Recent Research Highlights

Meerkats under pressure: Infections and climate change affect meerkat immune genetic and gut microbial diversity

Pathogens are among the most significant selective pressures on wildlife, particularly those infections that cause high mortality or strongly reduce reproductive success. Such infections drive host evolution through pathogen-mediated balancing selection**.** Immune genes, especially those of the major histocompatibility complex (MHC), are prime candidates for studying pathogen-mediated selection because of their central role in adaptive immune responses. Despite strong theoretical frameworks, detecting pathogen-mediated selection on host MHC and identifying the underlying mechanisms—such as heterozygote advantage, rare-allele advantage, or fluctuating selection - in natural populations remains challenging, leaving our understanding of host-pathogen coevolution limited.

Wildlife tuberculosis (TB), caused by pathogens in the *Mycobacterium tuberculosis* complex, poses a threat to many wildlife species. Infections are often latent and undetectable for long periods but usually irreversible and lethal once individuals develop clinical disease. Southern Africa is a global hotspot for wildlife TB, and the impact of the disease is worsened by hotter, sporadically drier conditions due to climate change. Within the long-term study population of wild meerkats (*Suricata suricatta*) monitored by the Kalahari Meerkat Project, TB significantly contributes to overall mortality and social group extinction. Given this strong selective pressure, we investigated TB-mediated selection on meerkat MHC using over 20 years of genetic and disease surveillance data from more than 1,500 individuals. Our analyses revealed strong evidence of pathogen-mediated selection on meerkat MHC: MHC genes showed faster differentiation than neutral markers over the study period. Rather than overall MHC diversity, selection appeared to act on specific alleles, suggesting mechanisms such as fluctuating selection or rare-allele advantage. One allele in particular, DRB*13, shifted from being associated with higher TB susceptibility to lower susceptibility, followed by an increase in its frequency. Carriers of DRB*13 also experienced higher reproductive success, slower progression to clinical TB, and longer survival after infection. We confirmed that climate variables - specifically higher temperatures and lower rainfall - accelerate TB progression and increase mortality. Given the combined pressures of infection and climate change, understanding how hosts adapt to such challenges is increasingly important. One proposed mechanism is rapid adaptation via shifts in the gut microbiome, which could mitigate external stressors. However, our results showed that TB infection and adverse climate conditions were associated with a loss of beneficial bacteria, particularly lactobacilli, rather than adaptive microbiome changes. This loss of gut mutualists further contributed to reduced survival, indicating that meerkats do not quickly compensate for environmental or pathogenic stress through microbiome adaptation. Overall, our findings suggest that both pathogens and climate change exert strong, compounding pressures on meerkat populations, driving selection on specific immune alleles while simultaneously undermining potential microbiome-mediated resilience.

In collaboration with Prof. Dr. Tim Clutton-Brock (University of Cambridge, UK) and Prof. Dr. Marta Manser (University of Zürich, Suisse). Funded by DFG (PI S. Sommer, SO 428/15-1).

Müller-Klein N, Risely A, Wilhelm K, Riegel V, Manser M, Clutton-Brock T, Silver L, Santos PSC, Melville DW, Sommer S (2025) Twenty years of tuberculosis-driven selection shaped the evolution of the meerkat major histocompatibility complex. *Nature Ecology and Evolution*. *https://doi.org/10.1038/s41559-025-02837-x.*

Müller-Klein N, Risely A, Schmid DW, Manser MB, Clutton-Brock T, Sommer S (2022) Two decades of tuberculosis surveillance reveal disease spread, high levels of exposure and mortality, and marked variation in disease progression in wild meerkats. *Transboundary and Emerging Diseases.* doi:*10.1111/tbed.14679.*

Risely A, Müller-Klein N, Schmid D, Wilhelm K, Clutton-Brock T, Manser M, Sommer S (2022) Climate change drives loss of bacterial gut mutualists at the expense of host survival in wild meerkats. *Global Change Biology*. https://doi.org/10.1111/gcb.16877.

Risely A, Schmid DW, Müller-Klein N, Wilhelm K, Clutton-Brock T, Manser MB, Sommer S (2022) Gut microbiota individuality is contingent on temporal scale and age in wild meerkats. *Proceedings of the Royal Society B*, 289, 20220609*.* https://doi.org/10.1098/rspb.2022.0609.

Donadio J, Risely A, Müller-Klein N, Wilhelm K, Clutton-Brock T, Manser MB, Sommer S (2022) Characterizing tuberculosis progression in wild meerkats (*Suricata suricatta*) from faecal samples and clinical signs. *Journal of Wildlife Diseases*, 58(2), 309–321. doi: 10.7589/JWD-D-21-00063.

Risely A, Wilhelm K, Clutton-Brock T, Manser MB, Sommer S (2021) Diurnal oscillations in gut bacterial load and composition eclipse seasonal and lifetime dynamics in wild meerkats, *Suricata suricatta. Nature Communications*, 12, 6017*.* https://doi.org/10.1038/s41467-021-26298-5.

Risely A, Gillingham MAF, Béchet A, Brändel S, Heni A, Heurich M, Menke S, Manser M, Schmid J, Tschapka M, Wasimuddin, Sommer S (2021) Phylogeny- and abundance-based metrics allow for the consistent comparison of core gut microbiome diversity indices across host species. Front Microbiol 12:659918. https://doi.org/10.3389/fmicb.2021.659918.

Assessing natural trace-amine associated receptor repertoires in wild meerkats

In addition to immune defences and microbiome dynamics, olfaction represents another crucial axis through which meerkats navigate ecological and social challenges. While olfaction has historically received less attention than other sensory modalities, it plays a central role in social communication, foraging, and predator avoidance, all of which directly affect survival and reproductive success. A recently discovered family of olfactory receptors, the trace amine-associated receptors (TAARs), mediates these behaviours in laboratory animals and has been shown to influence mate choice in bats and raccoons. This makes TAARs strong candidates for investigating the genetic basis of olfaction in wildlife under natural conditions. TAAR diversity varies widely both within and between species, largely due to gene duplication and pseudogenization, and the number of TAAR genes is thought to reflect the ecological importance of olfaction for a species. In meerkats, olfaction is key to social interactions, resource acquisition, and predator detection, making TAAR genes particularly relevant for understanding how sensory genetics shapes behavior and life-history strategies. Leveraging the extensive longitudinal data and genetic samples from the Kalahari Meerkat Project, we developed a high-throughput sequencing protocol for meerkat TAAR genes and genotyped nearly 400 individuals. We identified polymorphism at two loci—two copies of TAAR6 and three copies of TAAR8 - encompassing 25 alleles, placing meerkat TAAR diversity on par with other highly olfactory-dependent mammals, such as rats and mice. Analysis of 20 years of data revealed strong purifying selection on both loci: at least one amino-acid variant per locus was nearly universal, often encoded by multiple synonymous nucleotide alleles. We hypothesize that these conserved variants reflect the functional

importance of specific TAARs in meerkats, while the remaining diversity may contribute to behavioral and life-history variation. Building on these findings, we are now investigating how TAAR diversity influences life-history decisions, linking sensory genetics to ecological and evolutionary outcomes.
In collaboration with Prof. Dr. Tim Clutton-Brock (University of Cambridge, UK) and Prof. Dr. Marta Manser (University of Zürich, Suisse). Funded by DFG (PI S. Sommer, SO 428/15-1).

