Quantitative Risk Assessment of Cryptosporidium Species Infection in Dairy Calves

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ABSTRACT

Cryptosporidium parvum is a zoonotic protozoan that infects many different mammals including cattle and humans. Cryptosporidiosis has become a concern for dairy producers because of the direct losses due to calves not performing well and the potential for environmental contamination with C. parvum. Identifying modifiable control points in the dynamics of infection in dairy herds will help identify management strategies that mitigate its risk. The quantitative risk assessment approach provides estimates of the risk associated with these factors so that cost-effective strategies can be implemented. Using published data from epidemiologic studies and a stochastic approach, we modeled the risk that C. parvum presents to dairy calves in 2 geographic areas: 1) the New York City Watershed (NYCW) in southeastern New York, and 2) the entire United States. The approach focused on 2 possible areas of exposure—the rearing environment and the maternity environment. In addition, we evaluated the contribution of many risk factors (e.g., age, housing, flies) to the end-state (i.e., total) risk to identify areas of intervention to decrease the risk to dairy calves. Expected risks from C. parvum in US dairy herds in rearing and maternity environments were 41.7 and 33.9%, respectively. In the NYCW, the expected risks from C. parvum in the rearing and maternity environments were 0.36 and 0.33%, respectively. In the US scenarios, the immediate environment contributed most of the risk to calves, whereas in the NYCW scenario, it was new calf infection. Therefore, within the NYCW, risk management activities may be focused on preventing new calf infections, whereas in the general US population, cleaning of calf housing would be a good choice for resource allocation. Despite the many assumptions inherent with modeling techniques, its usefulness to quantify the likelihood of risk and identify risk management areas is illustrated.

(Key words: cattle, risk assessment, Cryptosporidium, watershed)

Abbreviation key: NYCW = New York City Watershed, P1, P2, P3 = probabilities of sources of C. parvum from infected calves (P1), oocysts in the calf rearing environment (P2), or oocysts on fomites (P3).

INTRODUCTION

Cryptosporidium parvum is a zoonotic protozoan recognized as one of the primary pathogens causing diarrhea in neonatal calves (de la Fuente et al., 1999; Naciri et al., 1999). The organism, depending on genotype (Morgan et al., 1997; Peng et al., 1997), causes usually self-limiting diarrhea in immunocompetent human patients, but causes life-threatening disease in those with immunodeficiencies (O'Donoghue, 1995). It has emerged as one of the most recognized causes of waterborne outbreaks of gastrointestinal illness (MacKenzie et al., 1994) as well as being associated with foodborne outbreaks (Quiroz et al., 2000) and sporadic cases (McLauchlin et al., 2000). By their location in watersheds, cattle have been implicated as a source of C. parvum associated with these examples (Smith and Rose, 1990), despite lack of direct evidence. The possible losses to a dairy operation from C. parvum are many. One is the direct loss in profitability from calves that do not perform as well due to morbidity. Other losses include less directly quantifiable losses that may arise from government restrictions on animal agriculture because of the zoonotic potential of the organism, as well as decreased consumer confidence in animal agricultural products.

It is necessary to find management approaches to prevent the risk of cryptosporidiosis. There are multiple reasons to take a preventive approach to this disease, not least among them is that there are no consistently effective and approved chemotherapeutics for cattle or humans (Woods et al., 1996; Blagburn and Soave, 1997). Furthermore, at recommended concentrations, most commercial disinfectants are not effective at killing C. parvum oocysts (Campbell et al., 1982; Ares-Mazas et al., 1997). Because of their small size, oocysts evade...
most water treatment facilities attempts to remove them and thus remain in finished water. To date, no vaccines have been marketed that have proven efficacious in preventing cryptosporidiosis, although there is current experimental work in this area (Perryman et al., 1999). Another reason to prevent the disease is that the life cycle of *C. parvum* is such that oocysts are immediately infective upon excretion and are transmitted via the fecal-oral route.

To design cost-effective strategies to minimize the associated risk of *Cryptosporidium* in dairy herds, a systematic approach of examining the dynamics of infection in the population and its environment is necessary. Quantitative risk assessment is one approach that provides a means to assess the risk and its impact (Vose, 2000), including microbial risk assessments for potentially zoonotic pathogens such as *Escherichia coli* O157:H7 and *Listeria monocytogenes* (Bemrah et al., 1998; Ebel et al., 2004). Two common risk assessment models are currently used of which an adaptation to animal health has been proposed by the Office Internationale des Epizooties (OIE, 2001). Carrying out a comprehensive risk assessment for cryptosporidiosis in watersheds is a complex task. A reasonable approach is the parsimonious one in which the complex risk scenario is partitioned into complementary units that can be integrated through multiple studies toward a comprehensive risk assessment.

The many factors associated with cryptosporidiosis and their complex interaction necessitates a systematic investigation of a multistep process that incorporates the inherent uncertainty involved at each step. Risk assessment, one of the components of risk analysis, offers a means to a systematic investigation. The present investigation focused on the risk *C. parvum* poses to dairy calves, on-farm, using data from 2 different geographic areas—the New York City Watershed (NYCW) and the United States as a whole. The process also identified some areas for potential risk mitigation activities that could decrease the likelihood of this protozoan on dairy farms.

