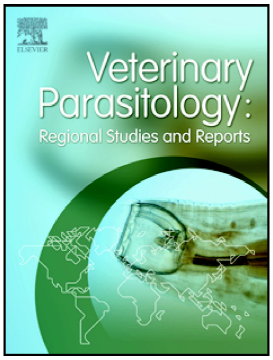

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Revealing the Northern Distribution of *Trichinella chanchalensis*: New Geographic Records from Nunavut and Ecological Perspectives

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Abstract

Trichinella is a genus of foodborne nematode parasites that comprises 13 taxa. In northern Canada three taxa, *T. nativa*, T6, and the recently discovered *T. chanchalensis*, are commonly found in wild carnivores. These parasites are of public health concern, particularly in northern Canada, where human infection rates are markedly higher. Our first objective was to determine whether *T. chanchalensis*, reported in Alaska, Yukon, and the Northwest Territories (NT), is present in wolverines from Nunavut. Our second objective was to determine the prevalence of co-infections and competition among *Trichinella* spp. Tongue samples were collected from 100 wolverines, from Nunavut and NT. *Trichinella* spp. larvae were isolated using the artificial digestion method, quantified (calculated as larvae per gram of muscle, LPG), and identified using next-generation sequencing (NGS). *Trichinella* spp. larvae were detected in 76/100 (76%) of wolverines, with higher prevalence and infection intensity in Nunavut (82%, 16.7 LPG) than in NT (70%, 8.0 LPG). We detected all three taxa in both territories, with co-infections more common in NT (90%) than in Nunavut (68%). We found no significant negative associations in the presence or abundance between *T. nativa* and T6, suggesting minimal competition in the host muscle tissue. We report a new geographic record for *T. chanchalensis* in Nunavut and demonstrate the utility of NGS for *Trichinella* spp. genotyping and detecting co-infections. Building on these findings and prior work, we propose hypotheses regarding the origin of *T. chanchalensis* and suggest approaches for clarifying the taxonomic status of T6.

Keywords:

Foodborne parasites, Northwest Territories, Nunavut, *Trichinella chanchalensis*, *Trichinella nativa*, *Trichinella* T6, Wolverines

1. Introduction

Members of the genus *Trichinella* are zoonotic foodborne parasites that are unique among nematodes, as their entire life cycle occurs within a single host infected through the consumption of infected muscle tissue (Gottstein et al., 2009). The genus currently comprises 13 recognized species or genotypes, along with two putative taxa (T14 and T15) whose status remains unresolved (Panda et al., 2025). Among the confirmed taxa, *T. chanchalensis* (T13) is the most recently described species, discovered in wolverines (*Gulo gulo*) in the Yukon and Northwest Territories, Canada (Sharma et al., 2020). Since then, *T. chanchalensis* has also been found in new hosts, including American marten (*Martes americana*) in the Northwest Territories (Lobanov et al., 2023), wolves (*Canis lupus*), lynx (*Lynx canadensis*), and a coyote (*Canis latrans*) in the Yukon (Malone et al., 2025), as well as in a new geographic area—Alaska, USA (Malone et al., In-press).

The predominant *Trichinella* taxa found in northern Canada, *T. nativa* (T2) and *Trichinella* T6 (hereafter T6) are freeze-tolerant, which allows the larvae to remain viable in frozen carcasses for months to years. The freeze-tolerance greatly facilitates *Trichinella* spp. transmission in the Holarctic (Pozio, 2016), and is also an important consideration for food safety as freezing meat will not inactivate the larvae. In Northern Canada and Alaska, consumption of wild game meat is high and may not be prepared in ways that reliably inactivate the larvae in muscle tissue. For those reasons, the incidence of and potential for human infection in northern Canada is considerably higher compared to southern Canada and the Continental United States (Gilbert et al., 2010; Wilson et al., 2015).