Fähnle J, Wilhelm K, Wiese B, Manser M, Clutton-Brock T, Sommer S, Müller-Klein N (2025) Natural variability of trace-amine associated receptors in wild meerkats. Front Zool 22, 37. https://doi.org/10.1186/s12983-025-00590-2.

Species community assemblages shape pathogen dynamics across disturbed landscapes

Changes in biodiversity caused by human land-use can restructure wildlife communities in ways that alter infection risk. We investigated how species assemblage and diversity translate into predictable shifts in pathogen prevalence, and why these relationships can differ between protected and human-impacted habitats.

In bat communities, we found that coronavirus prevalence is influenced not only by individual host species but also by the composition of the assemblage in which they occur. Across multiple roosts, infections were best predicted by bat community structure, with prevalence increasing in less diverse assemblages. This pattern suggests that changes in community composition favor a smaller set of highly competent hosts and certain demographic states (e.g., higher proportions of immunologically naïve individuals), thereby amplifying viral circulation at the community level.

Using wildlife communities in Panama as a model system, we showed that disturbance-driven changes in biodiversity can elevate protozoan infection risk. Trypanosome infections increased in altered landscapes primarily because disturbance promoted reservoir-dominated assemblages, particularly disturbance-tolerant generalists, and reduced genetic diversity in key host species. Notably, diversity–disease relationships were context-dependent: in protected systems, these relationships were weak or absent, whereas in disturbed, unprotected systems, higher diversity was associated with lower infection risk. These findings highlight that conservation and habitat protection can buffer disease dynamics by stabilizing community composition and enhancing host population resilience. Funded by the DFG (PI, S. Sommer).

Meyer M, Eibner G, Heni AC, Wilhelm K, Sommer S. (2025) Changes in biodiversity drive trypanosome infections of wildlife in Panama. *One Health*. https://doi.org/10.1016/j.onehlt.2025.101113

Meyer M*, Melville DW*, Baldwin H, Wilhelm K, Nkrumah EE, Badu EK, Oppong SK, Schwensow N, Vallo P, Corman VM, Tschapka M, Drosten C, Sommer S (2024) Bat species assemblage predicts coronavirus prevalence. *Nature Communications* 15, 2887. https://doi.org/10.1038/s41467-024-46979-1

Coronaviruses in Ghanaian bats: from community-level drivers to immunogenetics and microbiome consequences

Understanding coronavirus ecology in wildlife requires connecting processes operating at multiple biological levels: from communities, to host genomes, to within-host microbial symbionts. We combined longitudinal field sampling with high-throughput approaches to reveal how coronavirus infection risk emerges from bat assemblage structure, host immune gene variation, and infection-associated shifts in gut microbial communities. At the community level, we demonstrated that bat species assemblage composition predicts coronavirus prevalence. Infection patterns could not be explained by host identity alone: instead, prevalence varied systematically with assemblage structure, with higher infection levels in less diverse communities dominated by competent host species. Together, the findings imply that changes in community composition reshape transmission dynamics, thereby linking biodiversity patterns to coronavirus prevalence. Zooming in to host mechanisms, we showed that MHC class II immune gene variation mediates susceptibility and resistance to coronavirus infections within a closely related bat system. Specific functional immune variants were associated with contrasting outcomes across different coronaviruses, implying that immunogenetic diversity can shape which infections establish, persist, or co-occur - explaining why closely related host species living side-by-side can nevertheless show markedly different infection profiles. Finally, we linked infection to host-associated symbionts by showing that Hibecovirus (a *Betacoronavirus*) infection is associated with gut microbial dysbiosis. Only this one SARS-related coronavirus lineage showed a clear signature of microbiome disruption, with gut microbial diversity and composition shifting with infection intensity. These findings suggest that even in reservoir hosts, some coronavirus infections can be accompanied by measurable changes in physiological state and microbial homeostasis, with potential implications for host health and pathogen shedding dynamics. Together, these studies provide a more nuanced picture of coronavirus ecology in bats: community structure influences exposure and transmission opportunity, immune gene diversity shapes individual susceptibility, and infection can feed back onto host-microbiome homeostasis - all of which are essential for understanding disease dynamics in a rapidly changing world. Funded by the DFG (PI, S. Sommer).

Melville DW*, Meyer M*, Risely A, Wilhelm K, Baldwin HJ, Badu EK, Nkrumah EE, Oppong SK, Schwensow N, Tschapka M, Vallo P, Corman VM, Drosten C, Sommer S (2025) *Hibecovirus* (genus Betacoronavirus) infection linked to gut microbial dysbiosis in bats. *ISME Communications*, 5(1). *https://doi.org/10.1093/ismeco/ycae154.*

Meyer M*, Melville DW*, Baldwin H, Wilhelm K, Nkrumah EE, Badu EK, Oppong SK, Schwensow N, Vallo P, Corman VM, Tschapka M, Drosten C, Sommer S (2024) Bat species assemblage predicts coronavirus prevalence. *Nature Communications* 15, 2887. https://doi.org/10.1038/s41467-024-46979-1

Schmid DW*, Meyer M*, Wilhelm K, Tilley T, Link-Hessing T, Fleischer R, Badu EK, Nkrumah EE, Oppong SK, Schwensow N, Tschapka M, Baldwin HJ, Vallo P, Corman V, Dorsten C and Sommer S (2023) MHC class II genes mediate susceptibility and resistance to coronavirus infections in bats *Molecular Ecology*, 32, 24, 3989-4002. doi: 10.1111/mec.16983.

Anthropogenic disturbance, 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 anthropogenic disturbance and AdV on the gut microbiome of naturally infected Malagasy mouse lemurs (*Microcebus griseorufus*). Our study shows that habitat fragmentation and enteric AdV indeed disturbed the gut microbiome 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 the neotropical frugivorous generalist Jamaican fruit bat (*Artibeus jamaicensis*) and the *Piper*-specialist Sheba's short-tailed bat (*Carollia perspicillata*) 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. Funded by the DFG (PI, S. Sommer).

Brändel SD, Melville D, Wilhelm K, Corman VM, Page R, Drosten C, Tschapka M, Sommer S, Wasimuddin (2026) Gut microbial composition changes in an Astrovirus-infected Neotropical frugivorous bat – a one health perspective. Available at Research Square [https://doi.org/10.21203/rs.3.rs-8419449/v1]

Wasimuddin, Malik H, Ratovonamana YR, Rakotondranary SJ, Ganzhorn JU, Sommer S (2022) Anthropogenic disturbance impacts gut microbiome homeostasis in a Malagasy primate. *Frontiers Microbiology*, 13, 911275. doi: 10.1101/2022.04.02.486803

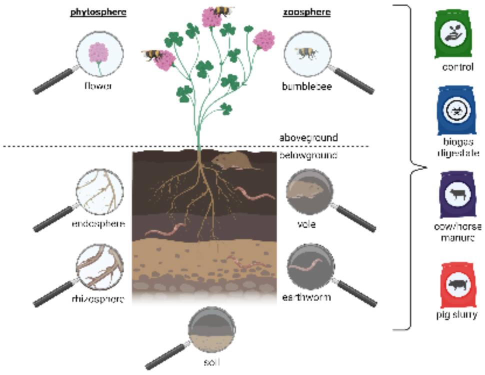
Wasimuddin, Victor M. Corman, Jörg U. Ganzhorn, Jacques Rakotondranary, Yedidya R. Ratovonamana, Christian Drosten & Simone Sommer (2019) Adenovirus infection is associated with altered gut microbial communities in a non-human primate. *Scientific Reports*, 9,13410. DOI: org/10.1038/s41598-019-49829-z.

