

# Microbiomes – the key to a healthier planet?

Microbiomes are communities of microorganisms living on or in animals, helping to keep them healthy. Changes in the composition of microbiomes could make wildlife more vulnerable to diseases which may be zoonotic – transmissible to humans – so monitoring them could help us to predict outbreaks of disease and protect global health. Dr Andrew Bartlow and colleagues at the Los Alamos National Laboratory, New Mexico, USA, have been studying screech owl microbiomes, analysing microbial DNA to further our understanding of the largely unexplored world of wildlife microbiomes.

Microbiomes are communities of tiny organisms, collectively known as microbiota. They are invisible to the human eye, living on and in all of us: layers of bacteria, viruses, and fungi covering our skin, gut, and every part of us. These 'friendly' microorganisms act as our body's first line of defence, helping keep us healthy by preventing their destructive counterparts from invading, as well as assisting with all sorts of different bodily processes.

## DEFENSIVE FLORA

These days we're better informed about the benefits of a healthy microbiome, whether it's to prevent acne, maintain our gut health, or even to benefit our mental health. Well-nurtured microbiota are better able to fend off unwanted pathogens (harmful microorganisms), helping to keep our skin clear and digestion smooth. If our microbial community is compromised, this defensive barrier can be breached, potentially leading to an all-out microbial

invasion which might escalate towards the entire body being overwhelmed by disease or infection.

All animals have their own microbiomes, yet the microbiomes of wildlife have received little investigation. Better understanding of this field could provide a much-needed insight into the ecology, distribution, and factors driving evolutionary changes in each species, as well as helping to prevent the spread of wildlife – and human – disease.

But because of our increasingly close relationships with wild animals – as we encroach on their habitats and trade wild species into captivity – when wildlife is at risk, so are humans. Zoonotic diseases, which can be transmitted from animals to humans (COVID-19, for example), are also potentially more likely to be contracted and spread by individuals with disrupted microbiomes.

## A ONE HEALTH APPROACH

Andrew Bartlow co-leads the Ecological Health Security Lab at Los Alamos National Laboratory, New Mexico, USA. Through research, training, and international collaboration, they take a 'One Health' approach which tackles health security challenges by recognising the connections between humans, animals, and the environment – and their microbiomes.

By monitoring the make-up of individuals' microbiomes and understanding what their usual, healthy balance is, we can detect potentially dangerous changes that could be a precursor to more serious issues developing – for example where rises in sea temperature alter the microbial composition of coral reefs preceding a bleaching event.



Western screech owls had a wider variety of bacteria in their microbiomes.



Less microbial diversity in the whiskered screech owls could be due to sex or foraging range.

All sorts of environmental changes can alter the composition of microbiomes, such as differences in temperature, food availability, pollutants, or geographical location. The microbiome's sensitivity to what may be unseen or subtle shifts in an individual's surroundings can be used as a detection system enabling us to better monitor wildlife health. Understanding this sensitivity can help determine the cause of the disruption, so we can attempt to prevent or mitigate the problem before things escalate and increasingly serious health problems arise – problems that are easier to see but harder to fix.

Bartlow and his team recognise that more research is needed in this growing field, and the degree to which microbiome health determines the spread of disease is not yet fully understood. But the fact that studies have found correlations between disrupted microbiomes and harmful physiological responses or increased susceptibility to disease, suggests that furthering our understanding will help us to improve global health.

## SCREECH OWL COMMUNITIES

To further their understanding of the

factors affecting wildlife microbiomes, Bartlow and his team compared the diversity and make-up of the bacterial communities of two owl species: the western screech owl (*Megascops kenicottii*) and the whiskered screech

The researchers took faecal samples and cloacal swabs (from the rear end of the birds). They then identified the different species in the microbial communities using next generation DNA sequencing of the 16S rRNA gene; the region of DNA that is sufficiently unique to most microbial species that it enables researchers to tell different kinds of bacteria apart.

Because the microbes can be very similar genetically,

owl (*Megascops trichopsis*). The study area was in the Peloncillo Mountains in south-east Arizona, where the ranges of the two species overlap. The team set up nesting boxes in one canyon. These species have much the same habitat and niche – feeding, nesting, and surviving using very similar resources.

