Seroprevalence and associated risk factors of Neospora caninum in cattle in the Khomas region of Namibia

Alaster Samkange (✉ alastersamkange@gmail.com)  
University of Namibia  https://orcid.org/0000-0003-0646-6250

Simbarashe Chitanga  
University of Namibia

Georgina Tjipura-Zaïre  
University of Namibia

Vimanuka Gibbs Mutjavikua  
University of Namibia

Jan Wilhelm Smith  
University of Namibia

Luis Neves  
University of Pretoria Faculty of Veterinary Science

Tshepo Matjila  
University of Pretoria Faculty of Veterinary Science

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Abstract

*Neospora caninum* is a coccidian parasite which occurs worldwide and is one of the most important causes of abortion, especially in cattle. However, no studies have been done in Namibia to determine the *N. caninum* status in livestock. Therefore, this study aimed to determine the seroprevalence level of *N. caninum* in cattle and the associated risk factors in the Khomas region of Namibia. Seven hundred thirty-six (736) serum samples were collected from female cattle in 32 farming establishments. These comprised 698 beef and 38 dairy cattle sera and were tested using a commercial IDEXX *Neospora X2®* ELISA kit. Questionnaires were concurrently administered to determine possible risk factors associated with *N. caninum* seropositivity. A total of 42 sera were positive (all beef), giving an animal-level seroprevalence rate of 5.7%. Eight of the 32 establishments had at least one positive animal, giving a herd-level seroprevalence of 25%. There was no significant association between seropositivity and the presence of dogs, jackals, history of abortions, farm size, number of cattle or average annual rainfall. The establishments with moderate to high numbers of Feliformia were 9.8 times more likely to be seropositive to *N. caninum* than those with none to low levels of the former (p = 0.0245). The authors concluded that the seroprevalence level of *N. caninum* in the Khomas region was relatively low compared to other parts of the world and that the role of Feliformia in the epidemiology of bovine neosporosis needed to be further investigated.

Introduction

*Neospora caninum* is an obligate intracellular coccidian parasite of the Apicomplexa phylum and Sarcocystidae family, which occurs worldwide (Dubey et al., 1988; Goodswen et al., 2013; Radostits et al., 2014). The parasite primarily infects dogs and cattle as well as all major domestic livestock species, companion animals, wildlife and captive animals, including deer, rhinoceros, rodents, rabbits, coyotes, wolves and foxes (Radostits et al., 2014; Donahoe et al., 2015; McAllister, 2020). The canids are considered the definitive hosts, in which infection results in polyradiculoneuritis and polymyositis in young dogs, with dermatitis and neurological manifestations being characteristic in adult dogs. Whilst no active human cases have been reported, the parasite is suspected to be zoonotic due to reports of evidence of genetic material and serological response in human beings (Duarte et al., 2020; Abo-Shehada et al., 2021), a suggestion to the zoonotic capability of the parasite (Karakavuk et al., 2021). If confirmed to be zoonotic, the parasite thus poses a danger to particularly immunocompromised individuals (Tranas et al., 1999; Lobato et al., 2006; Oshiro et al., 2015).

Neosporosis is of significant economic importance in livestock, particularly cattle, in which infection is characterised by abortions, stillbirths, the birth of weak neonates, congenital malformation, increased numbers of culled cows and decreased milk yield (Kierbić et al., 2019; Gharekhani et al., 2020), with associated annual losses running into hundreds of millions of United States dollars (Reichel et al., 2013; Demir et al., 2020). Infection in these intermediate hosts is through ingestion of food and water contaminated with sporulated oocyst (Dubey et al., 2007; McAllister, 2020), with the subsequent vertical transmission in infected herds playing a more significant role (Sinnott et al., 2017; Gharekhani et al.,
Several risk factors have been identified to be associated with infection in livestock, and these include the presence and number of farm dogs (Dubey and Schares, 2011), farm production systems and practices (Pare et al., 1998; Otranto et al., 2003; Bartels et al., 2006; Dubey et al., 2007; Ghalmi et al., 2012)(Moore et al., 2009), antibodies against other pathogens like BVD (Björkman et al., 2000), human population density (Schares et al., 2004) and the region within countries (Bartels et al., 2006).

