



RESEARCH BRIEF

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E. coli in Wildlife: What We Don't Know Might Hurt Us

Better understanding of animal-borne bacteria may help reduce transmission events to humans and improve food safety, biodiversity and conservation efforts.

Zoonotic disease emergence is a rising problem exacerbated by increasing human encroachment into wild areas through urbanization and resource extraction. Wild animals have also been cited as the source of outbreaks from harmful strains of the bacteria *Escherichia coli* – commonly known as *E. coli* – in food production. Although *E. coli* is normally present in the intestines of both animals and humans, certain strains of bacteria found in wildlife can have significant implications for human health. Wild animals play host to a range of genetically diverse *E. coli* and may serve either as vehicles of transmission or potential melting pots for the creation of new and possibly more dangerous strains that could threaten global health and food production. The broad genetic diversity of the *E. coli* found in wildlife also complicates source identification as well as outbreak control.

As human populations continue to expand into formerly natural areas, the potential for harmful microorganisms like *E. coli* to be transferred between humans and wildlife increases. The level of human impact on an environment directly corresponds with the pervasiveness of antibiotic resistant bacteria in wildlife. Severity of animal-to-human disease transmissions may increase when wildlife is exposed to antibiotics or human pathogens, often

POINTS FOR POLICYMAKERS

- ▶ **More research is required to understand the existence of *E. coli* in wildlife, especially given the potentially strong implications for global public health.** Increased data quantity combined with broader animal-hosted *E. coli* sampling across diverse species and in expanded geographic ranges is recommended. This will also clarify whether species that are significant carriers of *E. coli* differ from those that are threatened – an important consideration for disease management and wildlife conservation that ultimately aids in protecting global public health.
- ▶ **Future research funding should prioritize investigations into the routes and mechanisms of transmission.** This is especially critical at wildlife–livestock interfaces which offer significant opportunities for transmission of *E. coli* between domestic and wild animal populations. Resulting data will allow for better gauging the threat posed by wildlife-hosted *E. coli* to global public health.
- ▶ **A comprehensive and universal database of wildlife-hosted *E. coli* is needed.** A widely accessible source of information on wildlife-hosted *E. coli* will help address challenges of tracing contamination in food product outbreaks to a source point— a critical systemic shortcoming to properly monitoring foodborne pathogen transmission. This will also enable scientists to understand and track the extent and impact of global environmental antibiotic pollution.
- ▶ **Improving current protocols for contamination source tracking — even if difficult and expensive — will aid in the curtailment of future disease spillover into human populations.** *E. coli* outbreaks in agriculture production should be tracked. Crop contamination from harmful *E. coli* results in millions of dollars of produce losses in addition to costs related to treating foodborne illnesses and these infections lead to numerous deaths worldwide each year.

through contact with human waste such as garbage and sewage, contaminated waters, livestock or by consuming affected prey. Wildlife can also spread bacteria through fecal crop contamination, though few instances have been confirmed. Crop contamination results in millions of dollars of produce losses annually in addition to costs relating to the treatment of foodborne illness which lead to numerous deaths worldwide.

To better gauge the threat posed to global public health by wild animal-hosted *E. coli* and learn what key data was missing, Stanford researchers analyzed the current knowledge base. They examined factors including *E. coli* genetic diversity, animal hosts and their geographic distribution as well as the transmission pathways within and between wildlife and human populations. They identified three major knowledge gaps: lack of significant data within the existing studies; limitations in geographic locations chosen to date; and insufficient numbers of animal host species investigated. The gaps identified suggest that greater research efforts are needed to understand *E. coli* in wildlife, especially given the potentially strong implications for global public health.

The ability to classify *E. coli* across a broad range of animal species along with any knowledge gained about wildlife-harbored *E. coli* could allow for accurate contamination source tracking and intervention efforts as well as contain possible spillover of diseases into human populations. Universal access to this valuable information would result in multiple benefits for the environment, wildlife conservation efforts and agricultural production, while also protecting public health. It might also prevent wildlife from being wrongly blamed for certain disease outbreaks.



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This brief is based on the paper “**The under-investigated wild side of Escherichia coli: genetic diversity, pathogenicity and antimicrobial resistance in wild animals**” published in *Proceedings of the Royal Society B, Biological Sciences*.



FOR MORE INFORMATION

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