ESTIMATING TOXOPLASMA GONDIi EXPOSURE IN ARCTIC FOXES (VULPES LAGOPUS) WHILE NAVIGATING THE IMPERFECT WORLD OF WILDLIFE SEROLOGY

Stacey A. Elmore,1,5,7 Gustaf Samelius,2,3 Batol Al-Adhami,4 Kathryn P. Huyvaert,5 Larissa L. Bailey,2 Ray T. Alisauskas,6 Alvin A. Gajadhar,4 and Emily J. Jenkins1

1 University of Saskatchewan, Department of Veterinary Microbiology, 52 Campus Drive, Saskatoon, Saskatchewan S7N 5B4, Canada
2 Swedish University of Agricultural Sciences, Department of Ecology, Grimsö Wildlife Research Station, Riddarhyttan SE-730 91, Sweden
3 Snow Leopard Trust, 4649 Sunnyside Avenue N, Suite 325, Seattle, Washington 98103, USA
4 Canadian Food Inspection Agency, Centre for Foodborne and Animal Parasitology, 116 Veterinary Road, Saskatoon, Saskatchewan S7N 2R3, Canada
5 Colorado State University, Department of Fish, Wildlife, and Conservation Biology, 1474 Campus Delivery, Fort Collins, Colorado 80523-1474, USA
6 Environment Canada, Prairie and Northern Wildlife Research Centre, 115 Perimeter Road, Saskatoon, Saskatchewan S7N 0X4, Canada
7 Corresponding author (email: elmore.stacey@gmail.com)

ABSTRACT: Although the protozoan parasite Toxoplasma gondii is ubiquitous in birds and mammals worldwide, the full suite of hosts and transmission routes is not completely understood, especially in the Arctic. Toxoplasma gondii occurrence in humans and wildlife can be high in Arctic regions, despite apparently limited opportunities for transmission of oocysts shed by felid definitive hosts. Arctic foxes (Vulpes lagopus) are under increasing anthropogenic and ecologic pressure, leading to population declines in parts of their range. Our understanding of T. gondii occurrence in arctic foxes is limited to only a few regions, but mortality events caused by this parasite have been reported. We investigated the exposure of arctic foxes to T. gondii in the Karrak Lake goose colony, Queen Maud Gulf Migratory Bird Sanctuary, Nunavut, Canada. Following an occupancy-modeling framework, we performed replicated antibody testing on serum samples by direct agglutination test (DAT), indirect fluorescent antibody test (IFAT), and an indirect enzyme-linked immunosorbent assay (ELISA) that can be used in multiple mammalian host species. As a metric of test performance, we then estimated the probability of detecting T. gondii antibodies for each of the tests. Occupancy estimates for T. gondii antibodies in arctic foxes under this framework were between 0.430 and 0.758. Detection probability was highest for IFAT (0.716) and lower for DAT (0.611) and ELISA (0.464), indicating that the test of choice for antibody detection in arctic foxes might be the IFAT. We document a new geographic record of T. gondii exposure in arctic foxes and demonstrate an emerging application of ecologic modeling techniques to account for imperfect performance of diagnostic tests in wildlife species.

Key words: Arctic fox, DAT, ELISA, IFAT, Karrak Lake, MAT, occupancy modeling, Toxoplasma.

