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# A SEROLOGIC SURVEY OF *FRANCISELLA TULARENSIS* EXPOSURE IN WILDLIFE ON THE ARCTIC COASTAL PLAIN OF ALASKA, USA

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ABSTRACT: Tularemia is an infectious zoonotic disease caused by one of several subspecies of *Francisella tularensis* bacteria. Infections by *F. tularensis* are common throughout the northern hemisphere and have been detected in more than 250 wildlife species. In Alaska, US, where the pathogen was first identified in 1938, studies have identified *F. tularensis* antibodies in a diverse suite of taxa, including insects, birds, and mammals. However, few such investigations have been conducted recently and knowledge about the current distribution and disease ecology of *F. tularensis* is limited, particularly in Arctic Alaska, an area undergoing rapid environmental changes from climate warming. To help address these information gaps and provide insights about patterns of exposure among wildlife, we assessed the seroprevalence of *F. tularensis* antibodies in mammals and tundra-nesting geese from the Arctic Coastal Plain of Alaska, 2014–17. With a commercially available slide agglutination test, we detected antibodies in 14.7% of all individuals sampled ($n$=722), with titers ranging from 1:20 to 1:320. We detected significant differences in seroprevalence between family groups, with Canidae (foxes, *Vulpes* spp.) and Sciuridae (Arctic ground squirrel, *Spermophilus parryii*) having the highest seroprevalence at 21.5% and 33.3%, respectively. Mean seroprevalence for Ursidae (polar bears, *Ursus maritimus*) was 13.3%, whereas Cervidae (caribou, *Rangifer tarandus*) had comparatively low seroprevalence at 6.5%. Antibodies were detected in all Anatidae species sampled, with Black Brant (*Branta bernicla nigricans*) having the highest seroprevalence at 13.6%. The detection of *F. tularensis* antibodies across multiple taxa from the Arctic Coastal Plain and its nearshore marine region provides evidence of exposure to this pathogen throughout the region and highlights the need for renewed surveillance in Alaska.

*Key words:* Alaska, Arctic Coastal Plain, bacteria, *Francisella tularensis,* serology, tularemia, wildlife, zoonoses.

## INTRODUCTION

Tularemia is an infectious zoonotic disease caused by the bacterium *Francisella tularensis* (Friend 2006). Infections with *F. tularensis* are common throughout North America and have been documented in many vertebrate species, including mammals, birds, and amphibians (Mörner 1992; Ellis et al. 2002; Hansen et al. 2011; Hansen and Dresvyannikova 2022). Infection occurs when bacteria are transferred through the bite of an arthropod vector, contamination of an open wound, ingestion of contaminated water or food, or direct inhalation of the bacteria (Ellis et al. 2002; Petersen and Schriefer 2005; Keim et al. 2007). Lagomorphs and aquatic rodents are considered the primary reservoirs of *F. tularensis* and have been identified as possible sources of infection for humans and other wildlife (Mörner 1992; Ellis et al. 2002; Friend 2006; Hansen and Dresvyannikova 2022). Tularemia was first reported as a plague-like disease in a ground squirrel in California, US, in 1911 with the isolation of the *F. tularensis* bacterium in 1912 (McCoy 1911; McCoy and Chapin 1912). Since then, *F. tularensis* has been confirmed in >250 host species in the northern hemisphere (Keim et al. 2007). Clinical cases of *F. tularensis* infection are infrequently observed in wildlife, because individuals are either moribund or

dead when discovered, or infections are overlooked because of a lack of clinical signs in more resilient species (Friend 2006). In some wildlife species, however, infection with *F. tularensis* can cause acute pathogenic effects, with reports of death occurring in as little as 2–10 d in rabbits and hares (Mörner et al. 1988; Mörner 1992; Friend 2006). Among humans, *F. tularensis* infection can range from nearly benign to potentially fatal, depending on the route of entry and the bacterial subtype (Keim et al. 2007; Hansen et al. 2011).