**MATERIALS AND METHODS**

We adopted a risk assessment approach to address the stated objectives. This involves organizing and analyzing the information to arrive at an estimate of the probability of the risk occurring. The model we are following is based on the model of Covello and Merkhofer (1993) and adopted by the Office Internationale des Epizooties. The framework of the model consists of 4 steps: release assessment, exposure assessment, consequence assessment, and risk characterization. We used the scenario pathway analysis and event-tree methods to describe the dynamics of infection of *Cryptosporidium* in dairy calves. A conceptual framework for the event tree is presented in Figure 1. The end-state or final probability represents the risk (likelihood) of infection to susceptible calves in the dairy environment (Figure 1). Four different risk scenarios were investigated in this study: rearing environment on dairies in the NYCW (1a; Figure 2); maternity environment on dairies in the NYCW (1b); rearing areas on dairies in the United States at large (2a); and maternity environment on dairies in the United States (2b); each generating an end-state probability.

**Release Assessment**

The focus in this investigation was on *C. parvum* genotypes that are infective to calves. The primary source of *C. parvum* in the analysis was cattle; other potential sources of oocysts such as wildlife and humans...
were not included in the model. Several factors were identified that affect the release of *C. parvum* from the source (cattle) at the initiating event. Calves less than 30 d of age are at highest risk and shed oocysts if infected. If there were no infections at the source, then the likelihood of the release would equal zero (\(P_1\) for calf infection = 0). However, if the source (calf) was infected then there was a chance that *Cryptosporidium* would be released in the environment and the risk was equal to \(P_1\).

The second event in the pathway was that *Cryptosporidium* would be in the existing rearing or maternity areas (\(P_2\)). *Cryptosporidium* does not multiply in the external environment. If the probability of oocysts in the calves' environment was nonzero then there would be a risk equal to \(P_2\). Several factors that play a role in modifying this risk are explained below.

The risk of infection with *Cryptosporidium* was exacerbated by transmission through inanimate objects and fomites. Calves may be exposed to oocysts via fomites and the likelihood of that risk equals \(P_3\). The probability of fomites contributing to the likelihood of *Cryptosporidium* was calculated as described below and, again, if there were no oocysts on fomites, then there would be no risk to calf. This probability was modified by several factors that are explained below. The end-state risk was computed as the probability of the risk at the source, environment, and the transmission by fomites, \(P_1\), \(P_2\), and \(P_3\), respectively.

### Factors Operating at the Source Level (\(P_1\))

Calves are likely the primary source of *Cryptosporidium* in dairy herds. Although some studies have shown that adult cows and wildlife might contribute to the risk posed by this organism, we have not accounted for these 2 sources because either their role is not clear in the literature or was assumed to be negligible. Several factors modify the likelihood of release and perpetuation of *C. parvum* from a calf. Data for this level were obtained primarily from 2 sources (Garber et al., 1994; Mohammed et al., 1999). The study of Mohammed et al. (1999) was conducted in a watershed area that included the Catskill/Delaware portion of the NYCW in southeastern New York State, and was designated scenario 1. The study of Garber et al. (1999) was conducted...
Table 1. Description and distribution of the input variables for the various scenarios investigated.1

