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Regional Differences in the Prevalence of *Trichinella* spp. in Wolves in the Northwest Territories

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ABSTRACT

Trichinella (T.) is present in wolves of the Northwest Territories (NWT); however the prevalence of this zoonotic parasite varies across the landscape. As part of a wildlife disease monitoring program, tongue samples were collected from wolf carcasses that were provided to the Department of Environment and Natural Resources (ENR) by local hunters and trappers from different regions of the NWT. A total of 244 tongue samples were collected during 2001-2015. Location was a significant predictor of prevalence with prevalence being lowest (35.1%) in the South Slave (SS) and highest (79.3%) in the Mackenzie Mountains (MM). The location difference cannot be explained by differences in sex or age of wolves. However, prevalence increased with age plateauing at four years. Locations with a high prevalence of infection are cohabited by grizzly bears while locations with a low prevalence have limited access to garbage dumps and are not cohabited by grizzly bears. Levels of intensity of infection, measured in larvae per gram (LPG) of muscle tissue ranged from 0.07-100.77. Analysis of the intensity of infection suggests a weak relationship with age, but no effect of location or sex. Ninety-seven samples had an infection intensity of >1 LPG which is considered to be a human food safety concern, though wolf consumption is exceedingly rare. Genotyping of a limited number of positive samples (n=18) indicated that T2, T6, and *T. nativa* were present.

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INTRODUCTION

Trichinosis is caused by a parasitic roundworm of the genus *Trichinella* (T.) and is common in many species of wildlife, specifically mammalian predators and omnivores. Humans can get trichinosis by consuming undercooked meat from infected animals. A long term disease monitoring program in the Dehcho (DC) region reported on the prevalence of *Trichinella* spp. in a variety of wildlife species including bears, and wolves (Larter et al. 2011; 2016; Larter 2015 updated). Larter et al. (2016) reported wolves had the highest prevalence of *Trichinella* of all species of wildlife tested in the DC region and that prevalence was higher in wolves from the Mackenzie Mountains (MM).

From 2011-2013 wolf carcasses were provided to the Department of Environment and Natural Resources (ENR) through incentive programs to local hunters and trappers. This provided the opportunity to collect samples of wolf tongues from different locations of the Northwest Territories (NWT) and to explore the prevalence of *Trichinella* in wolves, and the intensity of the infection, over a much wider geographic area. Samples collected from wolves harvested in the South Slave (SS) and Sahtú (ST) regions were analyzed for the presence of *Trichinella* and pooled with those analyzed from wolves collected from the DC (Larter et al. 2016). This report documents the presence and infection intensity of *Trichinella* in wolves, and explores the effect of sex, age and location on the occurrence of *Trichinella* in wolves from the SS, DC, and ST regions and the MM (Figure 1).

Study Area

Harvested wolves came from throughout the ST, DC, and SS administrative regions including the MM which make up the western border with the Yukon of both the DC and ST (Figure 1.).

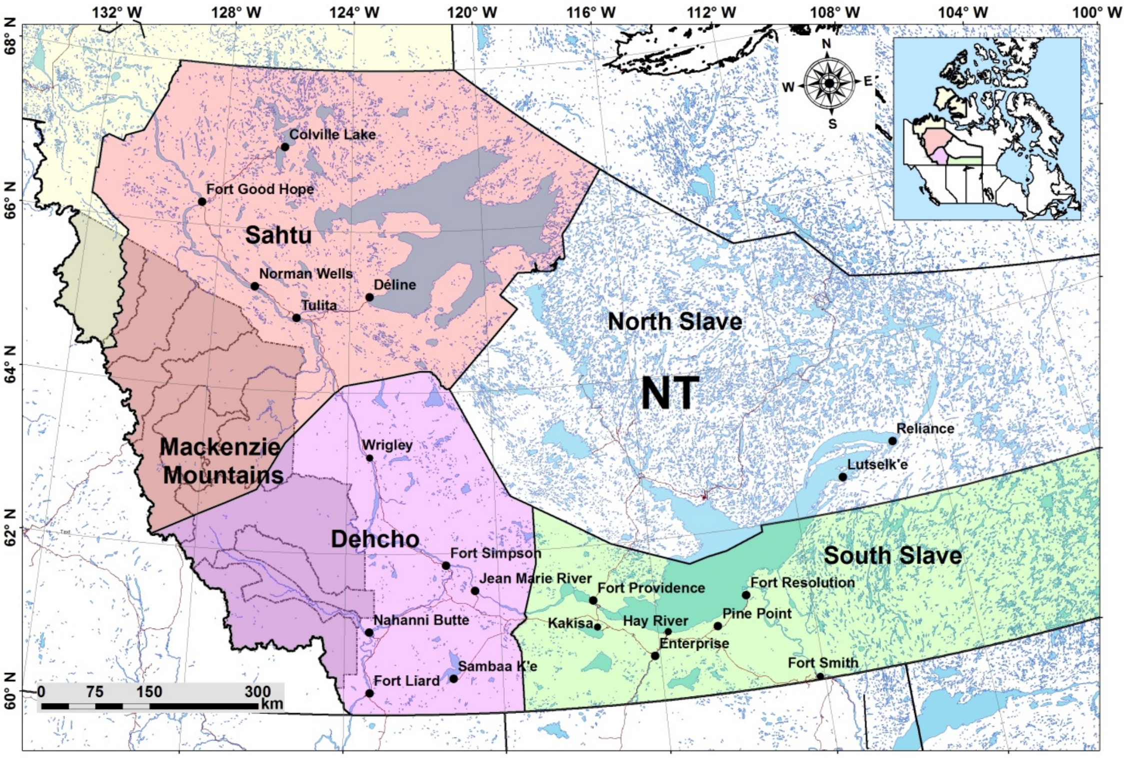

Figure 1. Study area including South Slave, Dehcho, and Sahtú administrative regions, the Mackenzie Mountains, and communities.