In Alaska, US, *F. tularensis* was first isolated from a rabbit tick (*Haemophysalis leporis-palustris*) collected near Fairbanks in 1938 (Philip and Parker 1938). Serologic surveys of Alaska wildlife have revealed the presence of *F. tularensis* antibodies in a broad range of species, including rodents, hares, birds, and large mammals (Zarnke and Ballard 1987; Chomel et al. 1998; Zarnke et al. 2004; Hansen et al. 2011; Hueffer et al. 2013; Ramey et al. 2019); another study detected the presence of *F. tularensis* DNA in insects (Triebenbach et al. 2010). Human cases of tularemia have also been documented in Alaska, with 38 cases reported in the state between 1946 and 2010, along with varying levels of seropositive individuals identified over the same time period (Hansen et al. 2011; Hansen and Dresvyannikova 2022). Detection of *F. tularensis* or its antibodies in wildlife and humans indicates active local transmission, although knowledge gaps remain regarding the geographic occurrence and transmission pathways of this bacterium within Alaska. The incidence of *F. tularensis* infection may also be affected by climate-related changes in wildlife distribution, particularly in regions subject to rapid warming.

The Arctic Coastal Plain (ACP) of Alaska, US, encompasses tundra and wetland habitats located between the northern slopes of the Brooks Range and the Beaufort Sea. The ACP supports large numbers of migratory birds during the breeding season and provides year-round habitat for a diversity of terrestrial and marine mammal species, including Arctic foxes (*Vulpes lagopus*), caribou (*Rangifer tarandus*), polar bears (*Ursus maritimus*), and multiple species of small mammals. This region is undergoing rapid environmental change, which has raised concern about the potential for increased prevalence and transmission of disease agents because of shifts in traditional wildlife ranges and possible increased interactions between species that historically had little contact (Burek et al. 2008; Post et al. 2013; Van Hemert et al. 2015). For example, because of reductions in sea ice, polar bears in northern Alaska are spending increasing amounts of time on land (Atwood et al. 2016), where they may come into more frequent contact with known hosts of *F. tularensis* (i.e., small mammals and foxes). Similarly, the abundance of four species of migratory geese breeding on the ACP has increased substantially in recent years (Flint et al. 2008; Amundson et al. 2019); geese feed and nest in close proximity to terrestrial mammals (caribou, foxes, and small mammals), thereby creating opportunities for transmission across taxa. However, occurrence of *F. tularensis* in this region is unknown, highlighting the need for more information about potential exposure and risks among wildlife.

We investigated the seroprevalence of *F. tularensis* antibodies in tundra-nesting geese and terrestrial and marine mammals sampled on and near the ACP, an area that has been largely excluded from previous *F. tularensis* surveys. Our primary objective was to identify general patterns of *F. tularensis* exposure in an Arctic wildlife community that is undergoing rapid changes because of warming. To do so, we screened for antibodies of *F. tularensis* in samples from 12 species representing six families across a broad suite of taxa. Although this study was exploratory in nature because of the dearth of information currently available about *F. tularensis* in Arctic Alaska, on the basis of prior knowledge about this pathogen, we expected to find highest seroprevalence among small mammals and their terrestrial predators (Friend 2006).