Whilst *N. caninum* is presumed to occur worldwide (Reichel et al., 2020), there is wide variation in prevalence across countries and regions, with some countries not having any data. Within the southern African region, evidence of bovine neosporosis has been reported in South Africa and Zimbabwe, with varied prevalence (Jardine and Last, 1993, 1995; Jardine and Wells, 1995; Njiro et al., 2011; Adesiyun et al., 2020). Other hosts which have been reported to show evidence of infection in southern Africa include dogs (Jardine and Dubey, 1992), birds (Lukášová et al., 2018) and wildlife (Seltmann et al., 2020). Despite the importance of the livestock sector in Namibia and the possible impact that *Neospora* infection can have on the productivity of this sector, there has been no study to determine the prevalence, distribution and potential risk factors associated with infection in commercial cattle production. Therefore, the purpose of this study was to fill this knowledge gap by determining the seroprevalence of *N. caninum* infection in cattle and the associated risk factors.

**Materials And Methods**

**Study area**

The study area was Namibia's Khomas region, located in the central part of the country (Fig. 1). Namibia's sub-tropical climate varies from arid to semi-arid and is the driest country in sub-Saharan Africa (Mwazi and Shamathe, 2007). The country's central highlands receive an annual rainfall of between 300 mm and 400 mm and have an altitude of up to 1900 metres (Kandiwa et al., 2017). The vegetation is predominantly shrub-veld, and ambient temperatures range from 7 °C in winter to 33 °C in summer (Kandiwa et al., 2019). The Khomas region has about 556 farming establishments with approximately 44,000 primarily commercial beef cattle (Directorate of Veterinary Services, 2018). Additionally, there are a few resettlement farms and communal settlements.

**Study animals**

The study animals were the cows and heifers in the Khomas region of Namibia. The females were targeted because vertical transmission is the most important in the epidemiology of *N. caninum* (Dubey et al., 2007; De Aquino Diniz et al., 2019). In addition, Wei and coworkers found that female cattle had a higher seroprevalence rate than males (Wei et al., 2022). Therefore, targeting females increased the probability of detecting positive animals. The 32 farming establishments selected for the study comprised 26 commercial beef farms, three communal beef herds, two dairy, and one resettlement farm.
Sampling and data collection

Sample size calculations were done according to the methods by Pfeiffer (Pfeiffer, 2002). For farm selection, estimated herd-level and individual animal-level prevalence rates of 20% and 10%, respectively, were used (Nasir et al., 2012; Fereig et al., 2016). A multistage sampling strategy was used to select the farming establishments included in this study. The Khomas region was first divided into clusters ranging from three to seven farming units. Seven clusters were chosen using convenience sampling, especially targeting farms that had previously reported abortions. Next, a stratified random sampling technique was used to select individual animals to be sampled at farm level, and a total of 736 heifers and cows were selected. A minimum of 10 cattle were sampled from each of the 32 farming establishments. A questionnaire was administered during the collection of serum samples to use that data to determine the possible risk factors of *N. caninum* in the Khomas region of Namibia.

Plain Vacutainer® blood tubes and 20-gauge needles were used to collect blood from the coccygeal or jugular veins. Sera were extracted by centrifugation at 6000 rpm for 10 minutes, after which they were stored at -20°C until testing.

Serological analysis

Indirect enzyme-linked immunosorbent assay (ELISA) (IDEXX Neospora X2® (IDEXX Laboratories, Inc, Maine 04092, USA) was used to detect specific anti-*N. caninum* IgG antibodies in the bovine sera as according to manufacturer's instructions. The assays were duplicated, with absorbance values measured at 650nm, with the S/P ratio of 0.50 as the cutoff value (negative < 0.50 & positive > 0.50).

Data analysis

The possible risk factors associated with *N. caninum* in sampled farming establishments were captured on questionnaires. The questionnaire and serology results were then captured in a Microsoft Excel 2013 spreadsheet. The captured data were analysed using descriptive statistics, chi-square test, odds ratios and multiple regression analysis at a 95% confidence level. Regression analysis was used on quantitative data to analyse the relationship between the dependent variable (number of *N. caninum* seropositive cases per establishment) and the independent variables (the numbers of cattle and dogs per establishment, farm size and average annual rainfall). The chi-square test and odds ratios were used to analyse the relationship between categorical data (the history of abortions, sightings of stray dogs, number of jackals, number of Feliforma and rain scores over the previous three seasons) and the *N. caninum* status of each establishment. Finally, descriptive statistics were used to calculate the seroprevalence rates. All the statistical analyses were done using Microsoft Excel 2013.

