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A circumpolar parasite: Evidence of a cryptic undescribed species of sucking louse, *Linognathus* sp., collected from Arctic foxes, *Vulpes lagopus*, in Nunavut (Canada) and Svalbard (Norway)

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[Correction added on 09 September 2023, after first online publication: The online open copyright line has been updated in this version.]

Abstract

The North has experienced unprecedented rates of warming over the past few decades, impacting the survival and development of insects and the pathogens that they carry. Since 2019, Arctic foxes from Canada (Nunavut) have been observed with fur loss inconsistent with natural shedding of fur. Adult lice were collected from Arctic foxes from Nunavut ($n = 1$) and Svalbard ($n = 2$; Norway) and were identified as sucking lice (suborder Anoplura). Using conventional PCR targeting the mitochondrial cytochrome c oxidase subunit 1 gene (*cox1*), lice from Canada and Svalbard were 100% similar (8 pooled samples from Nunavut and 3 pooled samples from Svalbard), indicating that there is potential gene flow between ectoparasites on Scandinavian and North American Arctic fox populations. The *cox1* sequences of Arctic fox lice and dog sucking lice (*Linognathus setosus*) had significant differences (87% identity), suggesting that foxes may harbour a cryptic species that has not previously been recognised. Conventional PCR targeting the *gltA* gene for *Bartonella* bacteria amplified DNA from an unknown gammaproteobacteria from two pooled louse samples collected from Svalbard foxes. The amplified sequences were 100% identical to each other but were only 78% like *Proteus mirabilis* reported in GenBank (CP053614), suggesting that lice on Arctic foxes may carry unique microorganisms that have yet to be described.

KEYWORDS
Arctic fox, Canada, ectoparasites, fur loss, lice, *Linognathus*, Norway

INTRODUCTION

Arctic regions have warmed nearly four times faster than other regions around the world (Rantanen et al., 2022). As temperatures continue to rise, northern ecosystems are actively changing, including shrinking of tundra habitat as boreal forests extend northward, reduced snow cover, decreased summer sea ice, and more extreme weather events (Arctic Council, 2005; Lu et al., 2021; Vincent, 2020). These environmental changes impact current Arctic fauna and are predicted to increase biodiversity as new species move further North (Wookey, 2007). Arthropods are highly sensitive to these changes and a warming Arctic is expected to increase the diversity of insects and the pathogens they carry (Samuel et al., 2016). For example, the biting rates of hematophagous arthropods, and the transmission of pathogens within these vectors, are significantly affected by temperature and generally increase as the conditions warm (Caminade et al., 2019). Little is known about the diversity and distribution of vector-borne pathogens in Arctic ecosystems, which highlights the need for targeted studies to characterise the current diversity of vectors and their associated pathogens (Parkinson et al., 2014).

The Arctic fox (*Vulpes lagopus*) has a circumpolar distribution and is capable of long-distance dispersal, which has resulted in little genetic variation among populations across a broad geographic range (Dalén et al., 2005). This species is well adapted to high Arctic tundra ecosystems and has a seasonally dimorphic coat. The thick winter coat begins to shed in the spring, with initial fur loss occurring on the legs, face, and sacral region (Buhler et al., 2021). Environmental variability is likely to have a significant effect on Arctic fox populations, including increased competition in the face of range expansion of southern species such as red fox (*Vulpes vulpes*) and selective pressures as Arctic rodent population cycles become more unstable (Fuglei & Ims, 2008; Gilg et al., 2009; Ims et al., 2008). In addition, a warming climate is likely to impact prevalence of disease in fox populations. For example, rising temperatures may increase survival of ectoparasites and transmission of zoonotic bacteria maintained by rodent reservoirs (Buhler et al., 2022; Parkinson et al., 2014; Parkinson & Evengard, 2009).

During the spring of 2019, fur loss was documented on Arctic foxes from the mainland of Nunavut (Canada) that deviated from normal moulting, including loss of guard hairs over the neck and shoulders (Figure 1; Buhler et al., 2021). Fur loss on these regions along with the presence of louse eggs on a fox with fur loss suggests that this may be the result of louse infestations (Buhler et al., 2021). Though lice were found on Arctic foxes in Nunavut during the 1990's (Buhler et al., 2021), observations of abnormal fur loss and lice infestations have increased significantly in Canada over the past few years. In the spring of 2021, Arctic foxes from Victoria Island (Cambridge Bay, Nunavut, Canada) were documented with the same fur loss on trail cameras and lice were collected from an Arctic fox on King William Island (Gjoa Haven, Nunavut, Canada) (Figure 1). Across the Arctic Ocean, harvested Arctic foxes from Svalbard (Norway) were also observed with lice and fur loss for the first time in 2019 (Fuglei et al., unpublished data). Arctic foxes are classified as "least concern" on the