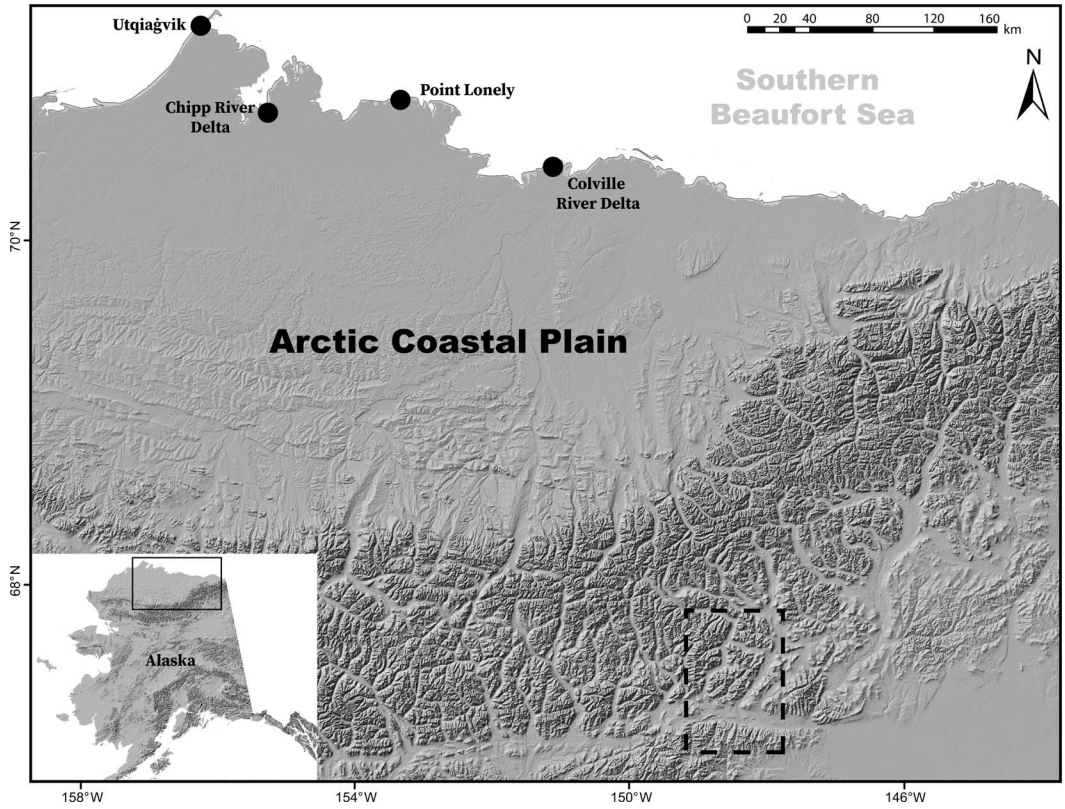


FIGURE 1. Map of the Arctic Coastal Plain of Alaska, USA, showing the specific locations where serum samples from tundra-nesting geese, foxes, caribou (*Rangifer tarandus*), and small mammals were collected. Dashed lines represent the area in the east-central Brooks Range where caribou were captured on their winter range. Polar bear (*Ursus maritimus*) capture locations are not shown.

## MATERIALS AND METHODS

We collected serum from multiple species that inhabit the ACP, including year-round residents and those that occur seasonally. Samples were collected in the spring, summer, and fall seasons during 2014–17, depending on species and site access. Study species consisted of Greater White-fronted Goose (*Anser albifrons*), Lesser Snow Goose (*Anser caerulescens caerulescens*), Black Brant (*Branta bernicla nigricans*), Arctic fox, red fox (*Vulpes vulpes*), caribou, polar bear, and five species of small mammals: Nearctic brown lemming (*Lemmus trimucronatus*), Nearctic collared lemming (*Dicrostonyx groenlandicus*), tundra vole (*Microtus oeconomus*), singing vole (*Microtus miurus*), and Arctic ground squirrel (*Spermophilus parryii*). Because of the remote nature of the ACP and difficult travel logistics, our sampling was conducted opportunistically at established field camps and in conjunction with ongoing research programs. Study locations covered a large geographic area and included regions where species are known to interact with one another (Fig. 1).

We captured nesting geese in June 2014 at the Colville River Delta (70.44°N, 150.68°W) and molting geese during July and August 2014–16 at the Colville River Delta, along the Chipp River (70.69°N, 155.31°W), and near Point Lonely, Alaska (70.91°N, 153.24°W); from each bird we collected 3.0–5.0 mL of whole blood from the jugular vein (US Geological Survey [USGS] Animal Care and Use Committee [ACUC] 2010-04, 2014-12, 2009-13, 2013-05). We collected whole blood samples from the heart post-euthanized from foxes that were shot or trapped near Utqiaġvik, Alaska (71.29° N, 156.79° W) during May and June in 2014–2016 as part of an ongoing US Fish and Wildlife Service predator control program. We shot or trapped small mammals near Point Lonely, Alaska, in 2014 and on the Colville River Delta during June and July in 2015–2016 and collected whole blood by cardiac puncture (USGS ACUC 2012-15). We captured caribou in April 2015 and 2017 on their winter range in the east-central

