoonotic coinfections. We investigate the health status of wildlife individuals by monitoring ecto- and endoparasites, bacterial, fungal and viral pathogen loads by amplicon sequencing, metagenomics, metabarcoding and viral genome assays. The combined data sets are analyzed by state-of-the art bioinformatics and statistical tools.



In a nutshell, working with an international team at the interface of evolutionary ecology, functional biodiversity, host-pathogen interactions, microbiome health functions, immune and conservation genetics, with the application to biodiversity conservation, our research uses an interdisciplinary, integrative approach to determine the effects of anthropogenic impact, land use change and environmental pollution on wildlife health and zoonotic diseases.