

AN ESTIMATION OF COYOTE POPULATION SIZE  
FOR EVIDENCE OF A TROPHIC CASCADE

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A Thesis Submitted to The Honors College  
In Partial Fulfillment of the Bachelor of Science with Honors degree in

ECOLOGY AND EVOLUTIONARY BIOLOGY

THE UNIVERSITY OF ARIZONA

August 2016

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## ABSTRACT

Following the re-introduction of gray wolves (*Canis lupus occidentalis*) into Yellowstone National Park in 1998, a dramatic influence of the wolves on the landscape of Yellowstone ecosystem was observed over the following x decades, termed a trophic cascade. Trophic cascade is defined as the reciprocal predator-prey effects that alter the abundance, biomass, or productivity of a population, community, or trophic level across more than one link in a food web, and this effect was has been well-documented from reintroduction efforts of apex predators in the United States. In the Yellowstone wolf example, the wolves have initiated both a traditional trophic cascade, which spans across trophic levels (predator-prey-vegetation), and a carnivore cascade, which spans across a predator guild (wolf-coyote-fox). A goal of the present study was to determine whether or not the Mexican gray wolf (*Canis lupus baileyi*) can initiate a carnivore cascade in Arizona and New Mexico, assessed by estimation of a coyote minimum population size on the White Mountain Apache Reservation in Arizona. This was accomplished by genotyping scats collected in 2008 and 2009 for polymorphic microsatellite DNA loci, to estimate the population size through a simple genetic minimum population size using all unique individuals. Sixty-one individual coyotes were estimated using minimum population estimate in 2008 and 28 individual coyotes in 2009, on the study plot, however, the estimate did not include the influence of Mexican gray wolves on coyotes population size, due to carnivore cascades in this region.

## ACKNOWLEDGEMENTS AND DEDICATION

Acknowledgements –

This is an effort to name each individual who has contributed in some way to the completion of this undergraduate senior thesis, to which I am grateful. With their help, I was able to complete my first scientific study to hopefully launch a successful scientific career in the fields of ecology, evolutionary biology, conservation biology, and genetics. First, I thank Dr. Melanie Culver for allowing a quite ambitious undergraduate to start a project in her lab and to continue as a Master's student in Ecology and Evolutionary Biology. Second, I thank Dr. Sarah E. Rinkevich of the United States Fish and Wildlife Service to substantially guide me through the beginnings of this project as well as take on an “unfinished” tangent of her PhD dissertation. Then I thank Karla Vargas and Emma Froehlich for their lab work assistance – without them I more than likely would have not been able to complete this project. Then there are my family members – Christina Hoskinson, Jeffery Hoskinson, Gina Hernandez, Daniel Hoskinson, and Matthew Hoskinson – to which I thank for their support through the stresses of this project. I also thank my friends – Lindsay Vicars, Maddie Carlson, and all others (there are too many to name), to which I am also quite thankful for their support. Then there are those family members that financially contributed to this project – Patricia MacLeod and Claudine Hickerson – which without their support I would not have been able to complete this project. In regards to financial contributions, I would also like to thank the The University of Arizona Honors College for the Alumni Legacy Grant, which also significantly helped in the completion of this effort. Lastly I thank and give credit to the White Mountain Apache, for letting Dr. Rinkevich complete her dissertation on their land and thus as a result I have the scat sample resources to complete my undergraduate senior thesis. Native American tribes are not recognized in Western science as much as they should be; I sincerely hope this effort is a start to minimize that transgression.

Dedication –

This undergraduate senior thesis is dedicated to two species in particular – the Mexican gray wolf (*Canis lupus baileyi*), and the coyote (*Canis latrans*) – the latter of which is the primary focus of this undergraduate senior thesis. These two species have been subjugated to the intense pressure of environmental anthropocentrism, in which the wishes of humans were violently placed onto predators of arguably the same ecological guild. This anthropocentrism continues, although not as violently, and thus hopefully one day wolves, coyotes, humans, and other predators will be able to live in ecological balance.