Brooks Range (67.02°–67.84°N, 147.75°–149.01°W) just before their annual migration to summer ranges on the ACP and collected blood from the jugular or cephalic vein (USGS ACUC 2015-5). We captured polar bears during March and April 2014–16 on the sea ice of the Southern Beaufort Sea between Utqiaġvik and the US–Canada border as described in Atwood et al. (2016) and collected blood from the femoral or jugular veins (USGS ACUC 2010-14). Ten individual bears were recaptured across subsequent seasons.

We tested sera for the presence of *F. tularensis* antibodies with a commercially available febrile antigen slide agglutination test per the manufacturer's recommended protocol (Becton, Dickinson and Company, Sparks, Maryland, USA). Serial dilutions of sera ranging from 1:20 to 1:320 were tested in parallel with *F. tularensis* antisera to serve as positive controls. Titers were scored according to the amount of agglutination present in each dilution during a visual scan 60 s after mixing. All titers that produced visible agglutination scored at ≥1:20 compared with positive controls were interpreted as containing *F. tularensis* antibodies. To ensure consistent seroprevalence results from our agglutination test and to account for possible bias in visual interpretation of titers between observers, we ran blind replicate tests on 10–20% of samples depending on species and serum availability. Only results from the first agglutination test were used for the calculation of seroprevalence among species and taxonomic families. Polar bear samples that represented recaptures were treated similarly, with only the first screening result being counted toward seroprevalence data.

To account for varying sample sizes between species and to evaluate potential differences in life history traits possibly leading to *F. tularensis* exposure, we pooled individuals into taxonomic families (Table 1) for analysis of differences in seroprevalence. Pearson's chi-square tests were used to determine independence between proportions of seropositive individuals across family groups. We used percent agreement and Cohen's kappa statistic to evaluate interrater reliability between replicate agglutination tests, which represents a coefficient of agreement between observations (Cohen 1960). All statistical analyses, including chi-square tests and computation of binomial 95% confidence intervals (CI), were conducted in R programming language (R Core Team 2022). Data produced during or referenced in this study are available in Smith and Van Hemert (2022).

## RESULTS

We collected and screened 732 serum samples from 722 individuals of 12 wildlife species belonging to six taxonomic families (Table 1). We detected antibodies in 10 species, with an estimated seroprevalence of 14.7% (95% CI, 12.3–17.5) across all samples (Table 1). Seroprevalence of *F. tularensis* varied significantly between taxonomic families ($\chi^2$=27.358; df=5; $P<0.001$), with Canidae (foxes; 21.5%; 95% CI, 16.7–27.2; $n$=233; Table 1) and Sciuridae (ground squirrels; 33.3%; 95% CI, 19.8–50.4; $n$=33) highest, followed by Ursidae (polar bears; 13.3%; 95% CI, 7.6–22.2; $n$=83), and Cricetidae (lemmings and voles; 9.1%; 95% CI, 3.1–23.6; $n$=33). The single representative of the Cervidae, caribou, had the lowest seroprevalence of all mammal species sampled (6.5%; 95% CI, 2.2–17.5; $n$=46). Overall seroprevalence for Anatidae (geese) samples was 9.5% (95% CI, 6.7–13.4; $n$=294: 13.6% in Black Brant (95% CI, 8.4–21.3; $n$=110), followed by Lesser Snow Geese (8.3%; 95% CI 4.4–15.1; $n$=108) and Greater White-fronted Geese (5.3%; 95% CI, 2.1–12.8; $n$=76). Of the subset of polar bears captured and sampled twice ($n$=10), all individuals retained the same status except one, which seroconverted (from antibody negative to positive) over an 11.5-mo period.