INTRODUCTION

Few parasites are known to infect as many vertebrate species as Toxoplasma gondii. This protozoan is ubiquitous in birds and mammals worldwide (Dubey 2009). Nevertheless, felids are the only known definitive hosts of the parasite and are responsible for environmental contamination by passing oocysts in their feces (Dubey et al. 1970). Because felids are rare visitors to arctic tundra, where logistics of ecosystem-wide observations are challenging, complete transmission routes and the full suite of hosts of T. gondii in the Arctic remain unknown. Presumably, the low density of felids in arctic regions reduces opportunities for oocyst transmission compared with subarctic and temperate regions. Although oocysts might travel from temperate and boreal regions through watersheds that drain into the Arctic Ocean (Simon et al. 2013), it is probable that arctic carnivores can also be exposed to T. gondii by consuming infected prey and by maternal transmission to fetuses during gestation.
Arctic foxes (*Vulpes lagopus*) are circumpolar canids with generalist diets (Audet et al. 2002). Although arctic foxes are common throughout northern Canada, rapid climatic change and increasing interspecific competition due to red fox (*Vulpes vulpes*) range expansion (Fuglei and Ims 2008) likely contribute to increasing stress on arctic fox populations. Red foxes restricted the southern limit of arctic foxes in Norway (Hersteinsson and Macdonald 1992) and competition between the two species negatively affected arctic fox occurrence and abundance during recolonization efforts in Fennoscandia (Hamel et al. 2013). Red foxes and other migrants from subarctic or temperate regions might introduce novel pathogens to an arctic ecosystem, which could affect the health of immunologically naïve arctic foxes. Although arctic foxes in Canada are not of apparent conservation concern, baseline data on a population in rapidly changing northern Canada can provide an important reference against which future comparisons can be made.

Arctic foxes are intermediate hosts of *T. gondii* and infection with this parasite can cause host mortality. For example, mortality has been reported in the Svalbard, Norway arctic fox population (Sorensen et al. 2005), in which an apparent antibody prevalence of 43% was observed (Prestrud et al. 2007). In North America, *T. gondii* detection in arctic foxes is rare, most likely due to lack of surveillance and the high cost of obtaining samples. Dubey et al. (2011) reported actual *T. gondii* infection in North American arctic foxes, isolating the parasite from five of 14 foxes in Alaska. However, antibodies have been detected in other canid species from the Northwest Territories and Alaska (Zarnke et al. 2000; Salb et al. 2008; Stieve et al. 2010), indicating that northern canids are likely routinely exposed to *T. gondii*.

Most studies that examined *T. gondii* in wildlife apply serologic assays as an alternative to direct demonstration of *T. gondii* infection in tissues by PCR, bioassay, histopathology, or immunohistochemistry (see Elmore et al. 2012; Jenkins et al. 2013). This is likely due to the difficulty of isolating the parasite ante mortem and the relative ease of accessing blood samples in live animals. These assays are rarely formally validated given the inaccessibility of known positive and negative control samples for many wildlife species (Elmore et al. 2012; Peel et al. 2013). As a result, assay details such as sensitivity and specificity are rarely available for the species of interest, creating uncertainty in the test results (Elmore et al. 2014) because the probabilities of false-negative and false-positive results are unknown. If sensitivity and specificity information are absent, data analysts have no measure of assay uncertainty using traditional naïve estimators of prevalence based solely on detections. Increasingly, this problem is being addressed by analyzing wildlife disease data within an occupancy-modeling framework, with which we can estimate and account for detection probability directly (e.g., Lachish et al. 2012; Eads et al. 2013; Elmore et al. 2014).

Occupancy-modeling approaches are analogous to mark–recapture analyses from wildlife biology and were initially used to estimate the occurrence of cryptic or rare species within habitat patches where they may be detected imperfectly (MacKenzie et al. 2006). These approaches are useful in wildlife disease ecology because they acknowledge that uncertainty exists when studying wild populations and when using imperfect and unvalidated diagnostic tests (McClintock et al. 2010; Lachish et al. 2012). Under a typical occupancy framework, randomly selected “sites” are surveyed on multiple occasions within a time frame where the occupancy state (species presence vs. absence) is assumed not to change. These repeated survey occasions at each site enable estimation of two parameters: occupancy (ψ), defined as the probability that a site is occupied by the species of interest (equal to prevalence in a wildlife disease context),
and detection probability ($p$), or probability that the species is detected during a given occasion, given the site is occupied (MacKenzie et al. 2006). In our application, diagnostic samples (i.e., serum samples from individual foxes) are analogous to sites, the “species of interest” are antibodies against $T. gondii$, and the repeated survey occasions are multiple replications of the test performed on each sample for each assay. Reinterpreting the model parameters for this study gives $\psi_i$ as the probability that serum sample $i$ is positive for $T. gondii$ antibodies and $p_d$ as the probability of detecting $T. gondii$ antibodies in sample $i$ from assay $t$, given that the serum sample is positive.