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## INTRODUCTION

### **APEX PREDATORS AND TROPHIC CASCADES**

Apex predators, or those species that occupy the highest trophic level upon which no species predate, have been repeatedly shown to have strong effects upon their respective communities and ecosystems. Attributes that can be ascribed to apex predators are female reproductive suppression, infanticide, territoriality, cooperative social behaviors, and alloparental care, which all of these characteristics can contribute to the main characteristic of apex predators which is self-regulation of their population size and densities (Wallach et al, 2015). However, apex predators have the capacity to extrinsically regulate the population sizes and densities of other species either within their guild or in lower trophic levels; this property of apex predators can influence the occurrence of an ecological phenomenon known as a trophic cascade. Trophic cascades, or cascades in general, are defined as reciprocal predator-prey effects that alter the abundance, biomass, or productivity of a population, community, or trophic level across more than one link in a food web (Pace et al 1999). For this particular discussion, it is important to illustrate this capacity due to the propensity of apex predators to initiate cascades either across trophic levels (predator-herbivore-vegetation) or across their predator guild (e.g. wolf-coyote-fox).

These trophic cascades have two mechanisms by which they operate, both of which are integral to the overall effect of the cascade. First is the N-driven cascade, in which the apex predator can influence the census population size of organisms. Second is the  $\mu$ -driven trophic cascades, by which apex predators can influence the foraging behavior of either carnivores within the guild or prey and thus influence the population density and distribution across a landscape (Brown, Laundre and Gurung 1999). It is namely this last mechanism that can be more important in terms of the optimal foraging strategy of either other carnivores or prey species, and this instills a landscape of fear for these species to incorporate predation risk into their optimal foraging

strategies (Brown, Laundre and Gurung 1999; Ripple and Beschta 2004a). Both of these mechanisms have been demonstrated to be equally important, with the  $\mu$ -driven mechanism perhaps being stronger due to the factor of predation risk being incorporated into the optimal foraging strategy with the presence of an apex predator (Lima and Dill 1990; Schmitz, Beckerman, and O'Brien 1997).

When these apex predators are missing from the community and ecosystem either through natural extinction or anthropogenic local extirpation, it can allow for irruptions of herbivores which can increase browsing rates and cause the trophic downgrading of local environments (Estes et al 2011) as well as the release of mesopredators to potentially assume an “apex predator-like” role in the environment although there have been cases which the mesopredator cannot attain the same ecological effect as a true apex predator (Ritchie et. al 2009; Ripple et. al 2013; Wallach et al 2015; Jones et. al 2016). In order to keep the ecosystem stable and limit trophic downgrading as much as possible, it is quite important to maintain the presence of apex predators within communities and ecosystems.

## **GRAY WOLVES (*CANIS LUPUS OCCIDENTALIS*) AND YELLOWSTONE NATIONAL PARK**

Perhaps one of the most well-known apex predators is the gray wolf (*Canis lupus sbspp.*). This species currently has 5 subspecies: the arctic wolf (*Canis lupus arctos*), the northwestern wolf (*Canis lupus occidentalis*), the plains wolf (*Canis lupus nubilus*), the eastern wolf (*Canis lupus lycaon*), and the Mexican wolf (*Canis lupus baileyi*), although the taxonomy of wolves is still controversial (Mech and Boitani 2003; Chambers et al 2012).

In the late 19<sup>th</sup> century and early 20<sup>th</sup> century, there was a misunderstanding and therefore fear of the wolf from the constant threat of the depredation of livestock from wolves and other

associated predators. Following from this fear, misunderstanding, and anthropocentrism, the United States Congress established the federal Bureau of Biological Survey with the Division of Predator and Rodent Control (PARC) in 1915 which had the expressed purpose of eliminating the wolves and large predators from the United States (Brown 1983; Mech and Boitani 2003).

One potential result of the reduction of large predators was an increase in ungulates including increased browsing rates. This increased rate of browsing by elk (*Cervus elaphus*) and deer (*Odocoileus virginianus* and *Odocoileus hemionus*) may have resulted in a trophic downgrade. A century later Americans grew to have a more favorable opinion of the wolves (Mech and Boitani 2003), and several members of *Canis lupus occidentalis* (Chambers et. al 2012) were captured in Canada and reintroduced into Yellowstone National Park in both 1995 and 1996 (Merkle et. al 2009). This particular reintroduction of gray wolves was studied quite extensively in terms of not only with the wolf and their interaction with the landscape (traditional trophic cascades), but carnivore cascades as well.