<table>
<thead>
<tr>
<th>Variable description</th>
<th>Distribution/model²</th>
<th>Scenario</th>
</tr>
</thead>
<tbody>
<tr>
<td>Preweaning management³</td>
<td>β = 0.19, Zᵢ = −1.596</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>General management³</td>
<td>β = 0.244, Zᵢ = 8.992</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>Age (15 d)³</td>
<td>β = 0.027, Zᵢ = 15</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>Season (summer)³</td>
<td>β = −1.15, Zᵢ = 1</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>Herd size (100 to 200 cows)³</td>
<td>β = 1.194, Zᵢ = 1</td>
<td>2a, 2b</td>
</tr>
<tr>
<td>Season (summer)³</td>
<td>β = 0.833, Zᵢ = 1</td>
<td>2a, 2b</td>
</tr>
<tr>
<td>Grouped calving cows³</td>
<td>β = 0.405, Zᵢ = 1</td>
<td>2a, 2b</td>
</tr>
<tr>
<td>Calf hutch</td>
<td>Beta [6, 5]</td>
<td>1a, 2a</td>
</tr>
<tr>
<td>Soil around rearing area</td>
<td>Beta [34, 15]</td>
<td>1a, 2a</td>
</tr>
<tr>
<td>Walls around calf area</td>
<td>Beta [10, 1]</td>
<td>1a, 2a</td>
</tr>
<tr>
<td>Soil around maternity area</td>
<td>Beta [20, 10]</td>
<td>1b, 2b</td>
</tr>
<tr>
<td>Aisle around maternity area</td>
<td>Beta [18, 4]</td>
<td>1b, 2b</td>
</tr>
<tr>
<td>Calf area</td>
<td>Beta [12, 7]</td>
<td>1b, 2b</td>
</tr>
<tr>
<td>Calf pen</td>
<td>Beta [9, 3]</td>
<td>1b, 2b</td>
</tr>
<tr>
<td>Feed buckets</td>
<td>Beta [20, 11]</td>
<td>1a, 2a, 1b, 2b</td>
</tr>
<tr>
<td>Flies</td>
<td>No model, 90%</td>
<td>1a, 2a, 1b, 2b</td>
</tr>
<tr>
<td>Existing Cryptosporidium parvum</td>
<td>No model, 6%</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>Existing C. parvum</td>
<td>No model, 11%</td>
<td>2a, 2b</td>
</tr>
<tr>
<td>P1</td>
<td>Pert [0.01, 0.042, 0.07]</td>
<td>1a, 1b</td>
</tr>
<tr>
<td>P1</td>
<td>Pert [0.70, 0.0765, 0.82]</td>
<td>2a, 2b</td>
</tr>
<tr>
<td>P2</td>
<td>Normal [0.148, 0.004]</td>
<td>1a</td>
</tr>
<tr>
<td>P2</td>
<td>Normal [0.264, 0.079]</td>
<td>2a</td>
</tr>
<tr>
<td>P2</td>
<td>Normal [0.011, 0.003]</td>
<td>1b</td>
</tr>
<tr>
<td>P2</td>
<td>Normal [0.198, 0.056]</td>
<td>2b</td>
</tr>
<tr>
<td>P3</td>
<td>Normal [0.070, 0.001]</td>
<td>1a</td>
</tr>
<tr>
<td>P3</td>
<td>Normal [0.281, 0.022]</td>
<td>2a</td>
</tr>
<tr>
<td>P3</td>
<td>Normal [0.067, 0.001]</td>
<td>1b</td>
</tr>
<tr>
<td>P3</td>
<td>Normal [0.244, 0.018]</td>
<td>2b</td>
</tr>
</tbody>
</table>

1Scenarios: 1a = New York City Watershed (NYCW) rearing environment, 2a = US rearing environment, 1b = NYCW maternity environment, 2b = US rearing environment, P1 = probability of calf infection, P2 = probability of oocysts in the environment, P3 = probability of oocysts on fomites and previously existing.

2β = Regression coefficient; Zᵢ = value of the factor; Beta = beta probability distribution defined by the 2 parameters in brackets; Pert = pert probability distribution defined by the 3 parameters in brackets; Normal = the normal distribution defined by the 2 parameters in brackets.

3Probabilities were computed using the logistic regression in equation 1.

over the entire United States and is designated as scenario 2.

Inputs to P1 in the NYCW (Scenario 1)

Estimates of the likelihood of Cryptosporidium at the source for the NYCW scenario were computed based on the findings reported by Mohammed et al. (1999). This likelihood was a function of 13 variables explained below and shown in Table 1 and Figure 2.

Preweaning Management

Preweaning management was significantly associated with the risk of infection of C. parvum in dairy herds in the NYCW (Mohammed et al., 1999) and consisted of 7 risk factors—manure disposal, bedding disposal frequency, type of liquid feed, ventilation, cleaning, use of antibiotics, and use of ionophores. These risk factors were combined using an indexing approach to determine the magnitude and directional relationship of the risk factor (Zᵢ) that represents the composite of the 7 preweaning management factors (Mohammed, 1991; Mohammed and Carpenter, 1991). This composite was then an input to the model. The effect of the preweaning management was estimated to be −1.596 using the indexing approach.

General Management

General management was significantly associated with the risk of infection of C. parvum in dairy herds in the NYCW and consisted of 4 risk factors—change of herd size, number of milking cows, presence of animals other than cattle on the farm, and the distance of the barn from the house septic system. Again, an indexing approach was used to determine the value of the risk factor (Zᵢ) that represents general management. The index value for general management was estimated at 8.992.

Age and Season

Age of the calf and the season in which the sample was taken were also significant in the final model and
thus contributed to the likelihood of calf infection (P1) in the scenario path. Summer was assigned a value of 1 in the model and the age of the calf was assigned a value of 15 d, mid-age of the highest risk.

**Inputs to P1 in the US (Scenario 2)**

Estimates of the likelihood of Cryptosporidium at the source level in the United States were computed based on the findings of Garber et al. (1994). It is a function of 3 variables at the farm level that were significantly associated with the likelihood of the oocyst and are presented in Table 1. These factors were herd size, the summer season, and grouping of calving cows in the maternity facility. A herd size of 100 to 200 cows was assigned a value of 1 in the computation, as were the summer season and multiple cow maternity facilities.

**Calculation of P1**

Probability P1 for both the NYCW and US scenarios was computed using the logistic regression model as follows (Kleinbaum et al., 1982; Hosmer and Lemeshow, 1989):

\[
P(C_p) = \frac{1}{1 + \exp((-\alpha + \sum \beta Z_i))}
\]

where P (Cp) is the probability a calf shedding Cryptosporidium, \(\alpha\) is the constant at standard conditions, and \(\beta\) is the change in the probability of infection due to the respective factor \(Z_i\).