Adding to the uncertainty of $T. gondii$ serology is the absence of a “gold standard” diagnostic test for wildlife hosts. The direct agglutination test (DAT; equivalent to the modified agglutination test [MAT]) is a commonly used serologic test for wildlife exposure to $T. gondii$ because it is flexible for use in multiple species (Prestrud et al. 2007), but it has not been formally validated for wildlife and performance can vary among host species (Macrì et al. 2008). Indirect fluorescent antibody tests (IFAT) are also used with wildlife sera (Dabritz et al. 2008; Miller et al. 2008), but their use has been limited to animals for which a taxon-specific secondary antibody has been produced. Both assays have subjective end-point criteria based on visual inspection, which suggests that the potential exists for misclassification and biased reporting of antibody prevalence. Commercially available enzyme-linked immunosorbent assays (ELISAs) can also be used to detect $T. gondii$ antibodies, but these assays are also limited by the requirement of a taxon-specific secondary conjugate antibody. To address this problem, Al-Adhami and Gajadhar (2014) developed an indirect ELISA using a protein A/G conjugate that can be used in multiple mammalian species, although the problem persists of obtaining known negative samples to determine cutoff values.

Herein we use occupancy-modeling approaches to: 1) estimate the antibody prevalence of $T. gondii$ in arctic foxes from Karrak Lake, Nunavut, Canada, and 2) determine which serologic assay gives the highest detection probability for $T. gondii$. Because canid prey and scavenged species that are common within our study area were reported to have anti-$T. gondii$ antibodies (Kutz et al. 2000, 2001; Elmore et al. 2014), we hypothesized that arctic foxes in the Karrak Lake ecosystem would demonstrate exposure to $T. gondii$. Because the IFAT has been demonstrated to have a higher detection probability than DAT in a previous study (Elmore et al. 2014) and the protein A/G ELISA had high agreement with the IFAT and DAT (Al-Adhami and Gajadhar 2014), we also predicted that either of these tests would have a higher detection probability than the DAT.

**MATERIALS AND METHODS**

**Study area**

Fieldwork took place in the Karrak Lake region (67°14′N, 100°15′W) of the Queen Maud Gulf Bird Sanctuary in the central Canadian Arctic (Fig. 1). This area is a large goose colony where over 1 million Ross’s Geese ($Chen rossii$) and Lesser Snow Geese ($Chen caerulescens$) have nested annually (Alisauskas et al. 2012). The landscape is characterized by rolling tundra with rock outcrops, sedge (Cyperaceae) meadows, marshes, and freshwater ponds (Ryder 1972).

**Field sample collection**

From mid-May to mid-June 2011–13, we live-captured 39 individual adult arctic foxes. Six foxes were trapped multiple times for a total of 46 capture events, but each fox was included only once in the occupancy analysis (see Data Analysis section). Foxes were captured in the original and central part of the goose colony (boxed area in Fig. 1) where the traps were located near den sites or prominent landscape features such as elevated knolls and large rocks. Foxes were sedated with 15 mg of Telazol® (tiletamine/zolazepam) following procedures of Samelius et al. (2003). We collected up to 3 mL of blood by cephalic venipuncture, placed
plastic ear tags in both ears for future identification, determined sex, and estimated age (on the basis of tooth-wear measurements; see upcoming text). After blood clot formation, we centrifuged the blood for 10 min, removed the serum, and stored it at −20°C. Foxes caught multiple times were sedated and had blood drawn at most once per year.