METHODS

Biological Sample Collection/Analysis

Tongue samples from the DC (n=54) and MM (n=27) were collected from harvested wolves, wolves killed for public safety, and wolves involved in motor vehicle collisions from 2001-2015 as described in Larter et al. (2016). Tongue samples from the SS (n=97), ST (n=64) and MM (n=2) were collected from wolf carcasses provided to the SS and ST regional ENR offices by local hunters and trappers from 2011-2013.

When at all possible a location, the date of death and the sex of the wolf was collected for each sample. When at all possible a first premolar tooth was collected. Tooth samples were forwarded to Matson's Laboratory (http://matsonslab.com) for aging. The age was determined by cementum age analysis of the first premolar tooth (Matson 1981).

Tongue samples were stored frozen in regional ENR offices prior to being shipped to southern laboratories. Fifty tongue samples (DC n=42; MM n=8) were forwarded to the Centre for Food-borne and Animal Parasitology, Canadian Food Inspection Agency, Saskatoon for analysis to detect *Trichinella*. The remaining 194 tongues (SS n=97; DC n=12; ST n=64; MM n=21) were forwarded to the Western College of Veterinary Medicine, Saskatoon for analysis to detect *Trichinella*.

Frozen tongue samples were thawed to room temperature and trimmed to remove fat and connective tissue. The digestion assay for the detection of *Trichinella* spp. larvae in muscle tissue followed Forbes and Gajadhar (1999) and Forbes et al. (2008). Weights of tested tongues varied. Positive results were converted to larvae/g (LPG) of muscle tested. The same analysis was done by both labs.

A limited number (n=18) of positive samples were genotyped into one of the eight species and four genotypes of *Trichinella*: species T. *spiralis* (T1), T. *nativa* (T2), T. *britovi* (T3), T.

pseudospiralis (T4), T. *murrelli* (T5), T. *nelsoni* (T7), T. *papuae* (T10), and T. *zimbabwensis* (T11) and genotypes T6, T8, T9, and T12 (Gottstein et al. 2009). Genotyping was done using a multiplex polymerase chain reaction (PCR) (Zarlenga et al. 1999; Gajadhar and Forbes, 2010).

Statistical Analyses

We used logistic regression (McCullough and Nelder 1989) to investigate the occurrence of *Trichinella* (prevalence) with binary occurrence as the response variable and location, age, and sex as covariate predictors. Age was modelled using polynomial terms and as a categorical variable [pups (age = 0), yearlings (age = 1), subadults (age = 2), adults (age $\geq$ 3)]. Because we were missing age data for most of the samples from the MM we ran an initial analysis without sex and age effects to determine if prevalence was higher in the MM than in the three other regions ST, DC, SS. The full analysis model was run on 209 samples. Six samples with unknown sex (ST = 2, DC = 1, SS = 3) as well as MM samples were excluded from the full analysis model (see Appendices 1-3).

We used contingency tests (Agresti 1990) to test for whether sex ratio and ages were independent of location (ST, DC, SS). Ages were pooled in two year intervals.

Many potential combinations of predictors were possible given that disease occurrence might affect different age or sex classes in the different locations. Additionally, non-linear relationships between age and disease occurrence might exist. Therefore, we used an information theoretic approach (Burnham and Anderson 1998) to find the most parsimonious model to predict the occurrence of *Trichinella.* The model with lowest AIC_c score was considered the most parsimonious. Models whose difference in AIC_c score from the most supported model was less than two (ΔAIC_c) were also considered (Appendices 1-3).

AIC_c scores indicate relative model fit but do not indicate absolute fit of the model to the data. Two goodness-of-fit tests were used to determine overall fit. First, receiver operating curve (ROC) scores were used to assess predictive ability of models (Fielding and Bell 1997). A model with a ROC score of >0.7 indicated that it had useful predictive ability. If ROC score was above 0.8 then the model had excellent predictive ability. In addition, the Hosmer-Lemenshow chi^2 goodness-of-fit test was used to assess goodness-of-fit based on observed and predicted binned data frequencies (Hosmer and Lemeshow 2000; Appendices 1-2).

Individual covariates were contrasted against an intercept-only model to assess base predictive ability (model 13, Appendix 1). We used an analysis of covariance (ANCOVA) approach (Milliken and Johnson 2002) to block the data by location with tests for age effects. The main objective of model building tested for locations-specific relationships between age and the probability of *Trichinella*. We also added a dump factor, wolves known to be harvested from community dumps, to the regression (Appendix 2).

We applied a piecewise regression model previously used for zone of influence analysis (Boulanger 2015) to estimate the exact threshold age when probability of *Trichinella* occurrence reached an asymptote. For this program we used segmented (Muggeo 2003; 2008) in program R (R_Development_Core_Team 2009). The ROC goodness of fit score for this model was determined using the pROC package (Robin et al. 2014).