In terms of documenting if a trophic cascade would occur at Yellowstone National Park as a result of the reintroduction of the gray wolf, Ripple and Larsen (2000) documented the historical trend of aspen (*Populus tremuloides*) recruitment in Yellowstone National Park and found that aspen recruitment was diminished during the years of wolf extirpation and that the age class of these aspen trees that would have been recruited during this time were missing (Larsen and Ripple 2003). Following the reintroduction of the wolf, studies have found that the reintroduction of the gray wolf contributed to the increased recruitment of aspen (Ripple et. al 2001), cottonwoods (*Populus spp.*) (Beschta 2003), willow (*Salix spp.*) (Ripple and Beschta 2004b), and alders (*Alnus incana tenuifoli*) (Ripple, Beschta and Painter 2015). This trend of increase in recruitment is still maintained even 15 years after the initial wolf reintroduction into Yellowstone National Park

(Ripple and Beschta 2012). In addition to the increased recruitment of these trees, studies have also found that due to the increase in recruitment of these trees, the morphology of the rivers in Yellowstone have changed as well (Beschta and Ripple 2006; Beschta and Ripple 2012), lending to the inference that the wolves even had an effect on the abiotic environment of Yellowstone National Park. Thus, in terms of traditional trophic cascades, the effect of the northwestern gray wolf on the Yellowstone National Park ecosystem was quite remarkable.

The trophic cascade mechanism by which these large trophic-scale effects (wolves-elk-vegetation) occurred was mostly the behavior driven mechanism. Through the reintroduction of the wolf into the environment, the elk (*Cervus elaphus*) was required to incorporate the risk of predation into its optimal foraging strategy and leave “plant refugia” in areas that have high predation risk (Ripple and Beschta 2004a). It is these “plant refugia” areas that have the greatest amount of recruitment of aspen, cottonwood, willow, and alder trees within Yellowstone National Park. The major mechanism for this trophic cascade was not through population reduction but through behavior modification such that the distribution and density of elk was altered post-reintroduction (Ripple and Beschta 2004a).

## **CARNIVORE CASCADES**

Carnivore cascades occur within a carnivore guild that occurs in sympatry with the apex predator (e.g. wolf-coyote-fox). Studies have shown that the mechanisms involves behavior modification instigated by competitors. For example, in Yellowstone it has been demonstrated that the reintroduction of wolves resulted in interference competition between coyotes and northwestern gray wolves (*Canis lupus occidentalis*), which caused a change in the population density and abundance of coyotes (Berger and Gese 2007; Berger, Gese and Berger 2008; Merkel et al 2009). This would be a form of a behavioral-driven carnivore cascade since it is altering the

density and abundance of a mesopredator within the carnivore guild. However, social rank within the coyotes has also been shown to influence the amount of risk the coyotes take at a carcass site - the location that they most frequently encounter wolves (Atwood and Gese 2008; Merkle et al 2009).

These behavioral-driven mechanisms from wolf reintroduction influence the distribution and abundance of coyotes but can also influence pronghorn distribution (Berger, Gese, and Berger 2008), and the irruption of small mammals such as rodents (Miller et al 2012) - main prey items of the coyote. Likewise, wolf reintroductions influence elk, limiting elk browsing on berry plants, which influences the distribution of grizzly bears (*Ursus arctos*) since grizzlies also depend on berry plants (Ripple et al 2014).

### **MEXICAN GRAY WOLVES (*Canis lupus baileyi*)**

The present study is focused primarily on the Mexican gray wolf, which is the smallest subspecies of gray wolf historically distributed in the American Southwest and Mexico (Brown 1983; Beschta and Ripple 2010; Hendricks et al 2016). In regards to trophic cascades, Beschta and Ripple (2010) analyzed the amount of aspen recruitment in the Blue Range Wolf Recovery Area (Apache-Sitgreaves National Forest, Alpine, Arizona) in three locals: a refugium site inaccessible to both elk and cattle, an old growth site accessible to elk, and a thinned site accessible to elk. In this area they found aspen recruitment in the refugium site consistent with climactic variation, however Beschta and Ripple did not find the increased aspen recruitment in the Blue Range Wolf Recovery Area. Since this was contradictory to what Ripple and Beschta had observed in previous trophic cascade studies, which primarily dealt with the reintroduction of the northwestern gray wolf in Yellowstone, their conclusion for this study was that there was no trophic cascade occurring in the Blue Range Wolf Recovery Area as of 2010.