We estimated age through tooth-wear classifications as “not worn” or “worn” (see Landon et al. 1998 for similar categories). Tooth wear of known-age foxes (n=7 marked as kits) and of foxes recaptured in more than 1 yr (n=38 recaptures of 26 foxes) showed the following: 1) five of five known yearlings had no tooth wear but one of 24 known to be at least 2 yr old was included in the not worn category; 2) 31 of 38 foxes known to be ≥2 yr had teeth showing minor to severe wear (G.S. unpubl. data). In accordance with these data, we structured our age categories as: <1 yr (n=19) = not worn and ≥2 yr (n=20) = worn.

Foxes were trapped under the following permits: Nunavut Department of Environment 2011-018, 2012-020, 2013-015 and Canadian Wildlife Service NUN-MBS-11-02, NUN-SCI-11-03, NUN-MBS-12-02, NUN-SCI-12-03. Blood was collected with permission from the University of Saskatchewan Committee on Animal Care and Supply (2009-0159).

**Laboratory analysis**

Following an occupancy-modeling framework (Elmore et al. 2014), we tested each serum sample (n=46 samples collected from the 39 individual foxes) using three replicates each of the DAT, IFAT, and ELISA, resulting in a detection/nondetection sequence consisting of nine replicates. Test results from each replicate were classified as antibodies clearly detected (denoted as 1), antibodies clearly not detected (denoted as 0), and equivocal results were ignored in the analysis (treated as missing observations, denoted as ‘.’).

Direct agglutination tests (Biomerieux, Saint-Laurent, Quebec, Canada) were performed on serum using a commercially available kit according to manufacturer’s instructions. Each serum sample was tested at 1:40 dilution (Jokelairen et al. 2013) on three discrete replications, or “site visits” (Elmore et al. 2014). Test wells indicating agglutination covering 50–100% of the well were recorded as “*T. gondii* antibodies clearly detected.” Following manufacturer’s instructions, test wells with a solid dot or small ring in the center were recorded as “no antibodies detected,” and wells with mild agglutination covering less than half of the test well were recorded as equivocal.

The IFAT was performed using anti-canine immunoglobulin (Ig)G–fluorescein isothiocyanate
Table 1. Candidate model set and model selection results of the occupancy analysis to estimate antibody prevalence ($\psi$) and detection probability ($p$) of Toxoplasma gondii antibodies in arctic foxes (Vulpes lagopus) from Karrak Lake, Nunavut, Canada. The number of parameters ($K$), $-2\log$ likelihood (-2LL), small sample size-corrected Akaike information criterion values (AICc), and Akaike weights ($w_i$) are presented for each model $i$.

<table>
<thead>
<tr>
<th>Model</th>
<th>$K$</th>
<th>-2LL</th>
<th>AICc</th>
<th>$\Delta$AICc</th>
<th>$w_i$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\psi(\text{age})p(\text{test})$</td>
<td>5</td>
<td>308.12</td>
<td>319.94</td>
<td>0.00</td>
<td>0.74</td>
</tr>
<tr>
<td>$\psi(\text{sex})p(\text{test})$</td>
<td>4</td>
<td>314.44</td>
<td>323.62</td>
<td>3.68</td>
<td>0.12</td>
</tr>
<tr>
<td>$\psi(\text{age} \times \text{sex})p(\text{test})$</td>
<td>7</td>
<td>307.98</td>
<td>325.59</td>
<td>5.66</td>
<td>0.04</td>
</tr>
<tr>
<td>$p(\text{test})$</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\psi(\text{sex})p(\text{test})$</td>
<td>5</td>
<td>314.28</td>
<td>326.10</td>
<td>6.16</td>
<td>0.05</td>
</tr>
<tr>
<td>$\psi(\text{age})p(\text{test})$</td>
<td>3</td>
<td>318.51</td>
<td>325.59</td>
<td>5.66</td>
<td>0.04</td>
</tr>
<tr>
<td>$\psi(\text{sex} \times \text{age})p(\text{test})$</td>
<td>5</td>
<td>318.37</td>
<td>330.19</td>
<td>10.26</td>
<td>0.01</td>
</tr>
</tbody>
</table>

