

Wildlife Services

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National Wildlife Research Center

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Ecology of Emerging Viral and Bacterial Diseases in Wildlife



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Major Cooperators:

- Colorado State University
- Colorado School of Public Health
- DOI/USGS/Biological Resources Division
- Private feedlot owners
- State Departments of Public Health
- The Ohio State University
- Wildlife Services Operations
- Wildlife Services National Disease Program
- USDA/APHIS/Veterinary Services

Groups Affected By These Problems:

- Consumers
- Federal, State, and local governments
- Livestock and poultry producers
- Public health organizations and hospitals
- U.S. military
- Wildlife and natural resource managers

National Wildlife Research Center Scientists Examine the Roles of Wildlife in the Transmission and Spread of Emerging Infectious Pathogens

Wildlife Services' (WS) National Wildlife Research Center (NWRC) is the only Federal research organization devoted exclusively to resolving conflicts between people and wildlife through the development of effective, selective, and socially responsible methods, tools, and techniques.

Considerable concern exists around the world about recent emerging infectious diseases, of which 75 percent are zoonotic, meaning the pathogens causing the disease can be transmitted between animals and humans. Wildlife plays a critical role in both the emergence and increased incidence of pathogens transmittable and causing disease in livestock and humans. In the last two decades, approximately 72 percent of emerging infectious diseases originated in wildlife, such as highly-pathogenic H5N1 avian influenza virus that originated in Asia and subsequently spread across the Eastern Hemisphere. In addition, wildlife has increasingly been implicated in the spread of re-emerging pathogens, such as antibiotic-resistant bacteria that are causing significant problems associated with agricultural, animal, and human health. Thus, wildlife populations often play a key role in diseases that directly impact humans and agriculture. NWRC is at the forefront of research and surveillance for many of these pathogens. Much of this effort has focused on avian influenza viruses and pathogenic bacteria, including antibiotic-resistant strains.

Avian influenza viruses (AIV) are found naturally in waterfowl and other wild bird species. There are 144 known subtypes of AIV but few of these subtypes cause serious diseases in birds. However, mutation of the virus can lead to infection of new wildlife species, domestic livestock (primarily poultry), and humans. These mutations can result in AIV strains that are highly pathogenic. For example, the highly pathogenic strain of H5N1 AIV originated from a low pathogenic strain of AIV in wild waterfowl and mutated into a highly pathogenic strain in Asia. This strain spread across the Eastern Hemisphere and caused considerable economic loss and mortality in domestic poultry, as well as human deaths. Thus, understanding the ecology of low pathogenic strains of AIV in the wild is critical for the prevention of future influenza epidemics and global pandemics that affect both livestock and humans. NWRC scientists have played a key role in understanding the ecology of AIV in wildlife and how they may transmit AIV from natural systems to agricultural operations and humans.

Pathogenic bacteria have become an increasing health risk to both livestock and humans. These bacteria can cause illness in humans, ranging from food poisoning to life-threatening disease. In livestock, such bacteria can cause considerable loss in production. An additional complication is when these strains become resistant to antibiotics and, hence, are difficult to treat with traditional means. These "superbugs" have recently become a problem in hospitals, where they often defeat the last line of defense, antibiotics, in a physician's arsenal of drugs. Recently, a number of antibiotic-resistant strains of pathogenic bacteria have been found in wildlife but the role of wildlife in transmitting and spreading these bacterial strains is largely unknown. Research at NWRC is beginning to unravel the role of wildlife in maintaining and spreading both pathogenic bacteria and antibiotic-resistant strains of those bacteria.

Applying Science and Expertise to Wildlife Challenges

Mallards Shed Light on Avian Influenza Viral Shedding and Transmission—NWRC scientists studied (1) how long, and at what levels mallard ducks shed AIV, (2) the best sampling methods (i.e., oral-pharyngeal swabs, cloacal swabs, and fecal swabs) for detecting the virus associated with mallards, and (3) whether the virus can be transmitted through a water source shared by infected and uninfected mallards. Researchers experimentally inoculated 3-month-old and 6-month-old mallards with a subtype of low pathogenic AIV commonly found in wild duck populations. Fecal samples had significantly higher



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virus concentrations than oral-pharyngeal or cloacal swabs, and the older ducks shed significantly more virus than younger ducks regardless of the sample type tested. Uninfected mallards became infected after using a water source that infected ducks had previously used. These results are important for surveillance purposes and suggest that water samples and fecal samples may be excellent alternatives to traditional cloacal and oral-pharyngeal swabbing of live-captured waterfowl. Furthermore, duck age may be important when interpreting viral shedding. Differential, age-related shedding could affect prevalence estimates, modeling of virus spread, and subsequent risk assessments. Epidemiologic modeling of disease dynamics can be used to develop control strategies that limit disease spread and ultimately control outbreaks. To elucidate important factors affecting avian influenza dynamics, NWRC scientists are studying the impact of viral dose on the subsequent course of infection in mallards to determine if the initial dose affects the duration of infection, the quantity of virus shed, and the time of peak viral load shed by an individual. Also of importance are the exposure histories of individual ducks. NWRC scientists are determining the duration of antibodies to avian influenza in mallards to ascertain whether an infection in 1 year will impact a subsequent exposure to the same virus the following year. These studies are revealing that the ability to detect antibodies to avian influenza in mallards may be relatively short-lived after an infection and that the duration of an elevated antibody titer may also be dependent on the exposure dose of the initial infection. NWRC scientists are also studying mallards to determine how many secondary infections are likely to occur from exposure to a single infected individual and how variable AIV transmission is among individuals.