Percent agreement between replicate sample results was 86.7% overall and varied among species from 71% to 100% (lowest in Cricetidae and Anatidae and highest in Cervidae, Ursidae, and Canidae). This result was supported by our Cohen's kappa statistic ($\kappa$=0.63; 95% CI, 0.47–0.78; $P<0.01$), indicating a moderate or substantial level of agreement between replicate observations (Cohen 1960; McHugh 2012). Antibody titers were highly variable by species and ranged from 1:20 to 1:320, with the majority scored as 1:20 (Table 1).

## DISCUSSION

Our study reports seroprevalence of *F. tularensis* in birds and mammals inhabiting the Arctic coast of Alaska, allowing inference about patterns of exposure across a diverse wildlife community. Although seroprevalence

TABLE 1. Seroprevalence of *Francisella tularensis* antibodies detected by a commercial febrile antigen slide agglutination test in sera collected from wildlife species on the Arctic Coastal Plain of Alaska, USA, 2014–17. Samples were collected from Arctic fox (*Vulpes lagopus*), Arctic ground squirrel (*Spermophilus parryii*), Black Brant (*Branta bernicla nigricans*), caribou (*Rangifer tarandus*), Greater White-fronted Goose (*Anser albifrons*), Lesser Snow Goose (*Anser caerulescens caerulescens*), Nearctic brown lemming (*Lemmus trimucronatus*), Nearctic collared lemming (*Dicrostonyx groenlandicus*), polar bear (*Ursus maritimus*), red fox (*Vulpes vulpes*), singing vole (*Microtus miurus*), and tundra vole (*Microtus oeconomus*).

| Species | *n* | Positive (%) | 95% CI | 1:20 Titer | 1:40 Titer | 1:80 Titer | 1:160 Titer | 1:320 Titer |
|---|---|---|---|---|---|---|---|---|
| Mammals | | | | | | | | |
| Canidae | 233 | 50 (21.5) | 16.7–27.2 | 20 | 17 | 6 | 4 | 3 |
| Arctic fox | 231 | 49 (21.2) | 16.4–27.0 | 20 | 17 | 5 | 4 | 3 |
| Red fox | 2 | 1 (50.0) | 2.6–97.4 | — | — | 1 | — | — |
| Cervidae | 46 | 3 (6.5) | 2.2–17.5 | 1 | 1 | 1 | — | — |
| Caribou | 46 | 3 (6.5) | 2.2–17.5 | 1 | 1 | 1 | — | — |
| Ursidae | 83 | 11 (13.3) | 7.6–22.2 | 6 | 3 | 2 | — | — |
| Polar bear | 83 | 11 (13.3) | 7.6–22.2 | 6 | 3 | 2 | — | — |
| Cricetidae | 33 | 3 (9.1) | 3.1–23.6 | 3 | — | — | — | — |
| Brown lemming | 11 | 2 (18.2) | 5.1–47.7 | 2 | — | — | — | — |
| Collard lemming | 2 | 1 (50.0) | 2.6–97.4 | 1 | — | — | — | — |
| Singing vole | 3 | 0 | — | — | — | — | — | — |
| Tundra vole | 17 | 0 | — | — | — | — | — | — |
| Sciuridae | 33 | 11 (33.3) | 19.8–50.4 | 3 | 4 | 2 | — | 2 |
| Arctic ground squirrel | 33 | 11 (33.3) | 19.8–50.4 | 3 | 4 | 2 | — | 2 |
| Birds | | | | | | | | |
| Anatidae | 294 | 28 (9.5) | 6.7–13.4 | 23 | 5 | — | — | — |
| Greater White-fronted Goose | 76 | 4 (5.3) | 2.1–12.8 | 4 | — | — | — | — |
| Lesser Snow Goose | 108 | 9 (8.3) | 4.4–15.1 | 9 | — | — | — | — |
| Black Brant | 110 | 15 (13.6) | 8.4–21.3 | 10 | 5 | — | — | — |
| Total | 722[a] | 106 (14.7) | 12.3–17.5 | 56 | 30 | 11 | 4 | 5 |

[a] Although 732 sera were collected, 10 polar bear samples were recaptures of the same individual and were excluded from any analysis.

