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# Utilizing animal gut microbiomes to mitigate biodiversity loss in the Anthropocene

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## ABSTRACT

**Background:** Microbial communities inhabiting animal gastrointestinal tracts play crucial roles in maintaining global biodiversity by contributing to the health of their hosts.

**Argument:** Ongoing biodiversity conservation efforts must consider associated gut microbial communities because they are integral to animal survival.

**Instruction:** Scientists, governing entities, and conservation practitioners must work together to protect and leverage gut microbial diversity to improve wild animal health.

**Conclusion:** Efforts to increase knowledge about, and protection for, animal microbiomes will aid in combating global biodiversity loss.

*Keywords*: gut microbiome, microbial diversity, conservation, wildlife, biodiversity, Anthropocene.

## THE STATE OF BIODIVERSITY DURING THE SIXTH MASS EXTINCTION

We are in the midst of the sixth mass extinction. The current rate of species loss is estimated to be hundreds to thousands of times higher than during the past tens of millions of years (Barnosky et al., 2011; Ceballos et al., 2020). Global efforts to measure extinction rates and identify species most at risk are underway. The IUCN's Red List of Threatened Species and the Living Planet Index track three-fourths of all vertebrate species, but only one-tenth of invertebrate and plant species have been assessed (Bachman et al., 2019). Decisions regarding which animals to protect often consider their cultural value and their roles in ecosystem functions with implications for humans, thus biasing assignments of endangered status to more studied and charismatic species (Colléony et al., 2017; OECD, 2019). Recently, the focus has shifted to include invertebrates, partially due to media reports on phenomena such as honeybee collapse disorder (Johnson, 2010) and "The Insect Apocalypse" (Jarvis, 2018). Thus, research and conservation efforts have begun to prioritize attention to the substantial importance of smaller life in Earth's ecosystems.

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## THE CASE FOR ANIMAL GUT MICROBIOMES

Symbiotic microbial communities are a key, yet often neglected conservation target. Research on wild animal microbiomes has been limited (less than 1% of wild species have been investigated), and tends to be focused on mammals, primarily in the Global North. However, all animals studied to date have relationships with unique communities of microbiota, many of yet unknown function or identity (Zaneveld et al., 2017). Gut microbiomes support digestion, nutrient acquisition, toxin degradation, immune system development and function, reproduction and fertility, behavior, and more (Davidson et al., 2020; Peixoto et al., 2021). There is considerable evidence that microbiome disruption has profound implications for animal health (Thaler, 2021), suggesting that the survival of Earth's macrofauna is tightly linked to their gut microbial communities. In fact, there is emerging evidence that the evolution of host species and their associated microbiota follow patterns of phylosymbiosis, wherein the phylogeny of host species is recapitulated in their microbiome composition, pointing to the deep significance of these relationships, maintained and co-evolved throughout time (Kohl, 2020; Mallott and Amato, 2021).

Microbial ecology studies have traditionally been conducted outside of a conservation context. Integration of these fields will equip conservationists with microbial approaches to improving animal health and thus help to mitigate biodiversity loss. We demonstrate the significant roles of microorganisms in wild animals and suggest how researchers, policy-makers, and conservationists can effectively leverage the microbiota in wild animal guts for biodiversity conservation.

## MICROBIOME COMPOSITION AND ANIMAL HEALTH

### What we know from human studies

The microbiome and its byproducts, as demonstrated extensively in humans and model organisms, are critical to host health, and include support of the integrity of the intestinal mucosal barrier, host immunomodulation, and nutrient metabolism (Jandhyala et al., 2015) (Fig. 1). The majority of gut microbiota reside at the intestinal mucosal barrier and help maintain its functions, including preventing pathogen expansion, modulating host-microbe communication, and ensuring appropriate nutrient uptake (Vancamelbeke and Vermeire, 2017). A degraded mucosal barrier can lead to diarrhea and chronic gastrointestinal disorders, bloodstream infections, and liver disease (Vancamelbeke and Vermeire, 2017). Additional health factors associated with the gut microbiome in humans include drug metabolism, obesity, diabetes, gastrointestinal and cardiovascular diseases, and mental health. Using analogies to human health, we infer a similar importance of the microbiome to wild animal health, although research on non-model organisms in wild settings is limited, with most studies to date focusing on mammals.