**Exposure Assessment**

Although the shedding of C. parvum has been observed in different age groups, we believe that the population at highest risk is calves between 1 and 30 d of age (O’Handley et al., 1999; Wade et al., 2000). Calves become exposed to the oocyst immediately after birth where the oocyst is prevalent in the surrounding environment (Sischo et al., 2000). Although no dose-response studies have been carried out in calves, it has been shown that all calves less than 30 d are at high risk of exposure to Cryptosporidium on farms where the infection is endemic (Moore et al., 2003). All calves that were exposed experimentally to C. parvum using different dosages (1 × 10⁴, 1.0 × 10⁶, 5 × 10⁶ oocysts) developed infection and shed the organism in their feces (Naciri et al., 1993; Harp and Goff, 1995; Fayer et al., 1998). Because infected animals shed significantly higher numbers of oocysts than the doses that were used in experimental infection, we believe that susceptible calves in endemic farms are at constant risk of exposure and that they will contract the infection if they are exposed (Fayer et al., 1998; Nydam et al., 2001).

**Risk of Cryptosporidium at Existing Rearing Area (P2)**

The calf rearing environment and the maternity environment risk factor categories were assumed to be the same for both the NYCW and US scenarios and were thus modeled similarly, but using input values specific to each population. The respective scenarios were designated 1a for the NYCW rearing environment, 2a for the US rearing environment, 1b for the NYCW maternity environment, and 2b for the US maternity environment (Table 1).

**Rearing Environment Scenario**

Data on the rearing environment were primarily obtained from Faubert and Litvinsky (2000). The probability that an infected calf contributes to the likelihood of the hazard in the existing environment was accounted for. Sites that also contributed to P2 included soil from the area around the calves, the calf hutches, and the walls of the calf area (Table 1 and Figure 2). The probability that a calf was shedding also contributed to the likelihood of the hazard in the rearing environment and was accounted for.

It was assumed that each of the 4 factors in the rearing environment and the 5 factors in the maternity environment contributed separately to the likelihood of Cryptosporidium at the respective P2 values. Thus, P2 was calculated as the joint probability of the independent events in both cases. The estimation of the true probability of each of the various sites in the environment contributing to P2 was assumed to follow the Beta distributions of the form \(\alpha_1 = r + 1\) and \(\alpha_2 = n - r + 1\), where \(r = \) the number of times C. parvum oocysts were found, and \(n = \) the number of trials in which they were looked for (Table 1; Vose, 2000).

**Maternity Environment Scenario**

Data on the maternity environment were again primarily obtained from Faubert and Litvinsky (2000). Sites that contributed to P2 in the maternity environment included the calving pen floor, the alleys near the calving pen, the calf area, and soil from the exercise area (Table 1). The probability that a calf was shedding also contributed to the likelihood of the hazard in the maternity environment and was accounted for.

It was assumed that each of the 4 factors in the rearing environment and the 5 factors in the maternity environment contributed separately to the likelihood of Cryptosporidium at the respective P2 values. Thus, P2 was calculated as the joint probability of the independent events in both cases. The estimation of the true probability of each of the various sites in the environment contributing to P2 was assumed to follow the Beta distributions of the form \(\alpha_1 = r + 1\) and \(\alpha_2 = n - r + 1\), where \(r = \) the number of times C. parvum oocysts were found, and \(n = \) the number of trials in which they were looked for (Table 1; Vose, 2000).

**Role of Fomites in the Risk of Cryptosporidium (P3)**

For all 4 scenarios modeled, P3 is comprised of the contribution of fomites [feed buckets (Faubert and Litvinsky, 2000) and flies (Graczyk et al., 1999)], the imme-
Consequence Assessment

The probability of existing *C. parvum* was obtained from the data of Garber et al. (1994) and Mohammed et al. (1999) less a factor of 50% that accounted for (approximately) routine cleaning of some surfaces where *C. parvum* may exist (Faubert and Litvinsky, 2000). The P3 was calculated as a joint probability of independent events (feed buckets, flies, and P2) and the disjoint probability of the existing *C. parvum*. The probability that the feed buckets contributed to P3 was modeled using a Beta distribution as above (Table 1).

### Consequence Assessment

Infected calves excrete oocysts in their feces for 3 to 13 d (average 7 d) postinfection (Fayer et al., 1998; Nydam et al., 2001). The number of oocysts excreted by an infected calf in the immediate environment varies between $4 \times 10^6$ and $4.15 \times 10^7$ oocysts/g per day (Fayer et al., 1998; Nydam et al., 2001). This amount is much higher than the reported infective dose used in experimental studies (Fayer et al., 1998; Moore et al., 2003). Because all calves less than 30 d old are at risk, irrespective of whether they were fed colostrum (Harp et al., 1989), we assumed that raising calves on farms with a history of *C. parvum* would put them at risk for infection. This risk was dependent on the presence of the infection on the farm. Experimental studies on the survival of *C. parvum* oocysts in the environment illustrated that changes in temperature and animal waste pile management affected its viability (Jenkins et al., 1999). An observational study showed that the likelihood of the oocyst being in environment samples is affected by pH and temperature of the soil (Barwick et al., 2003). In our analysis, we assumed that the oocysts would survive in the immediate environment of the calf for at least 30 d, the period during which the animal is at risk.