In northern North America, *T. nativa*, T6, and *T. chanchalensis* share hosts and an overlapping geographic range, but are genetically and ecologically distinct (Malone et al., In-press; Malone et al., 2025; Malone et al., 2024; Owsiacki et al., 2020; Pozio, 2016; Reichard et al., 2008; Sharma et al., 2020). These genetic and ecological differences reflect complex processes, including glacial cycles, episodic emergence of the Bering land bridge enabling the dispersal of host species from Eurasia to North America, host associations, and adaptation to the regional climate (Bilska-Zajac et al., 2021; Korhonen et al., 2016; Zarlenga et al., 2006). The presence and sympatry of these three *Trichinella* taxa across northern North America raise important questions about their historical biogeography, host associations, and potential niche partitioning. Prior to the discovery of *T. chanchalensis*, phylogenetic studies significantly advanced our understanding of the twelve recognized species within the genus of *Trichinella* (Korhonen et al., 2016). However, the evolutionary relationships and ecological characteristics of *T. chanchalensis* remain largely unexplored.

Trichinella nativa, T6, and *T. chanchalensis* have been found in the Northwest Territories (Gajadhar and Forbes, 2010; Larter et al., 2011; Owsiacki et al., 2020; Sharma et al., 2020), whereas only *T. nativa* and T6 have been found in Nunavut in previous studies (Gajadhar and Forbes, 2010; Owsiacki et al., 2020; Reichard et al., 2008). Traditional genotyping methods (multiplex PCR) used in these older studies cannot differentiate *T. nativa* and *T. chanchalensis*, and this may have prevented the detection of *T. chanchalensis* in Nunavut (Sharma et al., 2020). We therefore utilized a recently developed next-generation sequencing (NGS) method that can readily differentiate all

North American *Trichinella* taxa, including *T. chanchalensis*, and uses more larvae per sample, greatly improving the detection of underrepresented taxa (Lobanov et al., 2023).

Given that *T. chanchalensis* has been found in Alaska, Yukon, and the Northwest Territories, our primary objective was to determine whether this species was also present in Nunavut. We used NGS to quantify the prevalence and relative abundance of *Trichinella* spp. in co-infected hosts, enabling us to investigate interspecific interactions among sympatric *Trichinella* taxa.

2. Materials and methods

2.1 Study area

The Northwest Territories and Nunavut are two of Canada's three Territories and have a combined land area of 2,964,706 km^2 (Statistics Canada, 2022), which is one-third of Canada's entire land area, and have a combined population of 85,890 people and a population density of 0.03 people per km^2 (Statistics Canada, 2024). The Northwest Territories and Nunavut have three primary climate classifications, namely Subarctic with cool summer and year-round precipitation (Dfc), Continental subarctic – cold dry summer (Dsc), and a polar tundra climate (ET) (Beck et al., 2018).

2.2 Animal tissue sampling

One hundred wolverine carcasses or heads were collected between 2020 and 2023 from across mainland Nunavut (n = 50, subsampled from a larger collection) (Awan, 2025) and from the mainland portion of the Beaufort Delta region of the Northwest Territories (n = 50, representing all available samples) (Figure 1). Animals were legally harvested by hunters and fur trappers for purposes other than this research and voluntarily submitted to the Governments of the Northwest Territories or Nunavut. This study was therefore exempt from animal research ethics approval by the University of Saskatchewan (#010Exempt2025). This research was done in full collaboration with Territorial government personnel. Carcasses and heads were kept frozen until necropsy, and muscle samples collected during necropsy were then re-frozen at -20 °C until processing.

2.3 Recovery of *Trichinella* spp. larvae

Tongue tissue was used for all 100 animals as it has been shown to be the best predilection site for *Trichinella* spp. larvae in wolverines (Sharma et al., 2018). Muscle samples were trimmed to remove all connective tissue and mucosa, cut into small <0.5 cm pieces and combined for a median weight of 9.3 g per animal (range: 2.2-18.0 g). Larvae were recovered and quantified using the gold standard double separatory funnel digestion method with HCl and pepsin (Forbes and Gajadhar, 1999). Up to 100 recovered larvae per animal were stored in GeneAmp 1X PCR buffer (Thermo Fisher Scientific, Carlsbad, CA, USA) at -80 °C until DNA extraction.

2.4 Molecular identification of *Trichinella* larvae using NGS

DNA was extracted from pools of larvae from individual animals and five negative extraction controls (nuclease-free water) using the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific, Carlsbad, CA, USA) following the manufacturer’s instructions. Larval pools from each animal were genotyped using targeted deep amplicon sequencing of the internal transcribed spacer 1 (ITS-1) region of the ribosomal RNA cistron as described earlier (Lobanov et al., 2023; Malone et al., In-press; Malone et al., 2025). After determining the DNA concentration of each sample using the Qubit High Sensitivity dsDNA kit (Thermo Fisher Scientific) and analyzing the DNA fragment size distribution with the QIAxcel Advanced System (Qiagen), individual libraries were diluted to 4 nM and then pooled. Pooled libraries were further diluted to 8 or 12 pM, mixed 3:1 with PhiX control v3 (Illumina) at matching concentration, and sequenced using MiSeq 500-cycle v2 nano kits (Illumina) on the Illumina MiSeq platform.