per species varied between 0% and 50% (Table 1), among families, Canidae (foxes) and Sciuridae (arctic ground squirrels) had the highest proportions of seropositive individuals, supporting findings from other studies in Alaska that reported *F. tularensis* antibodies to be common among small mammal species and their predators (Hopla 1969; Zarnke and Ballard 1987; Chomel et al. 1998; Zarnke et al. 2004; Ramey et al. 2019). Surprisingly, the only two species in which *F. tularensis* was not detected were also small mammals (voles; Cricetidae). Detection of antibodies in 9.5% of tundra-nesting geese (Anatidae) is notable because it represents higher seroprevalence than previously reported for other avian taxa and provides the first serologic data for *F. tularensis* in these species. Additionally, the prevalence of 13.3% in polar bears is higher than that reported in a previous study from this region (Atwood et al. 2017) and provides additional evidence of the presence of a terrestrial and freshwater pathogen in an Arctic marine mammal species.

The specific mechanisms by which *F. tularensis* bacteria are transmitted on the ACP are largely unknown. However, observed differences in seroprevalence between both family groups and species within families might be attributed to unique life history traits that influence exposure to *F. tularensis*. Within the small mammals, seroprevalence was higher in Arctic ground squirrels that may live up to 6–10 yr (Wilbur et al. 2022), allowing more time for potential exposure than in voles and lemmings with lifespans of only several months (Poor 2005). Differences

in foraging habits, and hence of exposure to contaminated food or water, may also be a possible driver for this difference (Ellis et al. 2002; Petersen and Schriefer 2005). This scenario seems less likely, however, because members of both Sciuridae and Cricetidae are opportunistic foragers and feed on a similarly broad range of plants, berries, fungi, and small invertebrates (Poor 2005; Flower et al. 2019). Arvicoline species are also characterized by dramatic, multiannual fluctuations in population density, sometimes undergoing 40-fold changes in a 4-yr period (Wilson et al. 1999; Gruyer et al. 2008). Although these cyclic patterns vary by region and species, results of previous research on the ACP supports similar trends (Batzli and Jung 1980). We could not determine the population status of arvicoline species at the time of sample collection, but fluctuations in density might play a role in exposure to *F. tularensis*, including bottom-up trends of disease transmission among predators (Zarnke et al. 2004). Exposure to *F. tularensis* may increase in higher density rodent populations, and predators have been shown to prey heavily on arvicoline species at times of peak population densities (Gallant et al. 2012). These observations are speculative, however, and additional work involving more targeted sampling of individual species and further analysis by location and age and sex categories is warranted. This further work might provide finer resolution on apparent differences between groups of small mammals and may help to determine whether these species act as reservoir hosts in this region.

Mammalian predators have been the focus of many previous studies of tularemia in Alaska and other circumpolar regions because they are likely candidates for exposure through consumption of rodent and lagomorph prey species, which are commonly thought to act as reservoir hosts for *F. tularensis* (Zarnke and Ballard 1987; Zarnke et al. 2004; Hansen and Dresvyannikova 2022). The relatively high seroprevalence (21.5%) among foxes (Canidae) sampled in our study may be partially explained by their consumption of small mammals on the ACP, including Arctic ground squirrels (Flower et al. 2019) and highly cyclical arvicoline (lemming and vole) species (Roth 2002, 2003). A study of wolves captured in Alaska and the Yukon territory between 1984 and 2004 reported seroprevalence of *F. tularensis* antibodies ranging from 0% to >40% (Zarnke et al. 2004). The authors attributed patterns of *F. tularensis* in wolves to the cyclical availability of snowshoe hares (*Lepus americanus*), with the highest seroprevalence detected in wolves 1–2 yr after peak hare abundance (Zarnke et al. 2004). Foxes also prey on goslings and adult geese and consume goose eggs as a staple food source during summer months on the ACP (Roth 2002), leading to another potential pathway of exposure on the basis of our finding of 9.5% seroprevalence of *F. tularensis* antibodies in geese. Additional work is needed to determine the major exposure route of foxes on the ACP to *F. tularensis*. Examining the geographic occurrence of this bacterium in arvicoline rodents on the ACP, combined with information on the cyclical fluctuations of the abundance of these hosts and how this might act as a bottom-up exposure route to higher level predators, is warranted.