We analyzed detection histories for T. gondii antibodies using the single-season occupancy model in Program MARK (White and Burnham 1999) to estimate antibody prevalence within the arctic fox population at Karrak Lake. When multiple blood samples were available per fox (six individuals), only the serology results from the first year were included. We developed an a priori candidate model set (Table 1) to analyze the potential effects of sex and age class on the probability of being antibody positive ($\psi$) and the effect of serologic assay type on detection probability ($p$). We performed model selection using the small sample bias-corrected Akaike information criterion (AICc; Burnham and Anderson 2002). We ranked models by calculating the differences in AICc ($\Delta$AICc) between the highest-ranked model and remaining models; model weights ($w_i$) were then calculated for each model. Similar weights for multiple models indicated some model selection uncertainty, so we report model-averaged parameter estimates (Anderson 2008), unconditional variances, and associated 95% confidence intervals (CIs).

To estimate the naïve antibody prevalence from each assay, we counted the number of detections on the first repetition of each assay and divided by the number of serum samples tested (20 young foxes and 19 mature foxes). We also tested for overdispersion in our data using the median c-hat method, implemented in Program MARK, using the global model ($\psi [\text{sex} \times \text{age}]p[\text{test}]$).

RESULTS

We analyzed 46 serum samples from 39 foxes by DAT, IFAT, and ELISA for T. gondii antibodies. Although we only included serology results from the first blood sample from a fox in the occupancy analysis, laboratory analysis on the additional samples was performed. Of the six foxes that were tested on more than one occasion, one fox that was tested for two successive years after the first sample remained antibody negative throughout the study. Four samples was performed. Of the six foxes that were tested on more than one occasion, one fox that was tested for two successive years after the first sample remained antibody negative throughout the study. Four foxes were tested for two consecutive years; two of these were antibody positive in both years and two were negative in the first year and then positive in the second year. Naïve antibody prevalence estimates for each diagnostic assay in both young and mature...
foxes were lower than the occupancy estimates of antibody prevalence (Fig. 2). Age of foxes was an important determinant of being antibody positive ($\psi$), as it was in the top-ranked model and carried the most weight ($w=0.74$; Table 1). Mature foxes had higher antibody prevalence estimates than yearlings ($0.758$ vs. $0.430$; Table 2). Little evidence existed of sex-specific differences in antibody prevalence (Table 1). Serologic assay type ("test") influenced the probability of detecting T. gondii antibodies ($p$; Table 1), given that a fox was antibody positive; this effect was included in all models with Akaike weights $>0.10$. A comparison of model-averaged detection probabilities for the three diagnostic tests showed that detection probability was higher for the IFAT ($p=0.716$, 95% CI $=0.583$, $0.820$) than for both the DAT ($p=0.611$, 95% CI $=0.492$, $0.718$) and the ELISA ($p=0.464$, 95% CI $=0.333$, $0.600$; Table 2). Also, we found no evidence of overdispersion ($c=1$), indicating no lack of independence within the data set.

**DISCUSSION**

We document a new geographic record of T. gondii exposure in arctic foxes and show that arctic foxes within the Karrak Lake ecosystem in Nunavut are routinely exposed to T. gondii. At Karrak Lake, arctic foxes are probably exposed to T. gondii mostly by trophic transmission and vertical transmission. Oocyst transmission of T. gondii to arctic foxes in our study system is less likely because of the distance from lynx habitat (subarctic boreal ecosystems) and human communities where domestic cats (Felis catus) might be present. Alternatively, oocysts might enter terrestrial systems by traveling through watersheds from more southern latitudes followed by ingestion by wildlife (Simon et al. 2013). Arctic foxes in this population consume collared lemmings (Dicrostonyx groenlandicus), birds (including adult geese), and goose eggs; however, foxes also scavenge larger prey such as caribou and muskoxen and also show stable isotope signatures indicating consumption of prey from marine environments (Roth 2003; Samelius et al. 2007). All of these animals have the potential to serve as intermediate hosts of T. gondii, and antibodies have been reported in geese sympatric with the foxes in this study (Elmore et al. 2014), as well as caribou and muskoxen in the Canadian Arctic (Kutz et al. 2000, 2001). Geese and caribou conduct long-distance migrations between subarctic and temperate regions (where they might encounter T. gondii oocysts) and the Arctic. Also, arctic foxes can travel over long distances while dispersing.