The intensity of the infection of *Trichinella* was indexed as LPG of wolf muscle tissue. A natural log transformation of LPG resulted in a near normal distribution therefore LPG was log transformed for analysis using a generalized linear model with the AIC_c model selection similar to that done to explore disease occurrence (Appendix 3).

RESULTS

The prevalence of *Trichinella* was determined from 244 tongue samples collected from four different regions of the NWT; ages were determined for 89% (n=216) of samples and information on sex was available for 97% (n=237) of samples (Table 1).

Table 1. The number of tongue samples, age samples, and sex breakdown of samples for each different locations used in the analyses.

Location	N	♂	♀	Unk.	Ages
SS	97	46	48	3	97
ST	64	29	31	4	64
MM	29	16	13	0	7
DC	54	27	26	1	48
Total	**244**	**118**	**120**	**7**	**216**

Overall prevalence was 50.8% (n=244). Prevalence was highest in the MM (79.3%) and lowest in the SS (35.1%). Location was a significant predictor of occurrence (χ^2=22.0, df=3, $p<0.001$) when entered as the sole predictor in the logistic model. Predictive ability of this model was marginal with a ROC score of 0.66. The results are shown as odds ratios and mean probability levels (Table 2). The odds ratio is the relative odds of a wolf having *Trichinella* in each location compared to the other locations. For example, a wolf in the DC location has roughly baseline odds of having *Trichinella* compared to the other locations (odd ratio close to 1). Contrastingly, a wolf in the MM has 3.8 time higher odds of having *Trichinella*. These odds translate to mean probabilities with MM having the highest mean probability (0.79) followed by ST (0.61), DC (0.52), and SS having the lowest probability (0.35).

Table 2. Estimate of odds ratios and mean probabilities of the occurrence of *Trichinella* based upon a logistic regression using location only (McCullough and Nelder 1989).

Location	Odds Ratio Estimate	Lower Confidence Limit	Upper Confidence Limit	Mean Probability	Lower Confidence Limit	Upper Confidence Limit
SS	0.54	0.35	0.83	0.35	0.26	0.45
ST	1.57	0.93	2.64	0.61	0.48	0.73
MM	3.83	1.56	9.41	0.79	0.61	0.90
DC	1.08	0.63	1.86	0.52	0.39	0.65

Contingency tests suggested that both sex ratio (χ^2=3.6, df=6, p=0.74) and age (χ^2=9.8, df=8, p=0.27; Table 3, Figure 2.) were similar across locations. Sex ratios were 29♂:31♀ (ST), 27♂:26♀ (DC), and 46♂:48♀ (SS).

Table 3. Contingency test of age (in years) and location (ST, DC, SS) following Agresti (1990).

Age	ST	DC	SS	Total
0-1	45	24	57	126
2-3	10	12	15	37
4-5	6	4	13	23
6-7	2	5	5	12
>7	1	3	7	11
Total	64	48	97	209

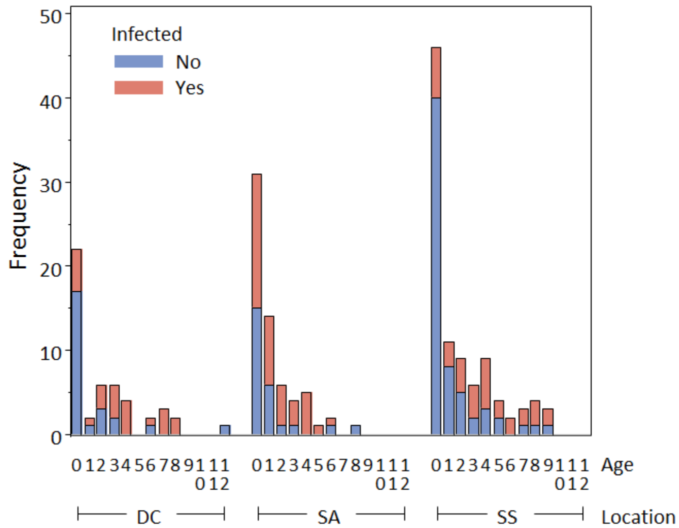

Figure 2. The distribution of all ages by location with presence of *Trichinella* indicated for each age.

Age and location were more supported than the intercept model (Models 11, 13, and Appendix 1) and all ANCOVA models were more supported than individual predictor models (Models 1-9, Appendix 1). Age effects were most supported by an additive model that had location as a block term, age as a linear term and cubic term (Model 3, Appendix 1). A model that constrained the occurrence of *Trichinella* to increase with age up to age six then asymptote (Model 4, Appendix 1) was virtually tied for support with this model.

The most supported model for locations-specific relationships between age and probability of *Trichinella* had location as a blocking term (unique intercept values for location), a linear term for age and then an interaction of the cubic term of age with location. This model basically assumed a similar increase in *Trichinella* with age but with different thresholds where disease transmission changed with age for each location (Model 1, Appendix 1).

We re-ran the logistic regression with two data points of older aged wolves not included (an eight year old from ST and a 12 year old from DC). These two older aged wolves were outliers compared to the younger ages of wolves collected (Figure 2), and therefore exhibited a high degree of influence on model results. Models that did not assume location-specific thresholds were most supported (Models 1-7, Appendix 2), with a model that assumed a common threshold age of four years at all locations being most supported (Model 1, Appendix 2, Figure 3). The addition of the dump term did not provide any significant predictor of *Trichinella* occurrence.