### Diet and the role of gut microbiota in nutrient acquisition

The quantity of food required to meet an animal's energy needs is determined by the efficacy and efficiency of nutrient metabolism by gut microbiota and varies with food type and availability. Thus, gut microbial composition oscillates with the seasons (Hicks et al., 2018; Xiao et al., 2019). Hibernating animals, such as the brown bear (*Ursus arctos*; Sommer et al., 2016), must cope with the transition from an excessive to a complete lack of nutrient intake upon entering hibernation. This change causes a shift in their gut microbial communities that results in a decrease of metabolic activity and thus energy expenditure. Nutrient acquisition is of particular interest in animals that have adopted a diet outside of their evolutionary niche, such as the now-herbivorous panda (*Ailuropoda melanoleuca*) in the order Carnivora. Pandas have poorly adapted microbial metabolic pathways for their diet compared to other carnivores (Guo et al., 2018). Given enough time and appropriate source microbiota, gut microbiomes can help animals shift to novel diets (Kohl et al., 2018). For example, dogs (*Canis lupus familiaris*), evolutionarily omnivores, have a highly adaptable microbiome to an all-meat diet (Bermingham et al., 2017). Conversely, animals deprived of their native dietary species and fed artificial diets can quickly lose their microbial diversity, affecting their future survival (Martínez-Mota et al., 2020), a finding that is highly relevant for captive populations of wild animals. Diet, and dietary change over time, affect microbiome composition and function in animals, with subsequent changes in host metabolism linked to health and disease (Albenberg and Wu, 2014).

### Gut microbiota and the immune system

Following birth, development of the gut microbial community and the host immune system are tightly linked. The gut microbiota protects animals from pathogen invasion via direct exclusion, cell-to-cell interactions, antimicrobial peptide and metabolite production, and immune defense priming through chemical signaling (Panwar et al., 2021). Many wildlife species have more effective innate immune responses than humans, often conferring the ability to quickly control or avoid infections. It is possible that specific gut microbiota in these species contribute to this improved disease resistance, but further investigation is required (Seal et al., 2021). Better understanding of the role of gut microbiota in wildlife immunity may also advise strategies for prevention and treatment of zoonotic diseases (Rajeev et al., 2020).

## GUT MICROBIOME DYSBIOSIS

### What we know from human studies

The gut microbiome is in dysbiosis when its community composition and species abundance deviates from that of healthy individuals. In humans, dysbiosis has been linked to irritable bowel syndrome, inflammatory bowel disease, ulcerative colitis, Crohn’s disease, obesity, liver disease, diabetes, cardiac disease, as well as a slew of neurological and psychiatric disorders associated with the gut-microbiome-brain axis (Gomaa, 2020). There are many factors that may lead to dysbiosis, including pathogenic infection, and following a course of antibiotics for example, microbiome reassembly in adults can take several months to years, and species richness often remains significantly diminished (Schwartz et al., 2020; Jurburg et al., 2021).

### Preliminary findings in wildlife

Gut microbiome dysbiosis has been associated with metabolic, gastrointestinal, and neurobehavioral disorders, as well as lower reproductive success in wild animals and has been linked to environmental exposure to chemicals such as antibiotics and other forms of pollution (Rosenfeld, 2017; Williams et al., 2018). For example, Asian elephants experience gut dysbiosis after translocation, captivity, and deworming (Chong et al., 2019; Moustafa et al., 2021). Reduced gut microbiome diversity is linked to iron overload disorder in Sumatran rhinoceros (*Dicerorhinus sumatrensis*) and black rhinoceros (*Diceros bicornis*), a condition that increases susceptibility to infectious diseases including salmonellosis and tuberculosis (Roth et al., 2019).

Gut microbial dysbiosis is associated with many disease states, but what constitutes a dysbiotic state may not always be predictable. This has led to the conception of the Anna Karenina principle (AKP), which posits that all healthy microbiomes have more similar community compositions, whereas dysbiotic microbiomes are more stochastic with high variability even among individuals experiencing the same perturbations (Zaneveld et al., 2017). Disrupting gut microbial communities may lead to a random dysbiotic state indirectly through the loss of host-managed regulatory controls rather than direct changes caused by diversity decline. As such, identifying the cause of a random dysbiotic state can be extremely challenging. The most effective solution, therefore, is to prevent wild animal microbiomes from entering dysbiosis in the first place.