**Table 2.** Model-averaged estimates of antibody prevalence ($\psi$) and detection probability ($p$) of Toxoplasma gondii antibodies in serum samples from arctic foxes (Vulpes lagopus) collected during May 2011–13 at Karrak Lake, Nunavut, Canada. Tests compared are direct agglutination test (DAT), indirect fluorescent antibody test (IFAT), and indirect enzyme-linked immunosorbent assay (ELISA).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>SE</th>
<th>95% Confidence interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\psi$Yearling</td>
<td>0.430</td>
<td>0.127</td>
<td>0.214–0.676</td>
</tr>
<tr>
<td>$\psi$Mature</td>
<td>0.758</td>
<td>0.117</td>
<td>0.472–0.916</td>
</tr>
<tr>
<td>$p$DAT</td>
<td>0.611</td>
<td>0.058</td>
<td>0.492–0.718</td>
</tr>
<tr>
<td>$p$IFAT</td>
<td>0.716</td>
<td>0.061</td>
<td>0.583–0.820</td>
</tr>
<tr>
<td>$p$ELISA</td>
<td>0.464</td>
<td>0.070</td>
<td>0.333–0.600</td>
</tr>
</tbody>
</table>
including travel through marine ecosystems on sea ice.

Observing T. gondii antibodies in a predator species such as arctic foxes might also serve as an indicator for potential human exposure and transmission of T. gondii in wildlife from this region. For example, caribou, muskoxen, and geese are important foods for both human subsistence hunters and foxes (Samelius et al. 2007), and exposure in these host species has been documented (Kutz et al. 2000, 2001; Elmore et al. 2014). We stress the importance of better understanding the distribution and transmission of T. gondii in arctic wildlife and the significance for wildlife and human health in northern Canada. In the recent Inuit Health Survey, Inuit populations in Nunavut had a higher antibody prevalence of T. gondii (32%) than Inuit in the west (Inuvialuit Settlement Region, 7.5%) and extreme east of Canada (Nunatsiavut, 11%), although this is still consistent with global estimates of about 33% infection of the general human population (Goyette et al. 2014). Although the Inuit Health Survey revealed that the consumption of seafood and marine mammals was a more important risk factor for human exposure to T. gondii than the consumption of birds and ungulates, our study serves as a reminder that this parasite circulates in terrestrial arctic ecosystems as well. Our current understanding of T. gondii in arctic foxes does not suggest direct transmission from foxes to humans, except possibly in cases of carcass handling or, rarely, consumption of foxes, but rather reflects the ubiquity of the parasite within a terrestrial food web.

In our study, mature foxes (≥2 yr) were most likely to be antibody positive. We had expected that the older age class would have the highest antibody prevalence because of the cumulative increased risk of exposure throughout the lifetime of a fox and previous observations (Mitchell et al. 1999). These results suggest that trophic or environmental transmission might be more likely to occur than vertical transmission, in which case we would expect more antibody-positive younger animals. However, the mature group might include a mixture of foxes where some were congenitally exposed and others exposed through trophic interactions. Despite having a lower probability of exposure, some young foxes were still antibody positive, suggesting that vertical transmission might occur, although these foxes might just be exposed to infected prey at a younger age than most. Future work includes a serologic study of neonate arctic foxes in the Karrak Lake population (E. Bouchard unpubl. data). A long-term study that follows the foxes throughout their lifespan would be useful to determine when foxes in the population become antibody positive, although this would be logistically difficult.