Wasimuddin, Brändel SD, Tschapka M, Page R, Rasche A, Corman VM, Drosten C, Sommer S (2018) Astrovirus infections induce age-dependent dysbiosis in gut microbiomes of bats. *The ISME Journal*, 12, 2883-2893. DOI: 10.1038/s41396-018-0239-1.

Impact of organic fertilization on microbial communities along the trophic chain in German agricultural grassland ecosystems (IMPALA)

Intensified land use is a major driver of biodiversity loss in grassland ecosystems. Such intensive management affects not only aboveground diversity but also soil properties and microbial communities. Since microbial communities interact continuously, changes in the lower trophic compartment (e.g., soil) can affect the microbiomes of organisms across multiple trophic levels. These shifts may impair essential health functions along the trophic chain, threatening individual hosts and potentially disrupting ecosystem balance.

The IMPALA project investigated how organic fertilization affects microbial communities across connected below- and aboveground trophic compartments of grasslands on the Swabian Alb in Baden-Württemberg, Germany. We found that the microbial communities of soil, roots, and flowers of *Trifolium pratense*, as well as the gut microbiomes of earthworms, voles, and bumblebees, shifted in response to fertilization, with effects varying by host species. Changes were more pronounced in belowground compartments, with pig slurry fertilization having the strongest impact. Overlapping bacterial genera among soil, roots, and higher trophic levels suggest strong cross-trophic interactions shaping microbial communities. Although pig slurry-derived microbial taxa were detected in all compartments, their low prevalence suggests that observed shifts are driven by changes in nutrient availability rather than direct establishment of fertilizer microbes. Mesocosm experiments showed that long-term fertilization history had a greater impact than short-term fertilization events. Plants, however, responded immediately to increased nutrient availability, adjusting their root microbial communities accordingly.



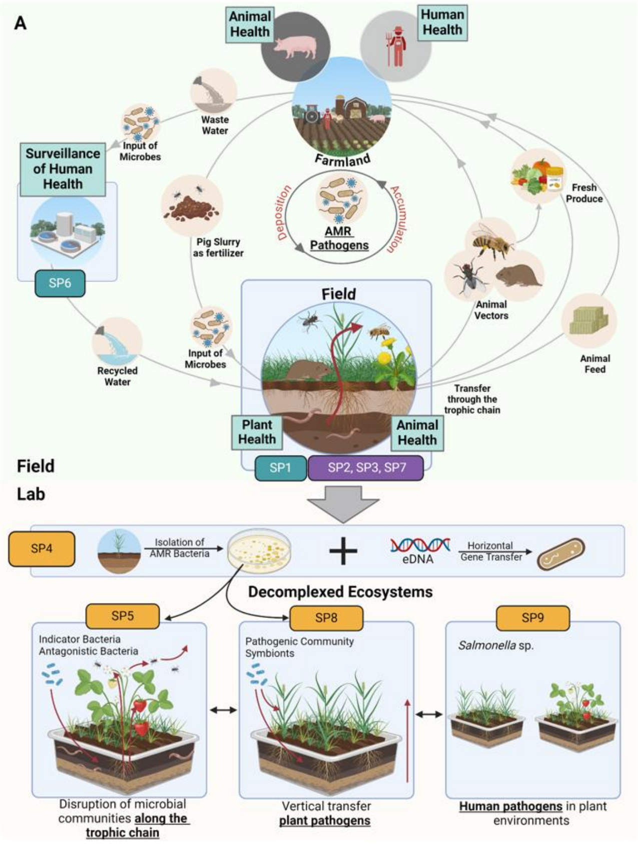
Metagenomic analysis indicated that fertilization led to reduced functional potential of microbial communities, although functional plasticity remained in belowground compartments. Fertilization increased the prevalence of antimicrobial resistance (AMR) genes and bacteriocin gene clusters (BGCs) along the trophic chain, though no direct correlation between AMR and BGC prevalence was found. Collaborations enabled the identification of soil-core microbiota as potential biomarkers of fertilization. Isolates carrying BGCs were tested in mesocosms, showing positive effects on plant growth, warranting further long-term studies. Our findings demonstrate that long-term organic fertilization affects all trophic compartments of grasslands, with potential ecological and health implications for animals and humans. These results underscore the need for mitigation strategies within a OneHealth framework.

Funded by the Baden-Württemberg-Stiftung program “Mikrobiom” (ID 18 IMPALA, PI S. Sommer).

Jetter K, Jani K, Wilhelm K, Stehle U, Chamedjeu RR, Riedel CU, Wilfert L, Schäfer P, Sommer S (2025) Fertilization impacts microbiomes along the grassland trophic chain. ISME communications, 5(1). https://doi.org/10.1093/ismeco/ycaf162.

Chamedjeu RR, Jani K, Jetter K, Wilhelm K, Schäfer P, Wilfert L, Sommer S, Riedel CU (2025) Impact of fertilization on the bacterial core microbiome of grassland soils: Abundance in the field and growth in vitro. Environmental Microbiology Reports. 17(6):e70235. https://doi.org/10.1111/1758-2229.70235.

Trophic Health: Effects of fertilization on AMR and zoonotic pathogen accumulation along the trophic chain – towards a One Health perspective in circular agriculture



In our new project (2026 – 2030), we aim to study how circular agriculture can spread AMR and zoonotic pathogens from livestock to the environment and back, and how ecosystem resilience may interrupt this cycle that threatens the health of humans, animals, plants, and our environment. We will combine a pan-microbiome approach with metagenomics in order to identify pathogens, AMR as well as antimicrobial peptide producers, which may in turn stabilize microbial ecosystems preventing the spread of harmful microbes. To address this detrimental cycle inherent to circular agriculture, we will survey microbial communities from soil, wastewater, plants and potential animal vectors, and experimentally verify the potential spread and mitigation of AMR and pathogens in a series of de-complexed mesocosm experiments. TrophicHealth will refine AMR and pathogen surveillance on our doorstep and in immediate food chain, as well as identify potential mitigation strategies significantly contributing to OneHealth by blocking the cycling of harmful microbes. This work will improve surveillance by the RKI and the Umweltbundesamt, and support veterinarian and farmers in their efforts to transition to sustainable and safe livestock farming.

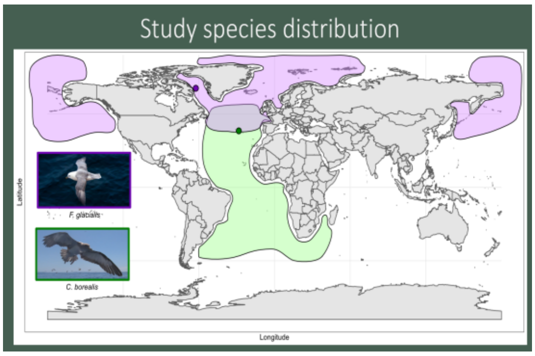
Funded by the BMFTR (Globale Gesundheit: Forschungsverbünde zum Thema „Pandemieprävention und -reaktion im Rahmen eines One-Health-Ansatzes“ (PI: S. Sommer)

TrophicHealth - Auswirkungen von Düngung auf die Akkumulation von AMR und Zoonoseerregern entlang der Nahrungskette - auf dem Weg zu einer One-Health-Perspektive in der zirkulären Landwirtschaft - Gesundheitsforschung BMFTR.

