

Dynamic of *Salmonella* spp. in Dairy Herds and the Risk to Watershed Ecosystem

Rebecca Bordonaro, Dr. Patrick McDonough, Dr. Hussni O. Mohammed
 Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University

ABSTRACT

We carried out a repeated cross-sectional study to determine the occurrence of *Salmonella* spp. in dairy herds in watersheds. Fecal samples were collected per rectum from a representative sample of cattle on these operations and tested for the presence of *Salmonella* spp. using a combination of bacteriological enrichment and molecular detection. Analyses of the data to date demonstrated that *Salmonella* spp. occurs at a relatively low proportion among animals in the study population.

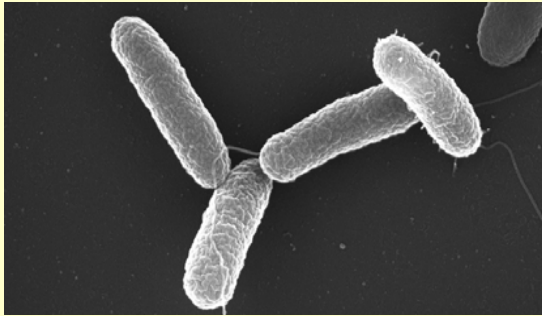


Fig. 1: *Salmonella*, A Novel Data-Mining Approach Systematically Links Genes to Traits. PLoS Biology Vol. 3/5/2005, e166

INTRODUCTION

Salmonella is a pathogen that can have serious effects on human health. The CDC approximates 40,000 reported cases of salmonellosis in the United States each year. *Salmonella* has a relatively low infective dose; it has been shown that as few as $10^5 - 10^8$ *Salmonella* cells are enough to produce infection in humans¹. Cows are a known reservoir for *Salmonella*, showing large variability in both shedding and genotype present². The influence of the interactions between the agent, host, and environmental factors on the virulence of pathogens is well illustrated in the emergence of antimicrobial resistant strains³. Factors influencing virulence and spread of *Salmonella* are of great importance because of the zoonotic potential of this pathogen and could help in mitigating the risk.

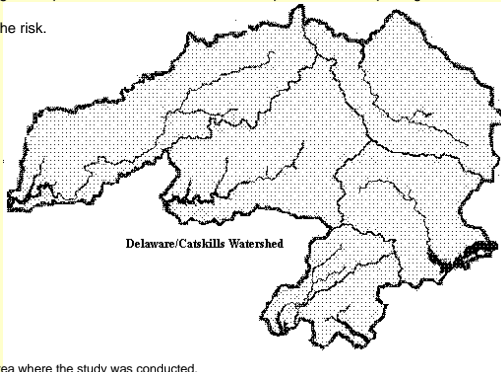


Fig. 2: The watershed area where the study was conducted.



Fig. 3: Rebecca Bordonaro collecting a fecal sample for the study.

MATERIALS AND METHODS

Sample collection

Fecal samples were collected during three seasons from 32 farms within New York watersheds. A total of 20 samples were collected at each visit, 9 from adult cows and 11 from calves.

Salmonella detection

Flasks of buffered peptone water with novobiocin were inoculated with feces. These flasks were incubated at 37°C for 24 hours. At the end of the incubation, this primary enrichment was used to inoculate a secondary enrichment of BHI in 2ml tubes. These were incubated for another 24 hours at 37°C. PCR detection of *Salmonella* in these samples was performed using the BAX Automated System.

Salmonella prevalence by season

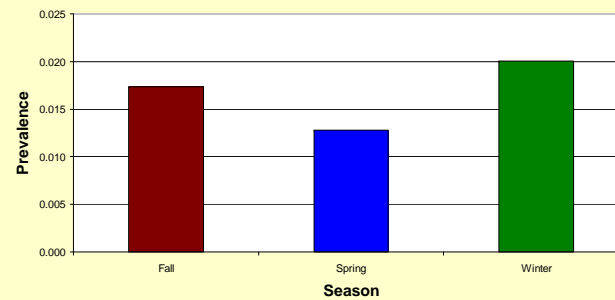


Fig. 4: The prevalence of *Salmonella* spp. among three seasons: fall, spring, and winter.

RESULTS

The overall prevalence of *Salmonella* spp. was 1.7% with a 95% confidence interval (1.10, 2.22). In a prevalence analysis by farm, 19 of 34 farms had 0% prevalence. Of the farms that were positive for *Salmonella*, 14 had a prevalence between 1.3% - 5% and one farm had a prevalence of 20.6%. In analysis by season, winter had the highest prevalence with 2%, followed by fall at 1.7%, and then summer at 1.3%.

Salmonella prevalence by farm

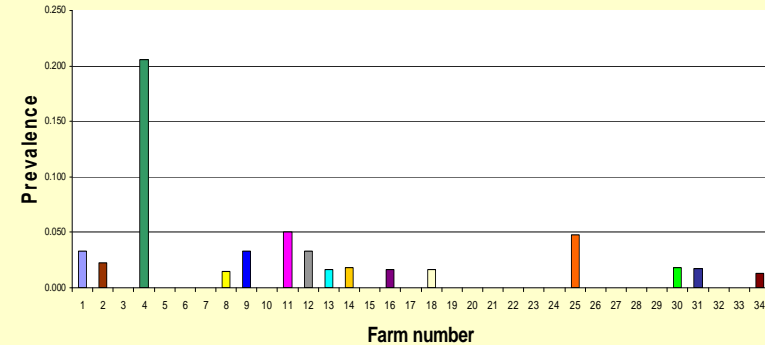


Fig. 5: The prevalence of *Salmonella* spp. by farm.

CONCLUSIONS AND DISCUSSION

Analysis with logistic regression statistics is currently being performed to determine risk factors associated with *Salmonella* infection. We have recently added waterborne pathogens including *Escherichia coli* and *Campylobacter* spp. to our research. Figure 6 shows the distribution of the different *Campylobacter* species that were screened for in the samples. To date, *C. jejuni* dominates the isolates.

Salmonella spp., *Campylobacter* spp., and *E. coli* O157:H7 are shed by cattle in watersheds; however, the shedding so far has been relatively low. Several management practices are associated with the shedding of these organisms and this knowledge could prove useful in designing risk mitigating practices.

Distribution of Campylobacter Species

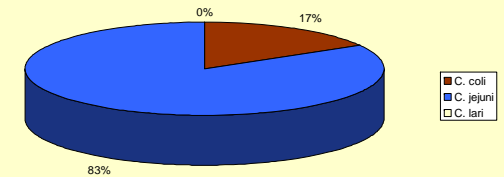


Fig. 6: The distribution of three *Campylobacter* species (*C. coli*, *C. jejuni*, and *C. lari*) among all samples positive for *Campylobacter* spp.

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