Results

In our study, 736 cattle (698 beef and 38 dairy) were sampled from 32 farming establishments, 30 of which were beef herds, and the remaining two were dairy. Eight of the 32 establishments had at least one
positive animal, giving an overall herd-level prevalence of 25% (8/32), and they were widely distributed across the sampling sites (Fig. 1). An overall animal-level prevalence of 5.71% (42/736) was observed, which varied widely across the farming establishments. For example, in the eight seropositive establishments, animal-level seroprevalence rates ranged from 3.03% (1/33) to 80.95% (17/21) (Table 1). The herd-level and animal-level seroprevalences for beef cattle only were 26.67% (8/30) and 6.02% (42/698), respectively. All the seropositive establishments were beef-producing commercial farms. The herd-level and animal-level seroprevalences for the two dairy farms sampled were 0% (0/2 & 0/38). Additionally, all three communal establishments and one resettlement farm sampled (all beef) were seronegative.

Table 1: A summary of the *N. caninum* ELISA test results for cattle sampled in the Khomas region of Namibia
<table>
<thead>
<tr>
<th>Farming establishment no.</th>
<th>Type of establishment</th>
<th>No. of cattle sera tested</th>
<th>No. seropositive</th>
<th>Prevalence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Beef commercial</td>
<td>12</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>2</td>
<td>Resettlement</td>
<td>32</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>3</td>
<td>Beef commercial</td>
<td>30</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>4</td>
<td>Beef commercial</td>
<td>18</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>5</td>
<td>Dairy</td>
<td>25</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>6</td>
<td>Beef commercial</td>
<td>39</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>7</td>
<td>Beef commercial</td>
<td>30</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>8</td>
<td>Beef commercial</td>
<td>43</td>
<td>3</td>
<td>6.98</td>
</tr>
<tr>
<td>9</td>
<td>Beef commercial</td>
<td>23</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>10</td>
<td>Beef commercial</td>
<td>33</td>
<td>1</td>
<td>3.03</td>
</tr>
<tr>
<td>11</td>
<td>Beef commercial</td>
<td>24</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>12</td>
<td>Beef commercial</td>
<td>40</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>13</td>
<td>Beef commercial</td>
<td>26</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>14</td>
<td>Beef commercial</td>
<td>25</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>15</td>
<td>Beef commercial</td>
<td>27</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>16</td>
<td>Dairy</td>
<td>13</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>17</td>
<td>Beef commercial</td>
<td>15</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>18</td>
<td>Beef commercial</td>
<td>25</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>19</td>
<td>Beef commercial</td>
<td>24</td>
<td>7</td>
<td>29.17</td>
</tr>
<tr>
<td>20</td>
<td>Beef commercial</td>
<td>18</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>21</td>
<td>Beef commercial</td>
<td>20</td>
<td>10</td>
<td>50.00</td>
</tr>
<tr>
<td>22</td>
<td>Beef commercial</td>
<td>21</td>
<td>17</td>
<td>80.95</td>
</tr>
<tr>
<td>23</td>
<td>Beef commercial</td>
<td>22</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>24</td>
<td>Beef commercial</td>
<td>20</td>
<td>2</td>
<td>10.00</td>
</tr>
<tr>
<td>25</td>
<td>Beef commercial</td>
<td>23</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>26</td>
<td>Communal</td>
<td>13</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>27</td>
<td>Communal</td>
<td>11</td>
<td>0</td>
<td>0.00</td>
</tr>
</tbody>
</table>
The results of possible risk factors for *N. caninum* seropositivity in cattle investigated using a questionnaire are shown in Table 2. The table summarises the results of the statistical analyses of the putative risk factors for seropositivity.

Eighteen of the 32 establishments (56.25%) sampled had a history of abortions during the previous five years, ranging from low levels of less than 10% (score 1), moderate levels of 10–15% (score 2) to at least one overt abortion outbreak (score 3) in the same period (Fig. 2). Eleven of the eighteen farms that reported at least one incident of abortions in the previous five years reported at least one incident of moderate to high abortion levels (scores between 2 & 3). Five of the eight farming establishments with at least one *N. caninum* seropositive animal had a history of previous abortions. However, this was not statistically significant on the chi-square test (p = 0.497).