Finally, the detection *F. tularensis* antibodies in 13.3% (95% CI, 7.6–22.2) of polar bears is noteworthy because information about exposure of Arctic marine mammals to what is commonly considered a terrestrial and freshwater pathogen is scarce. Atwood et al. (2017) published some of the first data on *F. tularensis* exposure in polar bears, reporting seroprevalence of 4.8% (95% CI, 1.9–10.8; $n$=108) for animals sampled 2007–2013. Increases in land use by polar bears in the Southern Beaufort Sea region has been documented in recent years (Atwood et al. 2016), potentially leading to more contact with terrestrial mammal populations, including scavenging foxes or grizzly bears (*Ursus arctos*), with which polar bears have had limited historical interaction. Several previous studies in Alaska detected *F. tularensis* antibodies in brown bears (Chomel et al. 1998; Ramey et al. 2019), and increases in time spent on land by polar bears may present a potential exposure pathway. Interactions

with nesting geese might also contribute to an increase in transmission of *F. tularensis*; in some regions, polar bears have been observed consuming tundra-nesting geese and their eggs (Iles et al. 2013; Prop et al. 2015). Similar assertions regarding possible increases in *F. tularensis* exposure because of time spent on land were made by Pilfold et al. (2021), who reported a mean seroprevalence of *F. tularensis* of 68.4% in western Hudson Bay polar bears. This elevated seroprevalence compared with bears sampled by Atwood et al. (2017) was attributed to historically greater amounts of time spent on land by western Hudson Bay polar bears compared with populations in the Southern Beaufort Sea, allowing more time for exposure to *F. tularensis* sources, including biting insects and terrestrial waterbodies, both of which are possible means of exposure to *F. tularensis* (Pilfold et al. 2021). The apparently higher seroprevalence in our samples (collected in 2014–16) compared with earlier results from Atwood et al. (2017) might indicate increasing cumulative exposure to *F. tularensis*, because sera screened in our study was collected from the same sampling region. However, given the interannual variability of *F. tularensis* reported in other studies and the challenges of interpreting serologic data, including unknown longevity of antibodies after initial infection, we can only speculate on potential explanations for this apparent difference and are unable draw any broad conclusions from this comparison. Additionally, the 95% CIs of polar bear seroprevalence between our study and those of Atwood et al. (2017) overlap slightly, indicating that sample size or other factors may play a role in the observed difference.

Caribou, the single representative of Cervidae, had relatively low seroprevalence (6.5%) compared with other taxa sampled in our study. Only three individuals had weak or moderate *F. tularensis* titers (1:20–1:80; Table 1). This species is arguably the most important on the ACP in terms of harvest by subsistence or personal use hunters and a potential pathway for human exposure through the consumption of undercooked or raw meat. Antibodies against *F. tularensis* previously have been identified in caribou in Alaska at similarly low prevalence and titers (Hopla 1969). The possibility exists for caribou to become infected by consuming contaminated water or vegetation because they feed in close proximity to nesting geese and small mammals. Caribou are also exposed to high densities of mosquitoes (Culicidae) during their summer movements (Morschel and Klein 1997; Fang 2010). Mosquitoes have been implicated as possible vectors of *F. tularensis* bacteria through blood meals in other parts of the northern hemisphere (Eliasson et al. 2002), but there is not yet evidence that this method of transmission occurs on the ACP. Triebenbach et al. (2010) examined the possibility for *Aedes* and *Anopheles* spp. mosquitoes collected near Fairbanks, Alaska, to act as vectors for *F. tularensis* and determined that transmission to mammalian hosts would be inefficient at best and may be limited by vector-pathogen dynamics. The authors did detect *F. tularensis* DNA in >30% of pooled samples, however, suggesting that these mosquito species may facilitate indirect transmission of this pathogen (Triebenbach et al. 2010).