Using the piecewise regression model, the estimated threshold age when probability of *Trichinella* occurrence reached an asymptote was 3.78 years (CI=1.9-5.6 years) with an ROC goodness-of-fit score of 0.79 (CI=0.73-85). This is similar to the estimate of four years based on regression model.

The intensity of infection from 124 tongues ranged from 0.074-100.77 LPG and when transformed with a natural log (ln) resulted in a near-normal distribution. The highest intensity of infection was recorded from a two year old male that had been frequenting garbage cans in Fort Simpson for months during winter 2014/15. The lowest intensity of infection was recorded from a two year old female that was harvested near Hay River in January 2012.

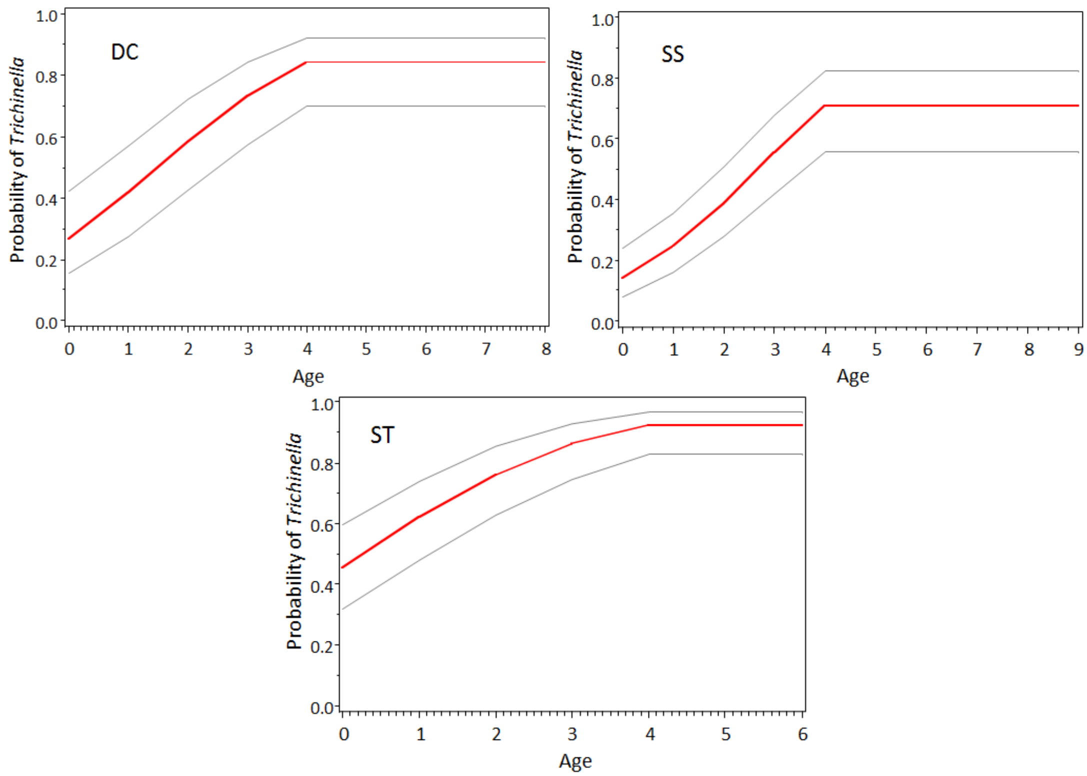

Figure 3. Predicted occurrence of *Trichinella* for each location (DC, SS, and ST) as a function of age with the removal of the two older aged wolves.

Only one model (Model 1, Appendix 3) on the intensity of the infection of *Trichinella* was more supported than the intercept model. Other covariates, combination of covariates, and threshold age models were not supported (Appendix 3, Figure 4). This suggests a weak relationship with age, but not sex or location (Figure 5.).

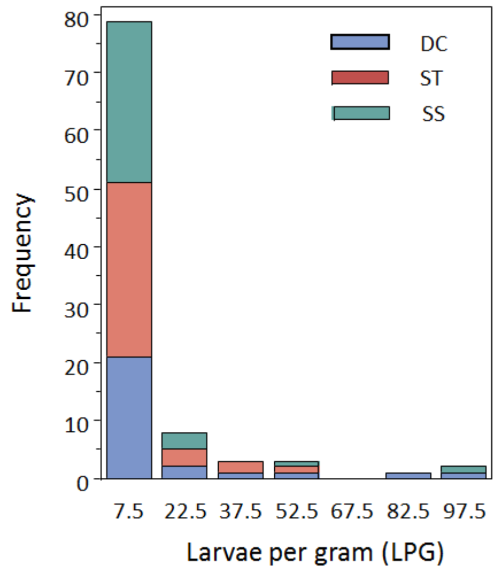

Figure 4. Distribution of larvae/g by location for wolves testing positive for *Trichinella*.