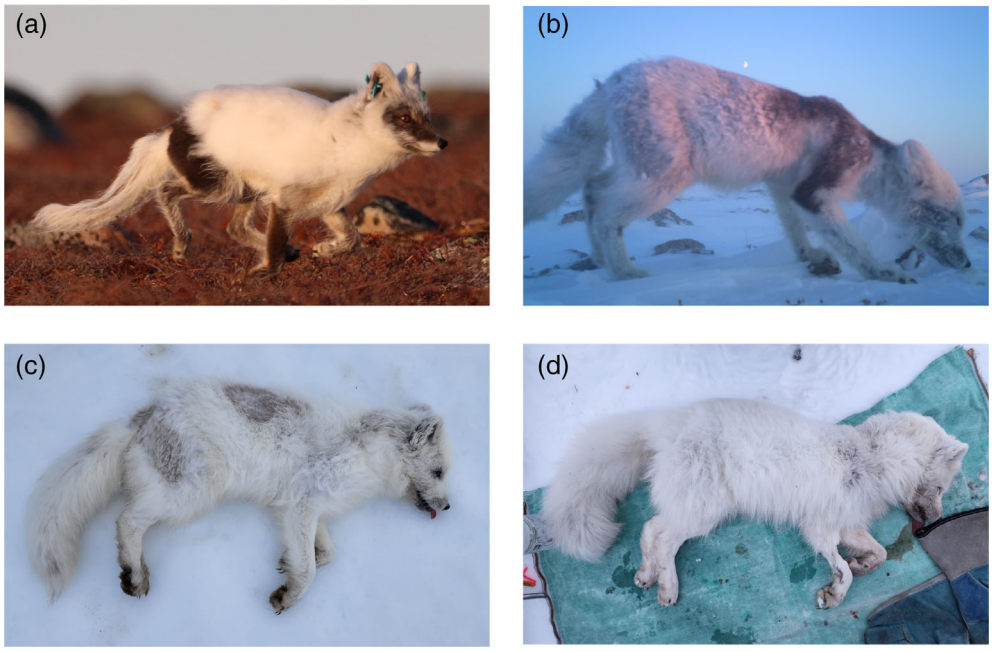

FIGURE 1 Comparison of normal moulting and varying degrees of abnormal fur loss on Arctic foxes in Nunavut, Canada. (a) Normal fox transitioning from winter to summer coat in June 2022 at Karrak Lake. (b) Fox with an extreme case of abnormal fur loss, including loss of almost all the winter fur across the shoulders and neck and significant loss of guard hairs on the face, back and rump, near Cambridge Bay (Iqaluktuuttiaq), Nunavut in May 2021. (c) Sedated fox with a moderate case of abnormal fur loss, including patches of fur loss on the back and rump, near Karrak Lake, Nunavut in May 2022. (d) Sedated fox with a mild case of abnormal fur loss, including thinning fur and loss of guard hairs on the shoulders, near Karrak Lake, Nunavut in May 2022.

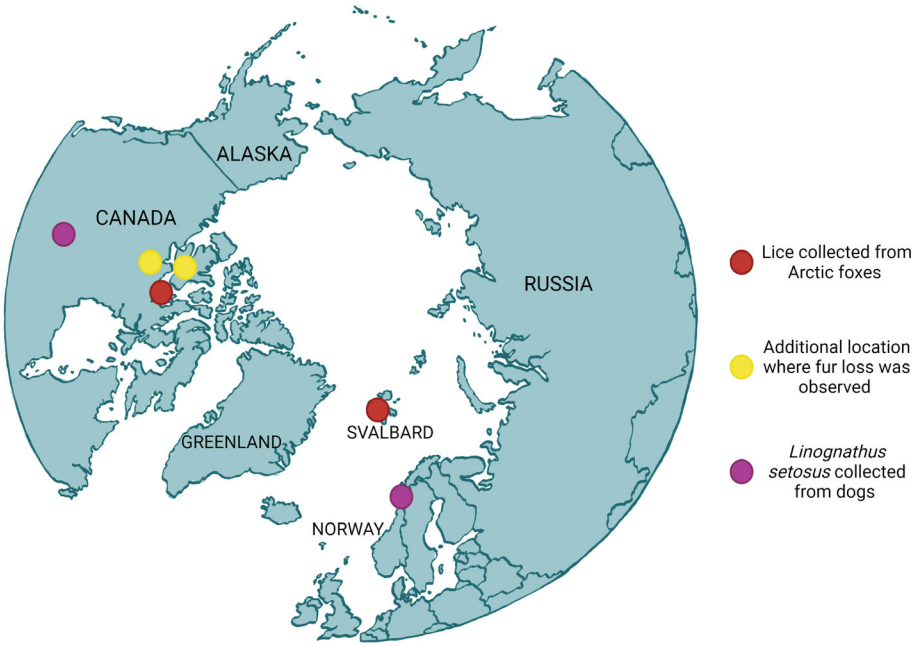

FIGURE 2 Locations where abnormal fur loss was documented on Arctic foxes in Nunavut and locations where lice were collected from Arctic foxes and dogs.

International Union for Conservation of Nature Red List and are listed as hosts for the canine sucking louse *Linognathus setosus* (von Olfers, 1816) (Durden & Musser, 1994). However, the parasite–host relationship is not well studied, and no attempt has been made for a morphological and molecular comparison between *L. setosus* specimens from Arctic foxes and those commonly found on domestic dogs or other canids. In fact, *L. setosus* has undergone very little recent taxonomic scrutiny and is still awaiting molecular characterisation. As Arctic foxes are important fur bearers in northern regions, it is imperative that these cases of fur loss are closely monitored. Morphological and molecular characterisation of lice from Arctic foxes may provide insight regarding host specificity, evolutionary history, and disease progression following infestation. In this study, we aim to investigate the genetic similarities between lice collected from Arctic foxes in Nunavut, Canada and Svalbard, Norway to determine if there is potential gene flow between fox lice from both locations and to identify genetic differences between Arctic fox lice and canine sucking lice, *L. setosus*. In addition, fox lice are screened for *Bartonella* DNA, a group of bacteria that are found in rodent reservoirs and are typically transmitted via flea and lice vectors (Buffet et al., 2013).

