Prey selection of wolves in the Columbia Mountains during a moose population decline

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Medula of an adult deer hair
(Photo: M. McLellan)

A lone wolf following a group of caribou at Bourne creek during the 2011 caribou census (Photo: C. Legebokow)

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SUMMARY

Mountain caribou are declining because of excessive predation resulting from changes to habitat and climate that facilitates the growth of alternate prey and associated predators. In the Columbia Mountains, the primary management action to reverse this trend has been to reduce moose density with the goal of indirectly reducing wolf numbers. However, it remains unknown what effect this reduction has on the diet composition of wolves in the area. We collected scats from 5 different packs from two time periods spanning the moose population decline. We documented a shift in species composition of wolf diet between 2004-2005 and 2008-2010. The number of scats containing moose declined by 13% while the number containing other species increased; beaver by 10%, deer by 7% and marmot by 6%. Mitochondrial DNA analysis revealed the potential for multiple species content in scat, particularly when the prey consists of juveniles. These results are preliminary and further analysis is necessary to obtain adequate sample size and sampling effort to confidently reflect the changes of wolf prey species.

Introduction

Mountain caribou (Rangifer tarandus caribou) living in the interior wet-belt of North America are endangered. The distribution of these animals has become highly fragmented (Wittmer et al. 2005a) and their current decline has been attributed to unsustainable predation rates (Seip 1992; Wittmer et al. 2005b, 2007). Expanding early seral conditions caused by forest harvesting is one factor that has led to increased numbers of other prey species such as moose (Alces alces) and deer (Odocoileus spp.) that thrive in early seral habitats (Rempel et al. 1997; Latham et al. 2011; Serrouya et al. in press). More of these ungulates have caused a numerical response in predators such as wolves (Canis lupus; Fuller et al. 1989) and more predators have led to greater encounter and kill rates of caribou (Latham et al. 2011). Because predator numbers depend on the abundance of prey species other than caribou, apparent competition can cause the extinction of caribou as their decline has little or no feed-back to predator numbers.
In the Columbia Mountains, the primary management action to reverse the decline of caribou numbers has been to reduce moose abundance with the goal of indirectly reducing wolf numbers. The moose population has declined by approximately 73% between 2003 and 2009 (Serrouya et al. in press), and wolf numbers have also declined by a similar proportion, but with a lag of 1-2 years (van Oort et al. 2010). A risk of reducing a predator’s primary prey without directly reducing predator numbers is that the predators may eat increasing amounts of rare prey, as the predator’s abundance declines (Norbury 2001, Courchamp et al. 2003). This pattern could occur whether or not there is a lag in the decline of predator numbers.

To help assess the risk of prey-switching by wolves, we have been monitoring predator consumption rates of collared wolves by visiting GPS locations where wolves have been foraging (*sensu* Webb et al. 2008). The specific goals of this work have been twofold: 1) to determine if wolves are shifting their diets as moose numbers decline, including whether they consume more caribou; and 2) to determine the moose density at which wolves are no longer satiated and thus trigger a numerical decline in wolf numbers (see Messier et al. 1994). However, these goals have been addressed using the GPS-based cluster approach (Webb et al. 2008), without independent validation. The method of using GPS-based forage estimates is new and has received considerable attention, but to our knowledge no published work exists to independently validate this method. Furthermore, we do not have abundant GPS-based data at the peak of the moose population. Fortunately, wolf scats were collected from 2004-05 and stored in a freezer as part of another research project (Stotyn 2008). Therefore, we proposed to analyse wolf scats as a means to independently validate the GPS-based work, and to have a temporal comparison of wolf diet composition when the moose population was high, relative to recent time when the moose population was much lower. Specifically for this project, we contrasted wolf diet composition at two time periods, 2004-2005 and 2008-2010, which we termed “high” and “low” moose density periods, respectively. A formal independent validation of the GPS cluster data is planned for the future, but was beyond the scope of this analysis.

**Methods**

**Study area**

The core study area was in southern British Columbia, from Revelstoke to Mica including watersheds that drain into the Revelstoke reservoir. This area is bounded by the Monashee Mountains to the west and the Selkirk Mountains to the east. Apps et al. (2001) provided a detailed description of the vegetation and the ecosystem. However, two wolf packs outside this core study area were also included for contrast (see Methods). These samples included the
Whatshan Lake pack, located 100 km south of the study area, and the Adams Lake Pack, located 50 km west of the study area.