## ANTHROPOGENIC CONTRIBUTIONS TO THE DISRUPTION OF ANIMAL MICROBIOMES

Human actions contribute to the disruption of wildlife gut microbial communities both directly (e.g., increased contact between humans and wildlife, antibiotic pollution) and indirectly (e.g., climate change, habitat degradation). Disruption of gut microbial communities may negatively affect wild animal health by impairing proper nutrient acquisition, interfering with immune regulation and response, and breaking down the gut mucosal barrier, thereby opening up the gut to pathogen invasion, for example (reviewed by Trevelline et al. 2019). These impacts are potentially far-reaching and may lead to the development and spread of antibiotic resistance, zoonotic disease, and ultimately declines in global biodiversity levels (Glidden et al., 2021) (Fig. 1).

### Direct anthropogenic impacts on animal microbiomes

#### *Contact with humans and their environments*

Human actions have been linked to gut microbiome perturbation in wild animals. Lower gut bacterial diversity, increased microbial variation among individuals, and higher prevalence of bacteria associated with domestic animals, including their pathogens, was found in individuals of Tome's spiny rat (*Proechimys semispinosus*) in disturbed areas (Fackelmann et al., 2021). Human-derived bacteria, including pathogens, have encroached into the guts of wild animals due to increased contact with humans and anthropogenic environmental contamination (Lee et al., 2019; Watson et al., 2019; Moustafa et al., 2021)—a phenomenon reviewed with respect to *Escherichia coli*, a highly transmissible and often pathogenic bacterium (Lagerstrom and Hadly, 2021). The transfer of microbiota goes both ways, and zoonotic spillover and spillback are becoming increasing concerns in the Anthropocene (Johnson et al., 2020).

#### *Environmental pollution by antibiotics*

Antibiotics are a major cause of gut microbiome dysbiosis in humans and livestock (Allen and Stanton, 2014; Schwartz et al., 2020). Few studies to date address their impacts on wild animal health, but they are likely similar. Susceptible gut bacteria are killed by antibiotics, creating opportunities for pathogenic invasion and colonization by resistant bacteria (Gomaa, 2020). Human infections by antibiotic-resistant (ABR) bacteria are becoming more common, as ABR is increasing globally at an alarming rate, causing an estimated 700,000 deaths per year worldwide and could reach 10 million by 2050 without successful intervention (O'Neill, 2014). The World Health Organization has thus identified ABR as one of the largest threats to global health, food security, and development (WHO, 2020). Environmental spread plays a significant role in the dissemination and creation of ABR (Skandalis et al., 2021). Antibiotics contaminate the environment through run-off from livestock