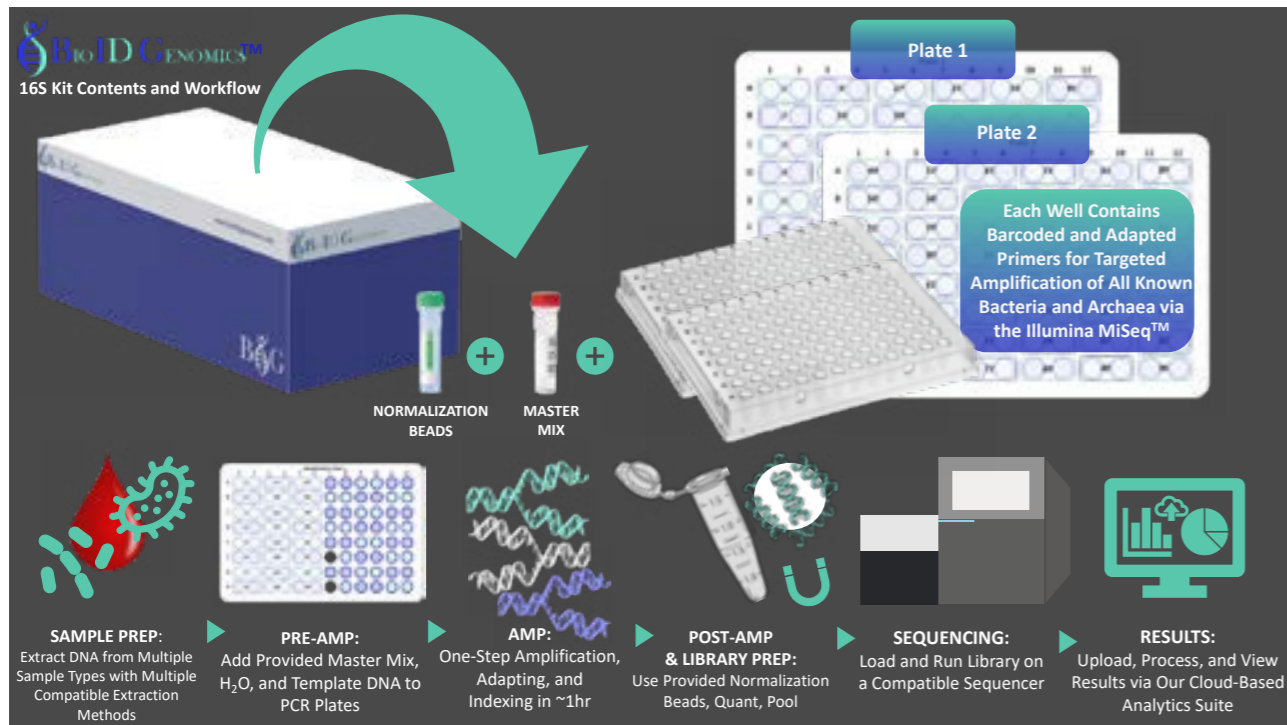
Bartlow wanted to use a different analysis than that typically used to tell them apart. So, the team targeted two separate locations within the DNA, improving their ability to identify each species or subspecies – known as taxonomic resolution – and enabling them to study microbiome diversity in greater detail.

**These 'friendly' microorganisms help to keep us healthy by acting as a barrier, preventing their destructive counterparts from invading.**

The power of the microbiome. Well-nurtured microbiota are better able to fend off harmful microorganisms.



The researchers targeted two locations within the DNA to enable them to study microbiome diversity in more detail.



16S rRNA sequencing. Bartlow and colleagues are the first to use this novel method to study wildlife microbiomes.

## The 'One Health' approach tackles health security challenges by recognising the connections between humans, animals, and the environment.

This is the first time that the microbiomes of either species of screech owl have been described, and the first use of this novel 16S rRNA sequencing method to observe wildlife microbiomes (until now it has largely only been used to examine pathogens in human blood). Though these methods still need refining for different study areas, these sequencing technologies have opened a new realm of microbial exploration.