### Risk Characterization

The risk presented to a calf, relative to the presence of oocysts, was estimated using the results of the previous steps as inputs (Table 1). The risk for each of the 4 scenarios is calculated as follows:

$$ P_{\text{end-state}} = P_1 \times (P_2 + P_3) $$

where $P_{\text{end-state}}$ is the final probability outcome and $P_i$ is the estimate of the probability at each event in Figure 1 or 1 of the other 3 corresponding scenarios (Table 1). This calculation assumes that the probability of P1 was independent from P2 and P3. However, this assumption is likely not true in this scenario. For example, the presence of oocysts in the environment is likely correlated with the probability of oocysts shed by calves. The degree of dependency is adjusted for in the final simulation using the RiskCorrmat function in @Risk (version 4; Palisade Corp., Newfield, NY), which produces a matrix of rank correlation coefficients between each of the input values.

To simulate the distribution of the end-state risk of *Cryptosporidium* to calves in the dairy environment, P1, P2, and P3 were assigned probability distributions (Table 1). For P1, a Pert distribution was assumed with values of (0.01, 0.042, 0.07) for scenario 1 and (0.7, 0.765, 0.82) for scenario 2. The Pert distribution is a version of the 4-parameter Beta and it allows the 4 parameters to be defined by inputs of minimum, most likely, and maximum values. Both P2 and P3 were assumed normally distributed and their distribution was approximated by the Poisson distribution (Vose, 2000). The Poisson distribution is often used to model events of microorganism concentrations, especially when the number of events is low (Bemrah et al., 1998). As the mean and variance get larger, the Poisson distribution approaches normal (Casella and Berger, 1990). The values of the mean and standard deviation for the risk at both P2 and P3 are given for each of the scenarios in Table 1.

The final probability distribution estimates the risk to a calf posed by *C. parvum* in each of the 4 scenarios. The distribution was generated using Monte Carlo simulation in @Risk software (version 4, Palisade Corp.) carried out with 10,000 iterations of the respective distributions for each probability with Latin Hypercube sampling. Monte Carlo simulation briefly involves using probability distributions, sampling from these distributions, repeatedly running the model (iterations), and then analyzing the sets of outputs. Latin Hypercube sampling uses stratified sampling without replacement and thus has advantages over Monte Carlo sampling when sample sizes are small. One such advantage is that it does not over- or undersample some parts of the input distribution and therefore better reproduces the shape of it, leading to statistics (e.g., mean and standard deviation) that are nearer to the theoretical values (Vose, 2000). When sample sizes are large, the results provided are similar.

### Sensitivity Analyses

Sensitivity analyses were performed to identify the impact of the inputs on the outcomes. This was accomplished by Spearman’s rank order correlation analysis because it makes no assumptions about the relationship of the composite of the distributions used.

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Table 2. Expected probabilities (mean and range in parentheses) for Cryptosporidium at the 3 levels of inputs to the 4 scenarios/models investigated (10,000 iterations) for the New York City watershed (NYCW) and the US dairy population.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Calf infection (P1)</th>
<th>Immediate environment (P2)</th>
<th>Fomites (P3)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NYCW rearing environment (1a)</td>
<td>0.042 (0.011–0.070)</td>
<td>0.015 (0.002–0.029)</td>
<td>0.069 (0.064–0.073)</td>
</tr>
<tr>
<td>US rearing environment (2a)</td>
<td>0.765 (0.703–0.820)</td>
<td>0.263 (0.029–0.054)</td>
<td>0.281 (0.18–0.354)</td>
</tr>
<tr>
<td>NYCW maternity environment (1b)</td>
<td>0.042 (0.013–0.070)</td>
<td>0.011 (0.003–0.024)</td>
<td>0.067 (0.063–0.070)</td>
</tr>
<tr>
<td>US maternity environment (2b)</td>
<td>0.765 (0.703–0.820)</td>
<td>0.198 (0.037–0.438)</td>
<td>0.244 (0.167–0.302)</td>
</tr>
</tbody>
</table>

RESULTS

Calf Infection (P1)

A simulated distribution of the risk of calf infection with C. parvum given the inputs above was obtained (Table 2). The risk for the calves in the NYCW was 1.1 to 7% with a mean of 4.2%. The model predicted that 90% of the probabilities of infection would be less than 5.7%. For the calves in the US scenario, the probability ranged from 70.3 to 82% with a mean of 76.5%. The 90% interval estimate for this probability was 73 to 79%.