Avian species in Alaska and other circumpolar regions have been consistently undersampled compared with mammals in previous studies investigating *F. tularensis* seroprevalence. Although often thought of as a mammalian pathogen, *F. tularensis* may cause disease in birds, and prior studies have implicated migratory species in the transportation of the bacteria, arthropod hosts such as ticks (Padeshki et al. 2010), or both. A study conducted in 1964–65 that screened >70 migratory and resident bird species in Alaska for the presence of *F. tularensis* antibodies reported only the "occasional antibody titer" and no isolates (Hopla 1969). Our results add to the sparse body of knowledge on *F. tularensis* in birds in this region and offer some of the first data on *F. tularensis* antibodies in tundra-nesting geese; *F. tularensis* antibodies have not been reported previously for any of the three species sampled as part of this investigation. A study

from 2018 examined fecal samples collected from 47 White-fronted Geese in Bulgaria but was unable to isolate *F. tularensis* from any samples (Najdenski et al. 2018). Although the detection of 9.5% seroprevalence in goose sera obtained from the ACP provides important baseline data, interpretation is difficult because of a dearth of information on *F. tularensis* ecology in these species. Nesting geese in this region spend a significant amount of time near many of the terrestrial mammal species known to harbor *F. tularensis*, so exposure through direct contact or contaminated food or water is plausible. All titers detected in tundra-nesting geese were low (1:20 or 1:40), possibly indicating low-level infections among geese or a relatively long duration since initial pathogen exposure, which might have occurred at stopover points during migration or on wintering grounds. However, documented increases in geese breeding on the ACP (Amundson et al. 2019), combined with additional projected increases (Hupp et al. 2017; Flint and Meixell 2021), make this an important area for future study.

One important caveat for interpreting our *F. tularensis* serologic data is that the slide agglutination test we relied on for this study was designed for human use and has not undergone rigorous validation tests with wildlife. Several previous studies have used this assay to detect *F. tularensis* antibodies with great success, however, supporting the use of this diagnostic method (Chomel et al. 1998; Atwood et al. 2017; Ramey et al. 2019). Like other serologic data, prevalence of *F. tularensis* antibodies provides useful information about general patterns of exposure and limited details on levels of infection (titers) but lacks the ability to provide inference on time since infection or bacterial subtype. This slide agglutination test has also been reported by the manufacturer to be subject to cross-reactions with antibodies to *Brucella* spp., a known pathogen of Arctic mammals and one that has been previously detected in polar bears from the Southern Beaufort Sea region (O'Hara et al. 2010) and foxes in northern Alaska (Neiland 1975; Morton 1989). Additionally, caribou are considered to be a likely reservoir for *Brucella suis* type 4 in Alaska (Zarnke and Ballard 1987). However, a concurrent study of *Brucella* exposure did not detect antibodies in any of the caribou or polar bear sera we tested for the current investigation, and *Brucella* antibodies were identified in relatively few (<4%) Arctic fox samples (Smith and Van Hemert 2022), indicating low probability of cross-reactivity. Thus, we infer our results to be indicative of probable *F. tularensis* exposure, further supported by an overall percent agreement of 86.7% between replicate tests and a moderate to substantial level of agreement according to a kappa statistic ($\kappa$) of 0.63 (Cohen 1960; McHugh 2012).

Our study provides important information about the presence of *F. tularensis* in wildlife inhabiting the ACP, an area undergoing rapid changes because of climate warming. The range of seroprevalence we observed among wildlife species emphasizes the need for renewed surveillance of this disease in Alaska, as has been suggested previously (Hansen et al. 2011; Atwood et al. 2017; Hansen and Dresvyannikova 2022). Although our results indicate exposure to *F. tularensis* among a diverse suite of birds and marine and terrestrial mammals in Arctic Alaska, future work is needed to answer specific questions about the ecology and epidemiology of this bacterium and resultant disease among wildlife. The definitive identification of reservoir species on the ACP and research into the possibility of transmission by arthropod vectors in this region is warranted, as are more systematic sampling of wildlife species; efforts to culture bacteria from animal and invertebrate hosts; and the use of molecular methods, including PCR analysis, that allow for confirmation of serologic results and characterization of *F. tularensis* subtypes.

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