Avian Influenza Viruses in Wild Mammals: Assessing the Risk to Agriculture—Anecdotal reports have suggested that select mammalian species may be periodically exposed to AIV. However, the viral shedding capability of most peridomestic (i.e., living in close contact to humans) mammalian species and their potential role(s) in AIV ecology are largely unknown. NWRC scientists studied the potential of several mammalian species to shed AIV by various routes. Of the three species tested (raccoons, cottontail rabbits, and striped skunks), all yielded evidence of shedding of a low pathogenic H4N6 AIV frequently found in waterfowl in the United States. The most prominent shedding was noted in striped skunks and cottontail rabbits through the nasal route, and, to a lesser extent, the oral route. Environmental transmission through virus-contaminated water was detected in raccoons. These three species are commonly associated with agricultural operations and suburban areas. Thus, when infected, these mammals could potentially play a role in the movement of AIV and subsequently pose a biosecurity risk to agricultural operations. Information pertaining to the virus shedding potential of these animals is essential for agricultural risk assessments.

Intercontinental Movement and Diversity of Avian Influenza Viruses in the U.S.—A national interagency avian influenza surveillance plan was initiated in 2006 for early detection of highly pathogenic avian influenza viruses (HPAIV) in wild birds. The plan included a variety of wild bird sampling strategies including the testing of fecal samples from aquatic areas throughout the United States from April 2006 through December 2007. Although HPAIV was not detected through this surveillance effort, NWRC researchers were able to obtain 759 waterfowl fecal samples from across the continental United States that were positive for low pathogenic avian influenza virus (LPAIV). Researchers used 136 DNA sequences obtained from these samples along with samples from a public influenza sequence database for a phylogenetic assessment of AIV diversity in the United States, based

on the hemagglutinin (HA) genes. Sequences from all HA subtypes, except H5, H7, H14 and H15, were analyzed to examine genetic variation, exchange between Eurasia and North America, and geographic distribution of LPAIV in wild U.S. birds. This study confirmed intercontinental exchange of some AIV HA subtypes (including a newly documented H9 exchange event), as well as identifying subtypes that do not regularly experience intercontinental gene flow but have been circulating and evolving in North America for at least the past 20 years. These HA subtypes have high levels of genetic diversity with many lineages co-circulating within the wild birds of North America. The surveillance effort that provided these samples demonstrates that such efforts provide important information about the ecology of AIV circulating in North America.

Wildlife and the Spread of Pathogenic and Antibiotic-resistant Bacteria—NWRC scientists have studied the potential spread of pathogenic bacteria to animals in agricultural facilities and humans in a variety of wildlife species ranging from European starlings to deer and elk. Scientists studied the local movements of European starlings and their potential role in carrying Salmonella among feedlots by sampling European starlings, cattle feed, cattle water troughs, and cattle feces on feedlots for Salmonella enteric. Results suggested that European starlings may be a source for *S. enterica* in cattle feed and water, which likely contributes to infections throughout the associated cattle herd. This finding suggests that European starlings not only are an important source for *S. enterica* infections in cattle but may also move pathogens within and among cattle feedlots.

In 2008, eight children playing on a soccer field in Evergreen, Colorado, were sickened with a strain of Shiga-toxin producing *E. coli* (STEC); five of these children were subsequently hospitalized. Ultimately, the source of these infections was genetically linked to feces from wild elk, which used the soccer field for foraging. STEC causes an estimated 265,000 enteric illnesses, 3,700 hospitalizations and 31 deaths in the United States each year with infection of people by one strain (STEC O157) alone costing an estimated \$405 million. This motivated public health officials to question whether wild elk were a source of STEC infections in Colorado. NWRC scientists studied this problem by sampling elk and deer feces in urban areas of Colorado in comparison with those sampled in wild areas and areas used by free-ranging cattle. Elk and deer using urban areas had much higher incidence of STEC (11 percent) than areas used by free-ranging cattle (2 percent) or wild areas (0 percent). This suggested that there is some connection between STEC incidence in elk and deer and their use of urban areas. While the reasons for this are currently unknown, NWRC scientists are working to unravel the sources of infection and the ultimate implications for human health. In addition to pathogenic bacteria, there is considerable concern about the spread of antibiotic-resistant strains of bacteria that are becoming increasingly prevalent. In health facilities, these are often referred to as “superbugs” that resist traditional medical treatment with antibiotics. NWRC scientists studied the role of wildlife in disseminating antibiotic-resistant bacteria to and from commercial livestock facilities. They found that a large percentage of wild raccoons using livestock facilities were infected with one or more strains of antibiotic-resistant bacteria and frequently visited feed troughs used by cattle on the livestock facilities. Thus, wild raccoons may be an alternate source of antibiotic-resistant bacteria entering the food chain and causing problems for agricultural, animal, and human health.

Selected Publications:

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SHRINER, S. A., K. K. VANDALEN, N. L. MOOERS, J. W. ELLIS, H. J. SULLIVAN, J. J. ROOT, A. M. PELZEL, and A. B. FRANKLIN. 2012. Low-pathogenic avian influenza viruses in wild house mice. *Plos ONE* 7:e39206.

Major Research Accomplishments:

- WS conducted research on the roles of wildlife in shedding avian influenza virus and related this information to the potential of subsequent transmission to domestic animals and humans.
- WS is evaluating the role of wildlife as transmitters of bacterial pathogens to and among livestock facilities and human populations.
- WS is elucidating the role of wildlife in the transmission and spread of antibiotic-resistant bacteria to and from commercial livestock facilities.
- WS sequenced wild bird fecal samples to study intercontinental movements of avian influenza virus and the implications for introduction of pandemic influenza strains into the United States.