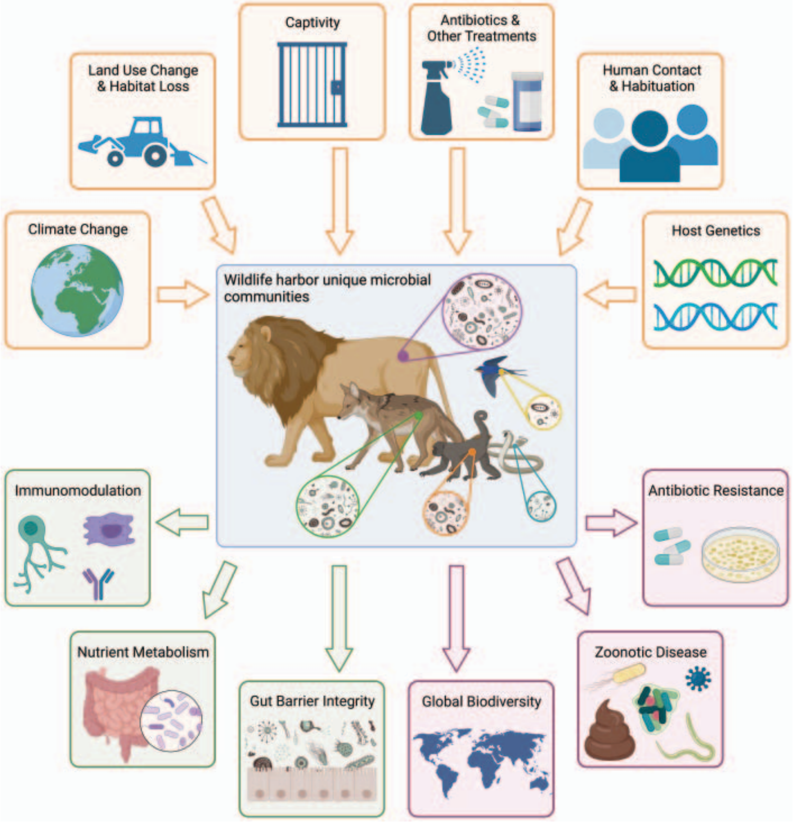

**Fig. 1.** All animals associate with unique gut microbial communities that may be susceptible to perturbation by a variety of external factors (yellow boxes). A complex web of interactions thus results in varying and often difficult-to-predict outcomes, including changes in individual hosts (green boxes) and impacts on the environment at large (purple boxes).

and aquaculture operations where antibiotics are used extensively and often prophylactically, as well as by improper landfill disposal of antibiotic medications and in effluent from wastewater treatment plants where removal of antibiotics is often incomplete (Berglund, 2015; Skandalis et al., 2021). Horizontal gene transfer (HGT) describes the capability of bacteria to share genes between populations and across bacterial species and is another major contributor to the spread of ABR (MacLean and San Millan, 2019). Due to their pervasiveness in the environment, containment remains challenging, and wildlife are often exposed to environmental antibiotic pollution. ABR has been detected in many wild birds and mammals globally, which likely contribute to the geographic expansion of ABR (Carroll et al., 2015; Swift et al., 2019).

Heavy use of chemicals (e.g., disinfectants, antibiotics, inorganic fertilizers, other agrochemicals) that directly target or otherwise impact microbes contribute to disrupted gut microbial diversity and function (Rosenfeld, 2017), the effects of which are worsened by climate change (Zandalinas et al., 2021). Notably, bacterial populations exposed to certain agrochemicals in combination with antibiotics may develop ABR up to 100,000 times faster than in the absence of agrochemicals (Kurenbach et al., 2018). Thus, human-sourced environmental pollutants can have compounding and unpredictable negative impacts on gut microbial biodiversity at a global scale.

### *Impacts of captivity on wild gut microbiomes*

Efforts to preserve vertebrate diversity through captive breeding, rearing, and rehabilitation can impact gut microbial communities and lead to downstream effects on host health and survival. Captive-breeding and rearing programs aid in the recovery of vulnerable populations, but challenges from inbreeding (Spielman et al., 2004; Yuan et al., 2015) and increased human contact (Ellenberg et al., 2009) have consequences for microbiome integrity. Factors common to captivity include manufactured enclosures, relatively sterile housing conditions, use of antibiotics, and non-native and/or low diversity diets, all of which potentially lead to captive host microbiomes that are substantially different from their wild counterparts. Resulting shifts in microbiome composition may impact host immunity (Flies et al., 2015; Seeber et al., 2020; San Juan et al., 2021), as it does in model organisms and humans. Studies have demonstrated the capacity of captivity to alter microbiomes in several mammalian and bird species (Clayton et al., 2016; McKenzie et al., 2017; San Juan et al., 2021). These documented alterations to the microbiome are host-specific, highlighting the need to investigate the biota of specific species subjected to captivity. These investigations are particularly important for confined, human-fed animals that will be reintroduced to their wild habitat with access to their native foods, or as insights into potential solutions for enhancing survival in anthropogenically-altered environments. Fostering native microbial diversity may also protect wildlife against diseases, enhancing species adaptive capacity in captivity (Lagerstrom et al., 2022]).

