

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

Disease caused by *Clostridium difficile* is linked most commonly to nosocomial (hospital-acquired) infections in humans, especially when antibiotics are administered that alter normal gastrointestinal flora. Humans develop a spectrum of disease after 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 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.

Dairy 2007 study

The U.S. Department of Agriculture's National Animal Health Monitoring System (NAHMS) conducted the Dairy 2007 study, which focused on dairy health and management practices in 17 States.¹ These States represented 79.5 percent of U.S. dairy operations and 82.5 percent of U.S. dairy cows. The operations were divided into 3 herd-size categories based on the number of milk cows present: small (fewer than 100 cows), medium (100 to 499 cows), and large (500 or more cows). One objective of the Dairy 2007 study was to determine the prevalence of *C. difficile* in the feces of dairy cows presumed to be healthy on U.S. dairy operations.

¹ States/Regions:

West: California, Idaho, New Mexico, Texas, Washington

East: Indiana, Iowa, Kentucky, Michigan, Minnesota, Missouri, New York, Ohio, Pennsylvania, Vermont, Virginia, and Wisconsin

***C. difficile* prevalence**

During the Dairy 2007 study, testing for *C. difficile* was performed on 118 dairy operations across the 17 participating States. Individual cow fecal samples were taken via rectal retrieval for culture.²

Overall, 1,858 fecal samples from dairy cows were tested for the presence of *C. difficile*. Of the 1,858 fecal samples tested, *C. difficile* was isolated from 29 samples (1.6 percent) [table 1]. At least 1 positive sample was found on 15 of the 118 operations (12.7 percent).

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

Test Result	Samples Tested		Operations Tested	
	Number	Percent	Number	Percent
Positive	29	1.6	15	12.7
Negative	1,829	98.4	103	87.3
Total	1,858	100.0	118	100.0

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

Sample-level results

Herd size and region

Sample-level prevalence estimates are shown in tables 2 and 3. Overall, the prevalence of *C. difficile* in fecal samples was low. Only 1.6 percent of fecal samples from cows were positive (table 2). The proportion of samples positive was different by herd size where a higher percentage of small herds were positive for *C. difficile* compared with medium herds ($p=0.04$).

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

	Herd Size (number of dairy cows)			Total
	Small (fewer than 100)	Medium (100–499)	Large (500 or more)	
Number samples tested	580	759	519	1,858
Number samples positive	19	3	7	29
Percent samples positive	3.3	0.4	1.4	1.6

There was no significant regional difference in the percentage of samples positive for *C. difficile* ($p=0.18$) [table 3].

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

	Region	
	West	East
Number samples tested	282	1,576
Number samples positive	8	21
Percent samples positive	2.8	1.3

Operation-level results

Herd size and region

The operation-level prevalence for *C. difficile* varied by herd size ($p=0.04$). A lower percentage of medium operations (4.3 percent) had at least one sample positive for *C. difficile* compared with small and large operations (22.2 and 14.3 percent, respectively) [table 4].

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 (number of dairy cows)			Total
	Small (fewer than 100)	Medium (100–499)	Large (500 or more)	
Number operations tested	36	47	35	118
Number operations positive	8	2	5	15
Percent operations positive	22.2	4.3	14.3	12.7

There was no significant regional difference in the percentage of operations positive for *C. difficile* ($p=0.07$) [table 5].

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

	Region	
	West	East
Number operations tested	19	99
Number operations positive	5	10
Percent operations positive	26.3	10.1

Summary

There was a difference in *C. difficile* results by herd size at the sample and herd levels. Because confounding factors may be present (e.g., average herd size differs by region), these univariate associations need to be explored further with statistical models or additional studies.

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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