

Prevalence of Calves' Cryptosporidiosis in Northern Kazakhstan

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Abstract. This work examines the prevalence of *Cryptosporidium* spp. infection of cattle in the Akmola region of Northern Kazakhstan. The research was carried out at 75 agricultural enterprises in 10 administrative districts where 894 calves aged from one month to 12 months were tested for cryptosporidiosis. The Bayesian inference method was used to predict the prevalence of cryptosporidiosis. The maximum likelihood estimate (MLE) of infestation of young animals in the region was 0.0391. To get a conjugate beta-posterior in Bayesian statistics, binomial and beta distributions were chosen for likelihood and prior respectively. A 95% credible interval for posterior prevalence was [0.0418, 0.0685]. Cryptosporidiosis was common in 22.7% of cattle farms in the Akmola region, mainly in large industrial enterprises, where there are more favourable conditions for maintaining the biotic potential of the disease pathogens. At the same time, calves up to one month of age are infested with cryptosporidia to a higher degree than animals of older age groups. The sex of animals had no correlation with the level of *Cryptosporidium* spp. invasion.

Keywords: Bayesian inference · *Cryptosporidium* · Prevalence

1 Introduction

Protozoa species of the *Cryptosporidium* Tyzzer, 1907 genus (Phylum Apicomplexa) are pathogens of many vertebrate animals, including humans [1]. The parasites have a global distribution and cause epidemiological outbreaks of the contagious disease – cryptosporidiosis – among people with symptoms of diarrhoea, abdominal pain, nausea, vomiting and fever [2]. It is an emergent zoonotic disease described in more than 90 countries and six continents. For those living in endemic areas, immunocompromised people such as infants, malnourished subjects or patients with T-cell immunodeficiency conditions (e.g. due to HIV infection), symptoms can be severe and even dangerous for life [3]. The recent occurrence of large outbreaks in several countries all over the world, as well as the results of many surveys of human and animal cryptosporidiosis, indicate that pathogens of this infection are widespread [4].

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Humans may acquire *Cryptosporidium* by direct con-tact with infected people or animals, and indirectly through contaminated water and food. Now, more than 20 species of *Crypt-osporidium* have been described [1, 2]. It was established that specific subtypes of the zoonotic *Cryptosporidium parvum* and the anthroponotic *C.hominis* are responsible for the majority of human cases. Furthermore, many surveys of cryptosporidiosis indicate that cattle may be the main source of *Cryptosporidium* infection of people, and transmission of *C.parvum* from calves is common in outbreaks in human populations [5]. The risk infection magnitude to camping in pastures people posed by contact with faeces, that produced by infected with *C.parvum* livestock, has been modelled. It was established that the time between grazing and camping is the most important control strategy, but increasing hand-washing frequency and the removal of cattle faeces before camping would also be beneficial [6]. However, in Central Asia there is only sporadic information about cases of human infection with cryptosporidiosis [7, 8], although prevalence of cattle's *Cryptosporidium* in northern regions of Kazakhstan is relatively high [9]. Therefore, studies of the epidemiology of the disease in the region in order to ensure the safety of livestock breeders and their families are considered relevant.

Because the calves in small and private farms are fed manually, it is important to study cattle infected with cryptosporidia, which can also infect people [10].

To date, cryptosporidiosis is an unexplored disease in Kazakhstan, and the risk it poses to the population is obvious. It is also known that modelling has become one of the main instruments of research in modern epidemiology. However, in Kazakhstan such study technology has only been used for limited zoonotic contagious diseases [11, 12].

This research, therefore, aimed to model the cryptosporidiosis distribution in calf populations in the farms of northern Kazakhstan using the Bayesian inference method.

2 Materials and Methods

Epidemiological data were collected in 2018–2019 in 10 districts of the Akmola region during expeditionary trips to 75 farms, including 16 dairy farms, 26 fattening farms and 33 small house-holding farms. In total, faeces were sampled from 894 calves of three age groups (257 animals were less than one month, 303 were one to three months and 344 were 4 to 12 months in age). Samples were examined microscopically for the presence of *Cryptosporidium* spp. oocysts after routine staining with carbolic fuchsin, according Heine (1982) [13].

The field data obtained on spontaneous infection of animals with *Cryptosporidium* spp. were processed by Bayesian statistics.