2.5 Sequence analysis and ecological modeling of *Trichinella* spp.

Sequences were analyzed using a customized Dada2 pipeline and three different classifiers (IDTaxa, AssignTaxonomy, and BLASTn) in RStudio (v. 2023.09.1+494) (Beaumelle et al., 2022; Callahan et al., 2016; Murali et al., 2018). For infected tissue samples, the intensity of *Trichinella* spp. infection was calculated by dividing the total number of larvae recovered by the weight of muscle tissue (in grams) analyzed.

To assess patterns of *Trichinella* spp. abundance and potential interspecific interactions, we analyzed species-specific parasite abundance across host samples. Parasite abundance was calculated by multiplying the larvae per gram for each muscle sample by the relative abundance of each *Trichinella* spp. as estimated from NGS. The species-specific parasite abundance included all samples (i.e. positive and negative samples), and values were log(X + 1)-transformed to normalize residuals and accommodate zero values. The log(X + 1) transformed species-specific parasite abundances were analyzed using linear models (LMs) with normal errors. For each *Trichinella* spp., we compared full models including the abundances of co-occurring *Trichinella* spp. as predictors to intercept-only models using ANOVA, and selected the best-fitting model based on statistical significance ($P \leq 0.05$).

To assess the potential associations between *Trichinella* spp. presence/absence, we used Firth’s logistic regression, which is appropriate for small sample sizes, to test whether infection status with one *Trichinella* taxon predicted infection status with another. Specifically, we modelled *T. nativa* as a function of T6, and vice versa, but not interactions with *T. chanchalensis* as it was too rare to accurately test competition. We calculated parasite richness as the number of *Trichinella* spp. detected per host and modeled it as a function of infection intensity (LPG). All models were fitted using R (v. 2023.09.1+494).

Results

3.1 Prevalence and intensity of *Trichinella* spp. infections

Trichinella spp. larvae were detected in 76% (76/100) of wolverines, with a prevalence of 82% (41/50) in Nunavut and 70% (35/50) in the Northwest Territories. Wolverines from Nunavut had higher infection intensities (median 16.7 LPG) than those from the Northwest Territories (median 8.0 LPG). These differences were further evaluated using quantile regression ($\tau = 0.5$), which estimated a median difference of -8.64 LPG (SE = -5.56, $t = -1.55$, $p = 0.12$), indicating that the observed differences in medians were not statistically significant.

3.2 Distributions of samples and positive animals

Location data was available for 97 of 100 animals; coordinates were available for 69 animals, and coordinates were estimated for 28 animals based on location names provided by hunters and harvesters. Wolverines in this study were found broadly across Nunavut, whereas sample submissions from the Northwest Territories were aggregated around the communities of Tuktoyaktuk, Inuvik, Aklavik, and Fort McPherson in the mainland Beaufort Delta Region (Figure 1).

3.3 Diversity of infections

The ITS-1 fragment from larval pools was successfully amplified in all 41 positive samples from Nunavut and from 31 of 35 positive samples from the Northwest Territories. Three *Trichinella* taxa were detected, *T. nativa*, T6, and *T. chanchalensis*. *Trichinella chanchalensis* was detected in two wolverines from the Northwest Territories (6.5%; 2/31) and nine wolverines from Nunavut (22%; 9/41). Most positive wolverines (78%; 56/72) were co-infected with two or three *Trichinella* taxa, while there were 16 single taxon infections (13 *T. nativa*, two T6, and one *T. chanchalensis* infection) (Table 1).

3.3.1 NGS output

We obtained 1,888,148 merged, quality-filtered reads from 72 samples in three separate sequencing runs, of which 1,850,658 were assigned to different *Trichinella* taxa. The numbers of reads assigned to *T. nativa*, T6, and *T. chanchalensis* were: 861,148;, 922,393, and 67,117, respectively. The median, average, and range of reads per sample were as follows: median 28,958, average 26,224, range 6,738-40,366. All negative DNA extraction controls had ≤ 20 reads assigned to *Trichinella* spp., which confirmed negligible carryover or contamination.