<table>
<thead>
<tr>
<th>Farming establishment no.</th>
<th>Type of establishment</th>
<th>No. of cattle sera tested</th>
<th>No. seropositive</th>
<th>Prevalence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>28</td>
<td>Communal</td>
<td>5</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>29</td>
<td>Beef commercial</td>
<td>18</td>
<td>1</td>
<td>5.56</td>
</tr>
<tr>
<td>30</td>
<td>Beef commercial</td>
<td>12</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>31</td>
<td>Beef commercial</td>
<td>26</td>
<td>1</td>
<td>3.85</td>
</tr>
<tr>
<td>32</td>
<td>Beef commercial</td>
<td>23</td>
<td>0</td>
<td>0.00</td>
</tr>
<tr>
<td>TOTALS</td>
<td></td>
<td>736</td>
<td>42</td>
<td>5.71</td>
</tr>
</tbody>
</table>

Table 2
summary of the statistical analyses results performed on the possible risk factors associated with *Neospora caninum* seropositivity

<table>
<thead>
<tr>
<th>POSSIBLE RISK FACTOR</th>
<th>ANALYSIS TOOL</th>
<th>P-VALUE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total no. of cattle</td>
<td>Multiple regression</td>
<td>0.946</td>
</tr>
<tr>
<td>No. of dogs</td>
<td>Multiple regression</td>
<td>0.433</td>
</tr>
<tr>
<td>Farm size</td>
<td>Multiple regression</td>
<td>0.713</td>
</tr>
<tr>
<td>Average annual rainfall</td>
<td>Multiple regression</td>
<td>0.143</td>
</tr>
<tr>
<td>No. of Feliformia</td>
<td>Chi-square &amp; odds ratio</td>
<td>0.024</td>
</tr>
<tr>
<td>Sighting of stray dogs</td>
<td>Chi-square</td>
<td>0.838</td>
</tr>
<tr>
<td>History of abortions</td>
<td>Chi-square</td>
<td>0.497</td>
</tr>
<tr>
<td>No. of jackals</td>
<td>Chi-square</td>
<td>0.854</td>
</tr>
</tbody>
</table>
The annual rainfall received per farming establishment averaged 344 mm per year and ranged from 224 mm to 600 mm annually. The average annual rainfall for 72% (23/32) of the establishments ranged between 301mm and 400mm per year, and 25% (8/32) of the establishments received 201mm to 300mm annually (Fig. 3). However, the average rainfall per establishment was not significantly associated with *N. caninum* seropositivity on multiple regression analysis (p = 0.143).

The sighting of Feliformia (primarily hyenas, cheetahs & leopards) at the farming establishments was significantly associated with *N. caninum* seropositivity amongst the cattle on the chi-square test and odds ratio analysis. The establishments with moderate to high numbers of Feliformia on their properties were 9.8 times more likely (OR = 9.8; 95% CI 0.061–4.504) to be seropositive to *N. caninum* than those with none to low levels (p = 0.0245) (Fig. 4).

Except for one, all the other 31 establishments had at least one dog, ranging in number from one to 41, with the latter being at a resettlement farm with many livestock owners and households (Fig. 5). The average number of dogs per establishment sampled was six. The presence of dogs in the establishments was not significantly associated with seropositivity on multiple regression analysis (p = 0.433). On chi-square analysis, there was also no significant association between *N. caninum* seropositivity and sightings of stray dogs in sampled establishments (p = 0.838).

All the farming establishments reported observing high numbers of jackals on their properties (score 3); this was, however, not significantly associated with *N. caninum* seropositivity on chi-square analysis (p = 0.854).

The average number of cattle per sampled establishment was 301, ranging from 13 to 1205 animals. The modal range was between 201 and 400 cattle (Fig. 6). On multiple regression analysis, there was no significant association between cattle numbers per establishment and seropositivity (p = 0.946). There was also no significant association between farm size and seropositivity on multiple regression analysis (p = 0.713).