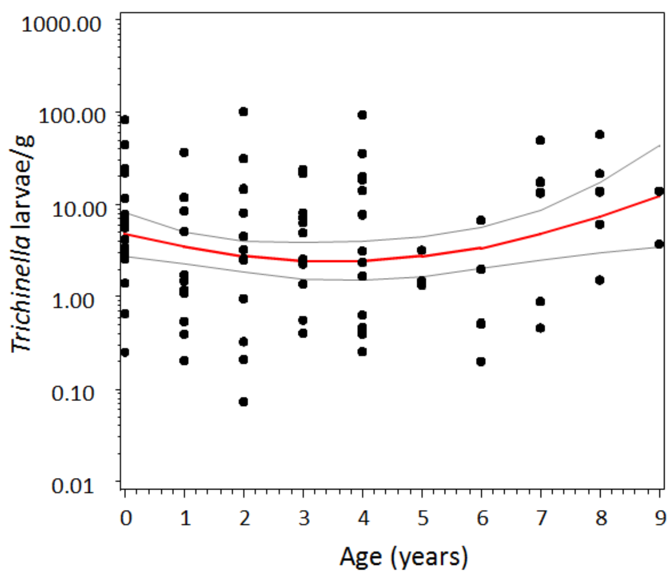

Figure 5. Predicted intensity of infection of *Trichinella* (ln (LPG)) as a function of age. Grey lines are confidence limits to the quadratic function.

Genotyping of a limited number of positive samples indicated that T2, T6, and *T. nativa* were present. For the SS (n=9) there were eight occurrences of T2, one of T6, and two of *T. nativa*. For the MM (n=8) there were six occurrences of T6, one of T2, and one of *T. nativa*. For the DC (n=1) genotyped as T2.

DISCUSSION

It is unfortunate that age data was lacking for wolves from the MM. Higher prevalence in the MM wolves may be a result of a different age distribution of sampled animals, rather than something more specific to the location. Wolves from the ST, DC, and SS were harvested by local trappers and show the expected distribution of mostly young/naïve animals and fewer older mature adults. This age distribution of samples was consistent between locations (Figure 2) therefore the difference in prevalence of *Trichinella* between locations is independent of sex and age. Most wolves from the MM were harvested by non-resident sport hunters who are more likely to be targeting larger and therefore probably somewhat older wolves. There is also the possibility that pack size is smaller in the MM than elsewhere. With smaller pack size the proportion of young naïve animals is reduced while the proportion of older animals is increased, again, resulting in a sample of harvested animals with an older age distribution.

In general, prevalence of *Trichinella* spp. infection is higher in carnivore and omnivore species that scavenge, hunt, or exhibit cannibalism than small mammal species such as rodents (Appelyard and Gajadhar 2000, Schmidt et al. 1978). The prevalence we report for wolves is consistent with expectations based upon their dietary patterns and the literature. Wolves consume a wide array of food items, including human garbage (Larter 2016). Many wolf tongues screened for *Trichinella* in the DC were from the same wolves used to document diet in the DC (Larter 2016). Cannibalism is rarely reported (Theberge and Theberge 1998) but may be common in wolves. Fights between packs over territory are often quite deadly and although carcasses are not ripped to shreds there is evidence of bites taken from them. In parts of Alaska up to 60% of wolf mortality has been attributed to other wolves (Mowry 2009).

Larter et al. (2016) reported a 59% prevalence of *Trichinella* for adult grizzly bears in the DC. Cannibalism and infanticide is well documented in grizzly bears (Mattson et al. 1992, McLellan 2005). Larter et al. (2016) speculated that a combination of cannibalism and ingesting infected wolf carrion could maintain the high prevalence of *Trichinella* in grizzly bears. The distribution of grizzly bears and wolves completely overlaps in the MM. Overlapping distribution of grizzly bears with wolves would be highest in ST and lowest in SS. The extent of cohabitation of grizzly bears and wolves may be a factor in the different prevalence of *Trichinella* in wolves we report between locations. Wolves are reported to attack and actively hunt grizzly bears (GSCI and GRRB 2014). This would expose them to individuals with a high prevalence of infection. However, other species like red fox and wolverine are known carriers of *Trichinella* (Larter et al. 2016), and there is substantial overlap in their distribution with wolves from all locations.

The prevalence of *Trichinella* increases with access to scavenging of garbage dumps and ingesting infected carrion. We added a dump term to the second logistic regression model (Appendix 2) in order to see if predictability of *Trichinella* improved. There was no improvement in the model likely because it was modelled as a binary occurrence (yes or no - the wolf was harvested at a community garbage dump site) and there were 27 missing values. It still could be argued that the order of *Trichinella* prevalence reported in wolves from highest to lowest for the three locations (ST, DC, SS) is consistent with the order of accessibility of the average wolf to human garbage dumps in the same three locations. Based upon the size of the region and the distribution of communities and garbage dumps within the region accessibility would be highest in ST and lowest in SS.

The asymptoting age for the prevalence of *Trichinella* was an interesting discovery, especially with the two different approaches providing similar results. This indicates that there is some small proportion of the wolf population that has not become infected by four years and once reaching that age they will not become infected. The proportion of wolves becoming infected was similar between locations, possibly slightly lower in SS than ST and DC (Figure 3). It would be interesting to see if this model holds with the inclusion of samples from MM. However, acquiring teeth for aging from wolves harvested in MM remains challenging. Interestingly, Larter et al. (2011) reported the average age of wolves testing positive for *Trichinella* (n=27) in the DC as approximately four years.