3.4 Interspecific interactions

The parasite abundance of *T. nativa*, T6, and *T. chanchalensis* was best explained by intercept-only models, (log-transformed scale:T2: $\beta = 0.78 \pm 0.06$, $p < 0.0001$; T6: $\beta = 0.75 \pm 0.08$, $p < 0.0001$; T13: $\beta = 0.13 \pm 0.05$, $p = 0.0046$), corresponding to estimated mean abundances of 5 LPG (95% CI: 3.50-6.98) for *T. nativa*, 4.62 LPG (95% CI: 2.98-6.92) for T6, and 0.36 LPG (95% CI: 0.11-0.66) for *T. chanchalensis*, indicating that there were no significant effects of co-occurring *Trichinella* taxa on each other. The association between *T. nativa* and T6 abundance was not significant (Pearson's correlation: $r = 0.16$,

$p = 0.17$). Parasite abundance did not significantly predict *Trichinella* spp. richness, as shown by both linear regression (slope = 0.074, $p = 0.457$) and Poisson GLM (slope = 0.037, $p = 0.801$). Firth's logistic regression models also found no significant predictive relationship between *T. nativa* and T6 infection status, indicating no evidence of negative or positive co-occurrence between *Trichinella* taxa.

4. Discussion

We report the first geographic record for *T. chanchalensis* in nine wolverines from mainland Nunavut (Figure 1). This expands the known range of *T. chanchalensis* from central Alaska all the way to western Hudson's Bay in Nunavut, an area spanning approximately 2700 kilometres. In this and previous studies, *T. chanchalensis* was detected near the southern border of the Territories and near the northern border of the Canadian provinces (British Columbia, Alberta, Saskatchewan, and Manitoba) (Malone et al., In-press; Malone et al., 2025; Sharma et al., 2020). However, there has been no surveillance in Canada's provinces (as opposed to the northern territories: the Yukon, Northwest Territories, and Nunavut) or the Continental United States using a method capable of identifying *T. chanchalensis*. Given the proximity of *T. chanchalensis*-positive samples to southern provinces, future studies should investigate the southern extent of the geographic range of *T. chanchalensis* in Canada and the Continental USA.

The prevalence of *T. chanchalensis* in wolverines from Nunavut was 9/50 (18.0%) which is lower but still comparable to the prevalence in this host species in the Yukon 36/125 (29.0%) (Malone et al., 2025). However, the *T. chanchalensis* prevalence in the Beaufort Delta Region of the Northwest Territories was much lower, 2/50 (4.0%), and more similar to the prevalence found in Alaskan wolverines, 1/32 (3.1%) (Malone et al., In-press). It does not appear that there is a westward prevalence gradient of *T. chanchalensis* in northern North America, as was once hypothesized (Sharma et al., 2020). In fact, prevalence is higher in Nunavut and the Yukon than in Alaska and the Northwest Territories (Malone et al., In-press; Malone et al., 2025). This finding may provide some insight into the origin of *T. chanchalensis*, suggesting that it is not of Beringian or Palearctic origin, but perhaps of a North American origin. However, the relatively limited geographic area sampled in the Northwest Territories may have contributed to a lower observed prevalence of *T. chanchalensis* (4.0%) in this study, which may not be representative of the prevalence across the entire Territory.

We found a high prevalence of *Trichinella* spp. (76%) in wolverines from Nunavut and the Northwest Territories, which is similar to previous reports in the region of 86% and 78% in the Yukon (Malone et al., 2025; Sharma et al., 2021), and 88% in Nunavut (Reichard et al., 2008). We found a higher median intensity of infection in Nunavut (16.7 LPG) compared to the Northwest Territories (8.0 LPG). However, these values are similar to previous intensities of 8.4-13.5 LPG reported across the region (Canadian Territories) (Malone et al., 2025; Reichard et al., 2008; Sharma et al., 2021). The higher infection intensity observed in Nunavut may be driven by regional differences in prey availability and scavenging behaviour. Wolverines in Nunavut may have greater access to infected carcasses of other carnivores, especially in the winter and early spring when scavenging is more frequent (Fisher et al., 2022). These repeated exposures can lead to elevated parasite burdens.