Immediate Environment (P2)

The estimated probability of oocysts in the rearing environment of calves in the NYCW was 1.5% with a range of 0.2 to 2.9%, whereas the rearing environment in the US scenario had a mean probability of oocysts of 26.3% and a range of 2.9 to 54% (Table 2). The maternity environment in both scenarios had a lower probability of contributing oocysts to a calf than did the rearing environment with a mean of 1.1% (0.3 to 2.4%) in the NYCW group and a mean of 19.8% (3.7 to 43.8%) in the US calves.

Fomites and Existing C. parvum (P3)

The probability of fomites contributing oocysts and of oocysts previously existing despite cleaning had a mean of 6.9% and a range of 6.4 to 7.3% in the NYCW rearing environment model (Table 2). The corresponding risk in the United States as a whole was 28.1% (18 to 35.4%). In the maternity environment scenarios, the estimated value of P3 in the NYCW was 6.7% with a range of 6.3 to 7.0%. The estimated value of P3 in the United States was 24.4% (range = 16.7 to 30.2%).

End-State Hazard (1a, 2a, 1b, 2b)

Our analysis showed that the risk to a calf in the NYCW in the rearing environment (1a) had a mean of 0.357% and the distribution of this probability ranged from 0.076 to 0.768%. (Table 3 and Figure 3). The corresponding risk to a calf in the US scenario ranged from 14.7 to 88.9% with a mean of 41.7%. Despite the wide range in scenario 2a, 90% of the values were between 31 and 55% (Figure 4). The end-state range of risk for calves in the maternity environment of the NYCW (1b) was 0.080 to 0.660% and the mean was 0.339% (Figure 3). For calves in the US maternity environment, the model predicted a range of 9.68 to 62.4% and a mean of 33.9% for the risk that C. parvum presents. For scenario 2b, 90% of the values were between 24.7 and 43.6% (Figure 4).

Sensitivity Analyses

The contribution of P1 (calf infection), P2 (immediate environment), and P3 (fomites and existing C. parvum) to the output (final risk) in each of the 4 scenarios is presented in Table 4. In the NYCW scenario, calf infection was the most influential input, whereas in the US scenario, the immediate environment made the largest contribution to the hazard presented to calves.

The relative contribution of the factors that comprised the risk the immediate environment (P2) posed is shown in Table 5 as a sensitivity analysis. Within the rearing environment, calf housing contributed most to the risk that the immediate environment posed, with the soil and walls of the enclosure being similar. Each of the 4 factors in the maternity environment contributed somewhat similarly to the risk (Table 5). None of the input factors that were used to calculate the estimates of P1 and P3 could have sensitivity analyses performed individually because we did not have access to the raw data for all of the input factors that contributed to those estimates. Thus, we could not model them stochastically, even though the uncertainty around the estimates of P1 and P3 was accounted for by probability distributions.
Table 3. Expected probabilities for the risk that Cryptosporidium parvum presents to a calf in each of the 4 scenarios investigated (10,000 iterations) in the New York City Watershed (NYCW) or the US dairy population.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Mean</th>
<th>Mode</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>NYCW rearing environment (1a)</td>
<td>0.0036</td>
<td>0.0042</td>
<td>0.0008–0.0077</td>
</tr>
<tr>
<td>US rearing environment (2a)</td>
<td>0.417</td>
<td>0.362</td>
<td>0.147–0.889</td>
</tr>
<tr>
<td>NYCW maternity environment (1b)</td>
<td>0.0033</td>
<td>0.0022</td>
<td>0.0008–0.0066</td>
</tr>
<tr>
<td>US maternity environment (2b)</td>
<td>0.339</td>
<td>0.225</td>
<td>0.097–0.624</td>
</tr>
</tbody>
</table>

Figure 3. Cumulative probability for the hazard of Cryptosporidium parvum as determined for the New York City Watershed rearing (scenario 1a, – – –) and maternity (scenario 1b, —) environments.

Figure 4. Cumulative probability for the hazard of Cryptosporidium parvum as determined for the US rearing (scenario 2a, – – –) and maternity (scenario 2b, —) environments.
Table 4. Influence (sensitivity analysis) of the input factors for the 4 scenarios on the output of each model for the New York City Watershed rearing and maternity environments and the US environments. The values are Spearman rank order correlation coefficients.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>P1 (calf infection)</th>
<th>P2 (immediate environment)</th>
<th>P3 (fomites)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NYCW rearing environment (1a)</td>
<td>0.986</td>
<td>0.61</td>
<td>0.56</td>
</tr>
<tr>
<td>US rearing environment (2a)</td>
<td>0.647</td>
<td>0.959</td>
<td>0.674</td>
</tr>
<tr>
<td>NYCW maternity environment (1b)</td>
<td>0.991</td>
<td>0.569</td>
<td>0.530</td>
</tr>
<tr>
<td>US maternity environment (2b)</td>
<td>0.644</td>
<td>0.951</td>
<td>0.679</td>
</tr>
</tbody>
</table>