Ingestion of current environmental levels of microplastics is associated with changes in the gut microbiome of two wild seabird species

Microplastic pollution is an increasing problem that society faces today. The lack of action to combat these pollutants likely stems from an absence of evidence that they do harm at environmentally-relevant concentrations and mixtures numerous relevant species, and potentially accumulate across the trophic train. We provided evidence that microplastic ingestion changes gut microbial communities throughout the gastrointestinal tract in two different wild seabird species feeding on marine mollusks, crustacea, and fish across both hemispheres, and therefore represent relevant marine plastic bioindicators. Moreover, we looked at not only one microbial community within the gastrointestinal tract, but at several such communities located anteriorly (in the proventriculus) and posteriorly (in the cloaca) and found that all these communities are changed by the ingestion of microplastics. Microbiomes showed signs of dysbiosis, with decreases in commensal microbes and increases in pathogens (even zoonotic pathogens), antibiotic resistant bacteria, and plastic-degrading microbes.

Photo courtesy of Y. Rodríguez

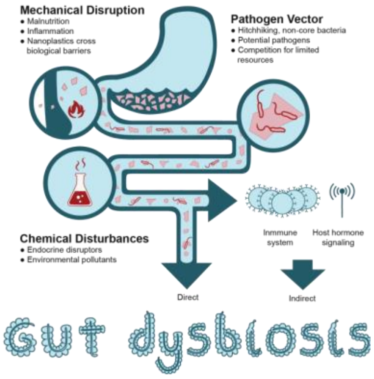


Our interdisciplinary approach differs from previous laboratory studies employing high concentrations of microplastics which often are not representative of the concentrations observed in the natural world. In our study, however, we show that changes to the microbiome are already occurring at current microplastic concentrations in the environment. The two seabird species we focused on (Northern fulmars and Cory's shearwaters) are highly relevant because they already chronically ingest microplastics and are not limited to small foraging areas, but instead migrate for thousands of kilometers across both hemispheres, putting the scale of these findings into global proportions.

Fackelmann G, Pham CK, Rodríguez Y, Mallory ML, Provencher JF, Baak JE, **Sommer S** (2023) Current levels of microplastic pollution impact wild seabird gut microbiomes. *Nature Ecology & Evolution*.

Fackelmann G, **Sommer S** (2019) Microplastics and the gut microbiome: how chronically exposed species may suffer from gut dysbiosis. *Marine Pollution Bulletin*, 143, 193-203.

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, 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 gut microbial symbionts. Given the gut microbiomes' vital standing in host health, microplastics could harm wildlife health in several ways: 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.

Fackelmann G, Sommer S (2019) Microplastics and the gut microbiome: how chronically exposed species may suffer from gut dysbiosis. *Marine Pollution Bulletin*, 143, 193-203.

Harnessing the microbiome for turtle conservation: investigating the protective effects of the eggshell microbiome against the emerging fungal disease fusariosis in an Amazonian freshwater turtle

The emergence of fungal pathogens threatening wildlife has increased exponentially, with well-documented catastrophic declines in amphibians and bats due to emerging fungal pathogens. However, high mortality in sea turtles due to the emerging fungal disease *Fusariosis* has received less attention. Fusariosis is caused by fungal pathogens within the *Fusarium solani* species complex (FSSC), representing important human, plant and animal pathogens, which has led to mass mortality in all seven sea turtle species by infecting turtle eggs during incubation, resulting in hatching failure. Alarmingly, we recently detected this pathogen in the Yellow-spotted Amazonian river turtle (*Podocnemis unifilis*) in the remote Ecuadorian Amazon (Carranco et al., 2022a), suggesting that this pathogen may also pose a threat to the 356 species of freshwater turtles and tortoises. Despite the imminent threat of this emerging pathogen towards turtle biodiversity, we have very little understanding of this fungal disease, including its transmission dynamics, pathogenicity, and long-term effects on the fitness of turtle hosts.

Our first aim has been to address this gap by investigating *Fusarium* disease dynamics using the Yellow-spotted Amazonian river turtle as a model system. We investigated fusariosis in unhatched eggs showing symptoms of *Fusarium* infection by using *Fusarium*-specific primers and by applying high throughput sequencing to detect FSSC pathogens. We could confirm the presence of three main FSSC pathogens causing egg fusariosis in turtle species. Moreover, we observed that a high proportion of eggs showing symptoms of fusariosis infection among nests was significantly associated with egg hatching success. However, since not all the eggs showing symptoms of fusariosis tested positive using a PCR FSSC test, we suggest the possibility of multiple causes of bacterial/fungal infection in turtle eggs (Carranco et al., 2022a).

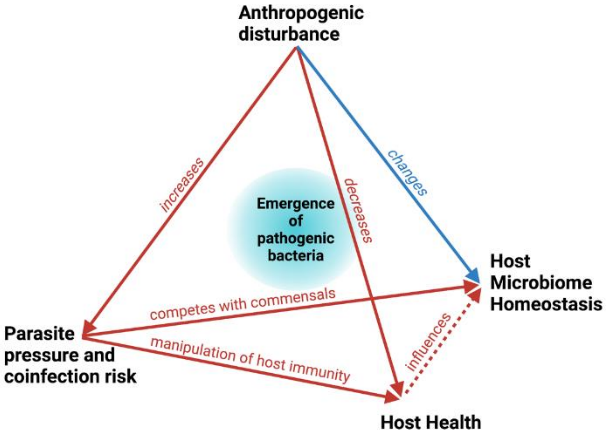
Infected turtle eggs

Since the host-associated microbiome is one of the key host traits for conferring resistance against pathogens, our next aim was to unveil the eggshell microbiome and microbial assemblages during turtle development. We investigated the internal eggshell microbiome and the cloaca microbiome of hatchlings and juveniles during the first month of development, together with the surrounding nest and river environment, using specific primers to amplify the V4 region of bacterial 16S rRNA on an Illumina platform. We first observed that the turtle eggs harbour an internal microbiome which is the seed for hatchlings' gut microbiome. We demonstrated that the nest environment has an influence on the egg and hatchling cloaca microbiome, which is the base of development for the cloacal microbiome of juveniles. During the first 20 days of juvenile turtle development, the gut microbiome changes and matures by the force of host selection processes and the interaction with the river environment. With these findings we could quantify for the first time the relative role of the environment and host-selection on gut microbial assemblages of oviparous reptiles, and expanded our understanding of *Fusarium* as an emerging infectious disease and the role of host-microbiome interactions in turtles (Carranco et al., 2022b). Our next project will allow us to investigate *Fusarium* epidemiology and the role of the host-associated micro and mycobiome in conferring resistance and resilience to fusariosis infection in turtle eggs in detail. Funded by the DFG (PI, S. Sommer).