The high prevalence of co-infections, 78% overall (68% in Nunavut and 94% in the Northwest Territories), detected in this study is lower than that in our previous study in the

Yukon, which also used the ITS-1 NGS method and found that 97% of wolverines were co-infected (Malone et al., 2025). Co-infection prevalence is generally much higher in NGS studies due to greater sensitivity and the use of more larvae, compared to multiplex PCR, which detected co-infection prevalence of 6% in Nunavut wolverines (Reichard et al., 2008), and 14% in Yukon wolverines (Sharma et al., 2021). Reichard et al. (2008) reported a high prevalence of T6 (97%; 35/36) in wolverines in Nunavut, whereas in the current study, we found a lower prevalence of 66%. Notably, most of the T6-infected animals from this current study were found in the northwestern mainland of Nunavut, which overlaps with the region sampled by Reichard et al. (2008).

The high frequency of co-infections with multiple *Trichinella* taxa within a single host raises the possibility of interspecific interactions among *Trichinella* taxa. We found no evidence of interspecific competition based on negative associations between *Trichinella* taxa, which agrees with our previous studies in the Yukon and Alaska (Malone et al., In-press; Malone et al., 2025). These results suggest that *T. nativa* and T6 do not compete within host tissues, at least under the conditions and muscle types sampled in this study. Ultimately, these results suggest that co-infection does not necessarily imply interaction and that host-level factors such as exposure risk, behaviour, and immunity are possibly the primary drivers of *Trichinella* spp. infection dynamics, rather than interspecific parasite interactions.

The biogeographic patterns of *T. nativa*, T6, and *T. chanchalensis* across northern North America suggest distinct evolution, possibly shaped by glacial cycles, host dispersal, and regional adaptation (Korhonen et al., 2016; Zarlenga et al., 2006). *Trichinella nativa* likely originated in Eurasia and colonized North America via Beringia more than 5 million years ago, before the onset of North American glaciation (Korhonen et al., 2016). In contrast, *T. chanchalensis* is phylogenetically distant from *T. nativa* and T6 and most closely related to *T. patagoniensis*, which occurs in South America (Krivokapich et al., 2012; Sharma et al., 2020). This relationship, combined with no documented presence of *T. chanchalensis* in Eurasia and low prevalence in Alaska (Malone et al., In-press), suggests that *T. chanchalensis* originated in the Americas, followed by northward expansion during interglacial periods or postglacial recolonization.

The current known distribution of *T. chanchalensis* includes Alaska, Yukon, the Northwest Territories, and now Nunavut. Given the phylogenetic distinctiveness and hypothetical origin of *T. chanchalensis* in the Americas, it is likely that the geographic range of this species extends beyond these documented regions. The northern regions of many provinces (British Columbia, Alberta, Saskatchewan, Manitoba, Ontario, Quebec) share similar ecological conditions and host assemblages, making the presence of *T. chanchalensis* likely (Figure 2). It is also possible that the range of *T. chanchalensis* could follow the Rocky Mountains southward into the United States as does T6 (Malone et al., 2024). Future population genetic analyses could be used to help determine whether *T. chanchalensis* populations are structured by geography, host movement, or historical isolation.

Trichinella T6 is closely related to *T. nativa* but has not been found in Eurasia (Malone et al., 2024; Sharma et al., 2020), either because of a lack of surveillance or its non-occurrence in the region. The absence of T6 in Eurasia suggests that it diverged from *T. nativa* following its dispersal into North America. The diversification of *T. nativa* and T6 reflects complex climate variation and changes in habitat during the emergence of the

Bering land bridge (2.5-2 million years ago), which altered host assemblages and facilitated the colonization of North America by important host species (ursids, canids, and mustelids) during the late Pliocene and early Quaternary periods (Bilska-Zajac et al., 2021; Korhonen et al., 2016; Zarlenga et al., 2006). Divergence between *T. nativa* and T6 may have also occurred from temporary (in evolutionary time) allopatry in glacial refugia (Zarlenga et al., 2006). Despite its genetic distinctiveness, T6 has not yet been formally described as a distinct species, leaving its taxonomic status unresolved. The consistent presence of T6 across northern North America, and its sympatric distribution and co-existence with *T. nativa* and *T. chanchalensis* may suggest niche partitioning. Further population genetic studies on *T. nativa* and T6 should be conducted to resolve the taxonomic status of T6.