DISCUSSION

Our goal was to understand the on-farm dynamics of the risk of cryptosporidiosis in calf populations and to determine where risk management strategies could be implemented. We believe this objective can be addressed by carrying out a risk assessment. Accounting for the multifaceted nature of decisions, many models have become complex and cumbersome. Our approach represents a parsimonious or disaggregated one for a complex process and focuses on the likelihood of the hazard for calves on the farm. The hazard identified for this study is exposure and infection of dairy calves to Cryptosporidium spp., and “hazard” here refers to an adverse event or outcome as defined in risk analysis nomenclature (Ahl et al., 1993). In the process, we estimated the risk that C. parvum presents to dairy calves in 2 different populations and in different areas of possible exposure. In addition, we identified factors for risk mitigation or management activities to decrease the risk posed to calves. To our knowledge, no similar studies have been undertaken.

Risk analysis is a methodological tool for supporting rational and systematic decision making in the face of uncertainty about the likelihood of various hazards occurring. The method used here combines a deterministic approach, which is based on actual observations collected on the study units, with stochastic Monte Carlo simulation. The stochastic approach complements the deterministic approach by providing insight to unobserved events. A limitation of an exclusively deterministic approach is that it only reports the average expected outcome. This limitation can be overcome by performing worst- and best-case scenarios, but this approach overemphasizes extreme situations because they are not as likely to occur as the expected scenario. An advantage of including deterministic inputs is that it allows for greater validity when generalizing the results to similar populations.

The 4 scenarios investigated represent different populations and different areas where the hazard, C. parvum, may present a risk to calves. The probability of the hazard was much higher in the broader US population than in the restricted NYCW population. Furthermore, the risk was higher in the rearing environment scenarios than in the maternity environment. Of the 3 broad probability inputs (P1, P2, and P3) that determined the end-state risk, the immediate environment (P2) contributed most to the final probability in the US population, whereas calf infection (P1) was the most important input in the NYCW scenario. This may indicate that if the endemic probability of shedding is already quite high, it is most important to focus risk management activities at the environment level to limit transmission and exposure of C. parvum. In contrast, if the level of calf infection is relatively low, it might be advantageous to take actions to prevent new calves from shedding oocysts. The initial prevalences of the C. parvum in animals in these 2 geographic areas, NYCW and the United States, were obtained from the published literature (Garber et al., 1994; Wade et al.,

Table 5. Influence (sensitivity analysis) of the input factors on the output of the 4 scenarios in P21 for the New York City Watershed (NYCW) and the more general US dairy population. The values are Spearman rank order correlation coefficients.

<table>
<thead>
<tr>
<th>Factors</th>
<th>Hutches</th>
<th>Soil</th>
<th>Walls of enclosure</th>
<th>Calf area</th>
<th>Pen floor</th>
<th>Soil</th>
<th>Aisle</th>
</tr>
</thead>
<tbody>
<tr>
<td>P2 NYCW rearing</td>
<td>0.884</td>
<td>0.282</td>
<td>0.252</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P2 US rearing</td>
<td>0.894</td>
<td>0.317</td>
<td>0.277</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P2 NYCW maternity</td>
<td></td>
<td></td>
<td></td>
<td>0.574</td>
<td>0.534</td>
<td>0.427</td>
<td>0.312</td>
</tr>
<tr>
<td>P2 US maternity</td>
<td></td>
<td></td>
<td></td>
<td>0.578</td>
<td>0.540</td>
<td>0.431</td>
<td>0.320</td>
</tr>
</tbody>
</table>

P2 = Probability of oocyst in the calf rearing environment.
risk in our current study. In addition to the difference in the target populations (initial prevalence, transmission parameters, animal density, etc.), there was a difference in the methods used to determine the prevalence of C. parvum. Each of these might have contributed to the observed differences in the computed risk in our current study.

Within the various factors that comprised the contribution of P2 (immediate environment) in the rearing environment, calf housing played the largest role in the end-state hazard. Thus, the logical risk management activity that would decrease the risk the most would be cleaning hutches between calves and placing hutches or pens on a surface that could be easily cleaned and which drains well. Examples of this include concrete, large gravel, and geotextile fabric. It is then necessary to provide clean, dry bedding over that surface (Harp and Goff, 1998). Washing the hutches or pens should be done with the hottest (~71°C) high-pressure water available followed by thorough drying (Harp and Goff, 1998).

In the maternity environments for both the NYCW and US scenarios, the area reserved for calves after birth and the calving pen floor were the most significant contributors to the P2 input. This is logical in that these areas provide more exposure to newborn calves than do the aisles around the maternity pens and the corresponding soil.

Many assumptions are necessarily made in this approach and therefore, the results should be interpreted with this in mind. The data used in this investigation were taken solely from peer-reviewed publications and thus, are as reliable as the scientific community allows. It cannot be assumed, however, that these data are equally applicable to all external populations. Further assumptions include the season of sampling (summer), the size of the herd (100 to 200 cows), and the approximate age of the calf (15 d).

