

Framework predicts endangered species' pathogen risk

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Dr. Wendy Beauvais is pictured with two saiga antelope calves in Central Asia. Beauvais developed a new framework to assess the risk of livestock pathogens jumping to wildlife, specifically endangered species. Credit: Cornell University

Four years ago, more than 200,000 endangered saiga antelope dropped dead on the remote steppe grassland of Central Asia in the species' worst recorded mass mortality event.

Dr. Wendy Beauvais, postdoctoral researcher in the College of Veterinary Medicine, was part of the team that pinpointed the cause of death—a deadly bacterium in the herd's bloodstream, triggered by environmental factors—and has used the saiga as a [case study](#) to develop a [framework](#) to rapidly assess and prioritize future risks of pathogens to wildlife.

"In general, events like this are likely to be rare and limited to small geographical areas," Beauvais said, "but their impact could be devastating to [endangered species](#) like the saiga."

The new framework builds on one developed by the World Organisation for Animal Health (OIE), which assesses the risk of [livestock](#) pathogens jumping to wildlife, specifically endangered species. They examine inherent randomness, natural variation and general lack of knowledge about such cases.

Beauvais' paper in *Royal Society Open Science*, "Rapidly Assessing the Risks of Infectious Diseases to Wildlife Species," adds key components to this framework: the seasonal movement of animals and their interactions with others as they traverse the globe.

"The saiga have this extreme life cycle where they migrate for long

distances," Beauvaisb said. "They're also in a remote area, so understanding what kind of contact they have with other animals and how [infectious diseases](#) might spread is quite challenging."

Interactions between the saiga and other animals—like livestock and free-ranging horses—are quite rare, which makes their occurrence more important because if they were to acquire an infectious disease, they might not have any immunity to it. "This makes them particularly vulnerable," Beauvais said.

The OIE's original framework is frequently used to examine the risk of importing or exporting animals for trade. After accounting for seasonal movement and cross-species interaction, Beauvais and her colleagues found that brucellosis (bacterial) and foot and mouth disease (viral) are two diseases most likely to be transmitted between livestock and wildlife.

Owners, local agencies and conservationists can use the new framework to monitor both livestock and wildlife like the saiga to predict the spread of infectious disease. Beauvais anticipates that the results of the study will be particularly useful for conservation groups as well as local stakeholders.

"My hope is that they'll be a bit more targeted in terms of the questions they ask and the diseases they need to be aware of in livestock," said Beauvais. The framework could also be used with other species, including caribou and bison, which like the saiga are migratory species living in remote areas.

The 2015 saiga event underscores the fact that not all outbreaks in [wildlife](#) come from [infectious diseases](#) transmitted by livestock. But, as Beauvais noted, they are still a risk; in addition to their findings regarding brucellosis and foot and mouth disease, she and her

collaborators have released a list of moderate-risk diseases with the paper.

"Infectious [disease](#) is really a livestock issue," said Beauvais. "It's about controlling and reporting diseases in livestock, and sharing information so that owners and government entities can tackle the problems together."

More information: Wendy Beauvais et al. Rapidly assessing the risks of infectious diseases to wildlife species, *Royal Society Open Science* (2019). [DOI: 10.1098/rsos.181043](https://doi.org/10.1098/rsos.181043)

Provided by Cornell University

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