The observations followed binomial distribution:

$$f(y|\theta) = C_n^{\sum y_i}\theta^{\sum y_i}(1-\theta)^{n-\sum y_i},$$

$$0 \le \theta \le 1,$$

where n – total number of examined animals, $\sum y_i$ - number of infected animals.

The concept of starting with the beta-prior and getting the beta-posterior is used when a posterior is in the same distribution family as a prior. The conjugate prior for

binomial likelihood is the beta-prior:

$$\theta \sim Beta(\alpha, \beta)$$

$$f(\theta|\alpha, \beta) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}\theta^{\alpha-1}(1-\theta)^{\beta-1}$$

where α, β – parameters of beta distribution.

It was assumed that each animal was independent and that the probability of being infected was the same for all animals.

The expected value of beta distribution is $\frac{\alpha}{\alpha+\beta}$. Thus the effective sample size of binomial likelihood is $\alpha + \beta$.

The posterior predictive mean is a weighted of the prior distribution mean and the data mean, with weights proportional to the sample size. The prior and the data contribute to the posterior distribution:

$$f(\theta|y) = \frac{f(y|\theta)\cdot f(\theta)}{\int_0^1 f(y|\theta)\cdot f(\theta)d\theta}$$

Rather than work out the integral in denominator we can use the Kernel of beta distribution. Then

$$\int_0^1 f(y|\theta)\cdot f(\theta)d\theta = C_n^{\sum y_i}\cdot\frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}\cdot\frac{\Gamma\left(\alpha+\sum y_i\right)\cdot\Gamma\left(\beta+n-\sum y_i\right)}{\Gamma(\alpha+\beta+n)}$$

Thus

$$f(\theta|y) = \frac{\Gamma(\alpha+\beta+n)}{\Gamma\left(\alpha+\sum y_i\right)\Gamma\left(\beta+n-\sum y_i\right)}\theta^{\alpha+\sum y_i-1}\cdot(1-\theta)^{\beta+n-\sum y_i-1}$$

or $Beta\left(\alpha+\sum y_i, \beta+n-\sum y_i\right)$.

R package functions dbeta, pbeta, qbeta, rbeta were used to implement Bayesian inference and find values for the credible intervals.

3 Results and Discussion

Although cryptosporidiosis is a dangerous zoonotic disease, a few studies of the parasitosis have been carried out in Central Asia. Results of these studies have indicated that *Cryptosporidium* is widespread in northern Kazakhstan. Infection by *Cryptosporidium* spp. was observed in 80% of Akmola region districts. The study showed a problem with cryptosporidiosis in 22.7% of farms studied, including 75.0% of dairy farms, 15.4% of fattening farms and 3% of small house-holding farms. It was indicated that the parasites of this genus were more widespread in large agricultural enterprises specialising in dairy production, compared to small producers and private farms.

In this cross-sectional epidemiological surveillance we often have had small sample sizes of faeces, which were depended to seasonality of calving and limited possibilities to collect and investigate enough and equal samples in different types of livestock

enterprises and house holding farms. Therefore we used the Bayesian inference which has an ability to do sequential updates. Using previous posterior as a prior to do another update makes straight forward a sequential analysis in Bayesian statistics. It is appealing and practical for predicting the prevalence and population dynamics of epidemically important diseases of people or animals [11].

As mentioned before, beta distribution is conjugate for the binomial distribution, and beta-prior will give beta-posterior. Parameters of beta-prior distribution were chosen according to a number of studies suggested that the mean of *Cryptosporidium* prevalence was between 0.05 and 0.28 [9]. Such practice is considered convenient for Bayesian modelling and used widely in mathematical epidemiology [11].

A total of 894 animals were tested, 35 of which were infected. The maximum likelihood (MLE) was 0.0391. The results of a numerical experiment showed that the posterior mean was 0.0543 (see Fig. 1).

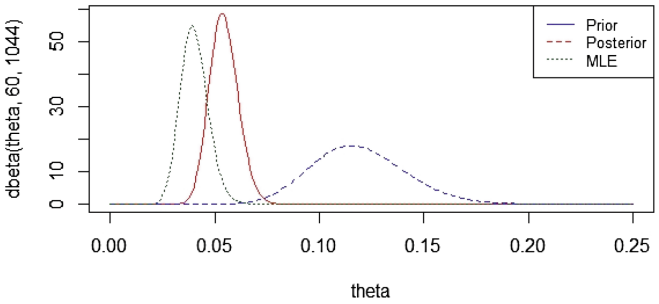

Fig. 1. Bayesian inference for total infection of animals.