**Discussion**

Our study reports an overall animal-level seroprevalence of 5.7%, and to the best of our knowledge, this is the first study on *N. caninum* seroprevalence in cattle reported from Namibia. This observed prevalence is comparable to that reported within the region in South Africa, where 5.17% seroprevalence was reported in beef cattle (Chisi et al., 2013). However, unlike in the latter study, where all the dairy farms sampled were positive (Chisi et al., 2013), the two small-scale dairy herds sampled in the current study were both negative. These results could be because the dairy industry in Namibia is still in its infancy, with an estimated herd of only 3000 cattle (Bieldt, 2005). In addition, the largest dairy farm in the country was not sampled because it fell outside of the study area.

A similarly low seroprevalence rate of 3.8% was also detected in one study in Iran, where it was attributed to a combination of warm and dry climate followed by cold and dry conditions (Noori et al., 2019). These
climatic conditions were deemed unfavourable for the survival of *N. caninum* oocysts in the environment (Noori et al., 2019). On the other hand, humid conditions coupled with mild to warm environmental temperatures are ideal for sporulation and survival of oocysts (Dubey et al., 2007) and have also been associated with higher incidences of *N. caninum* abortions (Wouda et al., 1999). Northwest China has a generally hot and dry climate with very little rainfall in the summer months compared to the other parts of the country, and the area has been found to have the lowest *N. caninum* seroprevalence rate of 9.4% in the country (Wei et al., 2022). These scenarios perfectly mirror the semi-arid conditions of the Khomas region of Namibia, where the current study was conducted.

A study on cattle in northern Tanzania (Arusha region) determined a seroprevalence rate of 21.5% (Semango et al., 2019), which is much higher than the current study. Given the semi-arid nature of Namibia's climate, it could affect the survival and sporulation of the *N. caninum* oocysts in the environment (Dubey et al., 2007; Noori et al., 2019) and therefore reduce transmission. On the other hand, northern Tanzania is more humid and has higher average annual rainfall (Kimaro et al., 2018) compared to Namibia, which provides a more conducive environment for the sporulation of *N. caninum* oocysts. The same argument could also explain the relatively low prevalence rate in Namibia compared to other countries like the northern part of Algeria (Ghalmi et al., 2012); Argentina (Moore et al., 2003), China (Qian et al., 2017), Colombia (Llano et al., 2018), North and Central America, Asia, Europe and India (Hebbar et al., 2022).

The low animal-level *N. caninum* seroprevalence rate in the current study could also be attributed to the fact that 95% (698/736) of the samples tested were from beef cattle compared to only 5% (38/736) from dairy cattle. Beef cattle are less susceptible to *N. caninum* than dairy cattle, and therefore they tend to have lower seroprevalence rates (Quintanilla-Gozalo et al., 1999; Haddad et al., 2005; Fort et al., 2015; Ribeiro et al., 2019; Gharekhani et al., 2020).

Communal, dairy & resettlement establishments were all negative, possibly because the number of herds sampled from this category was very small; a larger sample size might have given a different result. Additionally, feliforms are less likely to be found in this category of establishments due to higher human population densities. However, the dog population is also expected to be increased with the increased human population, especially in communal setups (Butler and Bingham, 2000).

The current study found no significant association between the number of dogs at the farming establishments and *N. caninum* seropositivity. Similar findings were also made in studies in Tanzania (Mathew, 2017; Semango et al., 2019). However, since dogs are the definitive hosts of *N. caninum* (McAllister et al., 1998; Goodswen et al., 2013), these findings are somewhat surprising. Other studies have indeed confirmed that the presence of farm dogs increases the risk of *N. caninum* infection in cattle (Dubey et al., 2007; Robbe et al., 2016; Fávero et al., 2017; Abdeltif et al., 2022) and goats (Rodrigues et al., 2020), most likely through faecal contamination of pastures and open water sources with oocysts. The lack of significant association with the number of dogs found in the present study might have been caused by the fact that most of the farm dogs were confined to the homesteads and therefore did not
have carte blanche access to livestock pastures. This, in turn, meant that the risk of pasture contamination, regardless of the number of dogs at the farming establishment, was markedly reduced.