**Scat Collection and Processing**

Scats were collected from kill sites identified from GPS data, from wolf den sites, and opportunistically while doing fieldwork in the study area. Opportunistic collection included along roads, trails, and while hiking off-trail. If prey remains were associated with the scat deposition, the species and age of prey was identified when possible. Scats were stored in ziplock bags, labelled and frozen until autoclaving.

Most scats were collected within the core study area, though scats from two packs were outside the core area were also analysed. These included the Whatshan Lake and Adams Lake packs. These packs were included in analyses for two reasons: 1) To include samples from areas outside the moose reduction treatment, as a spatial comparison to areas within the moose reduction area, and 2) To increase the diversity of potential prey in scats (i.e. deer), to help reduce bias of observers that were trained on moose-dominated scats from the core study area (and thus may miss other cervid scats, which was particularly important as the moose population declined because wolves may switch to eating other cervids).

Scats were autoclaved at 120° C for 90 minutes at the University of Alberta to kill any *Echinococcus granulosus* and *Echinococcus multilocularis* eggs. Scats were then individually washed to remove all fecal matter leaving hair, plant cellulose, bones, rocks, conifer needles and cones. These scats were then dried and frozen until microscopic analyses were conducted.

**Microscope Analysis**

To obtain representative samples from the high and low moose density periods, scats were stratified by year and then randomly selected for detailed analysis of vertebrate prey. However scat analysis is extremely challenging at first so initially scats were selected to accelerate learning and for immediate comparison with other similar scats, or scats from kill sites with known prey species. Thus, we did not strictly adhere to the stratified random design.

Scats were dissected entirely to reveal different hair types, bone fragments, hoof/dew claw remains and plant matter. Twenty hairs were randomly chosen from each scat and placed onto a slide with double-sided tape. The slide was numbered and filed for additional investigation if necessary. Hair microstructure, including the basal configuration, length, diameter, colour-band patterns and medulla pattern (Kennedy and Carbyn 1981, Moore et al. 1974, Jones et al. 2009), was examined for each hair at 100x magnification using a compound light microscope. Different hair types revealed the presence of multiple species. Examining
these hair characteristics at this power was often sufficient to identify some genuses such as leporids, marmots, beavers, squirrels, bears and separate them from cervids (Kennedy and Carbyn 1981, Moore et al 1974, Jones et al. 2009). Once the probable genus was identified, a few intact hairs, preferably guard hairs, were selected from the scat and imprinted onto a slide and removed. The imprint of the hair’s cuticle scale pattern was examined at 400x magnification to identify cervid species. Whitetail and mule deer could not be confidently differentiated. Juvenile cervids less than 5-months old could be differentiated from adults by looking at guard hair diameter and medulla structure. At approximately 5 months juveniles will grow mature guard hair (Kennedy and Carbyn 1981, Jones et al. 2009). Photographs and measurements of the microscopic image of ambiguous hairs were sent to colleagues at the University of Alberta for a second opinion.

DNA Analysis

For some samples containing cervid hair, particularly juveniles, it is difficult to confidently differentiate among species or even when multiple species occur in a scat. We selected a subsample of ambiguous scats for further testing using mitochondrial DNA (mtDNA) analysis for species (D. Paetkau, unpublished methods). Species ambiguity was often due to unclear or degenerated hair colour patterns and non-defining cuticle patterns. These hairs were likely from juveniles or possibly finer hairs from softer parts of adult cervids (e.g. abdomen, legs). Samples were sent to Wildlife Genetics International for analysis where they extracted mtDNA from hair roots and analyzed using ungulate-specific primers. Because of the methods used for mtDNA species analysis only relatively equal proportions of species content will arise as mixed species. Thus, in a mix of 90% moose and 10% deer, the deer signal wouldn’t even rise above the fluorescence baseline, and would thus go undetected (D. Paetkau, Wildlife Genetics International P. comm.).

Results

We collected, washed and autoclaved 313 scats. Of those scats, 81 were analyzed microscopically and 16 ambiguous samples containing cervid hair were selected from those for mtDNA analysis to differential among ungulate species. Four of the 81 samples did not contain enough material to identify species microscopically or genetically. Prey identified in scat samples included beaver, black bear, caribou, deer, elk, marmot, moose, mustelids, hares and squirrels. It is difficult to distinguish between whitetail and mule deer species genetically (D.
Paetkau, Pers. Comm.) or microscopically (Jones et al. 2009). Of the scats analyzed by microscope, 15 could not be confidently assigned a species, of which 9 were certainly cervids.

