

Risk of Drinking-water Outbreaks of Cryptosporidiosis in Humans Caused by Cattle in Watersheds^a

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Introduction

There are at least two genotypes of *Cryptosporidium parvum* in nature—one that has only been isolated from humans (the H genotype) and one that has been isolated from a large range of mammals, including cattle and humans (the C genotype). By virtue of their presence in watersheds and the potential for water contamination with manure, cattle have often been implicated as a source of oocysts for human outbreaks of cryptosporidiosis.

A recent review of drinking-water outbreaks in North America indicated that none in the United States and only one in British Columbia, Canada were associated with the C genotype. Thus, the objective of this study was to determine prevalence of *C. parvum* genotypes H and C in dairy herds in the New York City Watershed (NYCW) and illustrate the risk posed by cattle to water-drinkers in this area.

Materials and Methods

Fecal samples were collected from 437 calves at risk for *Cryptosporidium* in the NYCW. Concentration/flotation microscopy and direct DNA isolation were performed on all samples. Fragments of the SSU rRNA and TRAP C-2 genes were amplified by nested polymerase chain reaction (PCR). The SSU rRNA fragments were subjected to restriction digestion by the enzyme *VspI*,

and the TRAP C-2 fragments were digested by the restriction enzyme *Eco91I* to distinguish between the H and C genotypes. The power was calculated using the binomial probability for failure to reject the null hypothesis and the Poisson distribution for calculation of maximum risk.

Results

In 214 of the fecal samples, oocysts were detected by concentration/flotation microscopy and amplicons were generated by PCR from 200 of the samples. None of the 200 samples tested by this two-locus, nested PCR-restriction fragments length polymorphism approach has the H genotype. At this level, we are 99% confident that the cattle in the NYCW did not harbor the H genotype of *C. parvum*.

Conclusions

While cattle pose a risk as a source of cryptosporidiosis for humans, it more likely will occur in sporadic cases. It is unlikely that cattle in the NYCW pose a significant risk for a large drinking-water outbreak. Focusing solely on methods to decrease or eliminate watershed contamination with oocysts from cattle will likely miss important human sources of many urban drinking-water outbreaks caused by the H genotype.

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