However, *N. caninum* positive status was significantly associated (*p* < 0.05) with the presence of Feliformia (brown hyenas, leopards & cheetahs) but not black-backed jackals, despite most farmers reporting many sightings of jackals on their properties. Domestic dogs (*Canis familiaris*) and black-backed jackals (*Canis mesomelas*) look physically similar; therefore, the possibility of mistaking these two species in places where the presence of Feliformia was reported cannot be entirely disregarded. In a recent Namibian study, brown hyenas (*Hyaena brunnea*) and black-backed jackals (*Canis mesomelas*) were found to be seropositive to *N. caninum* (Seltmann et al., 2020); however, the significance of these findings in light of the results of the current study need to be further investigated. Furthermore, workers in Tanzania have also suggested the possible involvement of wildlife in the epidemiology of *N. caninum* after finding no association between dog ownership and cattle seropositivity (Semango et al., 2019).

In one study, self-rearing of replacement heifers was associated with an increased risk of bovine neosporosis (Otranto et al., 2003). However, the current study found no such association, despite all the establishments indicating that they self-reared replacement heifers. This could be explained by the low *N. caninum* seroprevalence rate in the Khomas region, which reduces the risk of vertical parasite transmission.

This study found no significant association between abortion history and *N. caninum* seropositivity. One study in Northeast Algeria made similar findings, and the authors concluded that those cows were resistant to *N. caninum* abortions (Abdeltif et al., 2022). However, further investigations would be needed, given the extreme biological importance of the latter findings. The same scenario could also be at play in the Khomas region of Namibia, especially considering that significant variations in seropositivity have been found between countries, within countries, regions in the same country, and breeds (Dubey et al., 2007). Another study in Southeastern Iran found no association between *N. caninum* seropositivity and a history of abortions (Noori et al., 2019). However, other studies have demonstrated a significant association between *N. caninum* seropositivity and a history of abortions (Moore et al., 2009; Ghalmi et al., 2012; Llano et al., 2018). As earlier noted, this discrepancy could be due to variations between countries or regions.

The findings in this study were generally in agreement with some studies in other parts of the world. However, the seroprevalence level of *N. caninum* in the Khomas region is much lower than in most other parts of the world. Furthermore, the role of Feliformia in the epidemiology of bovine neosporosis needs to be further investigated.

**Declarations**

**Acknowledgement**
The authors would like to thank the Meat Board of Namibia for funding the purchase of the ELISA kits used in this study and the Directorate of Veterinary Services in Namibia for availing their laboratory facilities and technical staff. Also, we sincerely thank Dr Vonai Charamba and Dr Alec Bishi for guiding the statistical analysis.

**Funding:** The Meat Board of Namibia funded the purchase of the IDEXX ELISA kits used in this study.

**Conflicts of interest:** The authors declare no conflict of interest.

**Ethics approval:** This study was approved by the University of Namibia Ethics Committee (reference no.: NEC0007) and the University of Pretoria’s Research Ethics Committees (reference no.: REC087-21 & HUM00/0322).

**Consent to participate:** All the respondents signed informed consent forms before participating in this study.

**Consent for publication:** All the participants in this research signed informed consent permitting the publication of this research.

**Availability of data and material**

The data gathered during this research is available upon reasonable request.

**Code availability:** Microsoft Office 2013

**Authors’ contributions:** All authors participated in the study’s conception, design, material preparation and data collection. Alaster Samkange did the data analysis and writing of the first draft of the manuscript. All authors commented on all previous versions and read and approved the final version of this manuscript.

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Figures
Figure 1

Map showing all the fourteen regions of Namibia in relation to the Khomas region which lies in the central area of the country. (Source: https://www.mappr.co/counties/namibia/, used with permission).
Figure 2

Figure 1: Google Earth map showing the distribution of the cattle farming establishments sampled in the Khomas region of Namibia, which is delineated in yellow. The eight positive farms are marked red, and the negative ones in blue.
Figure 3

Figure 2: Distribution of abortion of scores among sampled establishments
Figure 4

Figure 3: Average annual rainfall distribution among the sampled farming establishments
Figure 4: Feliformia score distribution among sampled establishments.

Figure 5: Distribution of Feliformia in sampled establishments.
Figure 5: Distribution of dogs in sampled farming establishments

Figure 6
Figure 7

Figure 6: Distribution of the numbers of cattle in sampled cattle herds