Summer diet composition varied much more than winter diets, however ungulate species remained the dominant component of prey in both seasons. In winter 74% of scats contained ungulate remains vs. 69% in summer (Table 1).

For scats collected within the core study area we found a general decline in the proportion of scat containing moose from the high to low moose density periods. During this time, there was a modest increase in scats containing beaver, deer and marmot (Figure 1). These scats included samples from the Goldstream, Downie and packs on the west side of Lake Revelstoke. One 2009 scat from the Goldstream pack contained what was likely juvenile caribou hair.

The Goldstream and Downie packs showed a decline in proportion of moose consumed however the decrease was much more substantial in the Downie pack from the high to low moose density period (Figure 2, 3). Likewise there was an increase in the number of scats containing beaver remains, particularly for the Goldstream pack. The Downie pack also showed an increase of the use of deer as prey from no deer in 2004-2005 to over 20% presence in 2008-2010 (Figure 3). At low moose density moose remain present in approximately 33% of wolf scats from both packs.

Wolves from outside the moose management area were less heavily sampled. The Adams lake pack had one scat containing moose and one containing caribou, whereas the Whatshan Lake wolves had 3 scats containing deer.

All cases analyzed using mtDNA confirmed the microscopic identification of cervids. However, three scats that were classified as caribou from microscopic analysis were identified as deer using the mtDNA analysis. Mitochondrial DNA prey species identification revealed that 40% (6 out of 15) of scat tested contained multiple species whereas microscopic analysis suggested only 5% occurrence of multiple species.

**Discussion**

Wolves in the core study area appeared to shift their diet as the moose population declined. The consumption of moose declined from 46% to 33% as moose densities were reduced, but the shift from moose to other prey was less pronounced for wolves in the Goldstream Valley (Fig. 2). Moose densities in the Goldstream Valley are higher than other
areas within the moose reduction treatment (Serrouya et al. in press), and this probably explains why wolves in the Goldstream had a less pronounced shift in diet. In a related study, Serrouya (2010) documented that wolves within the Goldstream Valley were consuming prey at a level consistent with what others researchers have documented as “satiation” (Messier et al. 1994, Hayes and Harestad 2000), whereas wolf packs outside the Goldstream Valley were killing prey at a lower rate (Serrouya 2010). Furthermore, Serrouya (2010) presented evidence suggesting that two wolf packs outside the Goldstream valley were not recruiting offspring into the packs in 2010, whereas the Goldstream pack successfully recruited pups at least until September, five months after birth.

The stable consumption of moose by the Goldstream pack suggests that the moose population in this area remains above a level that would necessitate shift in foraging behaviour, particularly in winter when moose are concentrated in the valley bottom and are relatively easy to encounter and kill. Yet, there was a notable increase in beaver consumption during the low-density period by this pack. The consumption of beaver was during summer, which coincides with the season when moose densities decline as they spread into the mountains. The shift to beaver during summer may be an indication that wolves, even in the productive Goldstream Valley, are beginning to have difficulty locating their primary prey during summer. Overall though, the findings of diet composition presented here support the conclusions of Serrouya (2010), that moose densities in the Goldstream remain above a level needed for recruitment and foraging efficiency (specifically, on the asymptote of the functional response). In contrast, wolves not in the Goldstream Valley have shifted their consumption from moose to other prey and this pattern may be translating into reduced recruitment and ultimately, abundance of wolves.

For packs outside the Goldstream Valley, the increased consumption of non-moose prey after the moose decline probably explains why there is a lag in the decline of wolf numbers to the moose reduction treatment. This pattern has at least two implications for management: 1) Predation risk to caribou may increase as wolves seek alternate prey, and 2) there may not be a proportional decline in wolf numbers relative to the decline in moose abundance. Direct removal of wolves would help address these issues.

Although this report does not include a formal validation of the GPS-cluster based consumption estimates, it is notable that 30% of wolf scats in the Goldstream contained beaver during the summer. This amount is approximately twice the amount (by frequency of prey items) consumed by wolves estimated by Serrouya (2010) using GPS data during the summer of 2010. The difference between the two methods would be even greater if converted to an index of biomass ingested. Because the handling time for small prey is relatively short compared to
larger prey, and because wolves will consume the entire animal if it is small and not leave remains (Floyd et al. 1978), it is difficult to detect the consumption of smaller prey by GPS cluster analysis. However, it is possible that smaller prey are an important part of wolf diet (e.g., Latham et al. 2011), particularly in an ecosystem where their primary prey has been greatly reduced. Fortunately small prey are easily identifiable in scat because they are composed of a relatively greater proportion of indigestible matter on a per kilogram basis (Floyd et al. 1978).

