

***Clostridium difficile* on U.S. Swine Operations**

Disease caused by *Clostridium difficile* is linked most commonly to nosocomial (hospital-acquired) infections in humans, especially after antibiotics are administered that alter normal gastrointestinal flora. Humans develop a spectrum of disease when infected with some strains of *C. difficile*. Symptoms range from mild diarrhea to life-threatening toxic megacolon and pseudo-membranous colitis (Weese, 2010). Even though *C. difficile* is typically seen as a nosocomial infection, there are increasing reports of community acquired infections.

C. difficile is a spore-forming organism which can survive in the environment for long periods and can, therefore, be ingested by animals or humans through contaminated foodstuffs and water (Yaeger et al., 2002). *C. difficile* has also been associated with clinical disease in young pigs and dairy calves (Yaeger et al., 2002; Hammitt et al., 2008). Shedding of *C. difficile* bacteria in animal feces can occur in the absence of clinical signs (Weese, 2010). In addition, some strains of *C. difficile* have been isolated from ground beef, ground pork, and ground veal purchased from retail markets in Canada which could serve as a source of infection in humans (Rodriguez-Palacios et al., 2007; Weese et al., 2009). To date, there has been little information available on the distribution and characteristics of *C. difficile* on various types of livestock operations across the United States.

Swine 2006 study

The U.S. Department of Agriculture's National Animal Health Monitoring System (NAHMS) conducted the Swine 2006 study, which focused on swine health and management practices in 17 States.¹ These States represented 94.2 percent of U.S. swine operations with 100 or more pigs and 94.0 percent of U.S. pig inventory for operations with more than 100 pigs on December 1, 2004. One objective of the Swine 2006 study was to determine if *C. difficile* could be found in the feces of grower/finisher pigs on U.S. swine operations and, if so, to determine the characteristics of the *C. difficile* isolates.

¹ **States/Regions:**

North: Michigan, Minnesota, Pennsylvania, Wisconsin
West Central: Colorado, Kansas, Missouri, Nebraska, South Dakota
East Central: Illinois, Indiana, Iowa, Ohio
South: Arkansas, North Carolina, Oklahoma, Texas

***C. difficile* prevalence**

During the Swine 2006 study, testing for *C. difficile* was performed on 63 swine operations from 15 of the 17 participating States. Overall, 867 fecal samples from pen floors (up to 10 samples per pen) of grower/finisher pigs (20+ weeks of age) were cultured² for the presence of *C. difficile*. All pens contained pigs that were presumed to be healthy and showing no clinical signs of disease. Of the 867 fecal samples tested, *C. difficile* was isolated from 99 (11.4 percent) [table 1]. At least 1 positive sample was found on 26 of the 63 operations tested for *C. difficile* (41.3 percent).

Table 1. Number and percentage of samples and operations tested for *C. difficile*, by test result

| Test Result | Samples Tested | | Operations Tested | |
|--------------------|-----------------------|-------------|--------------------------|-------------|
| | No. | Pct. | No. | Pct. |
| Positive | 99 | 11.4 | 26 | 41.3 |
| Negative | 768 | 88.6 | 37 | 58.7 |
| Total | 867 | 100 | 63 | 100 |

² Culture methods available in Thitaram et al. (2011).

Sample-level results

Herd size and region

There was no significant difference by herd size in the percentage of samples positive for *C. difficile* ($p=0.60$) [table 2].

Table 2. Number of samples tested and number and percentage of samples positive for *C. difficile*, by herd size

| | Herd Size (total inventory) | | | |
|--------------------------|-----------------------------|-------------|---------------|-------|
| | Fewer than 2,000 | 2,000–4,999 | 5,000 or More | Total |
| Number samples tested | 485 | 225 | 157 | 867 |
| Number samples positive | 66 | 19 | 14 | 99 |
| Percent samples positive | 13.6 | 8.4 | 8.9 | 11.4 |

The percentage of samples positive for *C. difficile* did not vary significantly by region ($p<0.42$) [table 3].

Table 3. Number of samples tested and number and percentage of samples positive for *C. difficile*, by region

| | Region | | | |
|--------------------------|--------|--------------|--------------|-------|
| | North | West Central | East Central | South |
| Number samples tested | 165 | 247 | 406 | 49 |
| Number samples positive | 18 | 40 | 29 | 12 |
| Percent samples positive | 10.9 | 16.2 | 7.1 | 24.5 |

Operation-level results

Herd size and region

There was no difference by herd size ($p=0.8$) [table 4] or by region ($p=0.2$) [table 5] in the percentage of operations with at least one positive sample.

Table 4. Number of operations tested and number and percentage of operations with at least one sample positive for *C. difficile*, by herd size

| | Herd Size (total inventory) | | | |
|-----------------------------|-----------------------------|-------------|---------------|-------|
| | Fewer than 2,000 | 2,000–4,999 | 5,000 or More | Total |
| Number operations tested | 36 | 15 | 12 | 63 |
| Number operations positive | 16 | 6 | 4 | 26 |
| Percent operations positive | 44.4 | 40.0 | 33.3 | 41.3 |

Table 5. Number and percentage of operations with at least one sample positive for *C. difficile*, by region

| | Region | | | |
|-----------------------------|--------|--------------|--------------|-------|
| | North | West Central | East Central | South |
| Number operations tested | 11 | 20 | 28 | 4 |
| Number operations positive | 6 | 11 | 8 | 1 |
| Percent operations positive | 54.5 | 55.0 | 28.6 | 25.0 |

Summary

Overall, the prevalence of *C. difficile* was relatively low (11.4 percent of samples positive) but the organism was widely distributed (41.3 percent of operations had at least one positive sample).

The recovery of *C. difficile* from feces on livestock operations warrants further investigation. Not all strains of *C. difficile* appear to have the same propensity to cause disease. Therefore, isolates from this study will be further characterized to determine how related these isolates are to those causing human disease. Further characterization of *C. difficile* isolates, including molecular typing and additional epidemiological studies, is needed to ascertain if a relationship exists between food animal isolates and those from humans in order to determine the potential for foodborne disease.

References

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