Carranco AS, Gillingham MAF, Wilhelm K, Torres M de L, **Sommer S***, Romo D* (2022). Transcending sea turtles: First report of hatching failure in eggs of an Amazonian freshwater turtle with symptoms of the fungal emerging disease fusariosis. *Transboundary and Emerging Diseases*, tbed.14596. https://doi.org/10.1111/tbed.14596. *Shared senior authors

Carranco AS, Romo D, de Lourdes Torres M, **Wilhelm K, Sommer S*, Gillingham MAF*** (2022). Egg microbiota is the starting point of hatchling gut microbiota in the endangered yellow-spotted Amazon river turtle. *Molecular Ecology*, mec.16548. https://doi.org/10.1111/mec.16548. *Shared senior authors

Predicting the impact of co-infections on host gut microbiomes

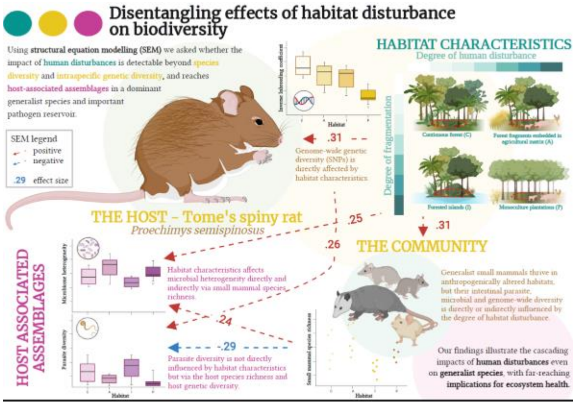


Co-infections are the norm in nature. Almost 50% of bank voles, for example, carry the tick-borne bacterium '*Candidatus* Neoehrlichia mikurensis' and the disease agent *Borrelia afyelii*, associated with Lyme disease in humans, and as many as 40% of bats are infected with more than one virus. Yet, we know very little about how co-infections, particularly with pathogens replicating enterically, impact the abundance and diversity of commensal gut microbiota. Since commensal bacteria take up important roles in hosts, including those related to nutrient breakdown and host immune defences, a better understanding of how pathogens shift their fragile balance was needed. In this work, we summarised findings that suggest that co-infecting pathogens can accentuate, undermine and disregard changes to the microbiome observed from single infections. We constructed a predictive framework that outlines how to test for precisely those synergistic, antagonistic or neutral effects of co-infecting pathogens and showcase our approach by re-analysing published microbiome data from a study on Malagasy mouse lemurs co-infected with an Adenovirus and helminths (Montero et al. 2021). It seems that co-infections may become more common in human encroached environments. In turn, this could raise the possibility of sicker wildlife populations owing to the disturbance of the gut microbiota and their functions, and risk the emergence and persistence of novel disease agents that jump the species barrier to infect domesticated animals or humans. Funded by the DFG (PI, S. Sommer).

Schmid DW, Fackelmann G, Wasimuddin, Rakotondranary J, Ratovonamana YR, Montero BK, Ganzhorn JU, **Sommer S** (2022) A framework for testing the impact of co-infections on host gut microbiomes. *Animal Microbiome*, 4(1). https://doi.org/10.1186/s42523-022-00198-5

Montero BK, **Wasimuddin, Schwensow N**, Gillingham MAF, Ratovonamana YR, Rakotondranary SJ, Corman V, Drosten C, Ganzhorn JU, **Sommer S** (2021) Evidence of MHC class I and II influencing viral and helminth infection via the microbiome in a non-human primate. PLOS Pathogens, 17(11): e1009675. doi: 10.1371/journal.ppat.1009675.

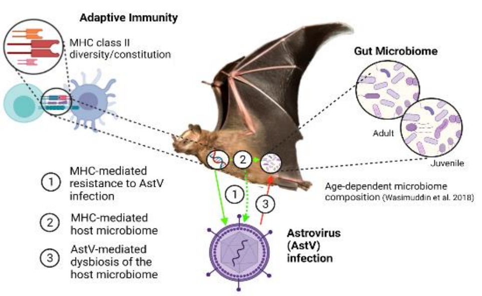
Disentangling effects of habitat disturbance on biodiversity



Changes in habitat characteristics following human disturbances are one of the most important factors influencing ecological communities and species abundance patterns. Yet, comparably little attention has been paid to the interconnectedness of biological communities at various levels of biodiversity, and whether their response differs. This study documents the nature and strength of both direct and indirect, and, at times, parallel effects of habitat disturbance on biodiversity: habitat characteristics associated with a gradient of human disturbance were the strongest predictors for small mammal species richness, and the genetic diversity and microbial heterogeneity of a dominant generalist. However, we also found clear evidence for indirect effects of human disturbance on host-associated species assemblages via small mammal species richness and host genetic diversity. Changes to host genetic diversity and the host species assemblage in connection with a reshuffling of the host associated micro- and macroorganisms may also explain why anthropogenically altered habitats become sources of diseases. Taken together, our study illustrates how human disturbance impacts multiple components of biodiversity in parallel, and causes cascading effects among them. Funded by the DFG (PI, S. Sommer).

Schwensow N*, Heni A*, Schmid J, Montero BK, **Brändel S**, Halczok TK, **Mayer G, Fackelmann G, Wilhelm K, Schmid D*, Sommer S*** (2022). Disentangling direct from indirect effects of habitat disturbance on multiple components of biodiversity. *Journal Animal Ecology,* 91, 2220-2234. * shared first / senior authors. doi: 10.1111/1365-2656.13802.

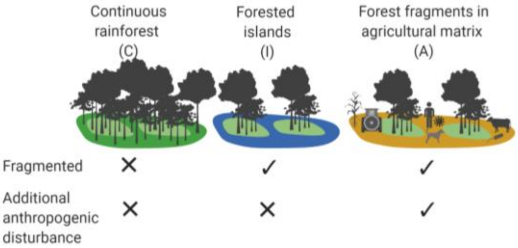
Interaction between MHC diversity and constitution, gut microbiota and Astrovirus infections in a neotropical bat



Astroviruses (AstVs) infect numerous mammalian species including reservoirs such as bats. Peptides encoded by the genes of the highly polymorphic Major Histocompatibility Complex (MHC) form the first line of host defence against pathogens. Aside from direct involvement in mounting adaptive immune responses, MHC class II genes are hypothesized to regulate gut commensal diversity and shape the production of immune-modulatory substances by microbes, indirectly affecting host susceptibility. Despite initial empirical evidence for the link between host MHC and the microbiota, associations among these factors remain largely unknown. To fill this gap, we examined MHC allelic/supertype diversity and constitution, the gut bacterial community and abundance pattern of a wild population of the neotropical bat (*Artibeus jamaicensis*) challenged by AstV infections. First, we show an age-dependent relationship between the host MHC class II diversity and constitution and the gut microbiota in AstV uninfected bats. Crucially, these associations changed in AstV infected bats. Additionally, we identify changes in abundance of specific bacterial taxa linked to the presence of certain MHC supertypes and AstV infection. We suggest changes in the microbiota to be either a result of AstV infection or the MHC-mediated modulation of microbial communities. The latter could subsequently affect microbe-mediated immunity and resistance against AstV infection. Our results underscore that the reciprocal nature of host immune genetics, gut microbial diversity and pathogen infection requires attention, which is particularly important given its repercussions for disease susceptibility and severity in wild animal populations with a history of zoonotic spillover and frequent human contact. Funded by the DFG (PI, S. Sommer).