We report a positive relationship with the intensity of infection of *Trichinella* with age past the approximate four year asymptote (Figure 5.). This is not unexpected because once an individual wolf has become infected we assume it maintains the infection throughout its lifetime. In all likelihood ingesting additional infected material during the course of its lifetime would likely increase the intensity of infection, a process similar to bioaccumulation.

The highest intensity of infection we report was 100.77 LPG, from two year old male that had been frequenting garbage cans in Fort Simpson for months during winter 2014/15. It is relatively rare that intensities are >100 LPG (Gajadhar and Forbes 2010). Quite possibly this extended period of time scavenging increased the probability of ingesting infected material resulting in a higher intensity of infection. Reported infection intensities for wolves are lacking. For black bears, Larter (2015) reported an infestation of 177.00 LPG. Schad et al. (1986) reported six black bears with intensities ≥300 LPG in Pennsylvania, with the highest being 912 LPG. Black bears in Pennsylvania had access to local slaughtering plants and garbage dumps where discarded offal could be scavenged.

Larter et al. (2011) genotyped 11 wolves and found six were infected with T. *nativa* and five were infected with T6. These samples could be from either DC or MM and are part of 244 samples used in this study. These same two genotypes, as well as the T2 genotype were reported from the 18 additional wolves genotyped as part of this study. *Trichinella* T2 is a cold-adapted genotype found in wild mammals from the arctic or subarctic zones of North America, Europe and Asia that is more resistant to freezing temperatures. *Trichinella* T6 is the most common genotype observed in sylvatic infections of Canadian wildlife and has a wider documented host distribution compared to T2 (Gajadhar and Forbes 2010). T6 from a black bear was responsible for a recent outbreak of trichinellosis in humans in northern Ontario (Daniel Dalcin, personal communication).

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PERSONAL COMMUNICATIONS

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APPENDIX 1

Logistic regression model selection results for wolf *Trichinella* analysis. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the ith model and the model with the lowest AIC_c value (Δ_i), Akaike weights (w_i), number of parameters (K) and log-likelihood (LL) of the model are presented. Goodness of fit includes ROC scores and results of the Hosmer-Lemenshow χ^2 goodness-of-fit test.

No	Model	Relative Model Fit					Goodness of Fit Tests			
		AIC_c	ΔAIC_c	w_i	K	LL	ROC	χ^2	df	p
1	location age location*age^3	240.72	0	0.40	7	-113.08	0.77	6.13	7	0.52
2	location age location*age^2	241.90	1.18	0.22	7	-113.67	0.76	14.27	7	0.05
3	location age age^3	243.19	2.47	0.12	5	116.59	0.78	2.75	8	0.95
4	location age (threshold = 6 years)	243.22	2.50	0.11	4	-117.51	0.77	3.88	7	0.79
5	location age age^2	243.41	2.69	0.10	5	-116.56	0.78	5.06	7	0.65
6	location age age^2 age^3	245.40	4.68	0.04	6	-116.49	0.78	5.86	8	0.66
7	location age	255.68	14.96	0.00	4	-123.74	0.76	12.81	7	0.08
8	location sex age	257.26	16.54	0.00	5	-123.48	0.77	7.08	7	0.42
9	location age location*age	258.70	17.98	0.00	6	-123.16	0.76	12.44	6	0.05
10	age(threshold=6 years)	264.50	23.78	0.00	2	-130.23	0.71	4.90	4	0.29
11	age	266.30	25.58	0.00	2	-131.11	0.72	9.70	4	0.05
12	location	282.10	41.38	0.00	3	-138.02	0.62	0.00	1	0.99
13	intercept only	287.89	47.17	0.00	1	-142.94	n/a			
14	sex	289.37	48.65	0.00	2	-142.67	0.52			

APPENDIX 2

Logistic regression model selection results for wolf *Trichinella* analysis with two older aged wolves removed and a dump factor included. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the *i*th model and the model with the lowest AIC_c value (Δ_i), Akaike weights (w_i), number of parameters (K) and log-likelihood (LL) of the model are presented. Goodness of fit includes ROC scores and results of the Hosmer-Lemenshow χ^2 goodness-of-fit test.

No	Model	Relative Model Fit					Goodness of Fit Tests			
		AIC_c	ΔAIC_c	w_i	K	LL	ROC	χ^2	df	p
1	location age(threshold=4yrs)	235.17	0.00	0.35	4	111.20	0.79	1.18	7	0.99
2	location age(threshold=3yrs)	236.10	0.93	0.22	4	-113.95	0.79	1.55	6	0.96
3	location age(threshold=5yrs)	237.18	2.01	0.13	4	-114.49	0.79	1.30	7	0.99
4	location age age^2	237.98	2.81	0.09	5	-113.84	0.79	0.40	6	1.00
5	location age age^3	238.42	3.25	0.07	5	238.42	0.78	1.64	6	0.95
6	location age(threshold=6yrs)	238.90	3.73	0.05	4	115.35	0.78	2.66	7	0.91
7	location age age^2 age^3	240.02	4.85	0.03	6	-113.80	0.79	0.57	7	1.00
8	location age location*age^3	240.32	5.15	0.03	6	-112.88	0.79	2.07	6	0.96
9	location age location*age^2	240.47	5.30	0.02	7	-112.95	0.78	1.64	7	0.95
10	location age (categorical)	240.56	5.39	0.02	7	-114.07	0.79	1.20	6	0.99
11	location age	241.29	6.12	0.01	4	-116.54	0.78	8.58	7	0.28
12	location sex age	243.25	8.08	0.00	5	-116.47	0.78	3.96	7	0.78
13	location age location*age	244.31	9.14	0.00	6	-115.94	0.78	7.87	7	0.34
14	age(threshold=4yrs)	248.75	13.58	0.00	2	-122.35	0.73	0.59	3	0.90
15	Location age(categorical) location* age(categorical)	252.45	17.28	0.00	11	-113.41	0.67	28.47	6	<0.001
16	age	255.23	20.06	0.00	2	-125.59	0.73	6.51	4	0.16
17	location	278.88	43.71	0.00	3	-136.38	0.62			
18	intercept only	285.39	50.22	0.00	1	-141.68				
19	sex	287.03	51.86	1.00	2	-141.49				
20	dump	287.17	52.00	0.00	3	-140.50	0.54			

