

Nonpoint Source Contamination-The Risk of *Cryptosporidium* spp. in Watersheds

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ABSTRACT

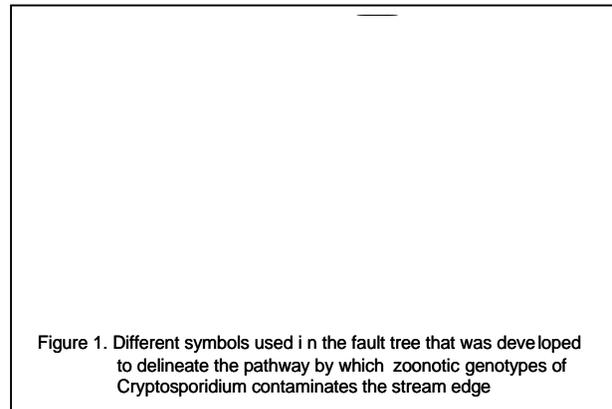
Cryptosporidium parvum is a coccidian protozoan that has zoonotic significance. Species of this protozoan are known to contribute significantly to calf morbidity and mortality and hence has become an economic liability to many dairy and beef herds. In addition to its negative impact on the efficiency of animal production, it has emerged as one of the most significant waterborne pathogens causing enterocolitis in humans worldwide. Because of the broad host spectrum of this protozoan, inefficiencies of the common drinking water treatment methods, and the lack of reliable drug therapy in humans, *Cryptosporidium parvum* is considered one of the major threats found in a water supply system.

We carried out a probabilistic risk assessment for the contamination of a drinking water supply system with zoonotic *Cryptosporidium* from nonpoint sources in a watershed in New York State. There are many agricultural sources that may contribute to the contamination of a water supply system including dairy cattle operations and associated farming activities, wildlife, and sewage treatment plants. The fault tree scenario pathway approach was used to assess the likelihood of contamination of the water supply in the watershed. Estimates of the parameters used in the risk assessment model were obtained from our studies and from the literature. The analysis demonstrated the importance of the farming activities in mitigating the risk of this protozoan associated with dairy cattle and highlighted the role of sewage treatment plants.

INTRODUCTION

Cryptosporidium is a protozoan that poses a public health threat and has long been regulated by the EPA through the National Primary Drinking Water Regulations. Under these regulations, the standard is 99% reduction for *Cryptosporidium*. The maximum contaminant level (MCL) goal for these organisms has been set at zero. That is, no *Cryptosporidium* may be found in drinking water after filtration and inactivation. In addition to the EPA regulations for this protozoan, have also identified this waterborne pathogen among their high priority organisms, since it can cause severe diarrhea in calves. In previous studies, we have found that if a farm has animals infected with *Cryptosporidium*, then the infection will be widespread among calves within the first 30 days of age (Barwick *et al.*, 2003; Wade *et al.*, 2000; Mohammed *et al.*, 1999). Moreover, *Cryptosporidium* infection is common among dairy farms in the U.S. (Fayer *et al.*, 2000; Chalmers *et al.*, 1997; Garber *et al.*, 1994).

As one of the emerging diseases, cryptosporidiosis has been associated with climatological changes in the U.S. and other countries around the world. Most of the reasons for the increased incidence of waterborne outbreaks attributed to this pathogen are speculative and supportive data is lacking. Because of a broad host spectrum, the large number of *Cryptosporidium*



oocysts shed by agricultural animals into the environment, and the resistance of the oocysts to environmental conditions, it is plausible that an increase in precipitation and snow melt might play a role in increased transmission of this protozoan from the sources into the water supply systems. Such increase in the rate of transmission of this protozoan may lead to an increase in the incidence of the infection among susceptible populations. Lending credence to this observation is the fact that *Cryptosporidium* oocysts have been isolated from 65 to 97% of surface waters tested throughout the United States (Juranek, 1998). The oocysts are known to be resistant to traditional water treatment methods that are commonly used in the world. In an attempt to delineate the pathway by which potential sources of zoonotic genotypes of *Cryptosporidium* may put humans at risk of infection, we carried out a risk assessment analysis. More specifically, we investigated the potential contamination of water supply systems with zoonotic genotypes of *Cryptosporidium* from agricultural activities, including dairy farming, in watersheds. There are several zoonotic genotypes of this protozoan that may originate from animals in watersheds. For the purpose of this paper, we will focus on *Cryptosporidium parvum* which has a broad host spectrum.