Curiously, there have been no studies examining if a carnivore cascade (or intraguild cascade) has occurred on the Blue Range Wolf Recovery Area or adjacent areas – which relates directly to whether or not Mexican gray wolves can influence the distribution and density of coyotes and foxes in these regions. With this it is important to establish if the Mexican gray wolves have achieved an ecologically effective density in these areas to influence the distribution and density of coyotes and foxes, and therefore a study to investigate this is necessary.

For the present study, the primary focus is whether or not the Mexican gray wolf influence the census population size of coyotes on the White Mountain Apache Reservation in Arizona, through a comparison of minimum population sizes. The hypothesis of this study is that Mexican wolves do have an influence on the census population size of coyotes in the plots described by Rinkevich (2012), and thus three predictions follow when relating the census population sizes to carnivore cascades.

## METHODS

*Samples* - For the purpose of the population estimate, coyote scats were collected on the White Mountain Apache Reservation, Arizona in 2008 and 2009 as part of the Rinkevich (2012) study. Methods for the collection of the scats as well as species identification of the scats can be found in Rinkevich (2012), and these scats were identified as coyote scats prior to the beginning of this study. Ninety coyote scats from Rinkevich (2012) were used in the present study (61 from 2008, and 29 from 2009).

*DNA extraction* – Sixty scat samples were provided already purified for DNA. DNA was extracted for 30 scat samples utilizing the Qiagen DNA extraction protocol (Qiagen Inc., Valencia, California).

Polymerase chain reaction (PCR) amplification was performed for ten canid microsatellite DNA loci known to be polymorphic in coyotes: FH2001, FH2096, FH2137, CX140, FH2054, FH2010, FH2159, CX2235, FH2100, and FH2062 (Lenney William et al 2003; Sacks et al 2004; Damm et al 2015). The PCR reagents and their concentrations are as follows: molecular grade PCR water, forward primer (0.4 uM), reverse primer (1 uM), Amplitaq 10X buffer solution, Amplitaq MgCl<sub>2</sub> (2.5 mM), Invitrogen dNTPs (0.2 mM), BSA (0.04%), M13 VIC-labeled dye (1 uM), and Amplitaq Taq polymerase enzyme (1 unit). Each reaction was a 10 uL reaction composed of 7 uL of PCR water and 3 uL DNA solution at a concentration of 5 ng/uL. The PCR conditions were as follows: initial denaturation step of 95°C for 10 minutes, denaturation of 94°C for 30 seconds, annealing step with a touchdown procedure from 70 °C to 53 °C, with 30 seconds for each temperature, elongation step of 72 °C for 45 seconds. 35 cycles of denaturation at 94 °C for 30 seconds -- 55 °C for 30 seconds for attachment of the M13 VIC-labeled dye – elongation of 72 °C for 30 seconds, with a final elongation step of 72 °C for 7 minutes.

PCR products were analyzed using the UAGC CORE facility at the University of Arizona, and the peaks were scored with GENEMARKER v.2.6.0. Peaks were selected based on the topology of the peak; that is, if a peak had a distinct form that was consistent with the description of the proper microsatellite peak in the manual for GENEMARKER v.2.6.0. Each of the loci were analyzed separately with 2 positive controls (DNA extracted from two different coyote tissues), 1 negative control (molecular-grade PCR water), and the 90 coyote scat samples. For the purposes of the peak analysis if one peak was present it was treated as a homozygous locus, whereas if two peaks were present it was treated as a heterozygous locus.

For the purposes of genotyping each of the scats, a simple minimum number of individuals was used to estimate the population size; that is, a scat that possessed a unique genotype was considered a unique individual. If two scats were analyzed and found to have the same genotypes for each of the loci, it was treated as the same individual. If data was missing for a particular locus (i.e. PCR amplification did not occur on that microsatellite region) it was not treated as a unique genotype, and if a scat had all of the loci missing it was not considered in the final analysis. Therefore, each scat was required to have a minimum of one locus that was amplified. This of course leads to a minimum population size that may be larger than the real census population size.

## RESULTS

Out of the 10 original microsatellite DNA loci amplified, only 4 were used in the final analysis, and those loci were FH2001, FH2096, FH2100, and FH2062. Scats must have had at least one locus amplify in order to be counted; this criteria was included because only 13 out of 61 scats in 2008 and only 5 out of 29 scats in 2009 amplified at all loci and thus would have greatly reduced our sample sizes. One scat sample from 2009 was removed from the final analysis since it did not amplify for any of the 4 loci included in this analysis, resulting in 28 scats from 2009, 61 scats from 2008, for a total of 89 scats. In further analyses, the 2008 census population size estimate was fully independent of the 2009 census population size estimate.