METHODS

Study populations

This study was carried out on lice collected from Arctic foxes in Nunavut, Canada and Svalbard, Norway. These populations occupy distinct ecosystems but are connected by sea ice (Fuglei & Tarroux, 2019). Coastal foxes, such as the Svalbard fox population, often rely on food sources from the marine food web and experience less variable litter sizes, while inland foxes, such as those on the mainland of Nunavut, exhibit population cycles that are largely associated with rodent population irruptions (Fuglei & Ims, 2008). A summary of the locations included in this study have been provided in Figure 2.

Lice collection

Arctic foxes from Nunavut were collected legally by trappers in Gjoa Haven during 2020–2021 These carcasses are typically submitted for disease testing after they have been skinned, so estimating prevalence is not possible in this study. One fox was submitted with the fur still present, as it was potentially rabid and had been shot near the community. Lice were collected opportunistically from this fox using a flea comb and stored in a 1.5 mL Eppendorf tube (Thermo Fisher Scientific, Waltham, USA) at −20°C until tested. Similarly, Arctic foxes from Svalbard were collected legally by trappers from trapping areas in Nordenskiöld Land, Spitsbergen during 2019–2020. Adult lice were collected opportunistically from these foxes, placed in microcentrifuge tubes containing 70% ethanol and frozen at −20°C until tested. All the foxes from which lice were collected exhibited varying degrees of fur loss (as described in Figure 1). The samples were sent to the Zoonotic Parasite Research Unit at the Western College of Veterinary Medicine (University of Saskatchewan) for molecular characterisation.

Morphological identification of lice

Lice were prepared on microscope slides using techniques described by Richards (1964) and identified as per Kim et al. (1986). As Arctic fox lice were in poor condition due to multiple freeze thaw cycles on

carcasses, a basic morphological cues along with host association was used for identification. Voucher specimens were deposited in the J.B. Wallis/R.E. Roughley Museum of Entomology, Department of Entomology, University of Manitoba.

Molecular characterisation of lice

Lice from two Arctic foxes from Svalbard and one Arctic fox from Nunavut were pooled for each individual and divided into microcentrifuge tubes containing three adult lice per tube ($n = 3$ pooled samples from Svalbard foxes and 8 pooled samples from the Nunavut fox). DNA was extracted from these pooled louse samples using the DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany). Molecular characterisation was completed using a conventional PCR targeting a 710 bp fragment of the mitochondrial cytochrome c oxidase subunit 1 gene (*cox1*) previously described by Folmer et al. (1994). Primers were LCO1490 (5′-GGTCAACAAATCATAAAGATATTGG-3′) and HC02198 (5′-TAAACTTCAGGGTGACCAAAAAATCA-3′). A 50 μL reaction mixture was used containing 5 μL 10X PCR buffer (200 mM Tris–HCl pH 8.4, 500 mM KCl; Invitrogen), 5 μL 50 mM MgCl2, 5 μL of dNTPs (Invitrogen), 2.5 μL of each primer, 0.1 μL of Taq DNA Polymerase (Invitrogen) and 5 μL of genomic DNA. PCRs were conducted using the following conditions: 95°C for 5 min followed by 35 cycles of 95° for 1 min, 40°C for 1 min, 72°C for 90 s and a final extension of 72°C for 7 min. Amplicons were run on a 1% agarose gel and products were purified using a PCR Purification Kit (Qiagen) and sent for Sanger sequencing (National Research Council, Saskatoon, Canada).

In addition, DNA was isolated from a pool of two adult *L. setosus* that originated from a dog brought to a veterinary clinic in Saskatoon (Canada) and a pool of three adult *L. setosus* collected from a dog brought to Nord University, Bodø (Norway). DNA extraction and PCR targeting the *cox1* gene were completed using the same methods outlined for fox lice. The sequences for Arctic fox lice from Svalbard and Nunavut and sequences from *L. setosus* specimens collected from dogs were compared using the align function in GenBanks Nucleotide BLAST (National Center for Biotechnology Information; Bethesda, United States).

Phylogeny

Sequences were assembled and viewed using CLC Main Workbench. Sequences were aligned to reference sequences available from GenBank and BOLD (Supplemental Table S2) using the online version of Mafft (http://mafft.cbrc.jp/alignment/server/) under default parameters. The aligned matrix was viewed, manually edited, and truncated in MEGA7 (Kumar et al., 2016). Mesquite 3.7 (Maddison & Maddison, 2021) was used to determine codon positions and to partition the matrix accordingly.

The partitioned dataset was analysed using the GTRCAT approximation in RAxML 8 (Stamatakis, 2014) for a maximum likelihood approach, calculating bootstrap support by invoking the autoMRE bootstopping criterion. For Bayesian Inference, MrBayes 3 (Ronquist & Huelsenbeck, 2003) was used for analysing the partitioned dataset employing a GTR + G model. Four chains searched for 10,000,000 iterations, saving every 1000th tree. The first 15% of the saved trees were discarded as burn-in, and the remaining trees were used to calculate the posterior probabilities. For a distance approach, a data-display network was constructed in SplitsTree4 (Huson & Bryant, 2006) using uncorrected p-distances derived from all characters using an unpartitioned dataset. Bootstrap support was calculated from 1000 replicates. A *Proechinophthirus fluctus* (Accession number MW803114) sequence was used as an outgroup.