Fleischer R, Schmid DW, Wasimuddin, Brändel SD, Rasche A, Corman VM, Drosten C, **Tschapka M, Sommer S** (2022) Interaction between MHC diversity and constitution, gut microbiome composition and Astrovirus infections in a neotropical bat. *Molecular Ecology*, 31, 3342–3359. doi: 10.1111/mec.16491.

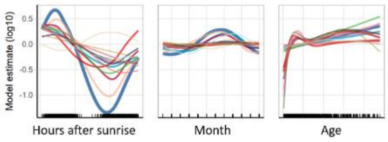
Effects of human encroachment into wildlife microbiomes



The gut microbiome is a symbiont consisting of a vast community of microbes and their genes, which play a key role in host health. Disturbances of this gut microbial community has been linked to many autoimmune diseases and infections, highlighting just how important a healthy gut microbiome is for the health of its host. Changes to wildlife gut microbiomes due to anthropogenic disturbances, such as habitat fragmentation, can disrupt natural gut microbiota homeostasis and make animals vulnerable to infections that may become zoonotic. In this study, we used the gut microbiome as an indicator for health in order to understand how zoonotic diseases can be transferred from wildlife to humans in the Anthropocene. Although anthropogenic disturbances are known to negatively impact the gut microbiome in a process known as dysbiosis, it is still unclear which anthropogenic factors drive these changes. Our study design in the Panama Canal area allows for the differentiation between habitat fragmentation *per se* and living in close proximity to humans, their domesticated animals, and agriculture. We found that 384 spiny rats (*Proechimys semispinosus*) living in fragmented habitats close to humans had greatly altered gut microbiomes, whereas spiny rats living in protected, fragmented habitats did not. This means habitat fragmentation *per se* did not drive the change in microbiome. Instead, the additional contact with humans shaped gut microbial composition and diversity. These findings are significant because spiny rats are generalist species expected to be more resilient to environmental changes. Yet, their microbiomes displayed two patters of change: The structural composition of the microbes that make up the gut microbiome became more irregular (heterogeneous) and shifted away from its natural composition. They also harbored more bacterial species that are found in domesticated animals and are known to cause disease in livestock. Our work suggests that gut microbiomes of spiny rats react to changes in their environment and offer the host a pathway to adapt or cope with anthropogenic alterations. Whether microbiome-mediated adaptations are fast and substantial enough to keep up with the rate and degree of change in the Anthropocene remains to be seen. Understanding that wild animals are struggling to cope with changes in the Anthropocene should serve as a warning that we may see more zoonosis-driven pandemics in the future.

Fackelmann G, Gillingham MAF, Schmid J, Heni AC, Wilhelm K, Schwensow N, Sommer S (2021) Human encroachment into wildlife gut microbiomes. *Communications Biology*.
wmf2021-asm.ipostersessions.com/Default.aspx?s=DF-7D-32-81-C3-F4-FD-35-24-9C-17-87-AF-F9-B3-6D

Meerkat gut microbiomes exhibit strong daily oscillations that do not decay with age



Gut bacterial communities are often incredibly dynamic over time, which makes them challenging to study. Microbes can fluctuate over the scale of hours, weeks, months and years, in response to feeding, seasonal climate, and host ageing, yet so far, we have not been able to disentangle these processes. We investigated gut microbiome dynamics in wild meerkats (*Suricata suricatta*) over a 20-year period to compare diurnal, seasonal, and lifetime processes in concert. We found that almost all common genera exhibited diurnal oscillations, and daily dynamics in bacterial load and diversity were stronger than seasonal and lifetime effects. Diurnal oscillations were driven by changes to the genus *Clostridium*, were better explained by light-dark cycles than foraging schedule, and did not decay with age. Across life, specific genera were associated with ageing and condition, and were more tightly linked to biological rather than chronological senescence. Our findings highlight that daily oscillations in the microbiome are probably more common than previously thought, and demonstrate that accounting for circadian rhythms is crucial for future gut microbiome research. Funded by the DFG (PI, S. Sommer).

Risely A, Wilhelm K, Clutton-Brock T, Manser M, Sommer S (2021) Diurnal oscillations in gut microbiome load and composition eclipse seasonal and lifetime dynamics in wild meerkats, *Suricata suricatta. Nature Communications.* 12, 6017. https://doi.org/10.1038/s41467-021-26298-5.

Foraging in monocultures with heavy pesticide input decreases the gut microbiota diversity of nectar-feeding bats

The health and physiology of native species can be negatively affected by agriculture, both due to habitat alteration and to pesticide use, and it is possible that gut microbiome disruption plays a role in these negative effects. We examined the association between management intensity of banana plantations and both the gut microbiota composition and body condition of one species of nectar-feeding bat (*Glossophaga soricina*, Phyllostomidae) in the Costa Rican Caribbean lowlands. We discovered that gut microbiota from bats foraging in conventional monocultures were overall less phylogenetically diverse than those from bats foraging in organic plantations or natural forests, both of which were characterized by diverse bacterial assemblages and individualized microbiota. Nonetheless, co-occurrence network complexity was higher in conventional monocultures, possibly indicating altered microbial interactions in agricultural landscapes. Bats from both banana plantations were larger and heavier than their forest counterparts, reflecting the higher and year-long food supply. With our study, we discovered that even if both banana plantations (conventional and organic) do provide a reliable food source for bats, conventional monocultures are associated with less diverse and potentially dysbiotic microbiota, while organic plantations promote diverse and individualized gut microbiota akin to their natural forest foraging counterparts. Whilst the long-term negative effects of anthropogenically-altered microbiota are unclear, our study provides evidence that organic agricultural practices are indeed more sustainable for wildlife health.

Alpízar P, Risely A, Tschapka M, Sommer S (2021) Agricultural fast food: Bats feeding in banana monocultures are heavier but have less diverse gut microbiota. *Frontiers in Ecology and Evolution*, 9,746783. DOI: 10.3389/fevo.2021.746783.

Impact of habitat disturbance and fungicides on homeostasis of amphibian skin microbiomes and abundance of protective bacteria against chydrid fungus infections - using endangered and rediscovered Costa Rican amphibians as natural model organisms

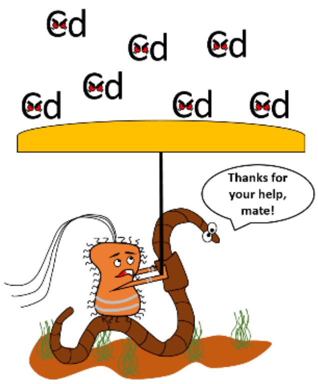
Some amphibians that were thought to be “extinct” have been found decades after population declines in the late 1980s. These species appear to have evolved resistance to the pathogen *Batrachochytrium dendrobatidis* (Bd), the likely causative agent of their declines, and raises the question how selection and diversity of protective skin microbiomes enabled these endangered neotropical amphibians to survive. 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. Unfortunately, these amphibian populations are still not “safe” due to ongoing anthropogenic threats, caused by habitat disturbance and overuse of pesticides. Alteration of the microbiome associated with environmental changes produced by anthropogenic activities may make the host more susceptible to pathogens. Our research showed that bacterial diversity of tadpoles of *L. vibicarius* from the disturbed habitats was lower than in those from the undisturbed habitats. Adults of *L. vibicarius* from disturbed habitats exhibited greater community dispersion than those from undisturbed habitats. These observed patterns could be associated to the presence of environmental stressors in our study sites, which can perturb a stable state leaving animals more susceptible to pathogen infections even beyond Bd. We could demonstrate that exposure to a widely used fungicide, chlorothalonil, changes the skin bacterial communities of tadpoles of *L. vibicarius*, potentially disrupting this protective trait against pathogens. With this research, we gained important information of the functional importance of the skin microbiomes, and the negative impacts of anthropogenic activities, especially agriochemicals, which can be used to develop management strategies that protect the health of these endangered amphibian populations.

