

Arcobacter abundant in Hurricane Florence floodwaters

October 2 2020, by Tracey Peake



Flooding near the Cape Fear River during Hurricane Florence in 2018. Credit: U.S. Army/Staff Sgt. Mary Junell

A North Carolina State University research team's search for *Campylobacter* in the floodwaters from Hurricane Florence instead uncovered an abundance of a related emerging pathogen: *Arcobacter*. The study raises questions about the prevalence of these understudied bacteria and demonstrates the ways in which floodwaters can amplify or

spread pathogens over a geographical area.

Campylobacter is a well-known group of foodborne bacteria, spread primarily through contact with contaminated fecal matter. In humans it causes symptoms commonly associated with "[food poisoning](#)," such as diarrhea, fever and cramps. However, Campylobacter infections also constitute one of the leading precursors of Guillain-Barré syndrome, a serious complication that can cause permanent disability and paralysis. Food animals—particularly poultry and hogs—are known reservoirs of Campylobacter bacteria.

By comparison, Arcobacter—which can look and behave similarly to Campylobacter—is an emerging, primarily waterborne, pathogen. Its prevalence in the environment is unknown and its role in human disease has only been confirmed in the past two decades.

In 2018, Hurricane Florence caused major flooding in eastern North Carolina, where much of the state's food animal production takes place. A team of NC State researchers including Sophia Kathariou, corresponding author of a paper describing the work, set out to determine whether the floodwaters contained Campylobacter that might have originated in poultry or hog farms. Kathariou is a professor of food science and microbiology at NC State.

"Very little is known about the impact of hurricanes on microbial communities," Kathariou says. "Although flooding could increase the exposure of surface waters to microbes, the large volumes of water associated with flooding may also dilute microbial agents, counteracting the effects. We had previously done surveys of turkey and hog farms in eastern North Carolina, and we knew that they were heavily colonized by Campylobacter," Kathariou says. "So we saw this as a good test case."

As soon as it was possible to safely access the floodwaters, the team took

96 samples of floodwater from the Neuse, Cape Fear, Lumbee and Waccamaw watersheds in North Carolina. Ryan E. Emanuel, paper co-author and professor of forestry and [environmental research](#) at NC State, coordinated the sample collection.

The researchers used growth media designed to culture *Campylobacter*, but of the 96 samples taken, only one yielded *Campylobacter*. However, more than 75% of the samples yielded genetically diverse strains of *Arcobacter*, which were all found to be the emerging pathogen *Arcobacter butzleri*.

The researchers hope to conduct further research to determine a baseline prevalence of *Campylobacter* and *Arcobacter* in the watersheds and their association with human illnesses before, during and after flood events.

"It is definitely a surprising result," Kathariou says. "We had not even looked for *Arcobacter* in farms. It could be more prevalent than we think."

The work appears in *Applied and Environmental Microbiology*.

More information: Jeffrey A. Niedermeyer et al. Search for *Campylobacter* spp. Reveals High Prevalence and Pronounced Genetic Diversity of *Arcobacter butzleri* in Floodwater Samples Associated with Hurricane Florence in North Carolina, USA, *Applied and Environmental Microbiology* (2020). [DOI: 10.1128/AEM.01118-20](https://doi.org/10.1128/AEM.01118-20)

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