By taking blood samples from recaptured animals, we might begin to understand the dynamics of antibody persistence and parasite colonization in arctic foxes, possibly using a robust design occupancy approach (e.g., Eads et al. 2013) if enough recapture data could be collected in a long-term study. It would also be beneficial to understand the movements of arctic foxes at Karrak Lake throughout the year to estimate where and when they become exposed to T. gondii. It is unknown whether Karrak Lake foxes maintain territories or emigrate during the winter, although they have a tendency to stay in an area once settled (Samelius et al. 2007). However, even foxes known to hold successful breeding dens in consecutive years will disperse during periods of low prey abundance, such as during a lemming population low point (G.S. unpubl. data), often traveling through marine environments. Also, because Karrak Lake is only approximately 60 km from the Arctic Ocean, foxes that immigrated to the ecosystem could have been exposed to T. gondii in a marine environment by scavenging marine mammals on sea ice or consuming marine food items that had washed to the shoreline. In a previous study, however, the stable isotope signatures of arctic fox blood suggested little use of marine habitats and a diet largely
composed of collared lemmings and goose eggs (Chen sp.) (Samelius et al. 2007). More research is needed to determine the origins of T. gondii exposure and infection at Karrak Lake.

We emphasize the utility of an occupancy-modeling framework for wildlife disease studies through a comparison of naïve and occupancy-based estimates of antibody prevalence. By reducing the uncertainty associated with diagnostic testing through repeated testing of our serum samples, we were able to produce more robust estimates of antibody prevalence than with traditional methods that do not account for nondetection.

Detection probability of T. gondii antibodies varied among the three serologic assays examined. The IFAT had a higher detection probability for antibodies \( (p=0.716) \) than the DAT and ELISA \( (p=0.611 \) and 0.406, respectively). This was consistent with results of Macrí et al. (2008) demonstrating higher sensitivity of the IFAT over DAT in canine serum samples. The lower detection probability of the ELISA might have been due to our conservative determination of a positive cutoff value, in the absence of known positive and negative controls. This suggests that the ELISA, as used in this study, might underestimate antibody prevalence in the absence of a more rigorous method of cutoff value determination using known positive and negative control samples from arctic foxes. This does not reflect the general value of the ELISA-A/G, however; when the appropriate controls were available, the ELISA was very effective and showed excellent agreement with the MAT, western blot, and an ELISA-IgG kit (Al-Adhami et al. 2014). Nonetheless, our work with replicate assays of the same samples demonstrated the utility of an occupancy framework to evaluate the performance of diagnostic tests in wildlife with unvalidated assays.

In summary, this study documents a new geographic record for T. gondii exposure in arctic foxes and demonstrates an emerging application of ecologic modeling techniques to account for uncertainty in serologic test results from wildlife. The logistic and financial challenges of pursuing arctic fieldwork also highlight the value of this data set. Future research bridging the occurrence of T. gondii with potential routes of exposure will be especially important to increase our understanding of T. gondii ecology in the Arctic.

**ACKNOWLEDGMENTS**

We thank R. Kerbes and K. Price for excellent assistance and great company in the field, D. Kellett for logistic support, D. Stern for help and hospitality in Cambridge Bay, and J. Benjamin for laboratory assistance. This study was supported by the Natural Science and Engineering Research Council Discovery Grant and Post Graduate Scholarship, Northern Studies Training Program, Western College of Veterinary Medicine Wildlife Health Fund, Environment Canada, Canadian Food Inspection Agency Centre for Food-Borne and Animal Parasites, Polar Continental Shelf Project, Swedish Polar Research Secretariat, the Colorado State University Department of Fish, Wildlife, and Conservation Biology, the University of Saskatchewan, and an equipment grant from the Canadian Foundation for Innovation Leaders Opportunity Fund for the Zoonotic Parasite Research Unit.

**LITERATURE CITED**


Hamel S, Killengreen ST, Henden JA, Yoccoz NG, Ims RA. 2013. Disentangling the importance of interspecific competition, food availability, and habitat in species occupancy: Recolonization of the endangered Fennoscandian arctic fox. Biol Conserv 160:114–120.


Submitted for publication 24 March 2015. Accepted 26 June 2015.