PCR for *Bartonella* bacteria

All pooled lice samples were tested. Positive controls included in the PCR were gBlocks™ gene fragments (Integrated DNA Technologies; Coralville, United States) created from the complete genome of *Bartonella quintana* (Accession number BX897700.1). The primers used to amplify a 767 bp region of the *gltA* (citrate synthase) gene were CS443f (5′ GCT ATG TCT GCA TTC TAT CA 3′) and CS1210r (5′ GAT CYT CAA TCA TTT CTTT CCA 3′) (Billeter et al., 2011). A 25 μL reaction mixture was used containing 2.5 μL 10X PCR buffer (200 mM Tris–HCl, pH 8.4, 500 mM KCl; Invitrogen), 1.25 μL 50 mM MgCl2, 1 μL of 2 mM dNTPs (Invitrogen), 1 μL of each primer (10 μM), 0.1 μL of Taq DNA Polymerase (Invitrogen) and 2.5 μL of genomic DNA. The gltA PCR was conducted using the following conditions: 94°C for 2 mins followed by 45 cycles of 94° for 30 s, 48°C for 1 min, 72°C for 1 min and a final extension of 72°C for 7 mins. Amplicons were run on a 1% agarose gel and products were purified using a PCR Purification Kit (Qiagen) and sent for Sanger sequencing (National Research Council, Saskatoon, Canada).

RESULTS

We report fur loss around Cambridge Bay (Iqaluktuuttiaq), Nunavut during the spring of 2021 (Figure 1). Abnormal fur loss was also documented in 18% ($n = 3/17$; CI_{95} 6–41) of live captured foxes at Karrak Lake (Nunavut, Canada) during the spring of 2022. Lice were collected opportunistically from foxes in both Nunavut and Svalbard, and all were most similar to *L. setosus*, with piercing mouthparts indicative of sucking lice (Figure 3). In short, the head is comparatively short and compact, lacking eyes, with sclerotized region surrounds mouthparts. The antennae contain five-segmented and unfused antennules; thoracic ventrum lack a distinct sternal plate, large intercoxal space; forelegs are comparatively small to subequal mid- and hind leg pair; setose abdomen lack of distinct paratergites, large spherical spiracles; in the male parameres well developed enclosing the aedeagus. (Durden & Musser, 1994; Ferris, 1951). (Figure 3). *Linognathus setosus* and arctic fox lice all measured between 1 and 2 mm in length.

DNA for the *cox1* gene was successfully amplified from three pooled louse samples from Svalbard and eight pooled louse samples from Nunavut. Sequences from all Arctic fox lice were 100% similar. There are no sequence data available for the barcoding segment of the *cox1* gene from *L. setosus* in GenBank or BOLD (https://www.

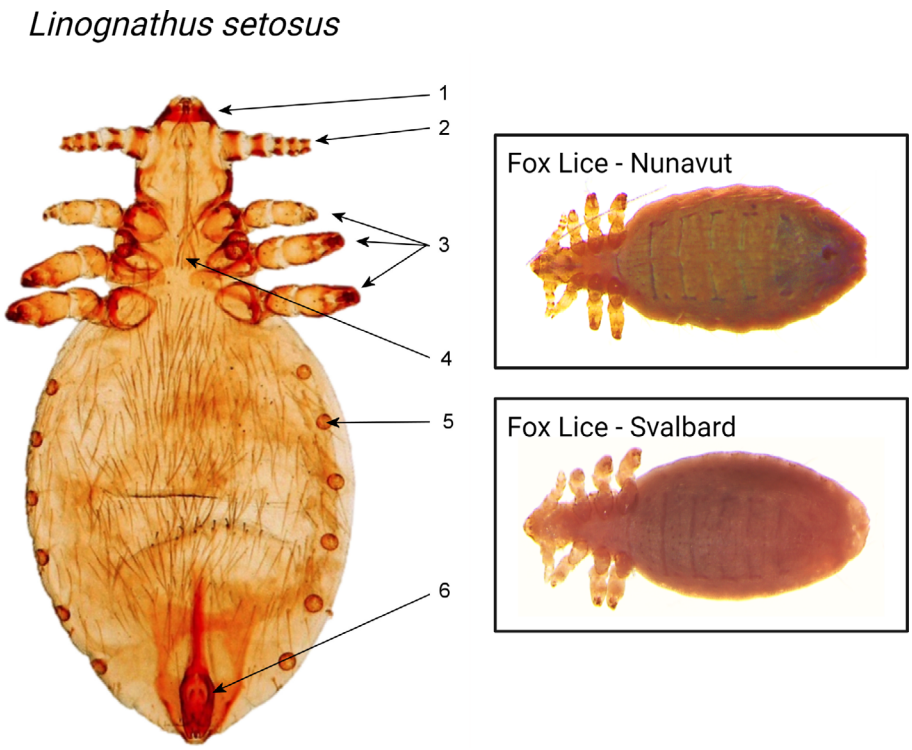

FIGURE 3 *Linognathus setosus* from a dog in Canada. Arrows indicate morphologically relevant characters including, (1) sclerotization of region surrounding mouthparts, (2) antennae, five unfused segments, (3) smaller foreleg compared to subequal mid-hind leg pair, (4) large intercoxal space lacking sternal plate, (5) conspicuous spherical abdominal spiracles, and (6) male genitalia with prominent parameres enclosing aedeagus. Arctic fox lice that have not been cleared have been provided for comparison (images not to scale with *L. setosus*).

TABLE 1 Molecular comparison of Arctic fox lice and *Linognathus setosus* from Canada and Norway.