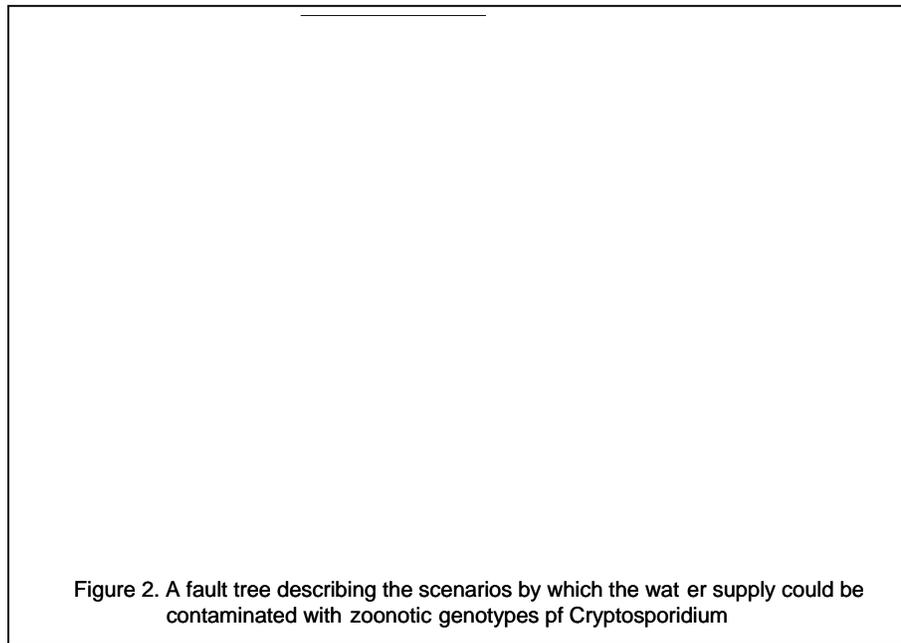
MATERIAL AND METHODS

To assess the risk of contamination of the water supply system we carried out quantitative risk assessment approach. A fault-tree pathway model was developed to capture the potential nonpoint agricultural sources of contamination in watersheds with zoonotic genotypes of this protozoan. Nonpoint sources (NPSs) are diffused sources of a hazard in a targeted population and hence are difficult to identify in comparison to point sources. In the current study we attempted to capture some of these NPSs of *C. parvum* in watersheds realizing that capturing all of these sources is a daunting task. Examples of NPS contamination of *C. parvum* from dairy farming and silvicultural activities include runoff from fields and leachate from septic tanks.

The fault tree analysis (FTA) is a deductive analytical approach of reliability and safety analyses of complex dynamics systems such as agricultural activities in watersheds. The FTA approach uses a tree to logically represent the various combinations of

possible events that are related to agricultural activities in watersheds which may result in a top undesired event, e.g., the presence of *C. parvum* in the water supply system. The tree delineates the pathway by which these events may lead to the failure, the hazard in the water, from the top to the root causes(s) at the bottom. There are several standard logic symbols that are connecting the branches of the tree to delineate the pathway from the bottom to the top (Figure 1). For example, the “gates” describe the relation between and among the “basic events” as they move up the tree towards the top event. In addition to the basic events, there are unknown or undeveloped relationships in the tree that can not be integrated for several reasons.

