

United States Department of Agriculture
Project Initiation

Project Data for Accession Number 1034747

Project Title

Using microbial transmission potential networks to identify and mitigate transmission of antimicrobial resistant bacteria among livestock and wild birds

Project Details

Sponsoring Institution National Institute of Food and Agriculture	Project Status ACTIVE
Funding Source NIFA Non Formula	Grant Year 2026
Grant No. 2026-68015-46673	Cumulative Award Amt. \$294,000.00
Proposal No. 2025-10369	Multistate No. (N/A)
Project Start Date Sep 01, 2026	Project End Date Aug 31, 2028
Program Code [A1366] Mitigating Antimicrobial Resistance Across the Food Chain	

Project Director

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Recipient Organization

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Non Technical Summary

Antimicrobial resistance (AMR) in the food chain threatens both human health and the stability of livestock-based agriculture. Annual livestock production losses due to AMR are projected up to 10%, while cumulative global GDP losses for 2025-2050 could reach US\$1 trillion. For farmers, AMR increases costs and reduces productivity by prolonging illness in livestock, raising veterinary expenses, and elevating morbidity and mortality rates. Wild birds have been implicated in spread of AMR among farms and may serve as reservoirs that facilitate continued emergence of novel AMR bacteria in farms. Our goals are to 1) identify reservoirs of AMR around livestock farms, 2) measure the extent to which wild birds transmit AMR within and among farms, and 3) identify factors contributing to AMR transmission among livestock and wild birds. We will sample the common bacterium E. coli from wild birds and livestock at 10 farms. To measure bacterial transmission among hosts, we will sequence E. coli isolates to identify

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sharing of bacterial genes, with a focus on genes associated with AMR. We will analyze networks of shared genes to identify farm and environmental factors associated with increased bacterial sharing and AMR transmission. By identifying factors contributing to increased prevalence and transmission of AMR within and among farms, this work will address the program area priorities of 1) identifying key AMR risks at a critical control point within the food chain, 2) identifying factors that impact AMR development, and 3) determining improved management practices in antibiotic stewardship and dispense this information to stakeholders.

Animal Health Component

Animal Health Component: 10%

Research Effort Categories

Basic	70%
Applied	30%
Developmental	0%

Classification

Knowledge Area (KA)	Subject of Investigation (SOI)	Field of Science (FOS)	Percent
311	4010	1070	30%
311	3410	1070	30%
311	0820	1070	30%
722	4010	1070	10%

Knowledge Area

[311] Animal Diseases

[722] Zoonotic Diseases and Parasites Affecting Humans

Subject Of Investigation

[4010] Bacteria

[3410] Dairy cattle, live animal

[0820] Wild birds

Field Of Science

[1070] Ecology

Keywords

Livestock, antimicrobial resistance, birds, transmission

Goals / Objectives

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Broadly, our goals are to (1) investigate bacterial sharing between livestock and wild birds, (2) identify environmental risk factors for inter-species antimicrobial resistance (AMR) transmission at the livestock-wild bird interface, and (3) quantify the extent of bird-mediated AMR spread among farms. To achieve this, we will sample wild birds, livestock, and environmental sources from Michigan farms across gradients of agricultural practices and landscape contexts. Using bacterial sharing of mobile genetic elements, including those carrying AMR genes, we will construct transmission potential networks to quantify epidemiological connectivity between wildlife and livestock hosts (Hassell et al. 2019, 2023). Specifically, we will address the following objectives:

- Identify on-farm and landscape-level environmental factors influencing AMR gene transmission between wild birds and livestock. At the farm level, we predict that there will be increased AMR prevalence and gene transmission on farms with greater presence and number of retention ponds or lagoons, greater access to livestock food and water resources for wild birds to exploit, and both higher livestock density and greater number of livestock. At the landscape level, we predict increased AMR prevalence and gene transmission on farms with a higher percentage of agricultural land and decreased natural habitat in a 1 km buffer around the farm.
- Identify the extent to which wild birds disseminate AMR among farms. We predict greater connectivity between livestock on farms and wild birds when inter-farm distances are shorter, farm density is higher, and bird abundance is greater.
- Identify key environmental interfaces that may be targeted as points of control for mitigating AMR spread into the food chain. We predict that retention ponds and water sources on livestock farms will be key interfaces with greater connectivity of AMR gene spread between wild birds and livestock due to the persistence of bacteria in water sources, and the high presence of birds exploiting these resources.

Project Methods

To understand the factors underlying AMR transmission dynamics and identify intervention points for AMR spillover, we will investigate bacterial sharing between livestock and wild birds on farms and identify landscape and on-farm environmental characteristics that influence patterns of AMR transmission at these interfaces. We will engage with 10 Michigan livestock farms to collect bacterial samples from wild birds and livestock animals. By isolating *E. coli* from these samples and performing whole genome sequencing, we will identify AMR-associated genes and evaluate patterns of gene sharing among birds and livestock, performing novel statistical network analyses to identify evidence of AMR transmission and test how this transmission is influenced by farm and environmental factors. Using this information, we will provide farmers with actionable information for mitigating wild bird-mediated AMR transmission on their farms.