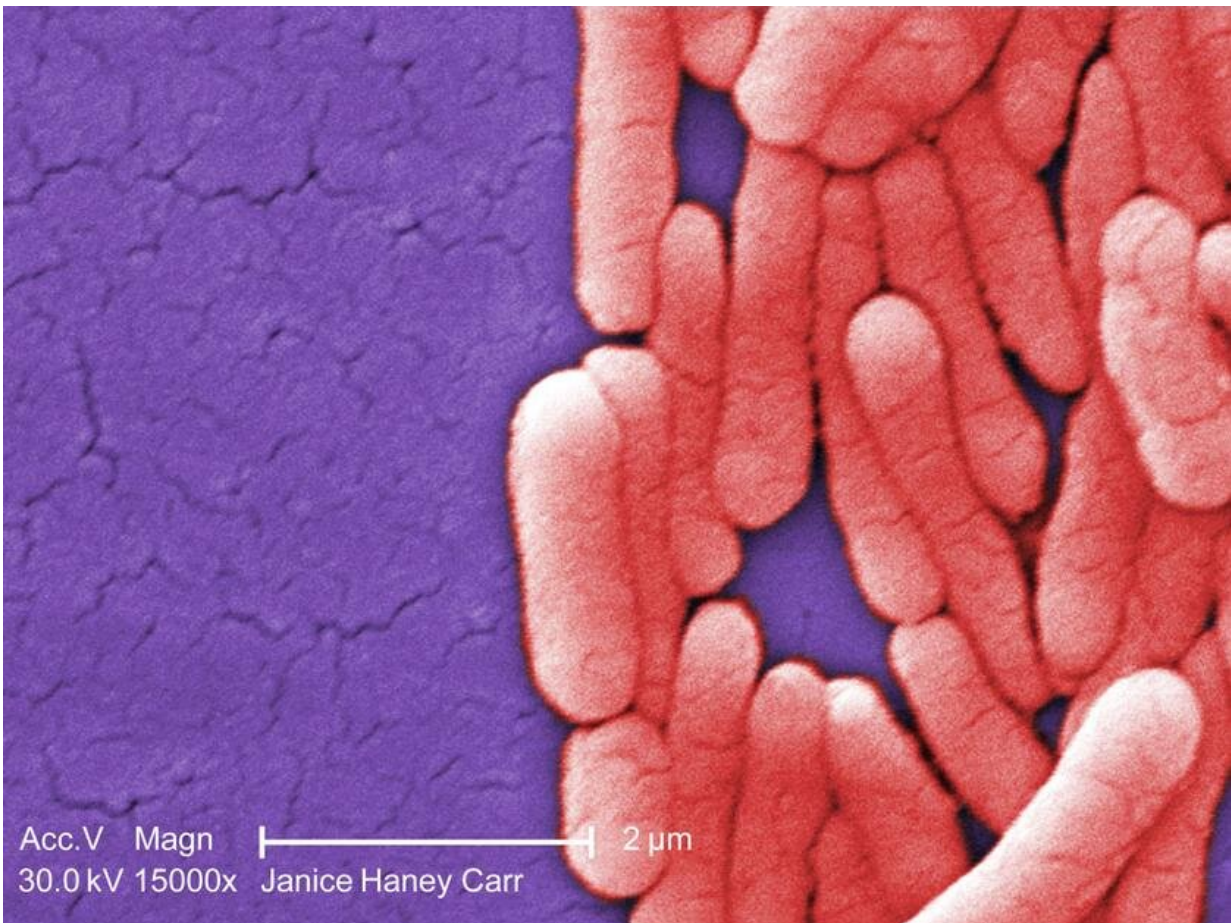


Antibiotic-resistant salmonella strains not seen in migrating wild birds

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To reach their conclusion, the researchers whole-genome sequenced 375 *Salmonella enterica* strains, like the one shown greatly enlarged under a microscope, from wild birds collected in 41 U.S. states from 1978 to 2019 to examine bacterial resistance to antibiotics and heavy metals. Credit: U.S. Centers for Disease Control and Prevention

Although many wild birds carry Salmonella, the strains of the bacteria they convey usually do not harbor antimicrobial-resistance genes, according to Penn State researchers, who led a team conducting a new, nationwide study.

That's good news, according to team leader Ed Dudley, professor of food science, Penn State.

"While we've known for a while that wild birds can carry Salmonella, the strains they carry appear to be of lesser concern to human health," he said. "The assumption was that these Salmonella—like the bacteria we can isolate from domesticated farm animals—would carry large numbers of antimicrobial-resistance genes. We found the opposite to be true."

