March of the Worms:
Using DNA to Map the Diversity and Distribution of Cervid GI Nematodes in Northwest Canada

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Background

Gastrointestinal (GI) nematodes can impact the health of ruminant hosts in subtle yet significant ways by altering body condition and fecundity. A current paucity of baseline information on GI nematode diversity and distribution in northern cervids is of concern to wildlife managers, veterinarians and communities relying on country foods. Traditional parasite surveillance techniques are expensive, laborious and often require post-mortem examination. In this study, we developed a rapid, non-invasive, fecal-based molecular tool to obtain baseline prevalence data for GI nematodes in western Canadian cervids.

Methods

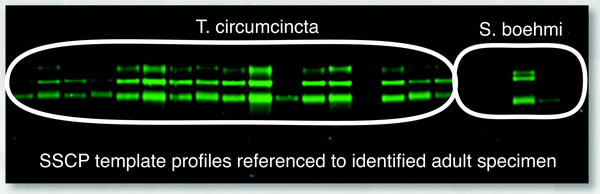
Step 1: Development of DNA Templates from Adult Worms

A. Collection of adult worms from GI tract.

B. ID adult to species level using morphological features.

C. PCR amplification of adult worm ITS-2 rDNA.

D. Development of SSCP template profiles.

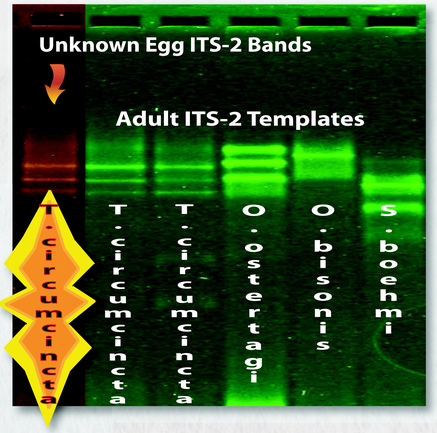


Step 2: Use of Adult Templates to ID Nematode Egg DNA

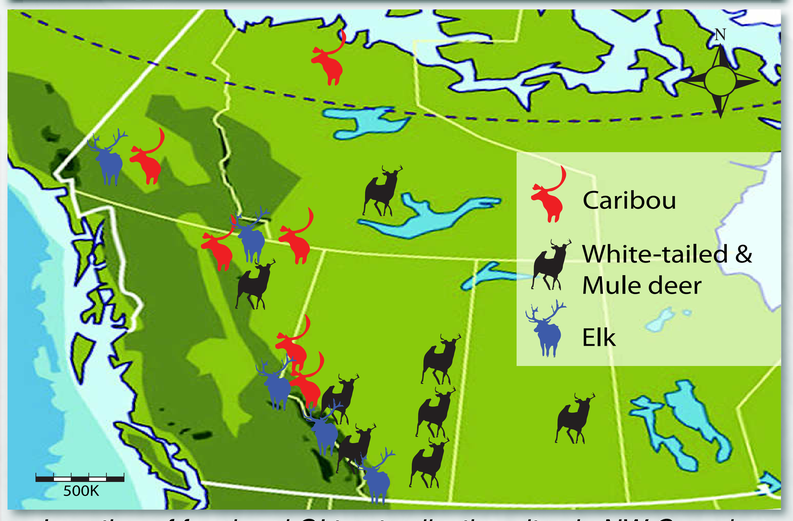
A. Collection of fresh (0 -24 hr) fecal pellets.

B. Isolation of egg(s) from pellets.

C. PCR amplification of egg ITS-2 rDNA & subsequent alignment of unknown egg SSCP profiles with those from known adults.

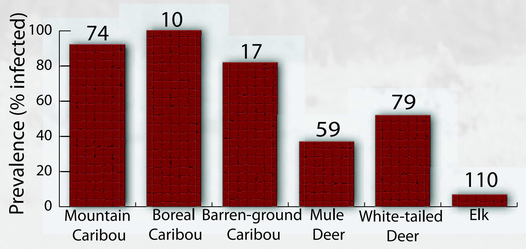


Survey Area



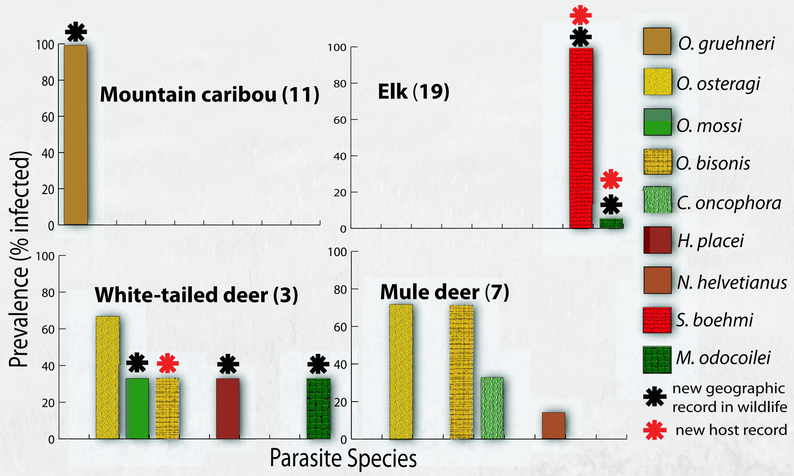
Location of fecal and GI tract collection sites in NW Canada

Results



*Prevalence of GI nematode infection in 2007/08 samples**

**mtn caribou, deer spp. & elk = spring & summer, boreal caribou = winter, BG caribou = fall; number of samples indicated above bar*



Preliminary results for GI nematode species prevalence in infected samples screened with SSCP

Conclusions

SSCP molecular techniques provids a simple, non-invasive, way to screen wildlife for GI nematodes. Using this tool, I have described three new host and six new geographic records for these parasites in northwest Canada. These records point to the paucity of basic information available for cervid host-parasite assemblages at northern latitudes.

To date, preliminary results show distinct patterns of overall infection prevalence and species diversity between caribou and other cervids. Caribou from all three ecotypes exhibited high prevalence of infection (82-100%) with one species (O. gruehneri), while deer sp. and elk displayed variable infection prevalence (7-52%) with multiple species of trichostrongyles. For southern regions where caribou and other cervids overlap spatiotemporally, these data suggest limited parasite-host switching between caribou and other cervids. New host and geographic records point to the paucity of basic information available for these host parasite assemblages.

Management Implications

1. The diagnostic tool provides wildlife managers and veterinarians a non-invasive way to monitor herd health, ideal for threatened or endangered species.
2. Rapid and efficient diagnoses are a powerful means to mitigate against the spread of parasites into non-endemic regions during animal translocation.
3. Distribution and diversity baselines obtained during this study can be used to monitor for, and respond to, expected emergence of novel GI parasites in Canadian cervids associated with shifts in climate and land use.

Future Analyses

We will look to elucidate latitudinal and habitat-type parasite diversity patterns among and between host taxa using generalized linear models and species similarity indices.

Acknowledgements

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