## Indirect anthropogenic impacts on animal microbiomes

### *Climate change*

Host-associated microbiome dysbiosis is linked to climate change via temperature and precipitation fluctuations (Greenspan et al., 2020; Hernandez-Gomez, 2020; Sepulveda and Moeller et al., 2020). For example, climate warming impacts microbial composition in the northern leopard frog (*Lithobates pipiens*; Kohl and Yahn, 2016). It also lowers abundances of beneficial bacteria and increases potential pathogens in western fence lizards (*Sceloporus occidentalis*; Moeller et al., 2020). Environmental warming may also help facilitate invasion by non-native species, including pathogens. For example, the gut microbiota of the invasive American bullfrog (*Lithobates catesbeianus*) responds more quickly to temperature increases than that of the green frog (*Lithobates clamitans*), allowing it to exploit new environments (Fontaine and Kohl, 2020). Increased precipitation aided in the recovery of a food item for Brandt's vole (*Lasiopodomys brandtii*), resulting in elevated abundances of the bacterium *Eubacterium hallii* that subsequently boosted growth and survival of the vole via fatty acid production (Li et al., 2020). Thus, climate change can modify gut microbiomes through changes in food availability as well as by exposure to different environmental sources of microbes.

### *Land-use change*

Access to both intact and functional habitat is vital to maintaining gut microbiome integrity. Land-use change can modify gut microbiomes by shifting soil microbial communities (a potential source of gut microbes; Berkelmann et al., 2020), as well as altering diets (Chang et al., 2016) and subjecting wildlife to human contact (Phillips et al., 2018). Converting landscapes from forests to agriculture leads to a decrease in dietary diversity, as observed in the associated reductions in microbial diversity in black howler monkeys (*Alouatta pigra*; Amato et al., 2013). Similar trends have been observed in other wildlife, such as several species of passerine birds (San Juan et al., 2020), the common vampire bat (*Desmodus rotundus*; Ingala et al., 2019), and the rice frog (*Fejervarya limnocharis*; Chang et al., 2016). Small, fragmented habitats are also likely to increase contact between humans and wildlife, allowing for the bidirectional transfer of human-associated microorganisms that may be detrimental to wild gut microbiome diversity (Fackelmann et al., 2021; Moustafa et al., 2021). Land-cover changes associated with urbanization also influence gut microbiota in the white-crowned sparrow (*Zonotrichia leucophrys*; Phillips et al., 2018) and through diet modifications in the house sparrow (*Passer domesticus*; Teyssier et al., 2020). The alarmingly fast rate of land-use change makes this area of research increasingly important (Winkler et al., 2021).

## USING MICROBIOMES TO BOLSTER BIODIVERSITY CONSERVATION EFFORTS

Given the breadth of direct and indirect anthropogenic impacts on symbiotic microbial communities, a broad response is required from a variety of stakeholders. Research scientists have much to do to understand the functions that gut microbiomes play in species ontogeny, diet, ecological interactions, and in overall animal health and survival. Governing bodies and conservation practitioners also have multiple responsibilities to contribute to the conservation of gut microbial diversity and consequently the biodiversity that depends upon it.

### Goals for research scientists

#### *Expanding and synchronizing the global database*

Efforts to catalog Earth's biodiversity should include any associated microbiota, arguably as an extension of their host species' biology (Bordenstein and Theis, 2015). Some institutions, including the US National Park Service and many US State Fish and Wildlife Departments, already have ongoing fecal collection efforts from the species they are charged with protecting. However, institutions often fail to prioritize, utilize, or curate these efforts post-collection, and information is not amassed in a central or open-access location. Research on host-associated microbiomes and their roles in host health and evolution would be greatly enhanced by curation of a global database of animal gut microbial communities, an effort recently championed by Yang et al. (2021). The curated database would include, for example, host physical metrics (e.g., body mass, gender, age), health status (e.g., parasite presence, stress hormone levels), plant and animal communities associated with the samples, and locality data (e.g., GPS coordinates of sample collection, land-use type, level of human impact). Integration of microbial diversity and function, and the ecology, evolution, and environment of host species is required to understand the full extent of how humans are tipping the planet into an extinction crisis, and to advise strategies for reversing this trend. Moving beyond a description of microbial richness to the functional linkages between the microbiome to host health, much of which requires an experimental approach, will lead to innovative treatments for those species in dysbiosis, particularly in captive-rearing, rehabilitation, or translocation efforts.