Wolverines are not commonly consumed by humans and therefore do not pose a direct food safety risk. However, all three *Trichinella* taxa detected in this study are, or presumed to be, freeze-tolerant, which prolongs the transmission window of the parasite via scavenging to other wildlife species of greater food importance, such as bears and lynx. The high infection prevalence in wolverines indicates that *Trichinella* spp. are circulating in terrestrial regions of the Canadian Arctic. For this reason, wild game meat should be cooked to an internal temperature of at least 71 °C (160 °F) to ensure that *Trichinella* spp. larvae have been inactivated (Canadian Food Inspection Agency, 2013). However, wild game meat in many Indigenous cultures is often coupled with a spiritual and cultural significance beyond purely nutritional value and is sometimes prepared in traditional ways such as raw, frozen, dried, smoked, or cured, which do not always inactivate the larvae (Noeckler et al., 2019). The findings of this study contribute to our understanding of *Trichinella* spp. ecology in northern ecosystems. The detection of *T. chanchalensis* in Nunavut greatly expands its known geographic range and challenges previous biogeographic hypotheses, suggesting the need for further geographic surveys (including provinces and Arctic islands in Canada, the continental USA, and the eastern Palearctic) using more sensitive NGS methods, population genetic studies, and phylogenetic studies to explore evolutionary history. The high prevalence and intensity of *Trichinella* spp. infections in wolverines highlight the importance of wolverines as a sentinel species. The high frequency of co-infections and lack of interspecific competition between *Trichinella* taxa suggest that host-mediated processes, rather than parasite interactions, are the primary determinants of infection success for *T. nativa* and T6. The findings from this study, alongside previous studies, raise important questions about the historical biogeography of *Trichinella* spp. diversity and ecology in North America.

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Figure captions

Figure 1. Distribution of *Trichinella* spp. in wildlife in the Beaufort Delta Region of the Northwest Territories and mainland Nunavut. Province and Territory abbreviations: AB = Alberta, BC = British Columbia, MB = Manitoba, NT = Northwest Territories, NU = Nunavut, QC = Quebec, SK = Saskatchewan, YT = Yukon. Map created using QGIS (v3.42.1-Münster).

Figure 2. Distribution of *T. nativa*, T6, and currently known and hypothesized geographic range of *T. chanchalensis* in Canada and the USA based on current ecological and epidemiological knowledge.

Tables

Revealing the Northern Distribution of *Trichinella chanchalensis*: New Geographic Records from Nunavut and Ecological Perspectives

Table 1. Proportion of single infections and co-infections with *Trichinella* spp. in wolverine (*Gulo gulo*) from Nunavut and the Northwest Territories determined using next-generation sequencing.

Composition of Infection	Proportion (%)
Mainland Nunavut	
T2 single infection	12/41 (29.2%)
T6 single infection	1/41 (2.4%)
T2/T6 co-infection	19/41 (46.3%)
T2/T6/T13 co-infection	7/41 (17%)
T2/T13 co-infection	2/41 (4.9%)
Northwest Territories (Mainland Beaufort Delta Region)	
T2 single infection	1/31 (3.2%)
T6 single infection	1/31 (3.2%)
T13 single infection	1/31 (3.2%)
T2/T6 co-infection	27/31 (87.2%)
T2/T13 co-infection	1/31 (3.2%)

Declaration of interests

☐ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☒ The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Cody J Malone reports financial support was provided by Weston Family Foundation. Cody J Malone reports financial support was provided by Polar Knowledge Canada. Cody J Malone reports financial support was provided by Natural Sciences and Engineering Research Council of Canada. Emily J Jenkins reports financial support was provided by Natural Sciences and Engineering Research Council of Canada. Emily J Jenkins reports financial support was provided by ArcticNet Inc. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Highlights

- New geographic record for *T. chanchalensis* in Nunavut
- High prevalence and intensity of infection in Nunavut and the Northwest Territories
- No evidence of interspecific competition between *T. nativa* and T6 in wolverines
- High frequency of co-infections with multiple *Trichinella* taxa detected by NGS
- Possible North American origin hypothesized for *T. chanchalensis*