Between 2008 and 2009, both the number of alleles present and the allele size range changed for each locus. This allele size range also differed slightly from the previously reported allele size ranges. The data for FH2001, FH2096, FH2100, and FH2062 are presented in Table 1, Table 2, Table 3, and Table 4, respectively.

Year	Number of Alleles	Allele Size Range	Previously Reported Allele Size Range
2008	37	121-213	122-158
2009	19	119-173	122-158

Table 1. Number of alleles, allele size range (number of repeats in the microsatellite), and the previously reported allele size range for locus FH2001 in *Canis latrans*.

Year	Number of Alleles	Allele Size Range	Previously Reported Allele Size Range
2008	30	88-154	89-109
2009	22	89-149	89-109

Table 2. Number of alleles, allele size range (number of repeats in the microsatellite), and the previously reported allele size range for locus FH2096 in *Canis latrans*.

Year	Number of Alleles	Allele Size Range	Previously Reported Allele Size Range
2008	43	86-182	142-176

2009	24	88-192	142-176
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Table 3. Number of alleles, allele size range (number of repeats in the microsatellite), and the previously reported allele size range for locus FH2100 in *Canis latrans*.

Year	Number of Alleles	Allele Size Range	Previously Reported Allele Size Range
2008	48	71-174	129-145
2009	23	89-178	129-145

Table 4. Number of alleles, allele size range (number of repeats in the microsatellite), and the previously reported allele size range for locus FH2062 in *Canis latrans*.

In the 2008 scat samples, there were 61 unique genotypes from 61 scats, and in the 2009 scat samples there were 28 unique genotypes from 28 scats. Therefore, preliminary analyses suggests that the coyote minimum population size in 2008 was 61 individuals, whereas in 2009 the coyote minimum population size was 28 individuals on the study plots described in Rinkevich (2012).

## DISCUSSION

In the Rinkevich (2012) study, it was found that there were 19 individuals of Mexican gray wolf (*Canis lupus baileyi*) between 2008 and 2009. Following from the results of the present study, it would be tempting to suggest an influence on coyotes by wolves since the minimum coyote population size declined from 61 to 28 from 2008 to 2009, however, this decline was probably due to a sampling effect, since more coyote individuals were detected as more individual scats were sampled, and half as many scats were sampled in 2009. Because of this sampling artifact, there is no evidence suggesting a trophic cascade.

Additionally, not all of the coyote scats yielded PCR amplifiable DNA. Additional sampling error may be present if not all of the coyote scats in the study area were collected, thus there could have been a higher population of coyotes if more scats were collected and found to have unique genotypes.

Also each of these PCR amplifications of these loci only occurred once, whereas they should have been done in triplicate to eliminate the possibility of misidentifying a peak. To be more conclusive on whether or not the correct peaks were identified for each of the scat samples, two more runs of PCR amplification need to be performed

The largest issue, and the issue that has direct implications on the final conclusion of the present study, is that there is no data on coyote population sizes before 2008 and 2009 and thus no inferences about changes in the coyote population size can be made. It is not known whether these coyote population sizes were smaller than years before, or larger than years before, or the population size has remained stable for years. From previous studies on the wolf-coyote-fox carnivore cascade, it normally takes several years for these kinds of inferences regarding carnivore cascades to be made. Since these analyses are essentially a “snapshot in time” on the census

population sizes of coyotes, it is not possible to suggest an answer to the original question of the present study. Therefore, it remains unknown as to whether or not a carnivore cascade is occurring on the White Mountain Apache Reservation in Arizona as a result of the reintroduction of the Mexican gray wolf onto the Blue Range Wolf Recovery Area in 1998.

To answer the question of whether or not a carnivore cascade is occurring, future studies are needed to not only look at the population sizes of both Mexican gray wolves and coyotes but to assess the distribution and density of both of these predators. Since carnivore cascades could occur with one or both of the trophic cascade mechanisms, the N-driven or  $\mu$ -driven mechanisms, it would be important to investigate which trophic cascade mechanism could be at play in Mexican wolf-inhabited areas.

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