Jiménez RR, Alvarado G, Mena F, Ruepert C, Ballestero E, Sommer S (2021) The fungicide chlorothalonil changes the amphibian skin microbiome: a potential factor disrupting a host disease- protective trait. *Applied Microbiology*, 1, 26–37.

Jiménez RR, Alvarado G, Sandoval J, Sommer S (2020) Habitat disturbance influences the skin microbiome of a rediscovered neotropical-montane frog. *BMC Microbiology*, 20, 292.

Jiménez RR, Alvarado G, Estrella J, Sommer S (2019) Moving beyond the host: unraveling the skin microbiome of endangered Costa Rican amphibians. *Frontiers in Microbiology*, 10, 2060.

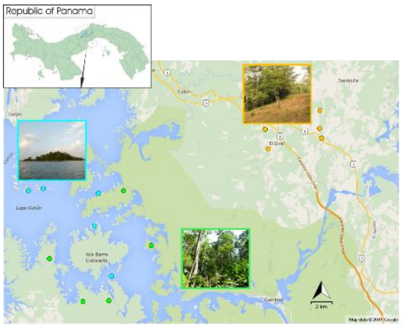
Gut microbiome as indicator of heavy metal pollution in soil



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.

Šrut M, Menke S, Höckner M, Sommer S (2019) Earthworms and cadmium – Heavy metal resistant gut bacteria as indicators for heavy metal pollution in soils? *Ecotoxicology and Environmental Safety*, 171, 843–853.

Human-induced landscape change disturb animal communities and species abundance pattern with significant effects on virus prevalence in wildlife



Anthropogenic environmental change can impact community traits such as species richness and population densities which have been shown to increase the prevalence of viral infections in wildlife reservoirs. It has been postulated that especially host species that are more resilient to changes of their natural habitat may increase in numbers which in turn may affect the prevalence of directly transmitted viruses. We have carried out an ecological survey of small mammal communities in three tropical landscapes differing in their degree of environmental change in Central Panama and investigated the effects of community changes on *Hepacivirus* prevalence, a virus closely related to human hepatitis C virus. The modification of continuous habitat into partly connected or isolated habitat patches during the past century was linked to changes in species richness and species assemblages, which in turn was associated with shifts in the abundance of generalist marsupial and rodent species. In particular, the spiny rat *Proechimys semispinosus* has become dominant in isolated habitat patches. Landscape-specific host density represents the most important ecological driver influencing local *Hepacivirus* prevalence. Our study provides important empirical data on how human-induced landscape changes may affect virus prevalence in wildlife and emphasizes the importance of a landscape scale approach considering the complex interactions between ecological factors driving host-virus interactions. Funded by the DFG (PI, S. Sommer).

Schmid J, Rasche A, Eibner G, Jeworowski L, Page RA, Corman VM, Drosten C, Sommer S (2018) Ecological drivers of *Hepacivirus* infection in a Neotropical rodent inhabiting landscapes with various degrees of human environmental change. *Oecologia*, 188(1), 289-302.

The best smellers make the best choosers: MHC-dependent mate choice is affected by female chemosensory receptor gene diversity

Sexual selection involving genetically disassortative mate choice is one of several evolutionary processes that can enhance population genetic variability and pathogen resistance. In many vertebrate species, females select mates depending on their major histocompatibility complex (MHC) genes. The products of the MHC genes are known to be drivers of pathogen resistance and sexual selection enhancing offspring genetic diversity. MHC further influences individual odor types and social communication. However, little is known about the receptors and their volatile ligands that are involved in this type of

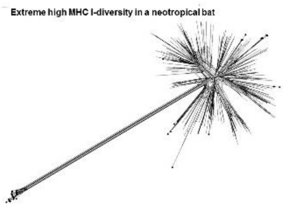
chemical communication. We investigated the effect of two groups of chemosensory receptor genes (trace-amine associated receptors (TAARs) and olfactory receptors (ORs)) on MHC-dependent mate choice. Our study is amongst the first to show a genetic link between behavior and chemosensory receptor genes. These results contribute to understanding the link between genetics, olfaction and associated life history decisions. Funded by the DFG (PI, S. Sommer).

Santos PSC, Mezger M, Kolar M, Michler F-U, Sommer S (2018) The best smellers make the best choosers: mate choice is affected by female chemosensory receptor gene diversity in a mammal. *Proceedings of the Royal Society London B*, 285, 20182426.

Santos PSC, Michler F-U, Sommer S (2017) Can MHC-assortative partner choice promote offspring diversity? A new combination of MHC-dependent behaviors among sexes in a highly successful invasive mammal. *Molecular Ecology*, 26, 2392-2404.

Santos PSC, Courtiol A, Heidel AJ, Höner OP, Heckmann I, Nagy M, Mayer F, Platzer M, Voigt CC, Sommer S (2016) MHC-dependent mate choice is linked to a trace-amine-associated receptor gene in a mammal. *Scientific Reports*, 6, 38490.

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. Funded by the DFG (PI, S. Sommer).

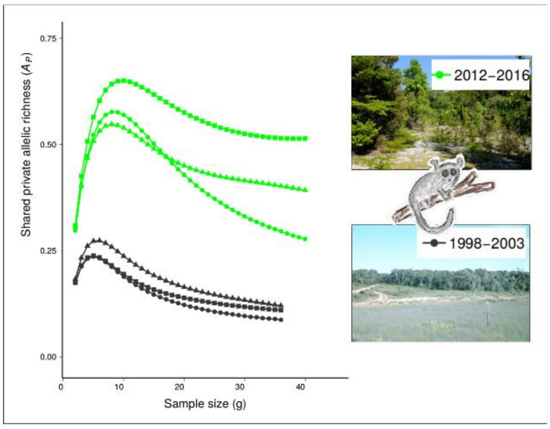
Qurkhuli T, Schwensow N, Brändel SD, Tschapka M, Sommer S (2019) Can extreme MHC class I diversity be a feature of a wide geographic range? The example of Seba's short-tailed bat (*Carollia perspicillata*). *Immunogenetics,* 71, 575. DOI: org/10.1007/s00251-019-01128-7.

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. Funded by the DFG (PI, S. Sommer).

Schwensow N, Castro-Prieto A, Wachter B, Sommer S (2019) Immunological MHC supertypes and allelic expression: how low is the functional MHC variability in wild endangered Namibian cheetahs? Conservation Genetics, 20, 65-80. DOI: org/10.1007/s10592-019-01143-x.

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 south-eastern 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 highlights 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. Funded by the DFG (PI, S. Sommer).