In the tested animal population the 95% credible interval for θ was [0.0418, 0.0685].

473 of total examined animals were females, 19 of which were infected. For females, the corresponding MLE was 0.0402, the posterior mean was 0.0644 and 95% credible interval for θ was [0.0473, 0.0839] (see Fig. 2).

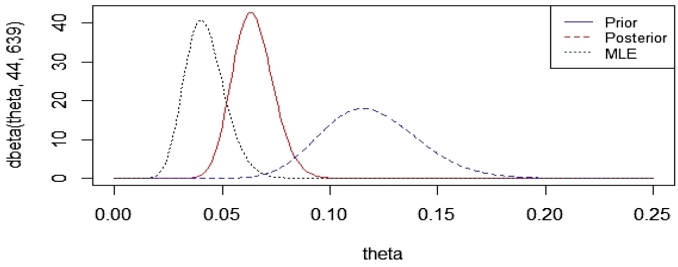

Fig. 2. Bayesian inference for infection of females.

16 of the 421 remaining males were infected. For males, the corresponding MLE was 0.0380, posterior mean was 0.0649, 95% credible interval for θ was [0.0471, 0.0855]

(see Fig. 3). The results showed that credible intervals for male and female animals were similar.

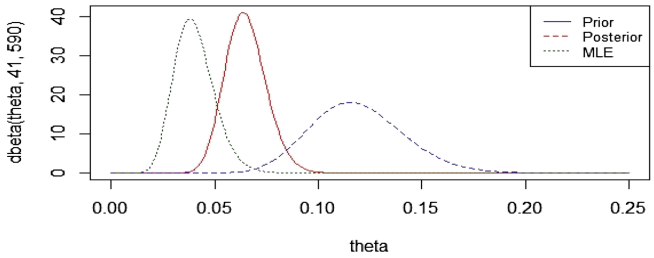

Fig. 3. Bayesian inference for infection of males.

The posterior distributions for females and males of 100,000 random samples were simulated. The results of a numerical experiment showed that the average empirical probabilities for females and males were 0.0644 and 0.0649, respectively. Therefore, the sex of animals does not affect infection with cryptosporidiosis.

Numerical experiments had shown that the highest infestation with cryptosporidia is observed in calves less than one month of age (see Table 1).

Table 1. Age fluctuations of infection with cryptosporidium of cattle in Akmola region

Age of calves	MLE	Posterior mean	95% CI for posterior mean	98% CI for posterior mean
Less than one month	0.0727	0.0953	[0.0695, 0.1248]	[0.0653, 0.1309]
One-three months	0.0293	0.0747	[0.0514, 0.1018]	[0.0478, 0.1076]
4–12 months	0.0244	0.0775	[0.0527, 0.1067]	[0.0488, 0.1129]

These characteristics of invasion suggest that the infection rate of calves at the first month of age is higher than that of older animals, and this is consistent with other studies [14–16].

It was established also that the pathogen's prevalence in livestock depended from season; however, larger differences have been associated with animal age, with younger animals showing a higher prevalence and shedding of oocysts [16, 17].

This is due to the fact that calves are born immunologically defenceless, and their immunity increases with time, so older animals can generate a more intense primary immune response than individuals under four weeks of age [18]. Apparently, the development of immunity leads to a relatively weak infection among animals of older age groups. However, the conditions for keeping and feeding animals of different ages maintain common sources and levels of infection in farms. In Kazakhstan, cow-calf-management in middle sized and small farms and large beef farms is described by the continuous contact between calves and dams that means also the development of natural colostral immunity

in neonatal animals. Calves with dams appear to be protective, as they have the continuous and longer consumption of maternal antibodies with colostrum in the first days and with the mother milk before weaning. In support of this, it was found that using dehydrated milk can make calves more susceptible to infection [19].

Preliminary results of our study also indicated that such technology could be assessed as protective against *Cryptosporidium* infection. Analogical results were shown in the Czech Republic. Here the incidence level of *Cryptosporidium* invasion showed a greater increase in dairy farms where newborn animals were grown individually from birth, in comparison with beef farms, where neonatal calves were kept with their dams [16].