Sample ID	Country	% Identity *L. setosus* from Canada (LS1)	Base pair length	% Identity *L. setosus* from Norway (LS2)	Base pair length
Svalbard – 1	Norway	86.94	537	87.69	642
Svalbard – 2	Norway	86.83	546	87.57	642
Svalbard – 3	Norway	86.63	531	87.38	642
Nunavut – 1	Canada	87.15	540	87.90	642
Nunavut – 2	Canada	87.16	622	87.68	642
Nunavut – 3	Canada	87.20	610	87.60	642
Nunavut – 4	Canada	87.12	650	87.38	642
Nunavut – 5	Canada	87.35	599	87.65	642
Nunavut – 6	Canada	87.29	600	87.90	642
Nunavut – 7	Canada	86.96	599	87.31	642
Nunavut – 8	Canada	87.29	654	87.54	642

Note: Sequences were compared using the align function in GenBanks Nucleotide BLAST.

boldsystems.org/). Thus, we included *L. setosus* collected dogs in Saskatchewan, Canada and Bodø, Norway as positive controls (Figure 2). The sequences for *L. setosus*, along with sequences from Nunavut and Svalbard fox lice, have been submitted to Genbank via BOLD, each grouping designated a unique barcoding index number (BIN): *L. setosus* — AEX0924; arctic fox lice — AEX3614. Genetic similarity between the 11 pooled samples of fox lice and *L. setosus* from dogs was relatively low (87% identity; 531–654 bp; Table 1). *Linognathus setosus* from dogs in Bodø (Norway) and Saskatoon (Canada) were 99% similar in their sequences (642 bp).

The final matrix used for phylogenetic and network reconstruction had a length of 685 characters and comprised 29 ingroup sequences (Figure 4). Across all methods, the intraspecific clusters of *Linognathus* had high support, with all sequences derived from fox lice

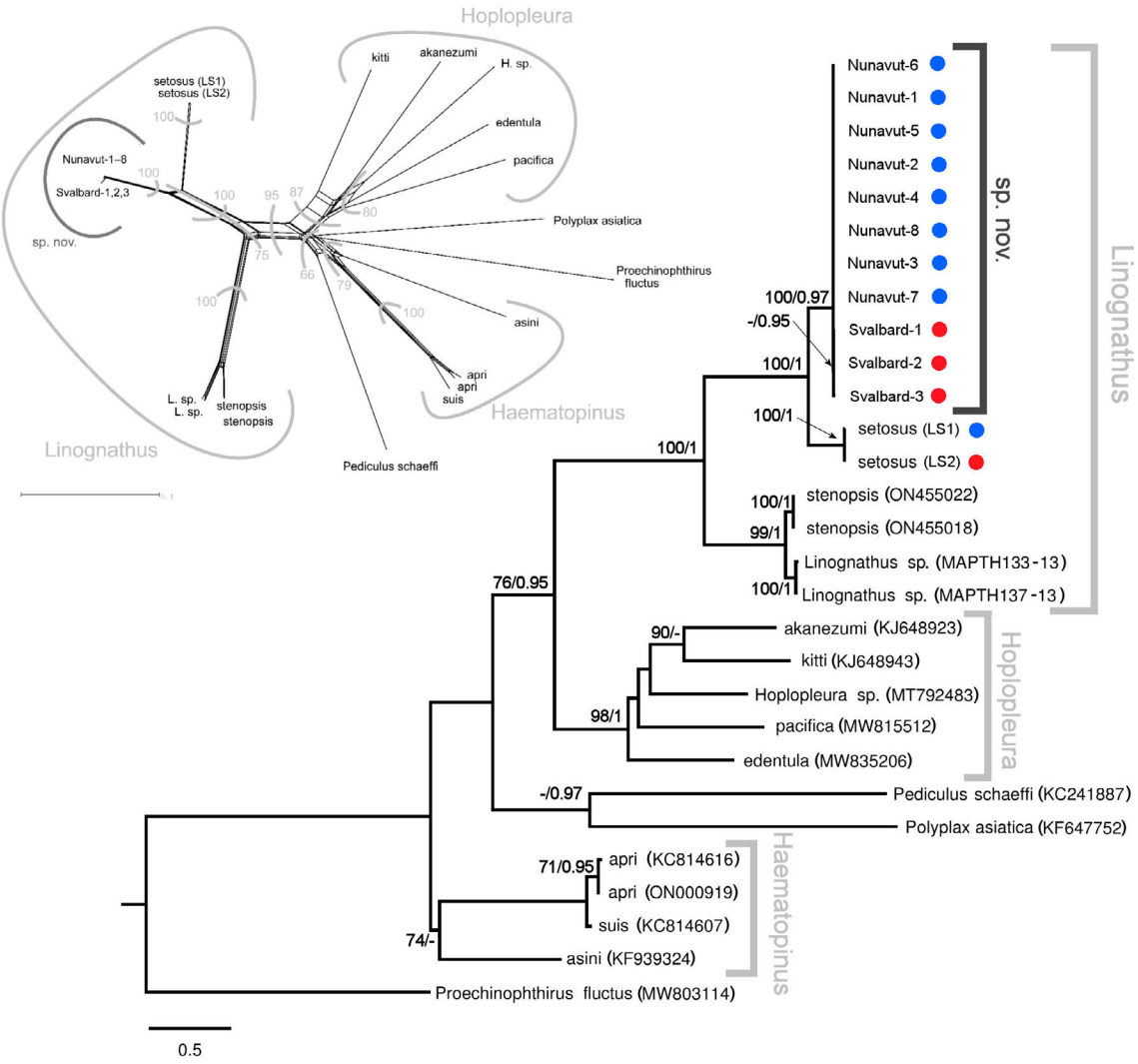

FIGURE 4 A phylogram from a maximum likelihood analysis on a codon partitioned cox1 dataset from RAxML8 using the GTRCAT approximation. Both bootstrap (>70) and posterior probabilities (>0.95) from a Bayesian inference are included as branch support (bootstrap/post. prob.). Specimens from Canada and Norway are indicated by a blue and red dot respectively. Inset is a data-display network generated from the same dataset, bootstraps (>60) are given in grey as support.

forming a clade sister to the sequences generated from dog lice, irrespective of origin (Figure 4). Even though the sequences from Norway formed an intraspecific monophyly within the *Linognathus* sp. nov. clade, the cluster had only posterior probability support from the Bayesian inference analysis.