Although moose is still the dominant prey species we were able to successfully identify beaver and deer as other important prey items, as well other less commonly preyed upon species that together amounted to as much as 21% of scats produced. The 30% decline of moose consumption in by the Downie pack was coupled with a 20% increase of deer consumption. The decline of moose consumption was expected as a result of the moose population decline, however, the increase in deer consumption may be a result of shifting prey selection due to availability, a change in pack dynamics or it may reflect an increase deer population. Further analysis, including changes in pack dynamics would be necessary to test these hypotheses.

This study was one of the first to use mtDNA for species identification in wolf scats. One surprising outcome was the proportion of scats containing multiple species. The hair in these scats were almost certainly from juvenile ungulates therefore it is reasonable that wolves were able to consume two different individuals before the remains of the first prey item was passed. However, it is possible that more rigorous microscopic analysis of scat may be required to successfully determine the presence of multiple species in the scat.

**Future Work**

We intentionally analysed scats that were from kill sites and scats that were likely to be deer or caribou in order to facilitate learning. The ambiguous scats were specifically sought for mtDNA analysis and likely over represented mixed scats and juvenile deer. To address this bias, we plan on analysing the remaining samples that were autoclaved but not analysed microscopically. We plan on using the remaining known kill site scats to test the researcher’s ability and provide a confidence measure for analysis. We will use mtDNA analysis to test remaining ambiguous scats containing cervids. Finally, scats were collected during the summer of 2010 and winter 2011, and analysing these samples would help confirm the preliminary trends reported here.
Acknowledgements

Funding was provided by the Fish and Wildlife Compensation Program, Columbia Basin. We would like to thank Patrick Jones for his help and guidance autoclaving, washing and analyzing scat samples. Corey Bird, Kelsey Furk, and many others helped with field data collection. We also thank Shannon Stotyn for allowing us to analyze the wolf scat samples she collected during the high moose density period.

Literature cited


**Table 1**: Proportion of scat by season and species. Summer 24 April - 20 October, winter 21 October –23 April. The number of scat containing that species in parenthesis.

<table>
<thead>
<tr>
<th>Prey</th>
<th>Summer</th>
<th>Winter</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beaver</td>
<td>12% (7)</td>
<td>4% (1)</td>
<td>10% (8)</td>
</tr>
<tr>
<td>Black bear</td>
<td>5% (3)</td>
<td></td>
<td>4% (3)</td>
</tr>
<tr>
<td>Caribou</td>
<td>3% (2)</td>
<td></td>
<td>2% (2)</td>
</tr>
<tr>
<td>Deer</td>
<td>15% (9)</td>
<td>26% (6)</td>
<td>10% (8)</td>
</tr>
<tr>
<td>Elk</td>
<td></td>
<td>4% (1)</td>
<td>1% (1)</td>
</tr>
<tr>
<td>Marmot</td>
<td>5% (3)</td>
<td></td>
<td>4% (3)</td>
</tr>
<tr>
<td>Moose</td>
<td>41% (24)</td>
<td>26% (6)</td>
<td>37% (30)</td>
</tr>
<tr>
<td>Mustelid</td>
<td>4% (1)</td>
<td></td>
<td>1% (1)</td>
</tr>
<tr>
<td>Hare</td>
<td>2% (1)</td>
<td></td>
<td>1% (1)</td>
</tr>
<tr>
<td>Squirrel</td>
<td>2% (1)</td>
<td>4% (1)</td>
<td>2% (2)</td>
</tr>
<tr>
<td>Unknown</td>
<td>2% (1)</td>
<td>4% (1)</td>
<td>2% (2)</td>
</tr>
<tr>
<td>Unknown cervid</td>
<td>10% (6)</td>
<td>17% (4)</td>
<td>11% (9)</td>
</tr>
<tr>
<td>Unknown not cervid</td>
<td>3% (2)</td>
<td>9% (2)</td>
<td>5% (4)</td>
</tr>
</tbody>
</table>

**Figure 1**: Prey species composition in wolf scat from within the Columbia Mountain moose management zones for 2004-2005 (n=26) and 2008-2010 (n=51). Nine scats contained two species.
**Figure 2:** Prey composition of scats from the Goldstream wolf pack. 2004-2005 (n=17) and 2008-2010 (n=19). Four scats had two species.

**Figure 3:** Prey composition of scats from the Downie wolf pack. 2004-2005 (n=8) and 2008-2010 (n=28). 4 scats had two species.