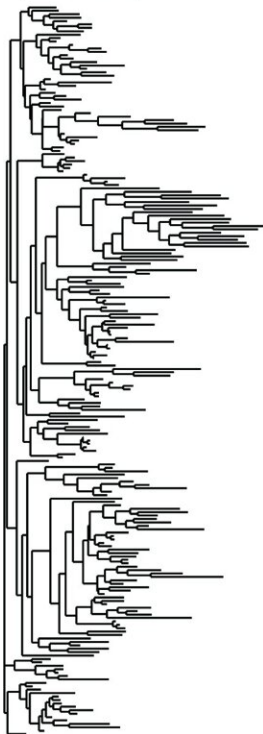


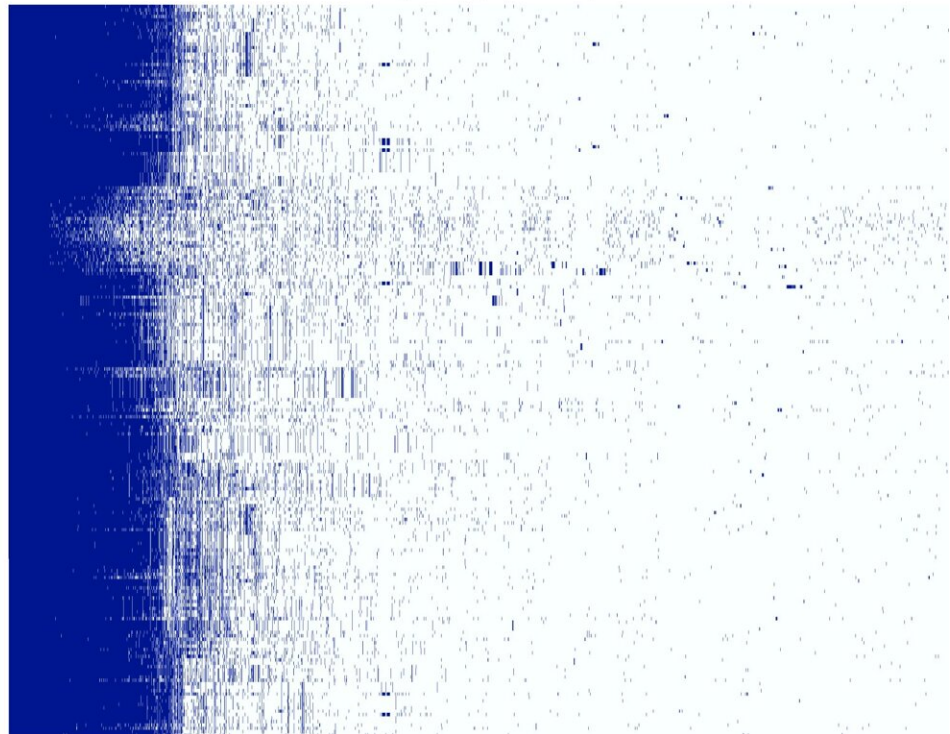
# Study finds a large proportion of Michigan's *C. jejuni* infections are caused by antibiotic resistant strains

August 31 2023, by Matt Davenport

Phylogenetic tree  
(n=214 strains)



Roary matrix  
(n=8,781 gene clusters)



Maximum-likelihood phylogeny of 214 *Campylobacter jejuni* strains reconstructed using the 615 core-gene sequences (550 736 bp) identified in the pangenomic analysis and rooted at the midpoint. The heat map shows the presence (dark blue shading) or absence (white shading) of the 8781 unique genes (arranged in columns) per strain based on placement in the phylogeny. Credit: *Microbial Genomics* (2023). DOI: 10.1099/mgen.0.001073

Working with the Michigan Department of Health and Human Services, Michigan State University researchers have shown that antibiotic resistance genes are prevalent in the bacterium *Campylobacter jejuni*, a leading cause of foodborne illness.

The team found that more than half of the *C. jejuni*, isolated from patients in Michigan, are genetically protected against at least one antibiotic used to fight bacterial infections. The team's full report is published in the journal *Microbial Genomics*.

"We know these pathogens have been around forever, but using more sophisticated genome sequencing tools lets us look at them differently," said Shannon Manning, the project's leader and an MSU Research Foundation Professor in the Department of Microbiology and Molecular Genetics. "We found that the genomes are extremely diverse and contain a lot of [genes](#) that can protect them from numerous antibiotics."

The team's report provides valuable technical insights to epidemiologists, [health care workers](#) and other specialists, but Manning also emphasized what the team's findings mean for the average person.

Although most otherwise [healthy adults](#) can fight off such stomach bugs without antibiotics, she said, there are people for whom *C. jejuni* presents a serious concern. Infections can lead to hospitalization, autoimmune and neurological complications, long-term disability and even death.

Understanding the extent of antibiotic resistance in this species, as well as which antibiotics different strains are resistant to, can help put patients on better treatment plans sooner.

"If we know the type of [antibiotic resistance genes](#) that *Campylobacter* has, then we know which antibiotics not to give a patient," Manning said.

This can lead to better patient outcomes and shorter hospital stays.

The finding also has broader implications. After people fight off an infection and the pathogen is killed—with or without antibiotics—its genes can linger, including those that provide antibiotic resistance. Other microbes can then pick up those genes, integrate them into their own genomes and gain resistance.

"That's really important. Foodborne pathogens are ubiquitous. They are found in the foods we eat but also in animals and environments that we come into contact with regularly," Manning said. "If they carry resistance genes, then not only can they make us sick, but they can also easily transfer the genes to other bacteria."

This underscores the importance of food hygiene and safety, Manning said, including avoiding cross-contamination of other foods and surfaces before cooking.

The team's genetic analysis also let the researchers pinpoint the host, or source, of specific strains. That is, they could predict whether the bacteria originated from specific animals or were generalists that are commonly found in multiple hosts.

"When we did this genomic analysis, we found that most patients in Michigan were infected with strains linked to chicken or cattle hosts," Manning said. Infections also were more likely to occur in [rural areas](#), the team found, suggesting that exposure to these animals and their environments could be important to monitor and potentially control.

Focusing on Michigan and working with hospitals around the state enabled the researchers to reveal more granular and local insights as well. Studying the 214 strains recovered from real patients, the researchers observed trends specific to Michigan that may otherwise

have gone unnoticed.

Although the Centers for Disease Control and Prevention operates a [nationwide network](#) surveilling foodborne pathogens, many states, including Michigan, are not part of this system.

"We have unique ecological and agricultural factors in Michigan that may impact how these pathogens survive and proliferate in certain hosts and environments," said Manning, whose team also studies other major contributors to foodborne illness, including E. coli, shigella and salmonella.

"If you don't look for them and assess, then you won't be able to identify which factors are most important for infections and antibiotic resistance or define how Michigan differs from other regions," she said.

**More information:** Jose A. Rodrigues et al, Pangenomic analyses of antibiotic-resistant *Campylobacter jejuni* reveal unique lineage distributions and epidemiological associations, *Microbial Genomics* (2023). [DOI: 10.1099/mgen.0.001073](https://doi.org/10.1099/mgen.0.001073)

Provided by Michigan State University

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