

Multistate Outbreak of Multidrug-Resistant *Campylobacter* Infections Linked to Contact with Pet Store Puppies

Posted October 3, 2017 2:00 PM ET

Outbreak Advisory

55 Cases

12 States

13 Hospitalizations

0 Deaths

- The Ohio Department of Health, several other states, the Centers for Disease Control and Prevention (CDC), and the U.S. Department of Agriculture Animal and Plant Health Inspection Service (USDA-APHIS) are investigating a multistate outbreak of human *Campylobacter* infections linked to puppies sold through Petland, a national pet store chain.
- 16 more ill people with a *Campylobacter* infection linked to the outbreak have been reported since September 11, 2017. The most recent illness began on September 12, 2017.
- As of October 3, a total of 55 people with laboratory-confirmed infections or symptoms consistent with *Campylobacter* infection who live in 12 states (Florida, Kansas, Maryland, Missouri, New Hampshire, New York, Ohio, Pennsylvania, Tennessee, Utah, Wisconsin, and Wyoming) have been linked to this outbreak.
 - 14 people are Petland employees from 5 states.
 - 35 people either recently purchased a puppy at Petland, visited a Petland, or visited or live in a home with a puppy sold through Petland before illness began.
 - 1 person had sexual contact with a person with a confirmed illness linked to Petland.
 - 4 people were exposed to puppies from various sources.
 - 1 person had unknown puppy exposure.
- Ill people range in age from <1 year to 86 years, with a median age of 23 years; 38 (69%) are female; and 13 (24%) report being hospitalized. No deaths have been reported.
- Epidemiologic and laboratory evidence indicates that puppies sold through Petland stores are a likely source of this outbreak. Petland is cooperating with public health and animal health officials to address this outbreak.
- [Whole genome sequencing](#) showed samples of *Campylobacter* isolated from the stool of puppies sold through Petland were closely related to *Campylobacter* samples isolated from the stool of ill people in multiple states.
- Clinical samples from people and puppies sickened in this outbreak appear to be resistant to commonly recommended, first-line antibiotics. This means infections with the outbreak strain may not respond well to oral antibiotics usually prescribed to treat *Campylobacter* infections.
 - CDC's [National Antimicrobial Resistance Monitoring System \(NARMS\)](#) team analyzed whole genome sequence data from *Campylobacter* isolated from stools of seven ill people and six ill puppies to look for genes that predict [antibiotic resistance](#).
 - Analysis suggests that all 13 isolates are resistant to azithromycin, ciprofloxacin, clindamycin, erythromycin, nalidixic acid, and telithromycin. In addition, 9 isolates appear resistant to gentamicin, and 12 isolates appear resistant to tetracycline.
 - Typically, predicted antibiotic resistance using whole genome sequence data matches the results of traditional antibiotic resistance testing for *Campylobacter*.*

- NARMS performed traditional [antibiotic resistance testing](#) on one isolate from an ill person. It showed resistance to the same antibiotics that analysis of whole genome sequence data predicted: azithromycin, ciprofloxacin, clindamycin, erythromycin, gentamicin, nalidixic acid, telithromycin, and tetracycline.
- *Campylobacter* can spread through contact with dog poop (feces). It usually does not spread from one person to another, however, activities such as changing an infected person's diapers or sexual contact with an infected person can lead to infection.
- Regardless of where they are from, any puppies and dogs may carry *Campylobacter* germs. Read [Advice to Pet Owners](#) and [Advice to Pet Store Workers](#) for illness prevention tips.
- This investigation is ongoing. CDC will provide updates as more information becomes available.

* Zhao, S., Tyson, G.H., Chen, Y., Li, C., Mukherjee, S., Young, S., et al. (2015). Whole genome sequencing accurately predicts antimicrobial resistance phenotypes in *Campylobacter* species. *Appl Environ Microbiol*, 82(2), 459 – 466.