APPENDIX 3

Model selection results for the intensity of *Trichinella* infection in larvae/g. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the *i*th model and the model with the lowest AIC_c value (Δ_i), Akaike weights (w_i), number of parameters (K) and log-likelihood (LL) of the model are presented.

No	Model	AIC_c	ΔAIC_c	w_i	K	LL
1	age age^2	366.73	0.00	0.22	4	-179.1
2	intercept	367.58	0.85	0.14	2	-181.7
3	Age(categorical)	368.65	1.92	0.08	5	-178.99
3	age age^2 age^3	368.77	2.04	0.08	5	-179.1
4	sex	369.14	2.41	0.07	3	-181.4
5	age(threshold=3yrs)	369.16	2.43	0.07	3	-181.5
6	age(threshold=4yrs)	369.50	2.78	0.06	3	-181.6
7	age	369.60	2.87	0.05	3	-179.4
8	age(threshold=5yrs)	369.62	2.89	0.05	3	-181.7
9	location age age^2	369.85	3.12	0.05	6	-178.5
10	dump age age2	369.97	3.24	0.04	5	-178.5
11	location	370.00	3.27	0.04	4	-180.8
12	dump	370.76	3.84	0.03	3	-181.2
13	location age	372.22	5.49	0.01	5	-180.8

APPENDIX 4

Tongue samples showing infestation intensities of >1 larvae/g with date and general location of sample collection, sex and age. SSR = South Slave, SA = Sahtú, DC = Dehcho, MM = Mackenzie Mountains.

Region	Infestation	Date	Location	Sex	Age
SSR-W-13-34	1.19	3-Apr-13	Caen Lake	F	1
SSR-W-13-62	5.13	12-Aug-12	Great Slave Lake by Hay River	M	1
SSR-W-13-73	4.93	12/13	Paradise Garden	M	3
SSR-W-13-32	8.22	31-Mar-13	Big Buffalo River	F	2
SSR-W-12-15	3.18	3-Dec-11	Swede Creek	F	5
SSR-W-13-75	6.78	15-Dec-12	Hook Lake	M	6
SSR-W-13-53	6.96	15-Dec-12	Hook Lake	M	0
SSR-W-12-02	14.26	Jan-12	Hwy 5 near Hay River	F	9
SSR-W-13-65	3.11	20-Nov-12	Dehcho Bridge	M	4
SSR-W-12-13	6.38	n/a	n/a	F	3
SSR-W-13-26	93.14	7-Feb-13	Mink Lake	M	4
SSR-W-13-31	21.58	14-Mar-13	The Hay River	M	8
SSR-W-13-45	1.42	28-Jan-13	Fort Smith	M	0
SSR-W-13-19	7.95	6-Jan-12	Hwy 5 km 244	F	4
SSR-W-12-39	15.92	2-Mar-13	n/a	F	2
SSR-W-12-04	13.88	12-Nov-11	Hwy 1 km 24	M	8
SSR-W-13-60	12.14	19-Feb-12	Rat River	F	1

Region	Infestation	Date	Location	Sex	Age
SSR-W-12-16	7.62	6-Feb-12	Sandy Lake	M	0
SSR-W-13-41	7.47	Feb-13	Mink Lake	F	0
SSR-W-13-70	7.61	27-Dec-12	Swede Creek	F	0
SSR-W-13-61	3.72	n/a	n/a	F	9
SSR-W-13-36	24.09	Feb-13	Mink Lake	M	3
SSR-W-13-58	50.29	26-Jan-12	Sandy Lake	F	7
SSR-W-13-13	5.61	16-Mar-13	Hook Lake	F	0
SSR-W-13-76	8.24	12/13	Point de Roche – Great Slave Lake	M	3
SSR-W-13-21	1.53	22-Feb-13	n/a	M	8
SSR-W-12-12	1.50	17-Dec-11	n/a	F	5
SSR-W-13-11	14.44	3-Apr-13	Caen Lake	F	4
SSR-W-13-48	20.00	16-Mar-13	Hook Lake	F	4
SSR-W-13-02	3.23	27-Dec-12	Hwy 1 km 24	M	2
SA-011 12/13	2.74	n/a	Fort Good Hope	F	0
SA-012 11/12	4.13	27-Jan-12	Colville Lake	M	0
SA-012 12/13	45.03	n/a	Fort Good Hope	M	0
SA-013 12/13	5.89	n/a	Fort Good Hope	M	0
SA-014 11/12	2.54	3-Jan-11	Norman Wells	M	3
SA-015 12/13	2.48	n/a	Colville Lake	U	0
SA-016 11/12	4.17	n/a	White Fish Lake	M	0
SA-016 12/13	19.57	Feb-13	Norman Wells	U	0