It is known that in the last decade, the number of reported human's cryptosporidiosis outbreaks has grown throughout the world [20]. The main source of the pathogen for people is water, and the huge amount of oocysts excreted by the infected host has defined the increasing of environmental contamination. Cattle have been involved in the epidemiological process as a source of *Cryptosporidium*, because cattle farms are located in watersheds [21]. Calves have the greatest prevalence and shedding intensity of *Cryptosporidium* at approximately first four weeks of age. In experiment, mean number of oocysts excreted by calves <30 days old was approximately 6×10^7 per g of faeces. These results indicated that one calf would excrete some 6×10^{11} oocysts in the first month after birth, taking both the quantity of faeces in a day and the period of excretion into consideration [22]. Thus, calving as the method of breeding management is important in relation to the peak numbers of pathogens released into the environment. It is known that calves produce less manure than adult animals, but the shedding intensity of pathogens by calves is greater and they realise more amount of cryptosporidia compared to the total cattle population.

In Kazakhstan, calving occurs mainly in the spring. Therefore, this period is potentially a critical time for contamination of water utilities.

Exposures to waterborne *Cryptosporidium* oocysts in recreational or drinking water are the global public health problem. Determining the sources of pathogens in the watershed and quantifying their environmental loading are very important from positions of biological safety for human and animals' populations. The natural variability of potentially pathogenic microorganisms in the environment from anthropogenic, natural, and livestock sources is large and difficult to quantify [23].

So, our research is the first step in characterizing the risk of contamination by non-point sources from pathogens of animal origin to determine the potential environmental impact based on the prevalence of animals in northern Kazakhstan.

Previously a probabilistic model was developed to evaluate the production of *Cryptosporidium* spp. from livestock sources within the watershed. For a real river watershed in a large geographic region, probability density functions were simulated, representing the daily rate of livestock pathogen production. The prevalence of cryptosporidia in cattle was modelled as a mixture of β-distributions. Analogically, Γ-distributions were obtained to describe the shedding intensity of animal pathogens. The methodology demonstrated possibilities to determine the initial terms for modelling the fate of pathogens and their transfer, as well as to identify and determine the regions that are most vulnerable to water pollution from pathogenic sources [23].

Results of our studies have shown that prevalence of *Cryptosporidium spp.* in calves of the studied region varies on different agricultural farms, in the range of 2.4 and 28.0% [9]. Average infection with cryptosporidia of calves in northern Kazakhstan was higher than in Canada [10], Mexico [24] and Spain [25], but lower than in Africa [14] and Germany [15]. This, apparently, reflects the influence of many factors, including the climate and the level of housing technologies used in farms (for example, individual boxes, hygienic conditions of calf housing places); physiological state of animals at the time of sampling (diarrhoeal and non-diarrhoeal); used research and coprological diagnostic methodologies. Furthermore, calves were more infected with *Cryptosporidium* on farms with large cow herds [25]. It was suggested that larger herds produce higher density of calf populations, which come to be infected *Cryptosporidium* and increased contamination of environment and risk infection to humans. It is also known that other numerous management characteristics (such as herd size, type of herd, water sources and weaning modality *etc.*) have been evaluated as potential risk factors for the transmission of these pathogens at farms, yet the results have been discordant [15, 26–28].

Therefore, further research would also be required to assess and modelling the risk factors in epidemiology of cattle's cryptosporidiosis for developing the optimal control management in farms of different types and preventing the environment contamination and infecting of people with the zoonosis in northern Kazakhstan.

4 Conclusions

Cryptosporidiosis is common in 22.7% of cattle farms in the Akmola region, mainly in large industrial enterprises, where there are more favourable conditions for maintaining the biotic potential of the disease pathogens. The maximum likelihood estimate (MLE) for the infestation of young animals in the region was 0.0391 and posterior mean was 0.0543. The credible interval for posterior prevalence was [0.0418, 0.0685]. At the same time, calves up to one month of age are infested with cryptosporidia to a higher degree than animals of older age groups. The sex of animals had no correlation with the level of *Cryptosporidium* spp. invasion.

The Bayesian inference technique allowed for predicting the prevalence of the disease and planning measures to control cattle cryptosporidiosis in the conditions of different types of enterprises in the Akmola region.

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