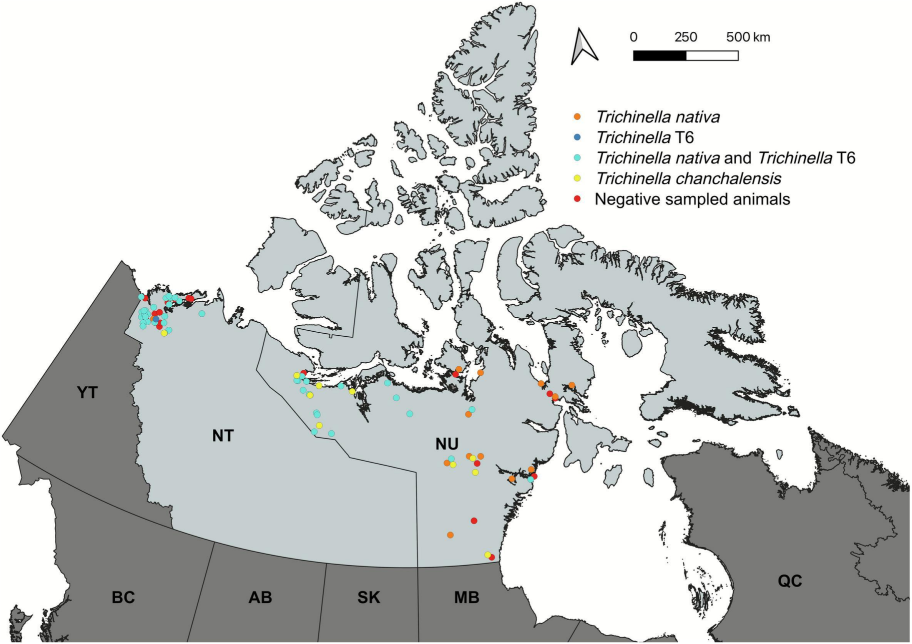
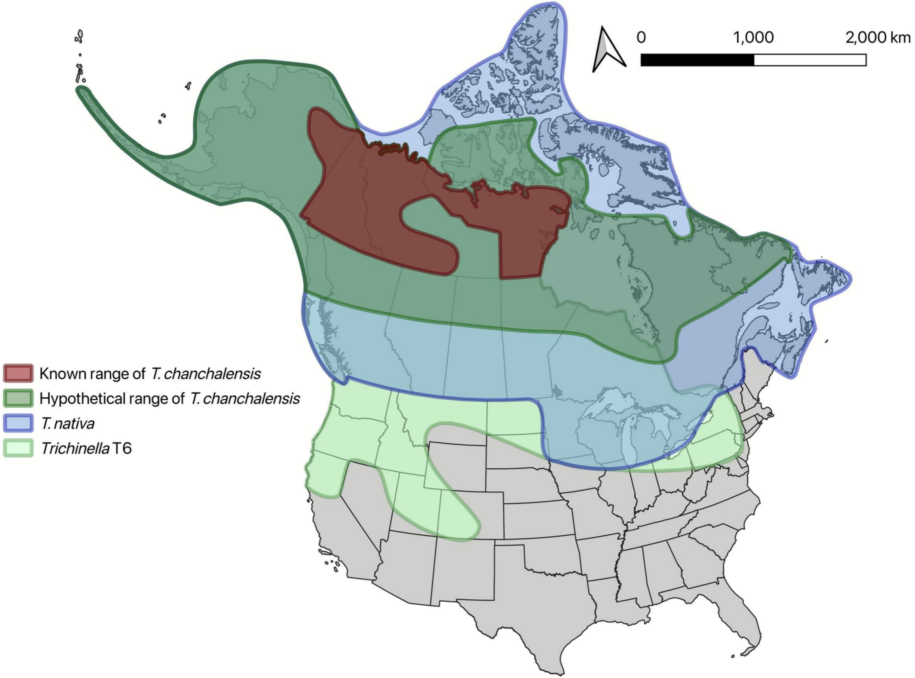

0
250
500 km
● *Trichinella nativa*
● *Trichinella* T6
● *Trichinella nativa* and *Trichinella* T6
● *Trichinella chanchalensis*
● Negative sampled animals
YT
NT
NU
BC
AB
SK
MB
QC

Figure 1



0
1,000
2,000 km
Known range of *T. chanchalensis*
Hypothetical range of *T. chanchalensis*
T. nativa
Trichinella T6

Figure 2