Region	Infestation	Date	Location	Sex	Age
SA-018 11/12	4.51	n/a	40 km N Colville Lake	F	2
SA-019 11/12	3.43	3-Jan-12	Colville Lake	F	0
SA-02 12/13	24.58	15-Dec-12	Norman Wells	F	0
SA-020 12/13	2.42	n/a	Colville Lake	F	4
SA-022 11/12	1.50	1-Dec-11	East Tedji Lake	M	1
SA-023 11/12	2.01	30-Nov-11	Tulít'a	F	6
SA-026 12/13	3.13	n/a	Colville Lake	U	1
SA-03 11/12	8.64	22-Feb-12	Fort Good Hope	M	1
SA-030 12/13	11.88	n/a	n/a	M	0
SA-031 12/13	6.92	n/a	n/a	M	0
SA-035 12/13	2.83	n/a	n/a	M	0
SA-036 12/13	1.10	n/a	n/a	F	1
SA-037 12/13	18.48	n/a	Colville Lake	F	4
SA-039 12/13	2.55	24-Nov-11	Norman Wells	F	2
SA-04 11/12	1.75	15-Feb-12	Fort Good Hope	M	1
SA-040 12/13	7.78	Dec-12	Fort Good Hope	M	4
SA-043 12/13	31.55	n/a	n/a	M	2
SA-044 12/13	1.70	n/a	Colville Lake	F	4
SA-045 12/13	37.15	n/a	Tulít'a	M	1
SA-046 12/13	1.39	28-Dec-12	Norman Wells	F	3
SA-06 12/13	7.33	Jan-13	Norman Wells	F	3

Region	Infestation	Date	Location	Sex	Age
SA-07 12/13	7.89	n/a	n/a	M	0
SA-08 12/13	22.05	Jan-13	Norman Wells	F	0
SA-09 11/12	1.35	n/a	White Fish Lake	M	5
MM-09 12/13	15.22	12-Apr-13	Canol Trail mile 70	F	0
MM-WOLF121	11.62	13-Apr12	Zone S/OT/01	M	0
MM-WOLF123	1.69	20-Sep-12	Zone D/OT/01 – Bunny Bar	F	n/a
MM-WOLF124	11.40	23-Sep-12	Zone D/OT/01	M	n/a
MM-WOLF131	1.39	31-Mar-13	Zone S/OT/01	F	n/a
MM-WOLF134	1.50	8-Apr-13	Canol Trail mile 70	F	n/a
MM-WOLF139	4.50	8-Sep-13	Zone D/OT/01	M	n/a
MM-WOLF141	4.33	1-Apr-14	Zone S/OT/01 – Palmer Lake	F	n/a
MM-WOLF143	23.14	2-Apr-14	Zone S/OT/01 – Palmer Lake	F	n/a
MM-WOLF144	1.92	2-Apr-14	Zone S/OT/01 – Palmer Lake	F	n/a
MM-WOLF78	8.80	16-Sep-09	Zone D/OT/01	M	4
MM-WOLF90	9.50	4-Oct-10	Zone D/OT/01	F	n/a
MM-WOLF109	76.84	24-Sep-11	Zone D/OT/01	M	n/a
MM-WOLF110	1.16	11-Sep-11	Zone D/OT/01	M	n/a
MM-WOLF111	4.81	4-Oct-11	Zone D/OT/01	F	n/a
MM-WOLF159	9.53	19-Sep-15	Zone D/OT/01	F	n/a
MM-WOLF160	10.76	6-Sep-15	Zone D/OT/01	M	n/a
MM-WOLF162	3.52	9-Sep-15	Zone D/OT/01	M	n/a

Region	Infestation	Date	Location	Sex	Age
DC-WOLF102	36.14	16-Mar-11	Manners Creek	M	4
DC-WOLF126	82.36	12-Dec-12	Jean Marie River	F	0
DC-WOLF129	6.15	19-Jan-13	Willow Lake River	F	8
DC-WOLF135	2.60	19-Apr-13	Fort Simpson	F	0
DC-WOLF11	2.30	20-Dec-03	9 km E Antoine Lake	F	3
DC-WOLF13	3.10	21-Mar-04	Martin River	F	0
DC-WOLF15	2.40	6-Apr-04	Fort Liard	U	n/a
DC-WOLF21	58.30	13-Feb-05	Poplar River	M	8
DC-WOLF25	21.60	27-Jul-05	Kakisa	M	3
DC-WOLF47	4.20	15-Feb-07	Trout Lake	F	0
DC-WOLF63	14.80	3-Aug-08	Nahanni Butte	F	2
DC-WOLF81	3.20	5-Jan-10	Wrigley	M	n/a
DC-WOLF83	1.50	2-Feb-10	Nahanni Butte	M	n/a
DC-WOLF91A	6.46	23-Nov-10	Wrigley	F	0
DC-WOLF94	13.48	28-Nov-10	Muskeg River	M	7
DC-WOLF96	17.67	22-Dec-10	Fort Simpson	M	7
DC-WOLF155	100.77	20-Jan-15	Fort Simpson	M	2