Wild birds are known to be common reservoirs of *Salmonella enterica*, a pathogen that sickens millions of people every year, Dudley explained, and scientists have worried that wild birds carrying antimicrobial-resistant *Salmonella enterica* pose a risk to public health because they can spread the resistant bacteria across large areas in a short time. This research indicates that wild birds do not serve as important reservoirs of resistant *Salmonella enterica* strains.

To reach their conclusion, researchers whole-genome sequenced 375 *Salmonella enterica* strains from wild birds collected in 41 U.S. states from 1978–2019 to examine bacterial resistance to antibiotics and heavy metals. The study—which was spearheaded by Yezhi Fu, a postdoctoral researcher in Dudley's research group in the College of Agricultural Sciences—answers important questions about the role migrating birds play in transmitting diseases to humans.

The researchers reported in *Environmental Microbiology* that they found Typhimurium was the dominant *Salmonella enterica* strain, accounting for 68% of the bird isolates. However, less than 2% of those isolates

were identified as multi-antimicrobial resistant or resistant to heavy metals. Interestingly, all the multi-resistant *Salmonella enterica* were isolated from water birds or raptors; none of them was isolated from songbirds.

The isolates tested in the study came from the National Wildlife Health Center, which is part of a U.S. Geological Survey lab. The federal connection resulted from Dudley's research group being part of the U.S. Food and Drug Administration's Genome Tracker program since 2016. That initiative's overarching goal, he noted, is to learn how to use the increasingly powerful ability to sequence bacterial genomes to learn more about food borne pathogens such as *Salmonella*.

"We worked with the National Wildlife Health Center because it has this genetically amazing collection of *Salmonella* isolates collected over more than 40 years from sick migratory birds," he said. "It is an opportunistic collection for us, and somebody just needed to analyze it. It yielded information we couldn't have gotten anywhere else."

Dudley's research group continued to analyze that federal collection of wild bird *Salmonella* isolates, making several other discoveries.

They reported in *Applied and Environmental Microbiology* that certain strains of *Salmonella* were associated with specific hosts. For example, after sequencing 131 *Salmonella* Typhimurium isolates from wild birds collected in 30 U.S. states, they found that songbirds and waterbirds were likely to host the same strains, while gulls and terns carried distinct, different lineages of the bacteria. The study indicates that *Salmonella* Typhimurium may have undergone evolution within wild birds in the United States.

"We also showed that lineages formed by wild bird isolates differed from most isolates originating from domestic animal sources," Dudley

said. "And by using a machine learning classifier, we were able to attribute Typhimurium genomes to various groups of [wild birds](#). That's important because identifying host-adapted genomic datasets can improve source prediction and facilitate future disease outbreak investigation."

A third paper added an international aspect to the research, Dudley said. In *Microbial Genomics*, the researchers reported that they found evidence of common ancestry and evolution of the Salmonella enterica strain Typhimurium in songbirds in the U.K. and U.S., presumably resulting from centuries of bird migration.

The researchers analyzed publicly available datasets from the U.K., Australia and New Zealand and found that Salmonella strains have been transmitted across the globe. The wild, migrating bird research provides insights into modern-day disease investigations, Dudley suggests.

"To find what antibiotics a particular Salmonella strain is resistant to, we don't have to run the traditional lab-based tests anymore—where you grow it on some type of media, expose it to antibiotics, and it either grows or it doesn't," he said. "Now, we can sequence the entire genome, and by identifying certain gene markers, we can predict—with almost perfect precision—what antibiotics the organism will be resistant to."

More information: Yezhi Fu et al, Evidence for common ancestry and microevolution of passerine-adapted Salmonella enterica serovar Typhimurium in the UK and USA, *Microbial Genomics* (2022). [DOI: 10.1099/mgen.0.000775](https://doi.org/10.1099/mgen.0.000775)

Yezhi Fu et al, Low occurrence of multi-antimicrobial and heavy metal resistance in Salmonella enterica from wild birds in the United States, *Environmental Microbiology* (2021). [DOI: 10.1111/1462-2920.15865](https://doi.org/10.1111/1462-2920.15865)

Yezhi Fu et al, Salmonella enterica Serovar Typhimurium Isolates from Wild Birds in the United States Represent Distinct Lineages Defined by Bird Type, *Applied and Environmental Microbiology* (2022). [DOI: 10.1128/aem.01979-21](https://doi.org/10.1128/aem.01979-21)

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