Figure 2 depicts the integrated putative model for the risk of *C. parvum* from NPSs in watersheds. Each of the basic events represents an initiating node for the source of the protozoan along the pathway and contains a mathematical expression or algorithm that is related to the connected nodes. The shape of the node represents the connecting relationship with the other nodes in the branch. For example, the calf



event is connected to the runoff from calves with an AND node. In other words there would be no *C. parvum* in the runoff if there is no *C. parvum* infection in calves. On the other hand, could *Cryptosporidium* enter the waterways if there is runoff from areas where the manure is stored on the farm, from composting areas, or from fomites, i.e., contaminated utensils, used on the farm since the three basic events are connected with an OR node? The potential role of the wildlife in the model is presented with a basic event that shows direct contamination from wildlife and a connector node (Figure 3) delineating the indirect pathway for the likelihood of contamination.

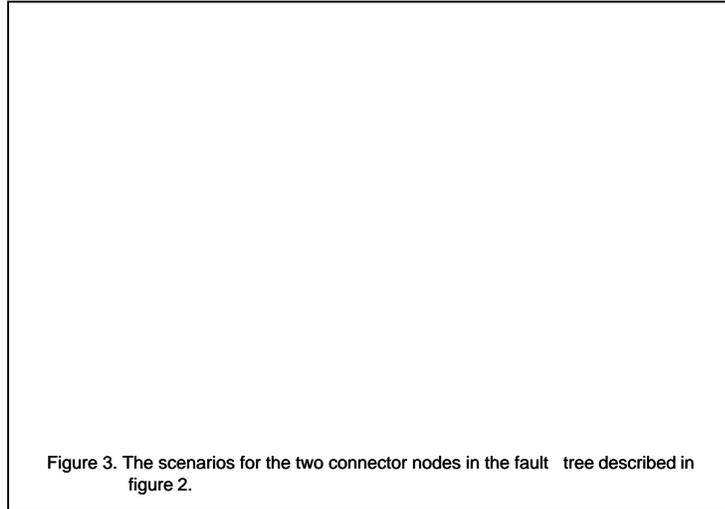


Figure 3. The scenarios for the two connector nodes in the fault tree described in figure 2.

Calves that are infected with the protozoan are likely to shed *C. parvum* into the surrounding environment and the likelihood of the oocysts is equal to the probability of infection of calves in the herd. However, some of these oocysts are likely to die in the environment as a result of several environmental factors

including heat, lack of moisture, and acidity of the soil. Estimates for these probabilities were obtained from our previous studies. Likewise, estimates of probability associated with the potential contribution from on-farm storage of manure, composting, and from perpetuation of the protozoan in the farm environment through fomites were obtained from our studies and from the literature.

The risk model presented above assumed that secondary transmission, i.e., direct transmission among animal hosts, is not applicable. This leads to an endemic level of infection circulating in a population through the environment. Because of the uncertainty associated with the estimates of the risk and quantities of oocysts at each level of the model obtained from the literature, several iterations were run using the Monte Carlo simulations in @RISK software to determine whether the probability of infection or transmission rate was altered if reasonable variations in each of the above parameters are made.

RESULTS AND DISCUSSIONS

Our results showed that the most important factors in the model were the level of infection in the calves and the presence of *C. parvum* in agricultural fields. This result is consistent with other observational studies that showed a high level of infection among calves in watersheds and a relatively low occurrence of oocysts in the environment of the respective farms. If efforts are to be made to control the risk of environmental degradation in watersheds, they have to be directed towards managing the likelihood of *Cryptosporidium* infection in the calves. Obviously calves pose a major risk to the environment by virtue of the amount of oocysts they shed in their feces and the potential role they play as amplifiers of low level infections in wildlife. Our analysis also indicated that the risk associated from either sewage treatment plants or seepage from septic tanks was relatively low in comparison to the risk from dairy farms. We are not sure if this conclusion is correct but we suspect that there are too many uncertainties associated with the low estimates used in this model because of the lack of data.

REFERENCES

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