### NESTLING NEIGHBOURS

The research team found a significant difference in the microbiomes of the western and whiskered screech owls and, within each species, nestlings from different nest boxes had different microbiomes than those from the same parents. This may be because siblings were eating the same food, though the researchers highlight that further studies are needed to establish any relationship between diet and microbiome composition – but nevertheless it's clear that studying siblings will be important for future studies of wild bird microbiomes.

Western screech owls also seemed to have a larger variety of bacterial species within their microbiomes than whiskered screech owls. Limited studies have been carried out on owl microbiomes but in another study on barn owls (*Tyto alba*) the microbiomes of females were found to be more diverse than those of males, and their larger foraging areas made their microbial communities more varied. So, sex and foraging range could also be affecting microbiome composition. By association this suggests that the greater variation in bacteria for western screech owls could be explained by a sexual bias or because their foraging areas are larger; again, future investigations would be needed to determine this.

In total the researchers found 3,404 different bacteria species, with 2,819 of these being found only in the nestlings. *Blautia hydrogenotrophica* was the most common species in many samples, together with similar species from within the same genus. These species are

associated with digesting plants, which suggests the owls had acquired these bacteria by eating herbivorous insects. A human pathogen, carried by ticks and found in blood, was the top species found in one adult bird's samples (and in lower quantities in other birds), perhaps due to this one individual eating (or being fed on by) infected ticks.

### MICROBIOME STUDIES FOR GLOBAL HEALTH

There are so many ways in which we and other animals develop our individual microbial communities. Microbes are transferred to animals whenever they eat, drink, breathe, or touch anything. Each individual's anatomy, physical condition, genetic makeup, diet, age, sex, behaviour, and a multitude of other factors also impact how their body interacts with these communities. There is much more we need to understand about the vast array of factors that can create and alter microbiomes, as well as the differences in microbial communities within and between species.

Bartlow and colleagues' work takes us a step closer to better understanding wildlife microbiomes and wildlife ecology, and their potential as indicators of environmental change and early-warning systems for disease outbreaks among wildlife and humans alike.



# Behind the Research

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### Research Objectives

Andrew Bartlow and colleagues are researching the importance of microbiomes to animal and human health.

### Detail

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#### Bio

Andrew Bartlow co-leads the Ecological Health Security Lab at Los Alamos National Laboratory, USA. They combine research, training, and international science networks to tackle local and global health security challenges. Their research focuses on the ecology, transboundary transmission, and biosurveillance of emerging zoonoses by taking a One Health approach to reduce disease risk.

#### Funding

Los Alamos National Laboratory's, Laboratory Directed Research and Development program

#### Collaborators

Jeanne Fair, Chuck Hathcock, Sarah Kane Moser, and Jeremy Ellis

#### Competing interests

Jeremy Ellis is employed by Fry Laboratories, LLC, a commercial clinical laboratory, and BioID Genomics, Inc, that manufactures the test kits used in this study.

### References

Bartlow, A, et al, (2022) Comparing western (*Megascops kennicottii*) and whiskered (*M. trichopsis*) screech-owl microbiomes in southern Arizona using a novel 16S rRNA sequencing method, *Animal Microbiome*, 4(45). [doi.org/10.1186/s42523-022-00196-7](https://doi.org/10.1186/s42523-022-00196-7)

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### Personal Response

**What species would you prioritise for future microbiome research, for example those more known for transmitting zoonotic diseases, or endangered species?**

Species with links to human infection and species that are endangered should both be prioritised in future wildlife microbiome research. We need to better understand how microbiomes regulate pathogen transmission to other species and, ultimately, to humans. For example, we could ask, do migratory birds with less diverse microbiomes have more pathogens, like avian influenza and Newcastle disease virus? We also need to incorporate microbiome research into wildlife conservation, especially in captive breeding programmes. Loss of host microbial diversity may result in species declines in disturbed habitats, which are becoming more frequent. Disturbed habitats are also correlated with spill-over events, demonstrating the need for research into species declines, microbiomes, and zoonotic disease transmission.