Montero K, Ramanamanjato J-B, Ernest R, Rakotondranary SJ, Ganzhorn JU, Sommer S (2019) Challenges of NGS in conservation management: insights from long-term monitoring of corridor effects on the genetic diversity of mouse lemurs in a fragmented landscape. *Evolutionary Applications*, 12, 425-442.

Method development for microbiome and MHC research

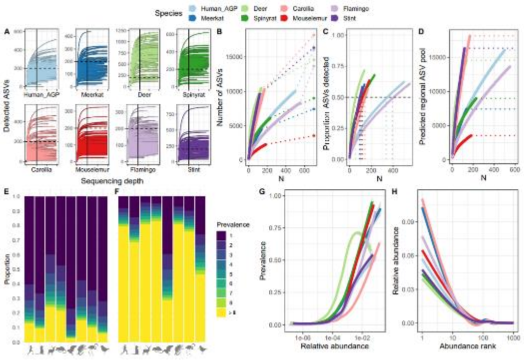
A novel workflow to improve multi-locus genotyping of wildlife species

ACACIA
Allele CAlling proCedure for Illumina
Amplicon sequencing

Genotyping novel complex multigene systems is particularly challenging in non-model organisms. Target primers frequently amplify simultaneously multiple loci leading to high PCR and sequencing artefacts such as chimeras and allele amplification bias. Most genotyping pipelines have been validated in non-model systems whereby the real genotype is unknown and the generation of artefacts may be highly repeatable. Further hindering accurate genotyping, the relationship between artefacts and copy number variation (CNV) within a PCR remains poorly described. We developed a novel open-source genotyping pipeline (ACACIA) to the data, and compared its performance with another, previously published, pipeline. ACACIA yielded very high allele calling accuracy (>98%). We discuss in detail the pitfalls researchers should avoid in order to reliably genotype complex multigene systems. Funded by the DFG (PI, S. Sommer).

Gillingham MAF, Montero BK, Wilhelm K, Grudzus K, Sommer S, Santos PSC (2021). A novel workflow to improve genotyping of multigene families in wildlife species: an experimental set-up with a known model system. *Molecular Ecology Resources,* 21, 982-998.

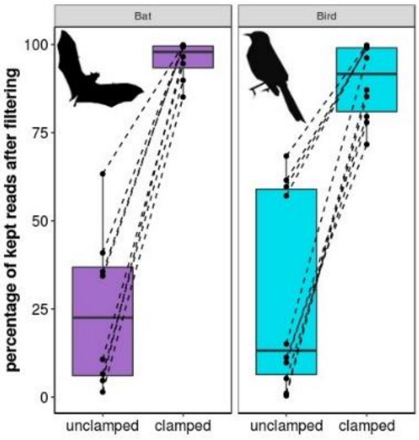
Can the estimation of core gut microbiomes be standardized across studies?



The filtering of faecal microbial datasets to retain high prevalence taxa is often performed to identify a common core microbiome that may be important for host biological functions. The common core gut microbiome is the subset of gut microbes that are particularly common across the host population, and are often identified based on prevalence (e.g. microbes that occur in over 50% of sampled individuals). However, these thresholds - though frequently used to compare results across studies and species - vary substantially across studies, and it is unclear whether gut microbial communities sourced from different host species demonstrate universal or species-specific responses to increasing prevalence thresholds. This has consequences for how comparable studies of core microbiomes are. We compared macroecological patterns in prevalence and abundance of eight gut microbial datasets from different mammal and bird species, and tested the effect of increasing prevalence thresholds on eight measures of alpha and beta diversity. Our results highlight some critical differences in macroecological patterns of rare taxa across the different datasets that can guide future sample collection and sample size, yet show that despite these differences, all microbial communities demonstrated similar responses in alpha diversity and beta dissimilarity to increasing prevalence thresholds. This suggests that most gut microbial communities exhibit similar patterns in prevalence and abundance distributions, especially of dominant taxa. Based on our results, we recommend methods that increase comparability of studies that identify a common core. Funded by the DFG (PI, S. Sommer).

Risely A, Gillingham MAF, Béchet A, Brändel S, Heni A, Heurich M, Menke S, Manser M, Schmid J, Tschapka M, Wasimuddin, Sommer S (2021) Phylogeny- and abundance-based metrics allows for consistent comparison of core gut microbiome diversity indices across host species. *Frontiers in Microbiology*, 12, 659918. doi: 10.3389/fmicb.2021.659918

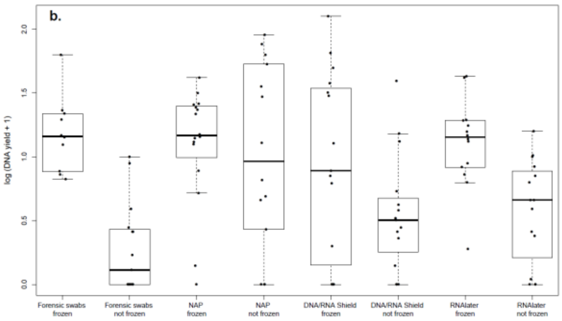
Jumping the green wall: the use of PNA-DNA clamps to enhance microbiome sampling depth in wildlife microbiome research



As microbiome research moves away from model organisms to wildlife, new challenges for microbiome high throughput sequencing arise caused by the variety of wildlife diets. Normally, high levels of contamination from the host (mitochondria) or diet (chloroplast) are commonly observed in wildlife samples. This contamination “hijacks” reads thus decreasing the overall sequencing depth of wildlife samples and reducing statistical power in downstream analysis. We developed an amplification protocol utilizing PNA-DNA clamps to maximize the use of resources and to increase the sampling depth of true microbiome sequences in samples with high levels of plastid contamination. The PNA-DNA clamps are DNA mimicking molecules that bind selectively to a target sequence. We used these clamps to block the sequences of chloroplast and mitochondria in fecal samples of birds and bats. Our protocol successfully blocks the signal organelle signals and provides a 13-fold increase in bacterial sequence amplification in comparison with the Earth Microbiome Protocol.

Víquez-R L, Fleischer R, Wilhelm K, Tschapka M, Sommer S (2020). Jumping the green wall: the use of PNA-DNA clamps to enhance microbiome sampling depth in wildlife microbiome research. *Ecology and Evolution*, 10, 11779-11786.

Home-made cost-effective preservation buffer stands the test against commercial preservation methods for microbiome research



The investigation of wildlife gastrointestinal microbiomes is a growing field in microbial ecology and conservation. Such studies often face difficulties in sample preservation if neither freezing facilities nor liquid nitrogen (LQN) are readily available. Thus, in order to prevent microbial community changes because of bacterial growth after sampling, preservation buffers need to be applied to samples. However, the amount of microbial community variation attributable to the different preservation treatments and potentially affecting biological interpretation is hardly known. Using sheep feces, we analyzed the effect of air-drying, an inexpensive self-made nucleic acid preservation buffer (NAP), DNA/RNA Shield™, and RNA*later*®, each together with freezing or storing at room temperature prior to 16S rRNA gene high-throughput sequencing to determine bacterial communities. Overall, NAP had better preservation qualities than RNA*later*® and DNA/RNA Shield™ making this self-made buffer a valuable solution in wildlife microbiome studies.

Menke S, Gillingham MAF, Wilhelm K, Sommer S (2017) Home-made cost-effective preservation buffer stands the test against commercial preservation methods for microbiome research. *Frontiers in Microbiology*, 8, 102.