In addition, two of the 11 pooled samples of fox lice (originating from Svalbard, Norway) amplified DNA with the *gltA* PCR (18%; CI_{95} 5–48). Both sequences for the *gltA* gene were 100% identical (GenBank: OQ472632). However, there were no sequence matches in GenBank and only 78% identity found with *Proteus mirabilis* (CP053614).

DISCUSSION

In this study, we document further cases of fur loss and louse infestations on Arctic foxes and identify a shared cryptic species of sucking lice on foxes from both Nunavut and Svalbard. Sucking lice are obligate ectoparasites that parasitize 12 of the 29 recognised mammalian orders (Hopkins, 1949; Kim, 1985; Light et al., 2010). The diversification of lice coincides with the diversification of all modern mammal orders (between 77 and 75 million years ago) and likely resulted from host-switching and extinction events (Light et al., 2010). They are transmitted via close contact with infected hosts, so the origin of the host-switching event for Arctic fox lice likely resulted during interactions with other canids. Though sucking lice had been partially identified via morphology on Arctic foxes from the mainland of Nunavut in 1997, no molecular or morphological comparison to *L. setosus* had been done to characterise these lice (Buhler et al., 2021).

A comparison of *cox1* sequences from *L. setosus* and fox lice revealed low identity (87%), congruent with the results of network, maximum likelihood, and Bayesian inference analyses that returned two well-supported, distinct clades, irrespective of the origin of the

voucher specimen. The unique BIN designation from BOLD is also congruent with the analyses presented here. This would suggest that there is limited gene-flow between lice on dogs and those on Arctic foxes. The *cox1* mitochondrial fragment is the most popular marker for molecular characterisation, as it has a wide range of data sets available and can provide information about population history over short time frames due to its elevated mutation rate (Galtier et al., 2009). Although *Linognathus setosus* and Arctic fox lice appear to be morphologically similar, sequence data from the barcoding region of *cox1* suggest that Arctic fox lice are likely to be an undescribed species. This suggests that the diversity of sucking lice found on the order Carnivora may be broader than initially thought. Future studies should aim to characterise the lice on Artic foxes and compare the morphology to that of *L. setosus* to assess its taxonomic status, as only small numbers of specimens were available for examination during this study.

Little intraspecific variation between Arctic fox lice collected from Nunavut and Svalbard was observed. This is also the case for *L. setosus* collected from Canada and Norway, which indicates potential for gene flow between Arctic fox lice populations from Canada and Svalbard or dog lice populations from Canada and Norway. Due to the direct transmission strategy of lice, this finding is not only supportive that Arctic foxes and dogs harbour different species of lice, but it is also consistent with previous observations of minimal genetic variation between Arctic fox populations across a broad geographic range (Dalén et al., 2005). In fact, a recent study (Fuglei & Tarroux, 2019) reported the first satellite tracking of natal dispersal of a young female Arctic fox from Svalbard to Canada, thus documenting one of the longest dispersal events ever recorded between continents (4415 km travelled). Gene flow between Arctic fox populations is largely dependent on polar sea ice (except for those in Iceland and in the Bering Strait), as sea ice minimises geographic barriers (Dalén et al., 2005). The extent of Arctic Ocean ice coverage has steadily declined since the 1970's and fox populations that are currently connected may become more isolated in the future, providing opportunities for genetic drift (Dahlke et al., 2020; Onarheim et al., 2018). Thus, warming temperatures are likely to increase the genetic variation between populations and their associated ectoparasites.

The canine sucking louse, *L. setosus*, feeds on blood and tissue fluid and causes pruritus (heavy itching) and excoriations when present on hosts. During severe infestations, dogs often damage the skin, which leads to alopecia and secondary bacterial infections (Angarano & Parish, 1994). Anaemia and more severe problems are generally seen in younger animals or those that are immunocompromised and in poor body condition (Angarano & Parish, 1994; Kohler-Aanesen et al., 2017). The abnormal fur loss on foxes from Nunavut was most often documented on younger animals and on the neck and shoulders, consistent with what is expected during *L. setosus* infestations (Figure 1; Buhler et al., 2021). Similar manifestations of disease commonly seen with dogs may be observed on Arctic foxes that are infested with sucking lice. The predilection sites for *L. setosus* are the head, neck and back of the dog, which is consistent with the areas of fur loss observed on Arctic foxes (Gunnarsson et al., 2005). Severity of fur loss on Arctic foxes varied and may reflect differences in the severity of louse infestations and/or individual biological factors, such as age and immunocompetence (Figure 1).