#### *Biobanking gut bacteria: a "frozen zoo" for gut microbiomes*

As we gain a better understanding of what constitutes a healthy microbiome for various wildlife, particularly highly endangered species, a concerted effort should be made to "biobank" feces and integral microorganisms. The Frozen Zoo in San Diego already biobanks living cell cultures, oocytes, sperm, and embryos of irreplaceable value from various at-risk species (Johnson, 1999). In the future, microbiome reserves drawn from these preserved samples could be used to inoculate the guts of individuals born from in vitro fertilization. This approach runs parallel to the goals of conserving the holistic health of endangered species as well as improving our tools for reintroducing locally extinct species with as close to the original microbiome conditions as possible. Maintaining biobanks of frozen feces will preserve entire microbial communities (Kerckhof et al., 2014), but will require a high volume of fecal samples from multiple individuals and populations, and thus extensive storage space. Isolating and storing stock cultures of only the essential microbes from wildlife stool would be a superior method, but would include the challenges of identifying those key species and culturing those that live under conditions hard to replicate in the lab. However, advances in microbiological techniques may increase the feasibility of such an endeavor (Vartoukian et al., 2010).

### *Studying the effects of host genetics on gut microbiomes*

Significant knowledge gaps remain about the role that host genetics play in the assembly and maintenance of gut microbial communities (Tabrett and Horton, 2020). Genome-wide association studies have been used to link human genotypes to microbiome assembly and show that up to 10% of microbiome dissimilarity can be explained by host genetics (Wang et al., 2016). Additionally, the symbiotic relationship between hosts and their gut microbiomes persists over evolutionary time such that patterns of phylosymbiosis are identifiable across many extant wild animal lineages (Mallott and Amato, 2021). In non-human primates, phylogeny has even been shown to outweigh dietary niche in microbiome composition and function (Amato et al., 2019). Because hosts' genomes encode mechanisms that control, to some extent, their gut microbial assemblies, it is crucial to address particular genetic stressors that wildlife face, namely inbreeding depression and hybridization.

Inbreeding depression results from matings between related individuals and is characterized by low genetic diversity within a population and a corresponding reduction in fitness. Significant inbreeding can result in lowered reproductive success, physical and mental disabilities, increased susceptibility to disease, and other health defects (Keller and Waller, 2002). Microbiomes of inbred Banna minipig (*Sus scrofa domesticus*) have reduced diversity, higher instances of a pathogenic bacteria, and altered metabolic function (Wei et al., 2020). However, the extent to which inbreeding affects the composition and function of the microbiome remains largely undescribed.

Hybridization is the interbreeding between species and has dramatically increased in the wild with growing anthropogenically-induced stress (Quilodrán et al., 2020). Research on the interplay between hybrids and their microbiomes is emerging, but remains in the early stages. Different gut microbiome compositions in hybrids have implications for their survival, potentially altering their ability to digest food items eaten by either parental species, and may impact host immunity, disease susceptibility, fertility, and even behavior (Brucker and Bordenstein, 2012). Hybrid individuals produced from pony and donkey mating pairs all possessed gut microbiomes that were significantly different from, and less diverse than, either parent (Edwards et al., 2020). Further investigations will help explain how host factors facilitate microbiome assembly and maintain its composition, as well as reveal the importance, and hint towards mechanisms, of phylosymbiosis and speciation (Miller et al., 2021).

## Priorities for government

### *Restriction and standardization on use of antibiotics*

Governmental bodies have an important role to play both in mitigating the overuse and misuse of antibiotics and regulating their use in general, thereby slowing the spread of antibiotics and ABR bacteria throughout ecosystems. It is estimated that over 80% of antibiotics sold in the US are used in animal production, primarily prophylactically and as growth promoters; up to 90% of those antibiotics are then excreted in stool and urine and subsequently disperse widely via surface water run-off, in manure-based fertilizers, or leach into groundwater (Ventola, 2015). Additionally, the use of antibiotics on crops is severely under-documented globally, but is a significant source of environmental antibiotic pollution, as they are prescribed prophylactically and even to treat insect infestations and other fungal and viral diseases against which antibiotics have no effect (Taylor and Reeder, 2020). Therefore, governments must increase efforts to track the use of, and synchronize and strengthen jurisdiction over, antibiotics in agricultural settings to prevent environmental contamination and consequently protect wild animal gut microbiomes from perturbation. Such governmental intervention has already succeeded in Sweden, where a decrease in detectable ABR in wild bears corresponded with regulations to control antibiotic use (Brealey et al., 2021).