To facilitate understanding the complex mathematical approach and explain the objectives to the stakeholders, including farmers, we opted to select simplified assumptions. In reality, the dynamics of this infection are more complex. There are more factors that contribute to the risk of exposure and infection that C. parvum poses to a calf, other than the ones modeled here—calves shedding oocysts, oocysts in the immediate environment, and fomites. For example, the role of other sources of this organism, for example, the contribution of wildlife in exposure of calves or environmental contamination, is not accurately known and thus is not included in the model, but could be a factor.

The probability distributions used constitute another group of assumptions. We used a Beta distribution, where the graphic plotting of the raw data was suggestive, to obtain the mean and standard deviation for the probabilities of P2 and P3. The Beta distribution returns an estimate of the true probability of an event occurring given the number of times that event occurs in a given number of trials (Vose, 2000). The Pert distribution was chosen to model P1 because we arrived at a valid most likely value via the logistic model, but wanted to incorporate some uncertainty around this value. The Pert distribution is 4 times more sensitive to the most likely value than to the minimum and maximum values when compared with the somewhat analogous Triangular distribution. In addition, choosing the Triangular distribution in this case would overemphasize the tails of the distribution or require knowing the absolute minimum and maximum values for calf infection. The Normal approximation to the Poisson distribution was chosen to account for our uncertainty and the variability in the data for P2 and P3. As the mean of the Poisson distribution gets larger and the coefficient of variability (standard deviation/mean) approaches 0, the Normal approximates the Poisson. This is the case in this analysis. A Poisson process is a good choice to model P2 and P3 because, in this process, the likelihood of occurrence of the event has a continuum of opportunity that ranges between zero and infinity and there is a probability of it occurring no matter how small the unit of exposure might be (Vose, 2000). Of the Poisson processes, the Normal approximation to the Poisson distribution is a good choice for this analysis because it is a continuous distribution that will return more than discrete probabilities.

Modeling this scenario is somewhat easier than a similar one might be for a bacterial pathogen that can readily multiply in the environment, changing the probability of its occurrence from one stage to another in a scenario path. In contrast, C. parvum cannot grow or multiply outside of the host; thus, the probability of their existence should not increase from one stage to another. Furthermore, because the oocysts are environmentally hardy, one would not expect a large loss in the viability of the oocysts that could take place if one were modeling the path from the calves, through the environment, and to a stream. Although the loss might not be great in the current scenario, some oocysts do die or are not viable for some other reason. Loss of viability data for each step could be added if it was more readily available for the environments modeled here.

The relatively large differences in outcomes between the NYCW and US scenarios reflect the large amount of variability that can occur between different populations. This further illustrates the danger of generalizing the results of this, or any other, study beyond the target population without taking great care. This also shows perhaps a more dangerous situation that can occur in
risk assessment and that is trying to arrive at a viable solution using only mathematical constructs and not basing the studies on observed data from the population to which one wishes to make inference. This illustrates the utility of our approach, showing that different risks are computed and different risk management strategies are highlighted depending on factors specific to the population from which one draws data and makes inferences.

The scenario in this model was limited to the risk that presence of C. parvum oocysts presents to calves and did not include formal modeling of a dose-response assessment. This was because there were not sufficient data to validly estimate the number of oocysts it would take to cause clinical disease in an average calf on a dairy farm. Furthermore, using the Beta-Poisson model to approximate it, as has been done in similar situations, may not be the correct approach (Teunis and Hovelaar, 2000). When such data become available, they can easily be incorporated into the model to extend the assessment. In addition, further risk assessments on this topic could take into account the number of oocysts at each stage and their genotype.

This model is just one step in a number of approaches or actions that can be used to find the best solutions for controlling C. parvum at the farm, environment, and watershed levels. It is logical to first attempt to model this risk at the only place where the pathogen can live and multiply—in the animal. Further models that could be considered include the transport of oocysts from the host to agricultural run-off and from run-off to consumers of water. Ideally, then, all models would be combined to yield a complete risk assessment of zoonotic cryptosporidiosis.

Even with the restrictions we have noted, this is, to our knowledge, the first attempt to model the risk that C. parvum presents to calves in the dairy environment. It shows some of the advantages and disadvantages of combining deterministic and stochastic approaches to risk assessment as well as some further avenues of investigation where data are lacking. Further, and most importantly, it illustrates some areas for possible actions to decrease the risk in dairy calves.

CONCLUSIONS

Potential risk of C. parvum to dairy calves in a specific watershed was compared with risk for the general calf population in the US. Youngstock is known to be at high risk for this zoonotic pathogen; therefore, our analysis focused on areas of probably highest exposure—maternity and rearing environments. Our analysis showed that calves are at a higher risk of infection with this organism in the general US population compared with animals in NYCW. This difference in the risk between the 2 regions was attributed to the expected endemic shedding rate of this water and foodborne pathogen among these cattle populations. If risk mitigation strategies were designed, they should be directed toward the hygiene of calf housing in the general US calf population, but toward preventing entry of new infected calves in the lower animal density NYCW population.

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REFERENCES