In addition, we also detected an unknown species of bacteria (likely a gammaproteobacteria) in two pooled lice samples from Svalbard during a PCR that was meant to amplify *Bartonella* DNA. The *gltA* gene is the most frequently used marker to differentiate between *Bartonella* and has the largest GenBank database (Kosoy et al., 2018). Despite this, a BLAST search resulted in no match, with the closest sequence being *Proteus mirabilis* (78% identity; CP053614). The unidentified bacteria are likely not symbiotic bacteria commonly found within the microbiome of fox lice, as only a few specimens from Svalbard amplified DNA. It is unclear if the bacteria are pathogenic and if transmission occurs between foxes and their associated lice. Disease progression observed on Arctic foxes following louse infestations (such as alopecia and excoriations) certainly provide additional opportunities for the transmission of vector-borne pathogens carried in the hindgut of insects, especially through the inoculation of infected faeces. Lice are largely host-specific when compared to other generalist ectoparasites such as fleas, which may suggest that there may be unique pathogens that cycle between foxes and their associated lice (Kim, 1985; Light et al., 2010). Thus, further studies are needed to characterise the microbiome of these lice and to identify potential vector-borne pathogens that may impact Arctic fox health.

In summary, abnormal patterns of fur loss continue to be observed on Arctic foxes. The fur loss is consistent with known predilection sites for canine sucking lice, occurring on the dorsum of the neck and back (Gunnarsson et al., 2005). Sucking lice collected from Arctic foxes in Nunavut and Svalbard have genetically identical *cox1* sequences, supporting large scale migrations and potential gene flow between populations and their associated ectoparasites (Dalén et al., 2005; Fuglei & Tarroux, 2019). These fox lice vary significantly in their *cox 1* sequences when compared to *L. setosus*, which suggests that a past host-switching event may have led to the emergence of a cryptic species. As sea ice continues to recede in northern regions, more opportunities for divergence should arise as Arctic fox populations become more isolated (Dahlke et al., 2020; Onarheim et al., 2018). Louse infestations and subsequent bacterial infections will likely impact survival for young foxes and the quality of fur available for trappers. Thus, it is important to continue monitoring Arctic fox populations for signs of fur loss and louse infestation. Future studies may aim to identify driving factors associated with outbreaks of lice, such as fox population cycles or den occupancy rate at breeding dens, as increased transmission may follow population peaks, or ectoparasite survival as temperatures continue to warm.

AUTHOR CONTRIBUTIONS

Kayla J. Buhler: Conceptualization; data curation; formal analysis; investigation; methodology; validation; visualization; writing – original draft; writing – review and editing. **Louwtjie P. Snyman:** Formal analysis; visualization; writing – review and editing. **Eva Fuglei:** Funding acquisition; investigation; writing – review and editing. **Rebecca Davidson:** Funding acquisition; investigation; writing – review and editing. **Sokratis Ptochos:** Investigation; writing – review and editing. **Terry Galloway:** Formal

analysis; investigation; methodology; writing – review and editing. **Emily Jenkins:** Conceptualization; funding acquisition; supervision; writing – review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no competing interests.

DATA AVAILABILITY STATEMENT

The sequence for *L. setosus*, along with sequences from Nunavut and Svalbard fox lice, have been made available in GenBank and BOLD (AEX0924 and AEX3614). Sequence for the *gltA* gene obtained from Svalbard fox lice is available in GenBank (OQ472632).

ETHICS STATEMENT

Research was approved by the Government of Nunavut (Wildlife Research Permit 2019–10 and 2021–19) and the University of Saskatchewan Animal Research Ethics Board (CofA 20,090,159 and 19,990,029) and adhered to the CCAC guidelines for humane animal use.

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REFERENCES

Angarano, D.W. & Parish, L.C. (1994) Comparative dermatology: parasitic disorders. *Clinics in Dermatology*, 12, 543–550.

Arctic Council. (2005) *Arctic climate impact assessment scientific report*. Cambridge: Cambridge University Press, pp. 863–960.

Billeter, S.A., Gundi, V.A., Rood, M.P. & Kosoy, M.Y. (2011) Molecular detection and identification of Bartonella species in Xenopsylla cheopis fleas (Siphonaptera: Pulicidae) collected from Rattus norvegicus rats in Los Angeles, California. *Applied and Environmental Microbiology*, 77, 7850–7852.

Buffet, J.P., Kosoy, M. & Vayssier-Taussat, M. (2013) Natural history of *Bartonella*-infecting rodents in light of new knowledge on genomics, diversity and evolution. *Future Microbiology*, 8, 1117–1128.

Buhler, K., Bouchard, É., Elmore, S., Samelius, G., Jackson, J., Tomaselli, M. et al. (2022) Tularemia above the Treeline: climate and rodent abundance influences exposure of a sentinel species, the Arctic fox (Vulpes lagopus), to Francisella tularensis. *Pathogens*, 12, 28.

Buhler, K.J., Samelius, G., Alisauskas, R. & Jenkins, E. (2021) Fur loss syndrome and lice infestations observed on Arctic foxes in Central Nunavut, Canada. *Arctic Science*, 7, 872–878.

Caminade, C., McIntyre, K.M. & Jones, A.E. (2019) Impact of recent and future climate change on vector-borne diseases. *Annals of the New York Academy of Sciences*, 1436, 157–173.

Dahlke, S., Hughes, N., Wagner, P., Gerland, S., Wawrzyniak, T., Ivanov, B. et al. (2020) The observed recent surface air temperature development across Svalbard and concurring footprints in local sea ice cover. *International Journal of Climatology*, 40, 5246–5265.

Dalén, L., Fuglei, E., Hersteinsson, P., Kapel, C., Roth, J., Samelius, G. et al. (2005) Population history and genetic structure of a circumpolar species: the arctic fox. *Biological Journal of the Linnean Society*, 84, 79–89.