### *Land-use management*

Habitat degradation and fragmentation can lead to gut dysbiosis in wildlife by decreasing the diversity of accessible dietary items (Amato et al., 2013) and introducing human-associated bacteria into wild populations through increased human-wildlife contact. Setting aside more lands as protected spaces can therefore alleviate negative impacts on wild animal microbiomes by maintaining ecosystem integrity and function and decreasing the level of contact with humans. For example, the science-driven initiative, 30×30, is an effort to address the climate and biodiversity crisis by protecting at least 30% of oceans and lands by 2030; protected areas would provide refugia for wildlife and corridors to increase landscape connectivity (Dinerstein et al., 2019). Land-use practices that enhance ecological integrity, including structural intactness and connectivity, support biological diversity and decrease human-wildlife contact and conflict. This will reduce the transmission of microbes, including pathogens and ABR bacteria, between humans and wildlife, ultimately protecting the health of both (Plowright et al., 2021).

## Actions for conservation practitioners

### *Management of captive animals*

Captive-rearing and rehabilitation are important for the conservation of vulnerable species, but some practices may lead to gut dysbiosis. Therefore, maintaining the similarity of gut microbial composition between captive animals and their wild counterparts will help preserve their unique microbial diversity. While it may not be possible to maintain all “native” gut microbes in captive environments, those that can be manipulated by diet should be prioritized, with an attempt made to re-inoculate with gut microbes that are inherited vertically. Subsequently, the maintenance of the microbiome may bolster the individual’s health, thus setting up a successful reintroduction into the wild.

Microbiome integrity can be achieved by minimizing human contact, maintaining a wild diet, exposing captive animals to plants, soil, and other individuals of their species, and avoiding antibiotic treatment whenever possible. If antibiotics must be administered to treat infection, pre- and probiotics may be given to the individual to stimulate diverse microbial regrowth (Trevelline et al., 2019).

### *Monitoring environmental pollution levels*

Measures to prevent antibiotic and other toxin exposure should also include careful environmental monitoring. Agriculture and human and veterinary medicine all use antibiotics and other pollutants such as rodenticides and pesticides extensively. Their widespread use means these toxins and resistant microbes have many opportunities to be carried via waterways and animal dispersal into new environments, negatively impacting natural microbial communities (Power et al., 2013). Longitudinal sampling of water sources and soil can aid toxin monitoring and guide intervention. These efforts would be especially recommended to monitor sensitive ecosystems or those home to endangered species downstream of livestock and other farming operations.

### *Fecal microbiota transplants*

In some cases, direct microbiome manipulation, such as fecal microbiota transplantation (FMT), may be helpful (Blyton et al., 2019). There are several ways to administer FMT treatments, including capsules (suppository or oral), enema, colonoscopy, or nasogastric tube (from nostril to stomach; Ramai et al., 2019). For wildlife, the least invasive option is oral delivery, either via capsule or coprophagy when possible. FMTs benefit animals no longer exposed to environmental factors that would have seeded their microbiomes, including juvenile mammals who have lost contact with their mother, social animals no longer interacting with individuals of their species, and coprophagic animals that no longer have access to feces when in captivity. FMTs should also be considered for cloned animals, which represent an important yet controversial advancement in conservation practice (Desalle and Amato, 2017). Caveats to consider when utilizing FMTs include the feasibility of obtaining access to a healthy, wild donor sample, and the ability to ensure this sample contains no harmful pathogens prior to transplantation, which has posed an issue in human patients (McSeveney, 2019). Other considerations include the invasiveness versus effectiveness of delivery methods, the number of treatments required, and the duration of the benefit to improving gut microbial diversity (Guo et al., 2020). FMT shows great potential in some cases, but requires further research before it can be recommended at broader scales.

## CONCLUSION

Earth's richness of microbial life not only helps sustain the human population, but a diversity of life on the planet via symbiotic interactions that function in a co-evolved global ecosystem. Gut microbial communities play a vital role in wild animal health, and many negative impacts may arise when diversity is lost or altered, often as a result of human actions. The most effective conservation efforts will include an understanding of the importance of protecting gut microbiomes for their promotion and preservation of animal health. Scientists, policy-makers, and conservationists must work together to both decrease the negative impacts of human activities on wild animal gut microbial communities, and to better understand and implement the application of animal microbiomes to bolster biodiversity conservation efforts into the future.

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