Durden, L.A. & Musser, G.G. (1994) *The sucking lice (Insecta; Anoplura) of the world: a taxonomic checklist with records of mammalian hosts and geographical distributions*. New York: American Museum of Natural History.

Ferris, G.F. (1951) The sucking lice. *Pacific Coast Entomological Society Memoir*, 1, 3–50.

Folmer, O., Black, M., Hoeh, W., Lutz, R. & Vrijenhoek, R. (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, 3, 294–299.

Fuglei, E. & Ims, R.A. (2008) Global warming and effects on the Arctic fox. *Science Progress*, 91, 175–191.

Fuglei, E. & Tarroux, A. (2019) Arctic fox dispersal from Svalbard to Canada: one female's long run across sea ice. *Polar Research*, 38, 1–7.

Galtier, N., Nabholz, B., Glémin, S. & Hurst, G.D. (2009) Mitochondrial DNA as a marker of molecular diversity: a reappraisal. *Molecular Ecology*, 18, 4541–4550.

Gilg, O., Sittler, B. & Hanski, I. (2009) Climate change and cyclic predator-prey population dynamics in the high Arctic. *Global Change Biology*, 15, 2634–2652.

Gunnarsson, L., Christensson, D. & Palmer, E. (2005) Clinical efficacy of selamectin in the treatment of naturally acquired infection of sucking lice (*Linognathus setosus*) in dogs. *Journal of the American Animal Hospital Association*, 41, 388–394.

Hopkins, G.H.E. (1949) The host-associations of the lice of mammals. *Proceedings of the Zoological Society of London*, 119, 387–581.

Huson, D.H. & Bryant, D. (2006) Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution*, 23, 254–267.

Ims, R.A., Henden, J.A. & Killengreen, S.T. (2008) Collapsing population cycles. *Trends in Ecology & Evolution*, 23, 79–86.

Kim, K.C. (1985) Evolution and host associations of Anoplura. In: Kim, K.C. (Ed.) *Coevolution of parasitic arthropods and mammals*. New York: John Wiley and Sons, pp. 197–231.

Kim, K.C., Pratt, H.D. & Stojanovich, C.J. (1986) *The sucking lice of North America*. An Illustrated Manual for Identification: State University Press, Pennsylvania.

Kohler-Aanesen, H., Saari, S., Armstrong, R., Péré, K., Taenzler, J., Zschiesche, E. et al. (2017) Efficacy of fluralaner (Bravecto™

chewable tablets) for the treatment of naturally acquired *Linognathus setosus* infestations on dogs. *Parasites & Vectors*, 10, 1–7.

Kosoy, M., McKee, C., Albayrak, L. & Fofanov, Y. (2018) Genotyping of *Bartonella* bacteria and their animal hosts: current status and perspectives. *Parasitology*, 145, 543–562.

Kumar, S., Stecher, G. & Tamura, K. (2016) MEGA7: molecular evolutionary genetics analysis version 7.0. *Molecular Biology and Evolution*, 33, 1870–1874.

Light, J.E., Smith, V.S., Allen, J.M., Durden, L.A. & Reed, D.L. (2010) Evolutionary history of mammalian sucking lice (Phthiraptera: Anoplura). *BMC Evolutionary Biology*, 10, 1–15.

Lu, X., Liang, E., Wang, Y., Babst, F. & Camarero, J.J. (2021) Mountain treelines climb slowly despite rapid climate warming. *Global Ecology and Biogeography*, 30, 305–315.

Maddison, W.P. & Maddison, D.R. (2021) Mesquite: a modular system for evolutionary analysis. Version 3. 70 http://www.mesquiteproject.org

Onarheim, I.H., Eldevik, T., Smedsrud, L.H. & Stroeve, J.C. (2018) Seasonal and regional manifestation of Arctic Sea ice loss. *Journal of Climate*, 31, 4917–4932.

Parkinson, A.J. & Evengard, B. (2009) Climate change, its impact on human health in the Arctic and the public health response to threats of emerging infectious diseases. *Global Health Action*, 2, 2075.

Parkinson, A.J., Evengard, B., Semenza, J.C., Ogden, N., Børresen, M.L., Berner, J. et al. (2014) Climate change and infectious diseases in the Arctic: establishment of a circumpolar working group. *International Journal of Circumpolar Health*, 73, 1.

Rantanen, M., Karpechko, A.Y., Lipponen, A., Nordling, K., Hyvärinen, O., Ruosteenoja, K. et al. (2022) The Arctic has warmed nearly four times faster than the globe since 1979. *Communications Earth & Environment*, 3, 168.

Richards, W.R. (1964) A short method for making balsam mounts of aphids and scale insects. *The Canadian Entomologist*, 96, 963–966.

Ronquist, F. & Huelsenbeck, J.P. (2003) MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19, 1572–1574.

Samuel, G.H., Adelman, Z.N. & Myles, K.M. (2016) Temperature-dependent effects on the replication and transmission of arthropod-borne viruses in their insect hosts. *Current Opinion in Insect Science*, 16, 108–113.

Stamatakis, A. (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, 30, 1312–1313.

Vincent, W.F. (2020) Arctic climate change: local impacts, global consequences, and policy implications. In: Coates, K. & Holroyd, C. (Eds.) *The Palgrave handbook of Arctic policy and politics*. Cham: Palgrave Macmillan, pp. 507–526.

Wookey, P.A. (2007) Climate change and biodiversity in the Arctic—Nordic perspectives. *Polar Research*, 26, 96–103.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Table S2. Sequences included in the phylogenetic analysis of sucking lice.

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